

Irene L. Hudson  
Marie R. Keatley  
*Editors*

# Phenological Research

*Methods for Environmental  
and Climate Change Analysis*



Springer

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Methods for Environmental and Climate  
Change Analysis

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*Editors*

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*Cover illustration: Eucalyptus leucoxylon "rosea", Pink Flowered Yellow Gum. Photograph by Tim D. Fletcher.*

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*To our partners, parents and children who have  
given much support and shown great practice*

# Foreword

Nearly 6 years have passed since the publication of my edited book, *Phenology: an integrative environmental science*, in late 2003. During this time phenological research has continued to increase both in visibility and importance within the broader scientific community. For example, the latest Intergovernmental Panel on Climate Change report stated that phenology “. . . is perhaps the simplest process in which to track changes in the ecology of species in response to climate change.” (IPCC 2007). Further, an initiative that has been a passion of mine for several decades has finally come to fruition over the past four years, namely the creation of a National Phenology Network in the United States (USA-NPN, which you can read more about in Chapter 2, Section 3.7).

However, not surprisingly, despite these and many other notable advances, phenological science still faces a number of long-term challenges. Thus, I was extremely pleased to learn of the plans to develop this book, focusing on phenological research methods, and to accept Marie Keatley and Irene Hudson’s invitation to write this foreword, as it affords me an opportunity to briefly review these challenges in the context of this volume’s contributions.

I see a three-fold set of major challenges facing phenology as we move forward in the coming decades:

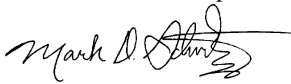
1. broadening the methodological “tool kit” used in phenological studies;
2. expanding the scope of research questions addressed by phenology; and
3. expanding the depth, diversity, and geographic extent of in situ and remotely sensed phenological data collection, as well as integration of existing (and creation of new) national phenology networks into a global monitoring system.

The first and the second challenges are really two aspects of the same issue. Phenological research is still very often conducted through regression-based studies that look for temporal trends. While there is power and elegance in these findings to-date, which underscore the impacts of a warming world on phenological timing, the scientific community needs the perspective of phenology to address other critical issues in species interactions, population dynamics, and ultimately adaptation strategies within managed and natural ecosystems. The majority of the chapters in this book are designed to broaden the “phenological thinking” of both students and

established scholars alike, not only through exposure to new methodologies, but also by expanding the range of research questions that they see possibilities to consider.

The third challenge is in many ways unending (i.e. you rarely have too much data), but Chapter 2 reports on the current status of phenological data collection around the world, and offers several worthwhile perspectives and approaches to advance the objectives of coordinated global phenological monitoring. In the near future, I want to use the structure of the International Society of Biometeorology (ISB) Phenology Commission (of which I am currently Chair) to help us continue moving forward with the long-term work of coordinating and expanding phenology observations and networks around the world. We (Elisabeth Koch, Jake Weltzin, and I) aim to lead this effort through a Group on Earth Observations (GEO) sub-Task, and possibly a World Meteorological Organization Expert Team.

So in conclusion, I call phenology an integrative (rather than integrated) environmental science, because I see it as a field of study that brings together researchers from many different disciplines, rather than being a unique discipline unto itself. Clearly, phenology's multi-disciplinary perspective is a powerful approach for addressing real-world problems. However, we can only achieve this objective fully if there is enough "cross-training" so everyone can "speak the same language." With this text, Marie, Irene, and their contributing colleagues have both broadened and deepened our world-wide phenological research "conversation."



Mark D. Schwartz  
Milwaukee, May 2009

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# Chapter 1

## Introduction and Overview

Marie R. Keatley and Irene L. Hudson

### 1.1 History

The term phenology was first introduced by Charles Morren in 1849 in a public lecture on the 16th of December entitled “Le globe, le temps et la vie” (Morren 1849, 1851). Phenology which he took from the Greek *φαινομοια*, (Morren 1849), was defined as “apparaître, se manifester: phénologie, la science des phénomènes qui apparaissent successivement sur le globe.” This translates as: to show, to appear: the science of phenomena that appear successively on the globe.

The term, phenology, grew out of Morren’s work on the “periodic phenomena of vegetation” with articles being published in the *Les Annales de la Société Royale d’agriculture et de botanique de Gand* (Annals of the Royal Society of Agriculture and Botany of Ghent). These articles were apparently compiled under one title “*Traité historique de Phénologie*” (de Selys-Longchamps 1853). It is, however, Morren’s paper “*Souvenirs phénologiques de l’hiver 1852–1853*” published in 1853 which is credited with the term’s introduction (Demarée and Curnel 2008) and the reason that 1853 is the date usually cited for this (Abbe 1905, Hopp 1974, Grove 1988, Puppi 2007).

Phenology, in its adjectival form, was introduced into the English language in 1875 (Lynn 1910, Egerton 1977) when instructions were issued by the Council of the Meteorological Society for recording phenological events (Anon 1875). The first definition of phenology published in English “is the observation of the first flowering and fruiting of plants, the foliation and defoliation of trees, the arrival, nesting, and departure of birds, and such like” was in 1884 (Anon 1884, Oxford English Dictionary 2008).

In 1972 as part of their contribution to the International Biological Program (IBP) the United States of America established a committee on phenology (Leith 1974). This Committee defined phenology as:

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*the study of the timing of recurring biological events, the causes of their timing with regard to biotic and abiotic forces and the interactions among phases of the same or different species (Leith 1974 p4).*

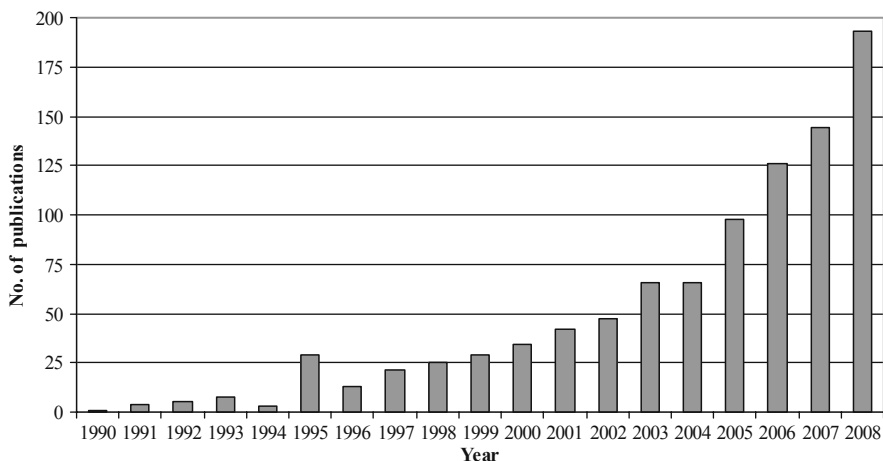
The committee suggested further refinements of the definition, to add a spatial and temporal framework:

*the unit of study may vary from a single species (or variety, clone etc.) to a complete ecosystem. The area involved may be small (for intensive studies on all phenostages of entire ecosystems) or very large (for interregional comparison of significant phenostages). The unit of time is usually the solar year with which the events to be studied are in phase. The events themselves may cover variable time spans, often shorter than the solar year (Leith 1974 p5).*

Regardless of its definition, and whether phenology includes seasonal events such as snow thaw (see Chapter 3 by Jeanneret and Rutishauser), phenology has a long history with agricultural phenological calendars dating from 1700 BC (Kramer 1963 in Aitken 1974), the longest phenological recording of flowering dating from 705 AD in Japan (Menzel 2003a) and Carl Linnaeus, outlining methods for collecting “calendrier florae” phenological data in 1751 (Linne 1751). Indeed, prior to the invention of thermometers the observation of agricultural phenological phases was used to judge whether a particular year’s climate was different to a so-called normal year (Pfister 1980).

In what follows we review and give the phenological, mathematical and statistical context of each chapter of this book (with broad references for the reader to glean the areas of research and publication and application; and choice what best interests him or her). This introduction and overview aims to inform the reader also of the scope of the topics discussed, as well as to provide a conceptual framework for past, new and ongoing and future developments in the field of phenological research.

With the exception of agricultural phenology, phenology has been regarded by the wider scientific community as the domain of natural historians (Sparks and Menzel 2002), and therefore lacking scientific rigour. This is despite many significant scientific contributions over the years to phenological methods and modelling (e.g. Bassett et al. 1961, Caprio 1966, Dierschke 1972, Caprio et al. 1974, Leith 1974, Idso et al. 1978, Pfister 1980, Alm et al. 1991, Kramer 1995, Degrandi-Hoffman et al. 1996, Linkosalo et al. 1996, Cenci et al. 1997, Chen et al. 1999). This view started to change in the 1990s (Fig. 1.1 and Schwartz 2003b) when the inherent value of phenology, primarily driven by the insights into the impacts of climate change which phenological observations and analyses can provide, was recognised (Sparks and Carey 1995, IPCC 2001, Root et al. 2003, Parmesan and Yohe 2003, Parmesan 2007). Changes in phenological processes have significant consequences for human health, biodiversity, forestry, agriculture, the economy etc (de Vries 1980, McMichael 1993, IPCC 2001, Walther et al. 2002, van Vliet et al. 2003, World Health Organisation 2003, Mackey 2007, Thuiller et al. 2008). Chapter 4 by van Vliet details these impacts on human health and primary production and presents



**Fig. 1.1** No. of papers published between 1990 and 2008 (indexed in the ISI web of science) in which both phenology and climate change are topics (ISI accessed on 26/02/09)

ways for these sectors to adapt to climate change. As noted by him in Chapter 4 the IPCC (Schneider et al. 2007) conclude that market and social systems have a considerable adaptation potential but that the economic costs are potentially large, for the most part unknown and unequally distributed, as is the adaptation potential itself. van Vliet also highlights the contribution that phenological monitoring continues to make, the need to improve the analysis of phenological time series and quantify both the societal and environmental impact, as well as the communication of the results.

Chapter 2 on phenological networks compiled by Elizabeth Koch, with contributions from authors from both hemispheres, confirms that there is now a worldwide recognition that phenology can be used as an integrative indicator not only for regional impacts of climate change but also at the global level (Donnelly et al. 2004, Parmesan 2006, Cleland et al. 2007, Rosenzweig et al. 2008). Chapter 2 supplements and updates the information on networks and databases provided in Schwartz (2003a) and Nekovář et al. (2008) as well as adding information for countries where phenological information was previously lacking (e.g. Africa and Russia).

The publication of “Phenology: An Integrative Environmental Science” (Schwartz 2003a) also heralded a new age of acceptance of phenological practice, application and research. This book builds on the book of Leith (1974) and following a similar format contains detailed information on: (1) phenological data, networks and research (2) the phenology of various bioclimatic zones, (3) phenological modelling, (4) remote sensing phenology; as well as (5) applications. It also highlights the multidisciplinary nature of phenology.



## 1.2 Current Issues in Phenology

The accelerated interest in phenology is highlighted by the fact that since the publication of “Phenology: An Integrative Environmental Science” (Schwartz 2003a), there has been a growing awareness, as expressed in the recent phenological literature, that popular analytical methods used in phenological research, whilst useful, have their limitations (Dose and Menzel 2004, Hudson et al. 2005, Sparks and Tryjanowski 2005, Cleland et al. 2007). Phenological studies almost certainly are observational and therefore often rely on correlation analysis for inference (Parmesan and Yohe 2003, Sparks and Tryjanowski 2005).

One example is the popular practice of analysing phenological records by simple linear regression (which has a correlational basis) - often used to determine whether there has been a change in the commencement time of a phenostage; indicated by a significant estimate of the slope. It has been highlighted (Sparks and Menzel 2002, Menzel 2003b, Hudson et al. 2005, Sparks and Tryjanowski 2005) that the slopes of the resultant regression lines are influenced by when the series commences and finishes and, also by the length of the series. Menzel et al. (2008) also noted that when utilising simple linear regression, the length of a time series and its start and end dates are crucial in correct detection of changes, and in estimating their magnitude. This is particularly so when highly variable, multi-decadal, phenological time series are analysed (Dose and Menzel 2004). As temperature in the last 12 years (1997–2008) encompasses the warmest period recorded (Goddard Institute for Space Studies 2009), this also impacts on the slope of the regression lines and on the ability of regression methods to accurately estimate the true rate of change over time of a phenological stage (Sparks and Tryjanowski 2005). However, this analysis is robust and has a role to play in phenology. In Chapter 6, Sparks and Tryjanowski present ways to ensure that the method is applied appropriately and provide examples of alternate methods: polynomial and multiple regression. Multiple linear regression (MLR) or stepwise regression (Draper and Smith 1981) are regularly used to investigate the influence of temperature on the first day of flowering or to relate a phenological response to weather measurements (Fitter et al. 1995, Sparks and Carey 1995, Keatley and Hudson 2000, Roy and Sparks 2000, Lu et al. 2006). To date, MLR or stepwise methods have delineated similar results across different regions (Fitter and Fitter 2002, Roberts et al. 2004). Stepwise regression is a procedure that selects the subset of the regressors that best explains the variation in the phenological response. Stepwise regression, however, has limitations in studies relating a phenological response to weather data. Firstly, it does not accommodate for large numbers of highly correlated regressors. This is an issue if daily or weekly measurements are used as regressors (see also Chapter 12 Roberts). In practice monthly aggregates of weather data are then used and clearly information is lost. Stepwise regression, like simple linear regression, does not take into account the marked auto-correlated structure in the regressors. Indeed what has not often been highlighted in the phenological literature is that phenological series (or fine time scale weather series) are correlated by nature, an aspect not accounted for by linear, MLR, nor stepwise regression methods (Chapter 13 Kelly, Hudson et al. 2005).

Roberts in Chapter 12 describes a recently introduced approach, penalized signal regression (PSR), to examine the relationship between phenology and weather (following Roberts 2008). PSR is based on linear regression, and thus retains the benefit of flexibility, but can be used with weekly or daily weather data and gives intuitively appealing and interpretable results. The penalised regression method avoids difficulties due to multicollinearity (correlated regressors) and illustrates the concept of penalising differences between regression coefficients so as to obtain a smooth profile. Roberts discusses how the PSR approach can also be expanded to investigate the effect of one or more covariates, for example latitude, on the regression coefficients (Eilers and Marx 2003) or to study how two or more banks of predictors, such as daily temperature and rainfall measurements, affect the phenological response.

Kelly in Chapter 13 points out that whilst multiple-location phenological data is reasonably uncommon, the impetus of expanding phenological networks will ensure data of this type will be available in the future (Cleland et al. 2007). Results from studies of trends in phenophases at a regional (rather than local) level provide more power to detect climate change. The representativeness of locations of phenophase observations is, however, an important issue (Rötzer et al. 2000, Thompson and Clark 2006, Siljamo et al. 2008), in that data from an individual location may unduly influence or bias models of phenological change, through factors that cannot be controlled for nor quantified. As Kelly cautions, data containing phenophase time series from multiple locations has an inherent correlated error structure which standard statistical methods cannot accommodate. She advocates and demonstrates alternative modelling approaches to account for both multiple localities and for the longitudinal nature of phenological data - data resolution and random effects modelling, both extensions of simple linear regression (see Verbeke and Molenberghs 2000 and Diggle et al. 2002).

Non-linear modelling has not been addressed much to date in phenology. Indeed it will be difficult to find a linear regression model that fits the data well for essentially non-linear processes. This is true particularly as the range of the data increases (Schleip et al. 2008). The pertinent question is how can we accommodate for non-linear responses of phenology to time and/or to climatic factors? This has been addressed by Hudson and her colleagues in Chapter 10, by the application of Generalised Additive Models for Location, Scale and Shape (GAMLSS) (see Rigby and Stasinopoulos 2005, and Hudson et al. 2009). Hudson et al. illustrate the advantages of GAMLSS to phenology is that GAMLSS: [1] can identify the main drivers of the event of interest from a multiplicity of predictors such as temperature and rainfall; [2] allow for non-linear impacts of time and/or the explanatory variables; [3] can statistically detect thresholds; for example, the lowest temperature for the commencement of flowering; and [4] can model the auto-correlated nature inherent in the phenological series (see also Chapter 13 of Kelly). In Chapter 19 MacGillivray's et al. present the GAMLSS approach to show its greater accuracy and relevance to the assessment of non-linear trends over time (year) for herbarium records.

Modelling nonlinear phenological responses with time have been addressed in the context of meta-analytic studies in phenology by Hudson (Chapter 20) and from

a Bayesian viewpoint by Schleip and his colleagues (Chapter 11). Bayesian analysis offers the possibility to overcome the pitfalls of linear regression models. Indeed Bayesian statistical methods have been applied to date in climate change detection, analysis and attribution (e.g. Hobbs 1997, Hasselmann 1998, Leroy 1998, Berliner et al. 2000), and also in climate reconstructions (Robertson et al. 1999, Schoelzel 2006). Recently various studies show that Bayesian analysis offers huge benefits in the analysis of varying changes, model probabilities and change-point probabilities of time series, when nonlinear changes in phenological and climate time series exist. Along with these rates of change, rigorously calculated uncertainties of model-averaged rates of change and linear trends can be described by Bayesian statistics (Dose and Menzel 2004, Menzel et al. 2008, Schleip et al. 2008).

A handful of papers have used other methods to account for the possible non-linearity and for the complex interdependencies and changing structure in phenological time series: namely dynamic factor analysis (by Gordo and Sanz 2005) and chronological clustering (Doi 2007, Doi and Katano 2008). These methods prove valuable in separating out underlying components of a univariate (single) time series that show significantly different patterns; aspects achievable by the techniques of wavelets and singular spectrum analysis discussed by Hudson and her colleagues in Chapters 17 and 18, respectively.

Much focus has gone into developing a better definition of phenophases and provision of greater precision and accuracy for data collected across phenological networks and stations (see Chapter 2; Meier 2003, COST 725 2008). However, the influence of sampling method, sample size and the frequency of observations on the analysis and interpretation of plant phenology has been rarely addressed in the phenological literature (Fournier and Carpentier 1975, Chapman et al. 1992, 1994, Hemingway and Overdorff 1999, D'Eça Neves and Morellato 2004). Such issues of sampling method, sample size and the frequency of observations are discussed by Morellato and her colleagues in Chapter 5 via a case study of tropical forest trees, where direct observations on transects are compared with those from litter traps. The lack of a coherent set of sampling rules and methods, if not analytic methods and procedures, is even more evident in tropical phenology, where there is a high diversity of species and complex ecosystems (Frankie et al. 1974, Newstrom et al. 1994, Sakai 2001, Morellato 2003). In Chapter 5 Morellato et al. advocate the combination of presence/absence data and a quantification method to estimate plant phenology, and recommend careful estimation of indices (Fournier intensity index (Fournier 1974) and activity index (Bencke and Morellato 2002)) and a cautious generalisation of pattern(s).

Reaching some consensus on design, method of collection and comparable analytic methods is much needed to advance the generalisability of phenological results. What has also been recently discussed is the need for the phenological community to reach a consensus on inclusion criterion for studies selected for phenological meta-analytic studies (Parmesan 2007). As noted by Hudson in Chapter 20 in a discussion of meta-analysis in phenology – these criteria likewise relate to sampling and observation frequency, that is length of observations (length of the time series) and pertain

to selection criteria of studies for inclusion into the synthetic analysis; this based in part on whether a reported neutral, negative or positive result was exhibited in regard to climate change impact on phenology (see Chapter 20 of this book and Parmesan 2007).

Phenological time series are often incomplete and of limited temporal range. As Schaber and his colleagues point out in Chapter 7 with ongoing efforts to expand the databases of phenological observations by data mining it is likely that more data sets with sparse data and data gaps will become available in the near future (see Aono and Kazui 2007). The problem of the uncertainty of individual time series and gaps is often accommodated for by averaging a set of phenological time series over a geographical area of interest or a time period of interest (Estrella and Menzel 2006, Menzel et al. 2006, 2008). To date, there are applications of methods for combining phenological time. One application is to obtain a reliable series from several time series (Häkkinen et al. 1995, Linkosalo et al. 1996, 2009, Linkosalo 1999, Schaber and Badeck 2002). Another is to construct a long time series for trend analysis, where data gap filling is of primary interest (Schaber and Badeck 2005). In addition combined time series can also be used to find outliers in individual time series (Linkosalo et al. 2000, Schaber and Badeck 2002, Doktor et al. 2005). Schaber and his colleagues in Chapter 7 present a method for combining phenological time series which imputes missing data within records as well as detecting outliers. Schaber et al. also quantify the effect of the extension of the outlier detection algorithm using Gaussian Mixture Models. Their outlier detection method is based on Gaussian Mixture Models (Doktor et al. 2005) and accounts for year-location interactions. The approach of Gaussian mixtures, discussed in Chapter 7 which allows for station  $\times$  year effects, can be further developed by assigning stations to tentative mixture components before checking for outliers. Schaber et al. (Chapter 7) point to the future application of Bayes statistics as an alternative way of analysing messy phenological datasets (see Dose and Menzel 2004), and suggest that further work would entail comparison of Bayes methods to the methods discussed in Chapter 7.

Recent technological advances in studying the earth from space have resulted in a new field of phenological research which concerns itself with observing the phenology of whole ecosystems and stands of vegetation on a global scale using proxy approaches (Reed et al. 2003, Stöckli and Vidale 2004). These remote sensing methods complement the traditional phenological methods which record the first occurrences of individual species and phenophases, and, in part, overcome one other limitation of phenological time series is that they have limited geographical range. But as de Beurs and Henebry in Chapter 9 point out, further research is required on the relationship between satellite derived metrics for the start and end of season with ground-based phenological observations. Jeanneret and Rutishauser in Chapter 8 on phenological mapping show also that technical and analytical challenges still remain, (e.g. the comparability of different data sources and/or frequent temporal gaps). These satellite derived phenological parameters are an approximation of the true biological growth stages; mainly due to the limitation of current space based remote sensing and the nature of vegetation index. As pointed out by Jeanneret and Rutishauser in Chapter 8 motivations to map phenology are often driven by

practical issues such as: regional planning (Jeanneret 1974, Messerli et al. 1978), aerobiology (pollen emission, Branzi and Zanotti 1989, García-Mozo et al. 2006), and agronomy (Mariani et al. 2007). They contend that “large-scale phenological maps are unequalled and irreplaceable in providing a maximum amount of topoclimatic information” and recommend that in a transition from cartographic intuition to future mapping algorithms we need to utilize and link all available sources of data, terrain information, knowledge and experience.

In Chapter 9 de Beur and Henebry present twelve methods commonly used in land surface phenology along with their limitations, in determining start and end of season, reiterating the point that, relating satellite observation with ground-based phenology, remains a significant challenge. The different spatio-temporal statistical methods are grouped into the following categories: [1] thresholds (Lloyd 1990, Fischer 1994, Myneni et al. 1997, White et al. 1997, Shabanov et al. 2002, Zhou et al. 2003, Karlsen et al. (2006, 2007), Delbart et al. 2005); [2] derivatives (White et al. 1997, Tateishi and Ebata 2004, Baltzer et al. 2007); [3] smoothing algorithms (e.g. moving average models (Reed et al. 1994)), discrete Fourier analysis (Moody and Johnson 2001), Principal component analysis (Eastman and Fulk 1993, Hall-Beyer 2003); and [4] fitted models (logistic models (Zhang et al. 2004)), Gaussian models or lower order Fourier estimates (Jönsson and Eklundh 2002), quadratic models with accumulated growing degree days (de Beurs and Henebry 2008). In Chapter 9 de Beur and Henebry also point to the as yet unresolved problems with a lack of statistical error structure from most of these methods and in oversmoothing.

In Chapter 3 Jeanneret and Rutishauser advocate that phenological observations are crucial as the basis for a description of a seasonal classification and seasonality. They show that a well designed phenological diagram can offer a comprehensive picture of the rhythm and amplitude of seasons and they detail the basic requirements of drawing up a phenological diagram. They suggest the inclusion of abiotic observations such as the timing of frost, thawing, icing, snow and fog provides seasonality descriptions beyond the vegetation period – offering thus a year-round, combined topoclimatic typology. In terms of utility Jeanneret and Rutishauser claim that phenological season diagrams are a compelling and cheap tool for extracting typologies of seasonal patterns based on an analysis of single years or of different stations; and have the potential for global application; despite phenology having, not as yet achieved international or global standardization (Bruns and van Vliet 2003).

Additionally given the increased worldwide momentum on reporting results from climate impact studies and now from phenological series, as the value of long-term data is being recognised, it seems that every attempt is being made to extract climate signals contained within these records (Stenseth et al. 2002, Walther et al. 2002, Parmesan and Yohe 2003, Root et al. 2003, Rosenzweig et al. 2008). However, it is still not fully appreciated, that the identification of points of significant change (change-points), in long-term phenological time series, is a prerequisite for the analysis and the interpretation of phenological observations as bio-indicators of climate change (Hudson et al 2005). Rapid shifts in climate can lead to, or be

contemporaneous with, abrupt phenological changes. These cannot be well detected by regression nor correlation, methods traditionally used to detect temporal changes in phenology (Cleland et al. 2007). The non-uniform periods of change that typify the climate of the twentieth century (Dose and Menzel 2004, Rutishauser et al. 2007) pose a particular challenge when linear regression analysis is used for the reconstruction of trends.

Indeed there are few studies to date determining change points in phenological series using precise statistical models (Dose and Menzel 2004, 2006, Hudson et al. 2004, 2005, Schleip et al. 2006, Keatley and Hudson 2008, Menzel et al. 2008). The Chapter (11) by Schliep and his colleagues presents a single change point method and the associated rates of change in flowering using nonparametric Bayesian functionals to time series. Bayesian analysis of the change-point probabilities as described by Schleip and his colleagues provides both visualisation and quantification of major changes in long-term time series (see also Dose and Menzel 2004, Menzel and Dose 2005, Menzel et al. 2008, Schleip et al. 2008, 2009). In Chapter 19 MacGillivray and her colleagues present the results from a multiple change point analytic approach, on herbarium records, following Moskvina and Zhigljavsky (2003), which is model free change point method, based on the sequential application of singular-spectrum analysis (SSA) (see Chapter 18) to subseries of the original series. They also determined, not only the significant points of change, but also the rates of change using both change point analysis and nonlinear modelling via Generalized Additive Models for Location, Scale and Shape (GAMLSS) (Chapter 10). MacGillivray's et al. (Chapter 19) advocate the combined use of both non-linear methods (GAMLSS) and change points methods in phenological analysis, particularly of herbarium records. The detection of change points has also been applied to the area of circular statistics (Jammalamadaka and SenGupta 2001), whose potential to phenology research is discussed in Chapter 16 by Morellato and her colleagues. Change point methods for linear scaled data are discussed in other chapters of this book (Chapter 11). Indeed the reconstructed subcomponents of phenological time series discussed by Hudson et al. (Chapter 18) point to significant points of change in cyclicity and amplitude of flowering in four species of eucalypt. Hudson also discusses the need for change point identification in phenological meta-analytic studies (Chapter 20); this is a problem not appreciated, nor accounted, for, to date, in phenology. The presence of significant and abrupt change points affects both the accuracy of the estimates of local climate impact and of the pooled estimates of climate effect from meta-analytic studies, which are traditionally conducted across wide geographical locations (Chapter 20).

It has been advocated for some time that statistical techniques used in phenology need to accommodate for the inherent complexity of phenological records (Dose and Menzel 2004, Hudson et al. 2005) which is often ignored. Complexity, such as their time series (correlated) nature, their often discrete and non-stationary properties, and the presence of excess zeros (non occurrence of a phenostage of interest). More sophisticated statistical methods for examining phenological time series are still needed. In Chapters 17 and 18 Hudson and her colleagues apply two such methods for time series decomposition and cross-correlation, namely wavelets analytic

methods (Percival and Walden 2000, Kang et al. 2004) and singular value decomposition (SVD) using singular spectrum analysis (SSA) (Golyandina et al. 2001, Hudson et al. 2004, Fukuda and Hudson 2005, Golyandina and Osipov 2007). It is noteworthy that whilst wavelet analysis has been used in a study of European spring temperatures (Paluš et al. 2005) and rainfall (Koch and Marković 2007) and changes in vegetation cover (Lu et al. 2007), it is as yet under utilised in traditional land based phenology. SSA is also not as yet very widely applied to phenological data (D'Odorico et al. 2002, Hudson et al. 2004, 2005, Studer et al. 2005, 2007). These chapters illustrate the worth of both wavelets and SSA, and associated cross correlational analysis to phenology, demonstrating that these methods offer us ways to: [1] identify spatial and climate niche across species; [2] decompose time series into its sub components (e.g. trends, oscillatory modes or seasonalities, change-points and noise); [3] establish whether a given species is uniquely influenced by climate through the year (i.e. has its own climatic signature); [4] determine the relationship between multiple climate indicators; [5] succinctly display how the association between the two processes, say climate and flowering, change with scale and time; and [6] identify the primary climatic drivers of flowering or of any phenophase.

Transitional state modelling, which assumes the existence of underlying heterogeneity (mixtures) in multivariate time series, is a novel technique developed by Hudson and her colleagues and applied to eucalypt flowering, as detailed in Chapter 14. Hudson et al.'s approach allows for modelling possible *interactive effects* of two or more climate variables on phenological response (where the phenological response and climatic predictors are discrete state processes). Interactive effects have as yet not been tested for in phenology; even though there is an appreciation that climate drivers, other than temperature, such as rainfall, and drought etc need to be modelled in addition to temperature forcing (Schleip et al. 2008).

Exploring the impacts of single and multiple climate variables, and even which temperatures impact from different months, or combinations and interactions of such variables, constitutes a significant modelling exercise (Sparks and Carey 1995, Keatley et al. 2002). Transitional state modelling (see e.g. Berchtold and Raftery 2002) has also, as yet, not been embraced in phenology. Hudson et al. (Chapter 14) develop the work of Kim et al. (2005, 2008, 2009), which uses mixed transition distribution (MTD) models (Berchtold 2006) to study the relationship between the probability of (on/off) eucalypt flowering with respect to two discrete states (high/low) of rainfall and of temperature. Allowing for interactive effects between climate predictors in modelling phenological response opens up new dimensions of interpretation of results. For example, the four eucalypt species examined in Chapter 14 are shown to be influenced by temperature (see also Keatley et al. 2002) and in some instances are influenced by rainfall and its interaction with temperature. Hudson et al. then conclude that as a consequence their flowering phenology will change in response to climate change, and propose that there may be a rainfall threshold required before flowering can occur (Hodgkinson and Freudenberger 1997).

Increased synchrony can mean less potential for genetic or demographic rescue effects (Brown and Kodric-Brown 1977, Tallmon et al. 2004). In the study of population dynamics the degree of synchrony (the temporal match of events in space and time) is frequently estimated by the cross-correlation of population sizes in two spatially distinct localities; with synchrony tending to decrease with distance (Ranta et al. 1997, 1999). In Chapter 15 Ranta and his colleagues demonstrate that phenological events can indeed be synchronized in a similar manner as population fluctuations. Ranta et al. show that the Moran effect (i.e. a common external perturbation) is capable of synchronizing two distinct life history events, that of leafing in European aspen (*Populus tremula*) and that of mast seeding in both Scotch pine (*Pinus sylvestris*) and Norway spruce (*Picea abies*) in Finland. Using a threshold-triggered phenology model Ranta et al. demonstrate that the conceptual framework of Moran effect may be extended to cover the timing of life history events, events not directly regulated by density-dependent feedback. Tests for synchrony based on circular statistics are also discussed by Morellato et al. (Chapter 16).

As mentioned cross-correlational methods underpin synchrony tests, but as yet, like testing for interaction effects of multiple climatic indicators, are underutilized in phenology. Schleip and his colleagues (Chapter 11) discuss correlational methods of phenological data with temperature (see also Dose and Menzel 2006 and Schleip et al. 2008). Wavelet cross correlation methods for bivariate time series are also discussed in Chapter 17 of this book when relating either bivariate phenological-series or say one phenological-series with climate time series indicators. See also the cross correlation methods based on the SSA reconstructions of both phenological and climate time series in this book (Chapter 18). Finally in the realm of circular statistics (Chapter 16) cross correlational methods are now available (Zimmerman et al. 2007).

In Chapter 16 Morellato et al. discuss circular statistics (Batschelet 1981, Fisher 1993, Zar 1999, Mardia and Jupp 2000), an area of statistics also not much used in phenology to date. This is possibly due to its difficult and less traditional mathematical and statistical formulation, and the lack of easily available software, till recently (see listing in Chapter 16). Most of the earlier animal and plant applications of circular statistics involved the analysis of directional data (e.g. the orientation and direction of movements of animals, such as flight direction of birds and butterflies and the orientation on salamanders and dragonflies (Batschelet 1981, Fisher 1993)). Morellato et al. show that the connection between the evaluation of temporal, recurring events and the analysis of directional data have converged in several papers (Herrera 1988, Milton 1991, Wolda 1988, 1989, Morellato et al. 1989, 2000, Alonso 1997, Davies and Ashton 1999, Hamer et al. 2005, Zimmerman et al. 2007) and show circular statistics to be a tool by which to better describe and to compare both plant and animal phenology. Morellato et al. advocate that circular statistics has particular value and application when flowering onset (or fruiting) occurs almost continuously in an annual cycle or where flowering time may not have a logical starting point, such as mid-winter dormancy. They conclude that circular statistics applies well to phenological research where one wants to test for relationships between flowering time and other phenological traits (e.g. shoot growth), or with



functional traits such as plant height. Circular statistical methods also allows grouping of species into annual, supra-annual, irregular and continuous reproducers; and for rigorous study of seasonality in reproduction and growth; and the assessment of synchronization of species (see also Chapter 15 for more discussion on synchrony methods).

Recently it has been appreciated that extending phenological records over time and particularly over geographical location is much needed (Chambers 2006, Sparks et al. 2006, Parmesan 2007, Sparks 2007, Bertin 2008). In Chapter 19 MacGillivray et al. present what Sparks (2007) calls “lateral thinking” – the use of herbaria specimens and photographs to examine the effects of climate change on phenology (see also Miller-Rushing et al. 2006, Lavoie and Lachance 2006, Miller-Rushing and Primack 2008, Loiselle et al. 2008, Gallagher et al. 2009). The relevance of such collections to a range of ecological conservation and biological studies has been, to date, largely underappreciated in Australia (Rumpff et al. 2008). MacGillivray et al. outline the constraints which need to be considered when linking phenological changes with climatic fluctuations and long-term trends. They offer some cautionary principles for analysis and interpretation - these include issues regarding sparsity of data and irregularity of records over time, as well as the need for more complex underlying distributions. How best, if possible, to infer first flowering dates and actual stage of flowering from snap records remains an issue for inference, modelling and interpretation. MacGillivray’s et al. (Chapter 19) also contend that to properly address the question of change, periods of no change must also be considered as important; vital also is the determination of events throughout periods of reasonably stable conditions.

In the final chapter, Hudson presents a review of the general methodology of meta-analysis, assesses its advantages and disadvantages, synthesizes its use in global climate change phenology and suggests new statistical directions and an underlying paradigm for a unified meta-analytic approach. Specifically Hudson proposes new statistical methods, as yet not applied to phenological research, and only recently applied, in part, in the health-climate-pollution epidemiological literature. Hudson discusses three approaches and applications to the modelling of *nonlinear* phenological response over time namely, Generalised additive models for location scale and shape (GAMLSS) (Stasinopoulos and Rigby 2007) (see Chapter 10 and Chapter 19 for GAMLSS analyses on eucalypt flowering and orchid peak flowering, respectively), penalised signal regression (Chapter 12 of Roberts) and Bayesian nonparametric function estimation (see Chapter 11 Schleip et al. and Chapter 19 by MacGillivray et al.). These are shown by Hudson to be inter-related to three recent epidemiological approaches of exposure (pollution/climate) to response (health/hospitalizations) modelling which Hudson contends hold much promise for future meta-analytic studies in phenology. These are nonlinear “dose/exposure to response” functionals in epidemiology (Gamborg et al. 2007, Baccini et al. 2008, Peng et al. 2009), Bayesian hierarchical meta-analysis (Baccini et al. 2008 and Michelozzi et al. 2009) and Bayesian hierarchical distributed lag models (BHDLMs) (Peng et al. 2009). Proof of concept of this application to phenology is an important area of future research, which we hope will be a challenge taken

up by mathematicians, phenologists, statisticians and others. Hudson shows that the overarching paradigm for all the meta-analytic methods suggested for phenological synthetic studies is the area of semiparametric regression (Ruppert et al. 2009); which she proposes as a possible way towards a unified meta-analytic approach in phenology.

### 1.3 Aims of This Book

There is both art and science in the analyzing and assessing of phenological impacts of climate change. Forecasting and anticipating such impacts remains an even greater challenge. A similar viewpoint with respect to climatological research and environmental change is espoused by von Storch et al. (2007). Von Storch and Zwiers have helped to inject statistical thinking and method into climatology research (von Storch and Zwiers 2001, Zwiers and von Storch 2004). Our book in a similar vein hopes firstly to build on Leith (1974) and of Schwartz (2003a), and thereby bring to readers the art and science, complexity and beauty of phenological research. It presents statistical, graphical, image analytic and sampling methods (via case studies and some theoretical exposition), both for those commencing in phenological research and for those more experienced in the area. In addition it embraces the call that “phenologists need to link with other disciplines” (Dunlop and Howden 2003, van Vliet et al. 2003), with contributions from botanists, ecologists, geographers, foresters, climatologists, meteorologists, GIS experts, phenologists, mathematical statisticians and health epidemiologists. We hope this book will also be valuable as a reference source for these disciplines and add rigour to and possibly change the focus of some directions of global climate change research towards a more mathematically and statistically rigorous exploration. We believe the book will add to the momentum and contribute to the robustness of the science, which is phenology; and bring together the disciplines needed to further advance this science. We shall then be better placed to propose future scenarios, so as to, in the words of von Storch et al. (2007), “confront stakeholders and policy makers with possible future conditions so that they can analyse the availability and usefulness of options to confront an unknown future”.

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# Chapter 2

## Global Framework for Data Collection – Data Bases, Data Availability, Future Networks, Online Databases

Elisabeth Koch

### 2.1 Rationale

Since the 1990s, phenology has regained scientific interest as a biological indicator for climate change (Schwartz 2003). Menzel and Fabian (1999) and Chmielewski and Rötzer (2001) were able to demonstrate with the observation series of the International Phenological Gardens' network that spring has advanced in Europe and autumn has come later. The autumn signal is not as significant as the earlier onset of spring, however, which results in a longer vegetation period in the middle and higher northern latitudes. The growing interest in, and importance of, phenology is also visible in the report of Working Group II, Assessment of observed changes and responses in natural and managed systems (Rosenzweig et al. 2007) of the 4th assessment report of the Intergovernmental Panel on Climate Change. The impact of warming on terrestrial species across the Northern Hemisphere is well documented by changes in the timing of growth stages (Rosenzweig et al. 2007). The data base for these impact studies is made up of long time series of phenological ground observations (e.g. Menzel et al. 2006) and/or satellite data (e.g. Zhou et al. 2001, Chen et al. 2005), thus reinforcing the necessity of sustainable phenological networks.

The growing interest in phenology has also triggered many new national and international network activities (e.g. <http://www.naturescalendar.org.uk>, <http://www.natuurkalender.nl/index.asp>). For examples of such activity in the US, South America and Australia, see Schwartz and Betancourt Pinto and Morellato, and Keatley and Chambers respectively, in this chapter.

The World Climate Research Programme (WCRP) has also published recommended methods for undertaking phenological observations (Koch et al. 2007). Additionally, one of the four priorities of the expert team on climate monitoring of the World Meteorological Organisation's (WMO) Commission for Climatology, is

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“to stimulate and coordinate phenological practices in climate monitoring activities” (WMO 2007).

In the following sections we will concentrate on ground networks whose main objective is phenological monitoring. There are of course many other observation networks, mainly biodiversity orientated, which also have aspects of phenology in their program for example the Long-Term Ecological Research (LTER) network, a good overview of which is presented at [www.lter.net](http://www.lter.net). In addition, there is a wide range of worldwide satellite data, contributing measures such as fAPAR (fraction of absorbed photosynthetically active radiation). Whilst these do need in-situ observations to determine their reliability and accuracy, they are becoming more important sources of data, as the higher spatial resolution of 250–300m of the new satellite generation begins to solve previous problems in comparability between point measurements at reference sites and satellite images (GCOS 2006).

This chapter will, however, focus on the data and resources available within ground-based phenological networks. The chapter describes the history of phenology in various locations, as well as describing the status and current activities of phenology in various regions around the world.

## 2.2 First Steps in the “Globalisation” of Phenology

Elisabeth Koch, Gaston Demarée, Susanne Zach, and Kirsten Zimmermann

### 2.2.1 Eighteenth Century

Phenological networks were established about one century, before the word “phenology” was created. Carolus Linnaeus is regarded as the father of modern phenology; in the middle of the 18th century he initiated the first known phenological network with 18 stations in today’s Sweden and Finland. Unfortunately, however, this network ran for only three years from 1750 to 1752 (Schnelle 1955).

About 30 years later the *Societas Meteorologica Palatina* at Mannheim, Germany founded and sponsored by Kurfürst Karl Theodor, and managed by his secretary Johann Jakob Hemmer, established the first pan European meteorological network (1781–1792) where phenological observations were also carried out at some locations. The results are published in *Ephemerides Societatis Meteorologicae Palatinae* 1783–1794 (Fig. 2.1). Among the stations with “*observationes botanicae*” were Rome, Saint Petersburg, Geneva and Mannheim, which had the most extensive dataset. The program was structured in *arbores et frutices* (trees and bushes), *fructus agrorum* (agricultural fruits) with the phases *gemmae* (buds), *folia* (leaves), *flos* (florescence), *maturitas* (ripeness). Columns were also reserved for *proventus* (description of appearance) and *morbi vel insecta nociva* (pests or diseases). Some

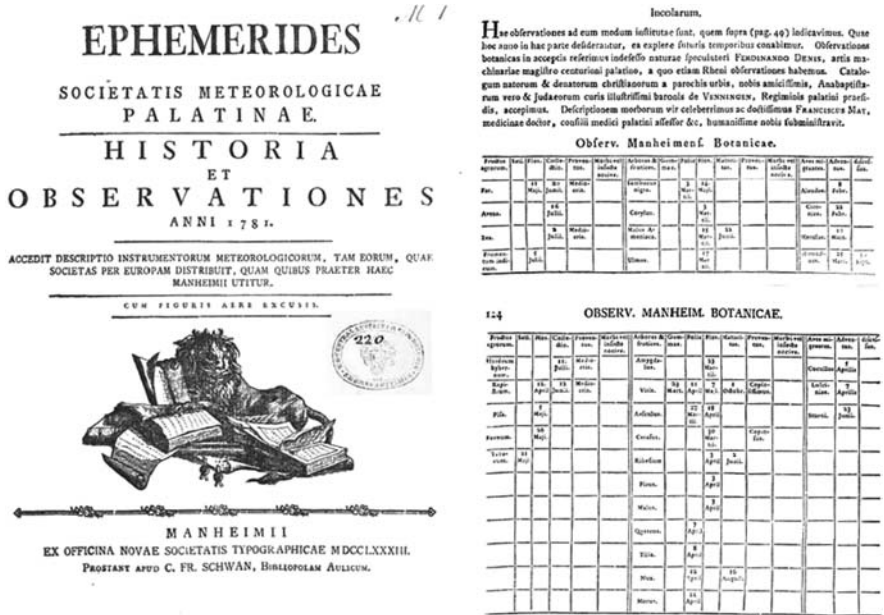


Fig. 2.1 Ephemerides (1783) first page and the table with “Observ. Manheim. Botanicæ”

animal phenology was also recorded, such as *aves migrantes* (migrating birds): *adventus* (arrival) and *discessus* (departure). The observers were highly educated people such as astronomers, botanists, doctors, pharmacists, teachers and clergymen and they were all male. The *Societas Meteorologica Palatina* founded as a result of the French Revolution (Lingelbach 1980).

### 2.2.2 Nineteenth Century

In the middle of the nineteenth century many networking activities were initiated. The Belgian astronomer Adolphe Quetelet, director of the Royal Observatory in Brussels, recruited observers in Belgium, The Netherlands, Germany, Italy, France, England and Switzerland. He collected data from approximately 80 stations for the period 1840 through to the 1870s and published them in the *Annals of the Observatory* and/or in the *Memoirs of the Belgian Academy* (Demaréé and Chuine 2006). Instructions for the observation of periodical phenomena were printed in 1853 by the Royal Academy of Sciences, the observations themselves published in the *Annals of the Observatory* and/or in the *Memoirs of the Belgian Academy*. Apparently, Quetelet’s instructions form inspired other meteorological services like the “*Bureau Central Météorologique*” of France where Eleuthère Mascart issued in

1880 the form “*Observations sur les phénomènes de la végétation et sur les animaux*” (Observations on phenomena of plants and animals). It was also Quetelet who encouraged Carl Fritsch to develop international phenological guidelines which he could present at an international conference on statistics in London in 1860. They were officially accepted but Fritsch was the only person who followed them (Schnelle 1955). Charles Morren (1853), professor of botany at the University of Liège and one of Quetelet’s observers coined the term “phenology” and it was very quickly adopted by the other scientists (Fritsch 1858)

From 1851 to 1877 Carl Fritsch from the *k.k. Centralanstalt für Meteorologie und Erdmagnetismus* (Centre for Meteorology and Geomagnetism) in Vienna administered a plant and animal phenological network in the Austrian Hungarian monarchy, which covered parts of today’s countries like Czech Republic, Croatia, Hungary, Italy, Poland, Romania, Slovenia and Slovakia. The number of stations varied from seven at the beginning up to approximately 70 in the 1860s (for the status of the network in 1857 see Fig. 2.2). The data are published in the Annals, the *Jahrbücher der Centralanstalt für Meteorologie und Erdmagnetismus* and it is planned to digitise them within the next few years and have them available on the webpage of ZAMG ([www.zamg.ac.at/phaeno\\_portal](http://www.zamg.ac.at/phaeno_portal)) as most of the Austrian phenological data from 1951 are already.

The United States network initiated by the Smithsonian Institute started in the same year in 1851, with plant and animal observations forming the program, spread across 320 locations in 33 states – but it ended after only 8 years in 1859 (Hopp 1974).

### 2.2.3 Nineteenth/Twentieth Century

A real success story was Ihne (1884) and Hoffmann’s call for phenological observations in 1884, which resulted in 59 years of data from the Southwest of Europe to the Northeast – collected according to common guidelines and published in a series (Ihne 1883–1941). The Deutscher Wetterdienst (DWD) digitised these data and they are available on demand from the Historical Phenological Database HPDB ([www.dwd.de](http://www.dwd.de)). In 1905 Ihne published the famous map: *Advance of spring in middle Europe*; a more recent publication dealing with the progress of spring across Europe is provided by Menzel et al. (2005). Figure 2.3 shows the map with stations from where at least 5 years of observation-data are stored in HPDB.

In 1953, the Commission for Agrometeorology (CAgM) of the WMO adopted regular phenological observations in the official agro-meteorological observation program to be carried out by each member country. This resolution triggered the (re-) establishment of (agro-) phenological observations in many national meteorological services after World War II and indeed the roots of the International Phenological Gardens in Europe (see Section 2.3.9) go back to that original resolution (Nekovář et al. 2008).

Karte der zu Ende Juni 1857 thätigen  
Stationen für phänologische Beobachtungen in Oesterreich.

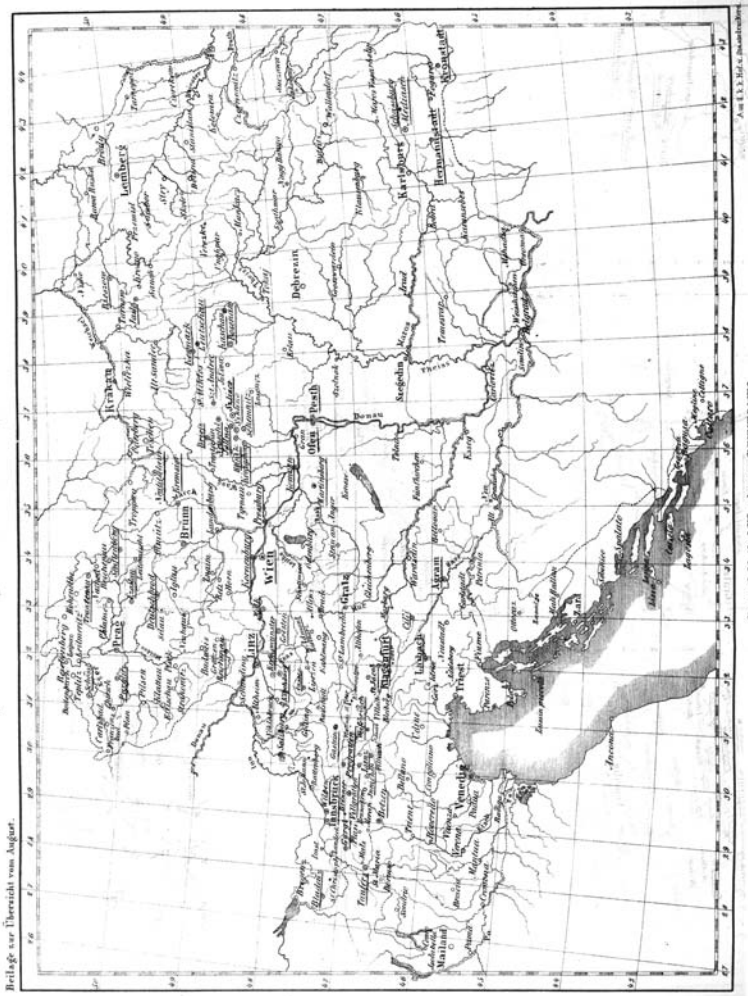
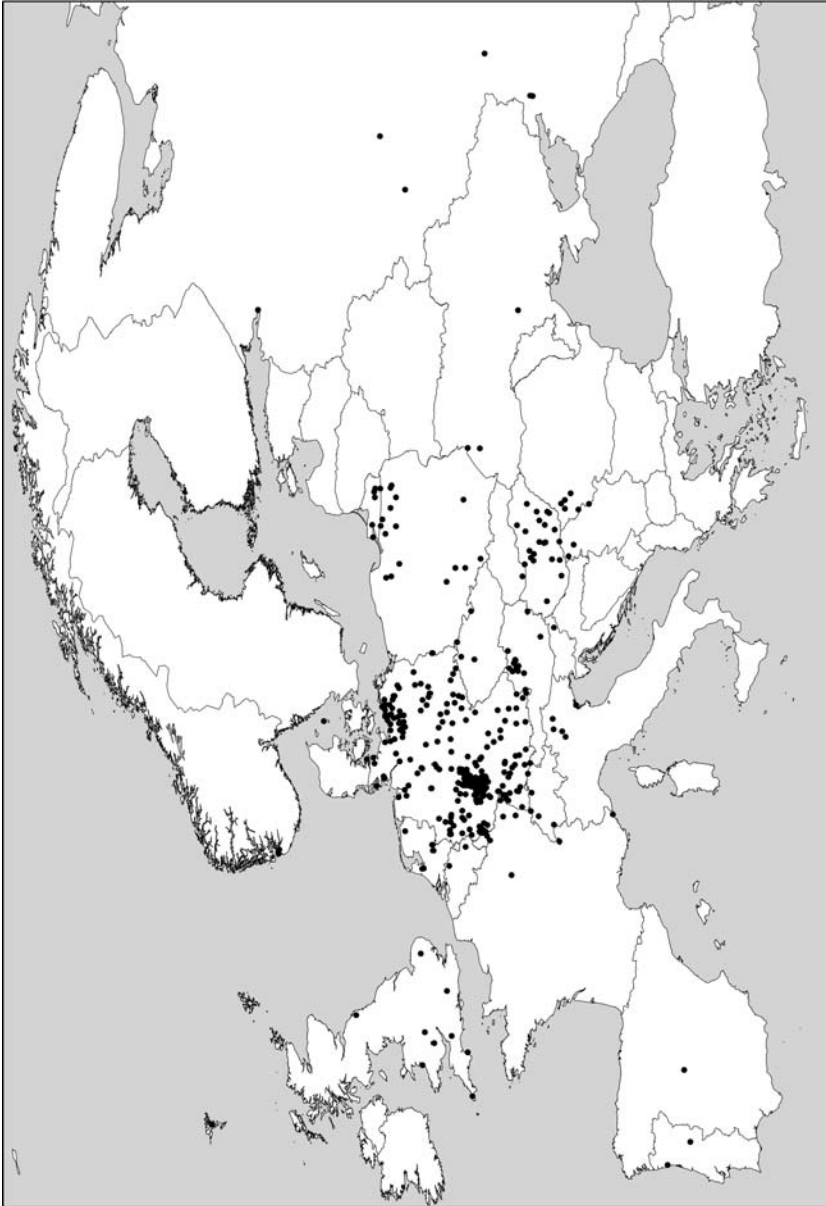


Fig. 2.2 Station map of the phenological network of "Oesterreich" active at end of June 1857. The station names are underlined (Fritsch and Löw 1859)





**Fig. 2.3** Phenological stations of the Hoffmann – Ihne network with a minimum of 5 years of observation data stored in the HPDB of DWD

## 2.3 Present Status and Future of Global Framework for Data Collection – Data Bases

### 2.3.1 Africa

**Amruta N. Rane, Poonam Gangaram, Carl Jones, Vikash Tatayah, and Elisabeth Koch**

Only a few phenological activities are known from Africa. The activities described here cover the status of activities in West Africa, and a significant ongoing study in Mauritius.

#### 2.3.1.1 West Africa

In nine West African countries (Burkina Fasso, Cape Verde, Chad, Gambia, Guinea Bissau, Mali, Mauritania, Niger and Senegal) agro-phenological network activities are undertaken. The agrometeorological and hydrometeorological (AGRHYMET) program which commenced operation in July 1975 (WMO 1986) publishes a monthly bulletin (<http://www.agrhymet.ne>). The bulletin details crop phenological phases along with weather conditions, soil moisture, crop pest phenological stages and damage caused by pests for each of the countries. The FAO also publishes regular reports about the food situation in West Sahelian countries which also mentions growth stages of different crops.

In 1991, the Commission of Agricultural Meteorology of the WMO edited guidelines on agro-phenology for Africa, but it has not been possible to find out more information on the networks, data bases etc.

In the IPCC AR4 report (IPCC 2007) the lack of geographical balance in the data on observed changes in natural and managed systems is stated. Evidence of observed changes is sparse in Africa. The Working group II report (Rosenzweig et al. 2007) points out many possible reasons for this imbalance, among them being a lack of data and published studies in this part of the world. Clearly, further attention and resources are needed to the collection of phenological data in Africa.

#### 2.3.1.2 Mauritius

In Mauritius a phenological study was initiated by the Mauritian Wildlife Foundation in 2001 to gain a greater understanding of food availability for Pink Pigeons (*Columba mayeri*) and Echo Parakeets (*Psittacula eques*) in the remnants of the native forest.

The native habitat on the island has been reduced to less than 2% since human colonisation in the 1600s (Strahm 1993, Swinnerton 2001). Since then 80 plant species (Strahm 1993) and at least 16 land bird species native to Mauritius have gone extinct (Baillie et al. 2004). A few Conservation Management Areas (CMAs); patches of native forest managed to exclude exotic mammal and plant species, have

supported small-scale habitat restoration. However, the native forest community is still heavily degraded by exotic plants and animals (Cheke 1987, Strahm 1993, Safford 1997). The Pink Pigeon and Echo Parakeet are the only extant, endemic pigeon and parakeet species in the Mascarenes (Cheke 1987). In the 1970s the populations of both these endangered species declined to less than 20 wild birds. However, subsequent intensive conservation management techniques (see Jones 2004) had increased the number of Pink Pigeons to approximately 380 wild birds across six subpopulations and Echo Parakeets to over 340 wild birds in two subpopulations, by April 2008 (Reuleaux and Wilmott pers. comm.). Habitat degradation and natural food shortages have been identified as two of the important limiting factors (Swinnerton 2001, Malham et al. 2007). Both species occur in remnant, native forest and their diet consists of leaves, flowers and fruits, mostly from native plants.

Hence, to ensure the ongoing recovery and long-term survival of these species, it is essential to understand the quality and quantity of natural food available in the forest throughout the year. Previous research (Cheke 1987, Jones 1995, Swinnerton 2001) and field observations have identified 37 native and 10 exotic plant species as important food species. Currently, very little is known about the phenological patterns of these species. In 2001 a phenology project was initiated (Atkinson and Sawmy 2003), which has been modified and restarted to address this information gap. At each subpopulation the project is aimed at understanding:

1. What time of the year do each of the species flower and fruit?
2. Is the flowering and fruiting for each species continual/sub-annual/annual/supra annual?
3. Is the flowering and fruiting for each species brief/intermediate/extended?,
4. How do rainfall, temperature, humidity, cyclones and soil quality affect plant phenology?

Ten individuals of each available food species is monitored at five sites (Plaine Lievre, Pigeon Wood, Combo, Bel Ombre and Ile aux Aigrettes). At sites where the CMAs occur, the 10 individuals have been distributed so that five are in the CMA and five outside the CMA in order to compare phenology between restored and degraded forest. All the field staff and volunteers (biologist/ecologists) are trained and a training manual has been created to ensure standard, good quality data collection. Monthly monitoring is carried out simultaneously at each subpopulation. All the data are recorded in a specifically designed observation sheet and entered electronically to be converted into a database in near future. This study will also monitor the reproductive phases in these birds such as the duration and timing of the Pink Pigeon non-breeding period and the start of Echo Parakeet breeding season which are believed to be linked to changing plant phenological activities.

### Conservation Implications

This phenological study will help identify the natural food availability throughout the year across fragmented remnants of native Mauritian forest and help understand

the link between the phenology of food plant species and the annual breeding trends in these endemic birds. It will not only benefit the long-term restoration of land-bird species but also assist in management plans for large-scale habitat restoration.

**Acknowledgments** This Mauritius project is supported by Mauritian Wildlife Foundation and National Parks and Conservation Services, Mauritius. The dedication of the field staff and volunteers make this project possible.

## 2.3.2 *Australia*

**Marie R. Keatley and Lynda E. Chambers**

### 2.3.2.1 Australian Phenological Networks

Many areas of the world have a long history of undertaking phenological observations (e.g. Britain (Sparks and Carey 1995) and Japan (Aono and Kazui 2008)) and have long-established phenological networks (e.g. Germany (Menzel et al. 2001) and Estonia (Ahas 1999)). Many of these data have been used to detail the impact of climate change (Menzel et al. 2006).

Australia is not in the same position with respect to networks. This is despite the first call for a phenological network being issued in 1891 (Prince 1891) and a network reportedly being established in 1949 by the “Meteorological Service”, which was implied to be still operating in 1967 (Wang 1967). However, further details of, and records from this network have not been located. A detailed history of early phenological work undertaken in Australia is provided by Keatley and Fletcher (2003).

In relation to long-term phenological datasets Australia has only a few that cover multiple decades (Chambers 2006). These range from snow cover to changes in the mating behaviour of lizards.

#### National Ecological Metadatabase

The National Ecological Meta Database (NEMD) commenced in 2005 ([www.bom.gov.au/nemd](http://www.bom.gov.au/nemd)) in response to the perceived lack of long-term datasets (Keatley et al. 2002, Westoby 1991), a perception that is borne out in part by the absence of any Australian studies reported in the third assessment report of the Intergovernmental Panel on Climate Change (IPCC 2001). In the IPCC 2007 report this improved slightly with six studies in the Australia/New Zealand region. The NEMD’s primary aim is to document such data sets, but also to:

- Improve the knowledge of the impacts of climate change on Australian natural systems and species;
- Provide information on baseline data for future monitoring programs;
- Promote sharing of knowledge between regions and institutions;

- Improve the capacity of natural resource managers to adapt to climate change through improved understanding of climate-species relationships;
- Assist in the identification of climate change indicator species (climate proxies).

The listing of records in the NEMD is voluntary. To supplement these contributions, a project “PhenoArc” was commenced in October 2007 (Keatley et al. 2008) to compile existing phenological data contained within the journals of Australian naturalist organisations which have been documenting the timing of phenological events in their journals and newsletters, in some instances for over 100 years (e.g. the Field Naturalists Club of Victoria whose first journal was published in 1884). This project had immediate success with additional records (1926 and 1943) detailing the nesting seasons of Western Australian birds located (Carnaby 1954, Robinson 1954).

Additionally, this project is examining annual reports and archives of government departments, for example departments of agriculture, which often contain records of harvest and production dates. Experimental farm data have been located in the New South Wales State Archives. The cards also represent some of the longest time series (1927–1969) in the PhenoArc database and are believed to be the first collation of agricultural phenological records for Australia. They provide a synopsis of experiments on wheat and oat varieties (e.g. seeding rates), but also list dates of seven phenophases (e.g. planting and harvesting start dates) along with rainfall and yield per plot. Records such as these have been useful in examining climate trends and impacts in Europe (Sparks et al. 2005, Menzel et al. 2006).

### ClimateWatch

Australia does not currently have any state or national programs for the systematic collection of real-time phenological data. The ClimateWatch (<http://www.climatewatch.org.au/>) project is the latest development in trying to establish a national network, using “citizen scientists” to build a national picture on natural resource management issues. Currently, one of the most prominent of these issues is climate change and its impacts. Phenological indicators will play a primary role in the identification and assessment of these. This project is in its trial stage and will build on and complement the National Ecological Meta Database. Trials will be established in three different locations in Australia. It is a collaborative project coordinated through the Earthwatch Institute – Australia in partnership with the Bureau of Meteorology, University of Melbourne, CSIRO and Birds Australia.

Earthwatch is coordinating three key steering groups that provide independent advice and guidance as to:

- The technical requirements needed to create appropriate web based systems to facilitate the uploading of data from the public and for the same public to query the data in order to generate displays of trends and patterns in natural resources nationwide.

- The best choice of indicator species or events that will provide the most robust data and the best nexus between the contributing public and useful indicator distribution.
- The best strategy to engage the media to ensure interest in the project is maintained and information disseminated to appropriate audiences.

### Terrestrial Ecosystem Research Network

The Terrestrial Ecosystem Research Network (TERN) is funded under the Australian Federal Government's initiative National Collaborative Research Infrastructure Strategy. <http://ncris.innovation.gov.au/Capabilities/Pages/TERN.aspx>. It is currently in its formative phase. It is not a phenological network per se, but it may have some phenological observations within it. Its aims are:

- to provide infrastructure that builds on the significant past and present investments of State, Territory and Commonwealth Governments to facilitate the development of an integrated approach to understanding Australia's ecosystems;
- to connect and integrate data relating to ecosystem components for a range of terrestrial ecosystems at different spatial and temporal scales;
- to develop and make available common sets of data on key ecosystem parameters and to establish, amongst other things, useful baseline and time-series data;
- to enable researchers to conduct experiments, undertake analyses, and construct models, that contribute to understanding of Australian ecosystems at both large (including national and regional) and small scales (such as catchments or habitat);
- to complement (and possibly integrate with) similar international networks where appropriate.
- Although the value of a phenological network for Australia has been recognised for over a hundred years, Australia is only now on the verge of implementing one.

### 2.3.3 *Canadian Phenological Networks*

#### **Elisabeth Beaubien**

A range of phenological observation activities are occurring in Canada. From 1987 to 2001 the Alberta Wildflower Survey gathered data on three bloom stages for 15 native plant species (Beaubien and Johnson 1994). It engaged about 200 Alberta volunteers annually. In 2002 the species and some phenophases were modified and the survey was renamed "Alberta Plantwatch".

In 1995, the author and assistant Ania Radziszewski launched a web-based "Plantwatch" to enlist observers mainly in Canada to track spring bloom times of eight plant species. Some international data for *Syringa vulgaris* was reported, especially from Poland and Japan; see archived data tables and maps of the available data at <http://plantwatch.sunsite.ualberta.ca>. This website is being updated as

an interactive site at [www.plantwatch.fanweb.ca](http://www.plantwatch.fanweb.ca), where observers have their own folders where they upload photographs and text.

By 2000 the federal government was interested in the potential of Plantwatch to involve “citizen scientists” in monitoring the effects of climate change. Canada Plantwatch then expanded with help from Environment Canada’s Ecological Monitoring and Assessment Network Coordinating Office (EMANCO) and Nature Canada. Volunteer coordinators were found for all 13 provinces and territories. See Schwartz and Beaubien (2003) for more information on coordinators and history of the program. A description of the program with a list of current coordinators is available at [www.plantwatch.ca](http://www.plantwatch.ca). Data reported to this webpage are mapped immediately and those data (dates and locations) are available to anyone to download. Researchers could also contact individual coordinators for additional data.

Some plant species are observed across Canada, while others are observed only in certain regions. See a list of most of the species observed in Canada under “scientific names” at [http://www.naturewatch.ca/english/plantwatch/learn\\_plants.asp](http://www.naturewatch.ca/english/plantwatch/learn_plants.asp).

Many of the species (or close relatives of the species) which are monitored in Canada are also monitored in Europe. These include Aspen Poplar (*Populus tremuloides*), Larch (*Larix laricina*), Coltsfoot (*Tussilago farfara*), Mountain Avens (*Dryas integrifolia/octopetala*), Common Purple Lilac (*Syringa vulgaris*), Prairie Crocus (*Anemone patens*, or *Pulsatilla ludoviciana*), Cranberry or Lingonberry (*Vaccinium vitis-idaea*), Purple Saxifrage (*Saxifraga oppositifolia*), Cloudberry (*Rubus chamaemorus*), Twinflower (*Linnaea borealis*), Dandelion (*Taraxacum officinale*) and Wild Strawberry (*Fragaria virginiana/vesca*).

### Details on Alberta Plantwatch

Observer training has been provided through printed program information with information on plant species identification (with colour photos and some sketches), observation site selection, and phenophase descriptions. Observers generally submit data before October annually. Most data are on paper forms, but reporting is also done by email, fax, or on the webpages listed above.

Who are the volunteer observers? They include farmers, ranchers, fire tower observers (Alberta Forest Service), volunteer weather observers (Environment Canada), biologists, foresters, naturalists, gardeners, urban dog-walkers and the occasional class of students. The list includes many retired people, who enjoy making plant observations part of their spring routine. Observers are recruited using many methods. Government departments are contacted to reach fire tower watchers and weather observers. Other volunteers are found from articles in naturalist society newsletters, by word of mouth from other observers, through radio interviews or newspaper articles or by their attendance at talks to naturalist groups around the province. Experienced volunteers are encouraged and retained through regular feedback and communication. They receive newsletters which recognize their contributions and summarize interesting comments on the season that observers submit.

**Table 2.1** Alberta plantwatch species

<b>Aspen poplar</b> ( <i>Populus tremuloides</i> )	Northern Bedstraw ( <i>Galium boreale</i> )
<b>Bearberry</b> ( <i>Arctostaphylos uva-ursi</i> )	<b>Prairie crocus</b> ( <i>Anemone patens</i> )
<b>Bunchberry</b> ( <i>Cornus canadensis</i> )	<b>Purple saxifrage</b> ( <i>Saxifraga oppositifolia</i> )
Choke Cherry ( <i>Prunus virginiana</i> )	<b>Saskatoon</b> ( <i>Amelanchier alnifolia</i> )
<b>Common Purple Lilac*</b> ( <i>Syringa vulgaris</i> )	Star-flowered Solomon's Seal ( <i>Maianthemum stellatum</i> )
Common Yarrow ( <i>Achillea millefolium</i> )	<b>Tamarack</b> ( <i>Larix laricina</i> )
<b>Dandelion*</b> ( <i>Taraxacum officinale</i> )	<b>Twinflower</b> ( <i>Linnaea borealis</i> )
Early Blue Violet ( <i>Viola adunca</i> )	<b>Wild Strawberry</b> ( <i>Fragaria virginiana/vesca</i> )
Golden Bean ( <i>Thermopsis rhombifolia</i> )	<b>White Dryad</b> ( <i>Dryas integrifolia/octopetala</i> )
<b>Labrador Tea</b> ( <i>Rhododendron groenlandicum</i> )	Wolf Willow ( <i>Elaeagnus commutata</i> )
<b>Lodgepole Pine</b> ( <i>Pinus contorta</i> )	

The Alberta Plantwatch species are listed in Table 2.1. All species are native, which means that they occurred in North America long before European settlement, except the introduced species marked with an asterisk (\*). Species in bold are also observed in other provinces and territories.

These are the current instructions given to Alberta observers:

“When choosing plants for observation, please keep in mind the following. You do not need to report on all species, just the plants near your home or those that are easy to visit regularly. Even one bloom date from one plant is useful. It is best to observe wild plants well away from buildings (heat sources), and in a flat area. If possible, choose plants to observe which reflect about the average for your area (i.e. not the earliest or latest to flower). Please observe the same individual shrubs or patch of plants from year to year”.

For non-woody herbs or “wildflowers,” *first bloom* is when the first flowers open in the plants under observation. For trees and large shrubs, first bloom is when the first flowers have opened in three different places on the observed plant. *Mid bloom* for most plants is when half of the flowers on the plant have opened. For *leaf-out* of aspen poplar, lilac and larch, please report the dates when, in at least three different places on the tree, the first leaves have emerged and unfolded completely. Note: see the information on your chosen plant species, for details on how to recognize first and mid bloom.”

Examination of the spatial and temporal trends in the 21 years of Alberta data has commenced, and this data should become available as the analyses are completed.

### 2.3.4 Phenological Observation in China

#### Xiaoqiu Chen

##### 2.3.4.1 Historical Background

Modern phenological observation and research in China started in the 1920s with Dr. Coching Chu (1890–1974). As early as 1921 he observed spring phenophases



of nine species of trees and two species of birds in Nanjing. In 1931, he summarized phenological knowledge from the last 3000 years in China and introduced phenological principles (e.g. species selection, criteria of phenological observations and phenology laws) developed in Europe and the United States from the middle of the eighteenth to the early twentieth century (Chu 1931). In 1934, he organized and established the first phenological network in China. Observations included some 21 species of wild plants, nine species of fauna, some crops, and several hydro- meteorological events, and were ceased in 1937 because of the War of Resistance against Japan (1937–1945). Twenty five years later the Chinese Academy of Sciences (CAS) established a countrywide phenological network under the guidance of Dr. Chu. The observations began in 1963 and continued until the first half year of 1997. In 2002 the phenological observation has been resumed again with reduced stations, species, and phenophases. In addition, the Chinese Meteorological Administration (CMA) also established a countrywide phenological network in 1980s.

#### **2.3.4.2 Networks and Data Collection**

The observation program of the CAS network included a total of 173 observed species. Of these, 127 species of woody and herbaceous plants had a localized distribution. Table 2.2 lists the 33 species of woody plants, two species of herbaceous plants, and 11 species of fauna that were observed across the network (Institute of Geography at Chinese Academy of Sciences 1965, Table 1). Since 1973, several stations added phenological observation of major crops. These observations were carried out mainly by botanical gardens, research institutes, universities and middle schools according to uniform observation criteria (Institute of Geography at Chinese Academy of Sciences 1965, Wan and Liu 1979). The phenophases of woody plants included bud-burst, first leaf unfolding, 50% leaf unfolding, flower bud or inflorescence appearance, first bloom, 50% bloom, the end of blooming, fruit or seed maturing, fruit or seed shedding, first leaf coloration, full leaf coloration, first defoliation and the end of defoliation etc.

The Institute of Geography at CAS took responsibility for collecting the phenological data and publishing them. Changes to the stations and in observers over the years resulted in data that were spatially and temporally heterogeneous. The number of active stations has varied over time. The largest number of stations operating was 69 in 1964 and the smallest number occurred between 1969 and 1972 with only 4–6 stations active. The phenological data from 1963 to 1988 were published in the form of Yearbooks of Chinese Animal and Plant Phenological Observation (volume 1–11). Currently, there are about 20 stations in the CAS network.

The CMA phenological network is affiliated with the national-level agrometeorological monitoring network and came into operation in 1980. The phenological observation criteria for woody and herbaceous plants, and fauna were adopted from the CAS network. There are 28 common species of woody plants, 1 common species of herbaceous plant and 11 common species of fauna. The main phenophases are the same as those of the CAS network. In addition to the

**Table 2.2** Common observation species of the CAS phenological network in China

Woody plants		
<i>Ginkgo biloba</i> L.	<i>Morus alba</i> L.	<i>Sophora japonica</i> L.
<i>Metasequoia glyptostroboides</i> Hu et Cheng	<i>Broussonetia papyrifera</i> (L.) Vent.	<i>Robinia pseudoacacia</i> L.
<i>Thuja orientalis</i> L.	<i>Paeonia suffruticosa</i> Andr.	<i>Wisteria sinensis</i> Sweet.
<i>Juniperus chinensis</i> L.	<i>Magnolia denudata</i> Desr.	<i>Melia azedarach</i> L.
<i>Populus simonii</i> Carr.	<i>Firmiana simplex</i> W. F. Wight.	<i>Koelreuteria paniculata</i> Laxm.
<i>Populus canadensis</i> Moench.	<i>Malus pumila</i> Mill.	<i>Zizyphus jujuba</i> Thunb.
<i>Salix babylonica</i> L.	<i>Prunus armeniaca</i> L.	<i>Hibiscus syriacus</i> L.
<i>Juglans regia</i> L.	<i>Prunus persica</i> Stokes.	<i>Lagerstroemia indica</i> L.
<i>Castanea mollissima</i> Blume.	<i>Prunus davidiana</i> (Carr.) Franch.	<i>Osmanthus fragrans</i> Lour.
<i>Quercus variabilis</i> Blume.	<i>Albizia julibrissin</i> Durazz.	<i>Syringa oblata</i> Lindl.
<i>Ulmus pumila</i> L.	<i>Cercis chinensis</i> Bge.	<i>Fraxinus chinensis</i> Roxb.
Herbaceous plants		
<i>Paeonia lactiflora</i> Pall.	<i>Chrysanthemum indicum</i> L.	
Fauna		
<i>Apis mellifera</i> L.	<i>Cryptotympana atrata</i> Fabr.	<i>Apus apus pekinensis</i> (Swinhoe)
<i>Gryllulus chinensis</i> Weber ( <i>Gryllus berthallus</i> Sauss.)	<i>Hirundo rustica gutturalis</i> Scopoli.	<i>Hirundo daurica japonica</i> Temminck et Schlegel.
<i>Anser fabalis</i> Subsp.	<i>Oriolus chinensis diffusus</i> Sharpe.	<i>Cuculus canorus</i> Subsp.
<i>Cuculus micropterus</i> <i>micropterus</i> Gould.	<i>Rana esculenta</i> L.	

natural phenological observations, the network also carries out professional phenological observation of crops on the basis of a specific observation criterion (National Meteorological Administration 1993). The main crop varieties include rice, wheat, corn, grain sorghum, millet, sweet potato, potato, cotton, soybean, rape, peanut, sesame, sunflower, sugarcane, sugar beet, and tobacco. In grassland areas, phenophases of dominant grass species, such as *Leymus chinensis* and *Stipa baicalensis*, are also observed. In Inner Mongolia, there are eight grassland meteorological monitoring stations with phenological observations.

The CMA network is the largest phenological observation system in China. There are about 640 agro-meteorological measurement stations currently, of these 446 stations are undertaking phenological observations (Fig. 2.4). The CMA-archives keep the original phenological observation records from 1981 to the present in hand writing and provide the data freely to research institutes and universities. As the phenological and meteorological observations are parallel in this network, the data are especially valuable for understanding phenology-climate relationships. These data can also be used to provide agro-meteorological service and prediction on crop phenophases and yields, irrigation amounts, plant diseases and insect pests, and forest fire danger (Cheng et al. 1993).

In addition, there were some regional phenological networks which previously existed. One example is the network established by Guodong Yang and Xiaoqiu

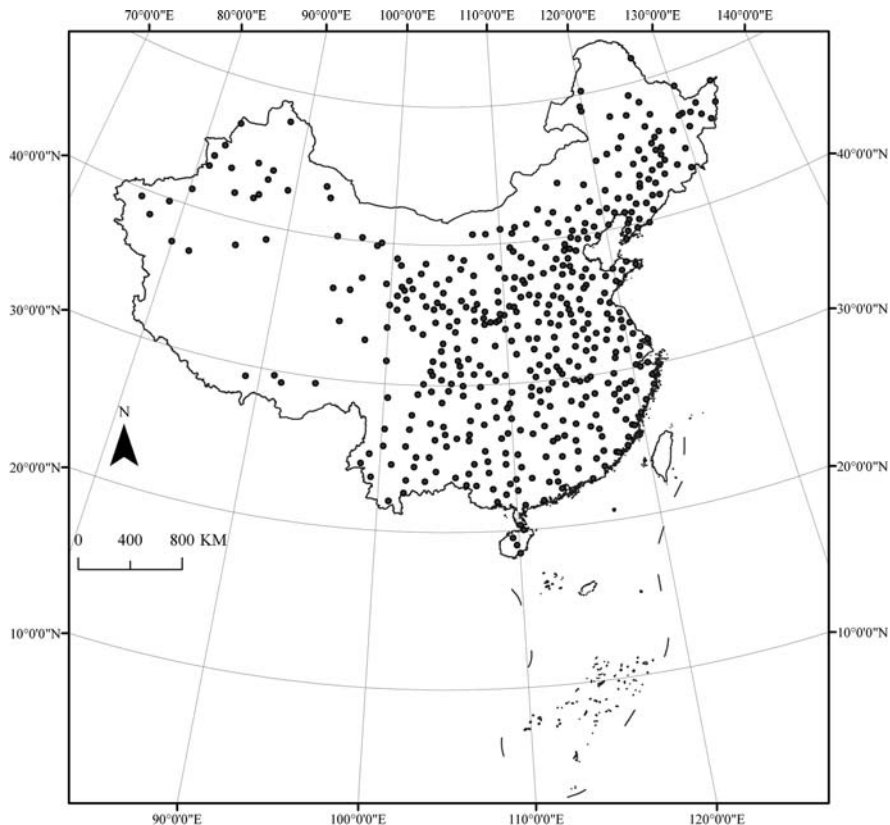


Fig. 2.4 Distribution of phenological stations of the CMA network

Chen during 1979–1990. The network consisted of approximately 30 stations in the Beijing area (about 16 410 km<sup>2</sup>). Using these data, they worked out and published a series of phenological calendars of the Beijing area (Yang and Chen 1995).

### 2.3.5 *Europe: Establishing a European Phenological Data Platform for Climatological Applications*

**Elisabeth Koch, Wolfgang Lipa, and Susanne Zach**

Europe has a long tradition in phenology and phenological networks (see Section 2.2).

The European phenological network EPN, which commenced in 2001 and ended (in terms of funding) in 2003, was a project funded by the European Union, with its

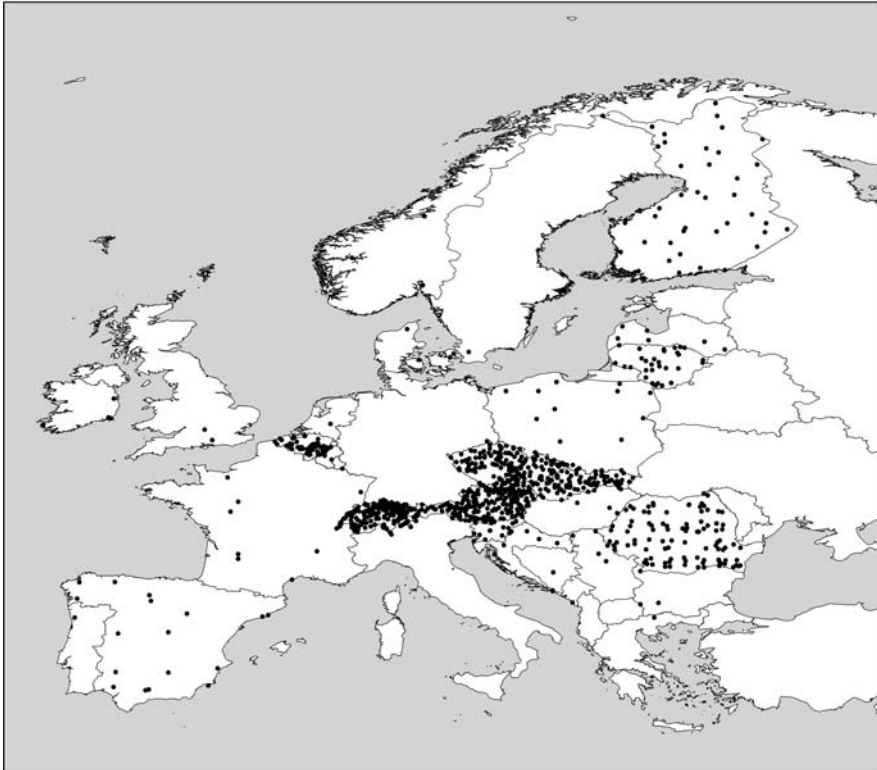
objectives being to facilitate integration and cooperation between existing phenological monitoring networks, to stimulate the expansion of existing and the creation of new monitoring networks, in order to improve integration of and access to phenological data in Europe (Vliet et al. 2003). After its funding period ended, the European phenological community searched for new ways to continue the cooperation of phenological network-providers and scientists on a pan European level. The phenological observation networks in European countries are organized by different institutions, having different objectives which result in different program with different observation guidelines and different formats and methods of data storage and archiving (Menzel 2003). All these facts have unfortunately hampered European wide phenological studies.

The need not only for the unification of the networks but also for the creation of one single database has been recognized for many years. For example, there have been several attempts at bilateral and multilateral cooperation (e.g. Bissolli et al. 2005, Horakova 2000). Finally in 2004, COST Action 725 was established with 27 participating countries (out of 34 COST members) with a funding period until 2009. COST is an inter-governmental framework for European Co-operation in the field of Scientific and Technical Research and works on the basis of so-called actions, that is networks of coordinated national research projects in fields, which are of interest to participants from at least five different member states (COST 2007).

The main objective of Action 725 is to establish a European reference data set of phenological observations that can be used for climatological purposes, especially climate monitoring and detection of changes. This data set is freely accessible for scientific purposes and [www.zamg.ac.at/cost725](http://www.zamg.ac.at/cost725) available via internet. Secondary objectives lie in the harmonization of techniques for the definition of phases and selection of species to be monitored. This involves developing guidelines to ensure that monitoring is undertaken in a harmonised way, developing data quality checking procedures, and applications of the datasets for mapping. The overall goal is to increase the knowledge of relations between weather/climate and phenological phases (Koch et al. 2005, 2009).

The action started with an inventory of all available phenological stations, including the national networks and the European International Phenological Gardens (IPGs), to determine what species and phases are being monitored. Not surprisingly it turned out that the stations are very unevenly distributed across Europe with the highest density in Germany (Figs. 2.5 and 2.6) with an even greater variability in the plant species and phases under observation. Altogether COST725 counted 9803 stations, where 306 different plants with 92 different phases are observed. These metadata build the fundamentals for the selection of plants and phases for the common database of COST725.

At a meeting in Vienna in April 2005 COST725 agreed on the list of plants and phases – derived from the metadata-results: 64 plants and 27 phases (which correspond to the Biologische Bundesanstalt, Bundessortenamt and Chemical Industry (BBCH) codes 0, 07, 10, 11, 31, 51, 55, 59, 60, 61, 65, 69, 75, 81, 85, 86, 87, 89, 92, 94, 95, 97 as well as

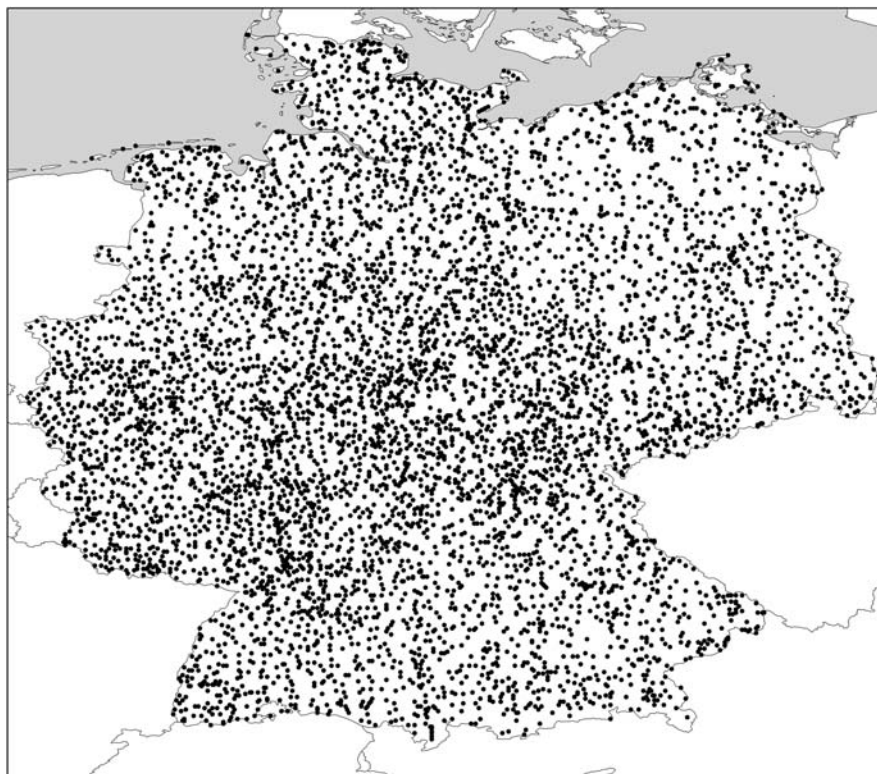


**Fig. 2.5** Stations of the COST725 database without Germany, status August 2007

- planting and harvest plus meadows: 25% green in spring, 1st cut for silage winning, 1st cut for hay winning
- the principal growth stages (the first digit of the selected BBCH code are shown in Table 2.4).

The main criterion for the selection was that the plants/phases are present in as many as possible of the observation programs.

Data quality assurance is one of the major concerns of the working group. The results of a questionnaire (Žust et al. 2006) on quality checking procedures applied by the different data owners revealed that the checking procedures differ widely. The most common methods visual control, followed by logical controls in terms of correct sequence of phases, threshold values or inter-phase duration. It is thus evident that common data quality procedures have to be developed and applied on the data set before it can be made widely available for use.



**Fig. 2.6** The COST725 database Germany only, as of August 2007

**Table 2.3** List of plants selected for the common database

Native plants	Fruit trees	Northern plants
<i>Aesculus hippocastanum</i>	<i>Malus x domestica</i> (early cultivar)	<i>Calluna vulgaris</i>
<i>Alnus glutinosa</i>	<i>Malus x domestica</i> (late cultivar)	<i>Cornus suecica</i>
<i>Alopecurus pratensis</i>	<i>Prunus avium</i> ( <i>Cerasus avium</i> ) (early cultivar)	<i>Epilobium angustifolium</i>
<i>Ambrosia artemisiifolia</i>	<i>Prunus avium</i> ( <i>Cerasus avium</i> ) (late cultivar)	<i>Fragaria vesca</i>
<i>Artemisia vulgaris</i>	<i>Vitis vinifera</i> (cultivar)	<i>Geranium sylvaticum</i>
<i>Betula pendula</i> ( <i>verrucosa, alba</i> )	<i>Prunus domestica</i> (early cultivar)	<i>Juniperis communis</i>
<i>Corylus avellana</i>	<i>Prunus domestica</i> (late cultivar)	<i>Vaccinium myrtillus</i>
<i>Fagus sylvatica</i>	<i>Pyrus communis</i> (early cultivar)	<i>Populus tremula</i>
<i>Forsythia suspensa</i>	<i>Pyrus communis</i> (late cultivar)	
<i>Picea abies</i> ( <i>P. excelsa</i> )	<i>Ribes rubrum</i>	
<i>Quercus robur</i> ( <i>Q. peduncula</i> )		
<i>Sambucus nigra</i>		

**Table 2.3** (continued)

Native plants	Agricultural plants	Southern plants
<i>Dactylis glomerata</i>	<i>Hordeum vulgare</i> (spring cultivar)	<i>Laurus nobilis</i>
<i>Tussilago farfara</i>	<i>Hordeum vulgare</i> (winter cultivar)	<i>Olea europea</i>
<i>Acer platanoides</i>	<i>Secale cereale</i> (spring cultivar)	<i>Prunus amygdalis/dulcis</i>
<i>Acer pseudoplatanus</i>	<i>Secale cereale</i> (winter cultivar)	<i>Rosmarinus officinalis</i>
<i>Alnus incana</i>	<i>Triticum aestivum</i> (winter cultivar)	
<i>Anemone nemorosa</i>	<i>Avena sativa</i> (spring cultivar)	
<i>Betula pubescens</i>	<i>Avena sativa</i> (winter cultivar)	
<i>Fraxinus excelsior</i>	<i>Beta vulgaris</i> (cultivar)	
<i>Galanthus nivalis</i>	<i>Helianthus annuus</i> (cultivar)	
<i>Larix decidua</i>	<i>Solanum tuberosum</i> (early cultivar)	
<i>Prunus spinosa</i>	<i>Solanum tuberosum</i> (late cultivar)	
<i>Robinia pseudoacacia</i>	<i>Zea mays</i>	
<i>Salix caprea</i>	Meadow	
<i>Sorbus aucuparia</i>		
<i>Syringa vulgaris</i>		
<i>Taraxacum officinale</i>		
<i>Tilia cordata</i>		

**Table 2.4** Principal growth stages of the BBCH code

Principal Growth Stages	Description
0	germination/sprouting/bud development
1	leaf development (main shoot)
2	formation of side shoots/tillering
3	stem elongation or rosette growth/shoot development (mainshoot)
4	development of harvestable vegetative plant parts or vegetatively propagated organs/booting (main shoot)
5	inflorescence emergence (main shoot)/heading
6	flowering (main shoot)
7	development of fruit
8	Ripening or maturity of fruit and seed

Besides the creation of the database, a comprehensive historical overview of the European networks and the present status including station maps and observation program has been published (Nekovář et al. 2008). A milestone in the work of COST725 was the publication of the meta-analysis of phenological trends in Europe (Menzel et al. 2006). An enormous data set with more than 125,000 series of 542 plants and 19 animal species from 21 European countries from the period 1971 to 2000 was available and could be evaluated: 78% of the time series of spring and ripening phases showed a negative trend towards earlier dates, only 3% were significantly delayed. Autumn phases characterized by leaf colouring and leaf fall data were ambiguous. The average advance of spring advance was 2.5 days per decade in Europe. This large valuable dataset will allow further analyses of this type, thus informing the changes in phenological behaviour as a result of climate change.

### ***2.3.6 The INPA Long-Term Phenology Project Monitoring Amazon Forest Trees: Tracking the Effects of Climate Changes on Tree Phenology***

**Antonio Moçambique Pinto and L. Patricia C. Morellato**

#### **2.3.6.1 Introduction**

This section presents a brief overview of phenological studies in Brazil, followed by a more detailed description of the INPA (the National Institute for Amazon Research, located in Manaus city, Amazon State, North Brazil) long-term phenology project monitoring Amazon forest trees.

Brazil is the largest South American country. The main vegetation types are: tropical evergreen moist forest including Amazon forest, Atlantic rainforest, Atlantic seasonal forest or semi-deciduous forest, cerrado or woody savanna, open grassy savanna, pantanal (a seasonally inundated vegetation), caatinga (semi-desert vegetation), sub-tropical Araucaria forest and natural fields. Some vegetation types are among the most diverse in the world (e.g. Amazon forest and Atlantic forest) and have been recognized as biodiversity “hotspots” for conservation priorities. All this diversity of species and vegetation types has not been completely studied in respect to its floristic diversity. Consequently, just a small percentage of its species and vegetation have been examined from the point of view of their seasonal changes.

A survey of phenological works undertaken in Brazilian native vegetation, considering just community studies including information on flowering and fruiting patterns, identified that tropical forest is the best studied ecosystem, with Amazon (terra-firma) forest and Atlantic forest of Southeastern Brazil being the best studied vegetation types (Morellato 2003). Cerrado (woody savanna) is the second-most studied vegetation type. Trees (forest) and woody plants (cerrado) are the life-forms observed in almost all papers surveyed. Most papers cover a short time span, usually about 1–3 years of observation, and just a few long-term phenology databases were surveyed (Morellato 2003). Besides the INPA project presented here, a similar program of long-term phenological data collection was established by Companhia Vale do Rio Doce (CVRD), a mining company at Espírito Santo State, Northeast Brazil. They observe lowland evergreen forest trees, employing the same methodology proposed by INPA project. The project started in 1982 and still seems to be active today. Another long-term observation of Amazon trees is carried out by EMBRAPA (Brazilian enterprise for Agricultural and Cattle Breeding Research), but no data are publicly available. According to Morellato (2003), the number of phenology papers published has increased over the last 20 years. The last five years show that more vegetation types have been studied. However, long-term phenological observations are uncommon.

The INPA project represents the first and oldest as well as possibly unique long-term phenological data collection for South American tropical forest trees. The phenological work started in 1962, at the Florestal Reserve Ducke, (Manaus,



Amazonas State, Brazil), headed by Dr. V.C. Araújo, Centro de Pesquisas em Silvicultura Tropical, with regular, phenological observations from 1965 until today. A second study site was established in 1974 at the Silviculture Experimental Station. The original goals of the project were: to know more about the biology of tree species of great or potential economic importance, and to determine the best time for seed or fruit collection to support silvicultural procedures such as planting and fruit harvesting. Further goals are now being added to the project, with current objectives being: to investigate the effects of climatic changes on plant phenology over the 35 years of observations; to compare the phenological patterns of the species that are common between the two research stations involved in the project; to explore the potential applications of this long-term phenological data, and to monitor the effects of climatic cycles and climatic changes on tropical forest trees.

## Methods

The phenological monitoring system was set up in 1962, at the Florestal Reserve Ducke in Manaus, Amazonas State, Brazil. Trees were selected from 1962 until 1965, up to a total number of 300 trees (approximately three per species) and 100 species marked over an area of 140.5 hectares of native Amazon lowland tropical forest (terra-firme forest). The regular observations started in 1965. In 1970 the sample size was extended to 500 trees (five per species), which are still monitored today. In 1974, INPA replicated the phenology study at a second site. They marked 500 trees of another 100 species from an Amazon lowland forest at the INPA Experimental Station situated approximately 30 km from the Ducke Reserve.

The choice of species was carried out according to some basic rules of forestry: actual or potential economic value of timber, and potential source of gums, resins and oils (wood or seed). Both studies perform monthly observations for changes on reproductive and vegetative phenology.

They defined 10 phases:

1. flower buds,
2. flowering (open flowers),
3. end of flowering,
4. beginning of fruiting (new fruits starting development),
5. ripe fruits,
6. end of fruiting,
7. leaf fall,
8. beginning of leaf flushing,
9. new leaves,
10. old leaves.

The database is a dbase – DOS database. The output is the mean of phenology data over a specific period. It does not produce a year by year output.

### 2.3.6.2 Research Results and Implications

The Phenology Project has produced a good number of papers over the last 30 years. All papers to date deal with data from the Ducke Reserve. No paper has been published with data from the Experimental Station, the second study site. Most papers are focused on one species or family (e.g. Alencar 1994), and just two papers have analyzed community phenological changes (Araujo 1970, Alencar et al. 1979). The papers analyse mean phenological data over 6–12 years. A few papers have studied time series and trends. The strongest observed correlation was between flowering phenology and temperature (Alencar 1994). The papers never take into account effects of climatic change and its evaluation using plant phenology.

After the migration of the data from the dbase – DOS database to a relational data bank, the data is being analysed by comparing the phenological patterns of some species in common between the two study sites and tracking the effects of natural climatic changes. Some results are in press and other are under review. Current work involves analysing the community patterns and the relationship to El Niño events, extreme dry seasons and other climatic changes affecting Amazon forests.

The very preliminary analyses of data from this project showed that the long-term phenology observations reveal the irregularity of the reproductive patterns of tropical forest trees. It highlights the importance of taking into account phenology data when planning the management of forest trees, especially fruit and tree harvesting, and that the influence of natural climatic change on tropical tree phenology is difficult to detect. Future steps in the project will include the building of a new, more friendly online data base, to store, organize and share the phenology information, and examine species and community data from different perspectives.

**Acknowledgments** This project is supported by CNPq – Brazilian National Council for Science. AMP and LPCM receive, respectively, a doctoral and research productivity fellowship from CNPq.

### 2.3.7 *Genesis and Progress Toward a National Phenology Network for the USA*

#### **Mark D. Schwartz and Julio Betancourt**

The idea for a USA-National Phenology Network (USA-NPN) has a long history and many contributors. In 1956, Joseph M. Caprio (Montana State University) initiated lilac phenological research in the USA. He developed a network of volunteer observers (~1000, growing to 2500 by 1972) reporting from 12 Western states (Caprio 1957, 1966). Caprio's program stimulated development of a similar program in the Eastern USA in 1961, initially under the direction of W. L. Colville (University of Nebraska; ~300 observers in 1970). The Eastern network lost funding in 1986, but was continued at ~40–50 stations by Mark D. Schwartz (University of Wisconsin-Milwaukee; Schwartz 1994). The Western States Phenological Network was terminated upon Caprio's retirement in 1993, but was reactivated at a handful of

sites by Dan Cayan (Scripps Institution of Oceanography [Scripps]/U.S. Geological Survey [USGS]) and Mike Dettinger (USGS/Scripps) to complement their studies on changes in timing of snowmelt discharge (Cayan et al. 2001). Cloned lilacs (and models developed from them) now serve as “anchor points” binding together commonalities among phenological observations from native species in diverse ecoregions, climate data, and remote sensing observations across a continent-wide network (Schwartz 1998, Schwartz et al. 2006). In the absence of other continental phenological monitoring, legacy lilac data provide the most logical tie to the mid-twentieth century before the major inflection in temperature and growing season trends.

More recently, Schwartz foresaw the need for a national network that would revitalize and broaden the lilac network, while extending phenological observations to other native and non-native species, drawing in part on co-location with a subset of National Weather Service Cooperative Observer stations and cooperation with other existing networks. In summer 2004, Julio Betancourt of the U.S. Geological Survey independently arrived at the same conclusion after co-chairing an AIBS Grand Challenge Workshop that explored the National Ecological Observatory Network’s (NEON) role in studying ecological responses to climate (AIBS 2004). When it appeared that NEON might be designed around intensively-sampled regional nodes, Betancourt teamed up with Schwartz to begin organizing a spatially-distributed network that would achieve “wall-to-wall” continental coverage for phenological observations and operate independently but ultimately in collaboration with NEON.

In August 2005, Betancourt, Schwartz and a steering committee of diverse scientists convened a workshop in Tucson, Arizona, to initiate an implementation plan for a USA-NPN. The workshop was funded by the USA National Science Foundation (NSF) and four other federal agencies (USGS, National Park Service [NPS], Environmental Protection Agency [EPA], and U.S. Dept. of Agriculture-Forest Service [USDA-FS]), and included 40 scientists from across the country and the globe (Betancourt et al. 2005). The 2005 workshop reinforced the need for the broader scientific community to organize a nationwide network of phenological observations with simple and effective means to input, report, and utilize these observations, including the resources to provide the right information at the right time for a wide range of decisions made routinely by individual citizens and by the Nation as a whole. Separate breakout groups converged on a framework of four expandable components or tiers (Fig. 2.7), each representing a different level of spatial coverage and quality/quantity of phenological and environmental information: (1) locally intensive sites focused on process studies (e.g. Long-Term Ecological Research [LTER], AmeriFlux, and AgriFlux sites); (2) spatially extensive science networks focused on large-scale phenomena (e.g. National Weather Service Cooperative [COOP] stations, NPS Inventory & Monitoring sites); (3) volunteer and education networks (e.g. garden clubs, bird and butterfly monitoring networks, college campuses); and (4) Remote sensing data that can be ground-truthed and assimilated to extend surface phenological observations to the continental-scale. Workshop participants emphasized that observations be entered into a database management system and be made available to the public in mapped

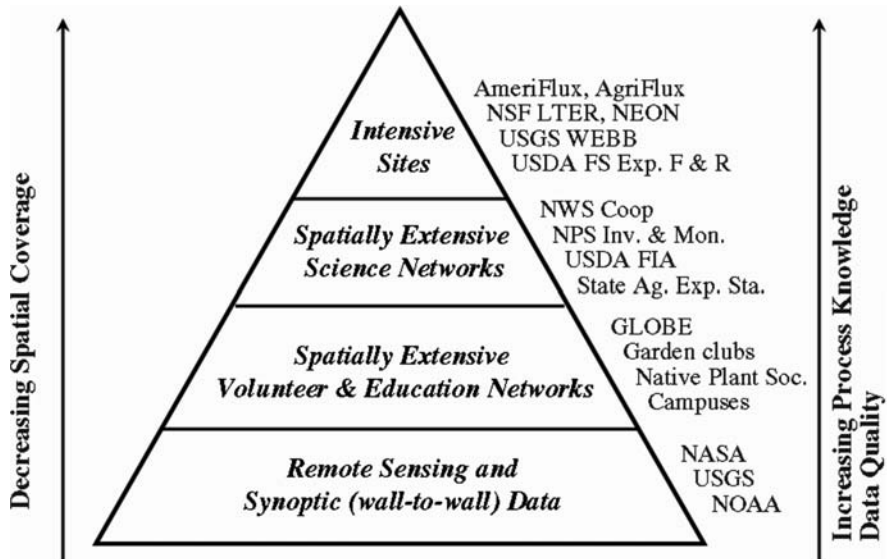


Fig. 2.7 Organizational components of USA-NPN

form and near real time (see USA-NPN Plant Phenology Programs web page at <http://www.npn.uwm.edu>).

At the 2005 Workshop, an Implementation Team (IT) was recruited with representation across disciplines, institutions, and existing environmental networks that already incorporate or could adopt phenological monitoring, with the goal of launching the first monitoring activities in 2007. The USA-NPN IT met in Tucson, Arizona in March 2006 to draft an implementation report and continue to organize the network. The IT was tasked with aspects of network development such as securing stable support from federal agencies for a national coordinating office; renewal and expansion of the lilac network; and adoption of phenological monitoring across existing environmental networks (LTER, AmeriFlux, NPS Inventory & Monitoring, and the National Weather Services COOP Network). The IT was also charged with developing mechanisms and funding for coordinating research across the network.

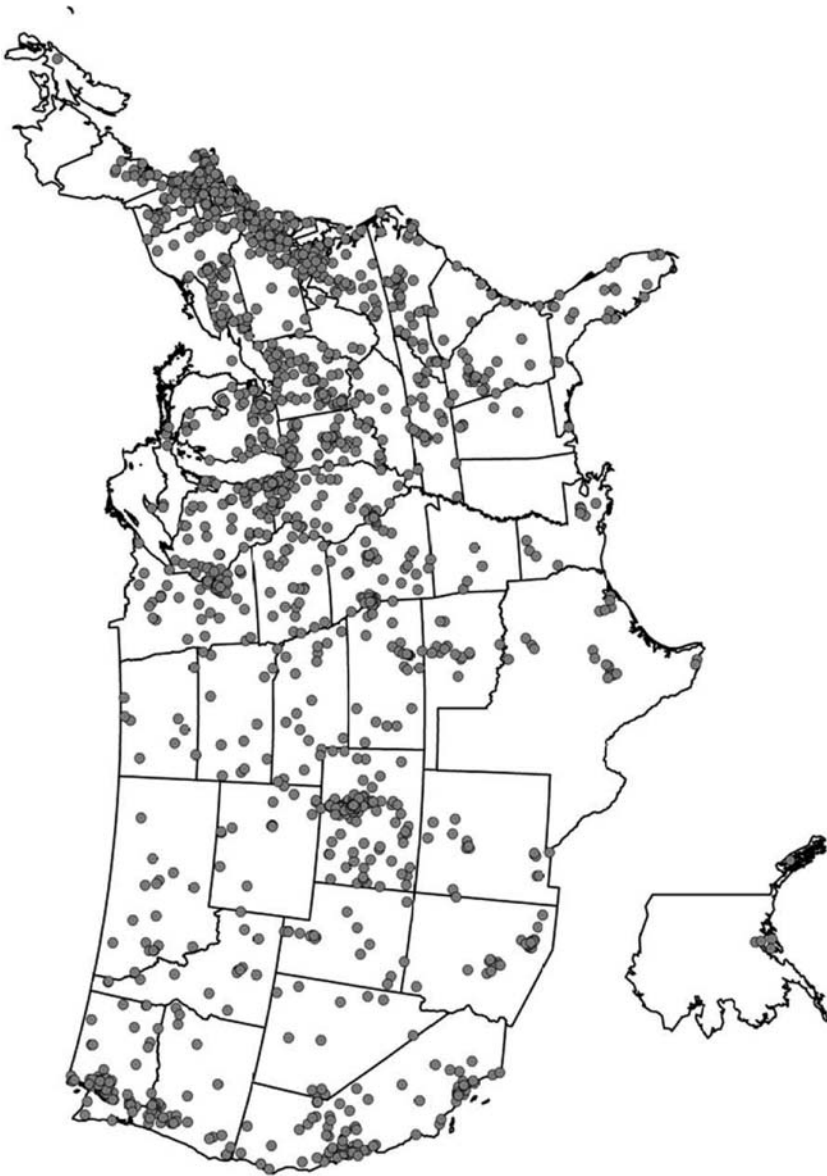
In summer 2006 the IT leadership identified the need for another workshop to resolve remaining planning and implementation issues. Furthermore, progress had been so rapid that it was thought a workshop in autumn 2006 would permit the USA-NPN to launch initial data collection in spring 2007. The second workshop was held in October 2006 (Milwaukee, WI), and addressed issues revolving around the selection/prioritization of appropriate plant species (including lists of target species representative of the Nation's ecoregions), and development/review of observation protocols. It also dealt with logistical issues connected to data collection for each of four network tiers, proposed to start in spring 2007 (Betancourt et al. 2007).

Given some practical issues (such as cloned lilacs requiring a year of acclimation before observations commence, and different levels of organization in the various

regions across the country), observations were launched in 2007, but limited to a smaller set of species overall, with more detailed protocols at some sites, and across some regions. However, by June 2007, over 750 individuals had registered as USA-NPN observers (Fig. 2.8). Project Budburst, a USA-NPN Citizen Science Field Campaign, was also highly successful in recruiting many participants. Technical issues that remain to be resolved will first require a review of web page/reporting systems for observers, and assessment of desired modifications that can be resourced and implemented in time for spring 2008. Equally important will be the development of an initial data management plan that will address data archiving and access issues. The organizational issues include station location, public participation, and cooperative agreements with existing sites and networks. In order to be most effective in the short-term the USA-NPN must maximize the number of phenological observation stations and their geographical coverage. The best strategy for accomplishing this is for USA-NPN to develop some form of co-location agreements with existing observation networks, such as the National Weather Service Co-Operative Observer Program (COOP), AmeriFlux, NPS Inventory and Monitoring, and LTER sites.

In March 2007, Schwartz received a US\$ 500,000 for a Research Coordination Network (RCN) that will cover USA-NPN meeting expenses for the next 5 years. A National Coordinating Office of the NPN has been developed, through an agreement between the U.S. Geological Survey and the University of Arizona.

The products of the first and second RCN meeting, several focused workshops, partnership with a web development group, and countless volunteer hours by many individuals allowed the design and full implementation of data collection with the USA-NPN Plant Phenology Program (PPP) starting in spring 2009. Genetic variation among individuals from the same native species affects their phenological responses to environmental variation. For example, when trees from across eastern North America are gathered and grown at a common location, trees from northern regions achieve spring budburst earlier each year than southern-origin trees, because they have adapted to growing in a region with less solar-thermal energy available. Therefore, a continental-scale phenological monitoring network using only native/introduced/naturalized species would produce a “mixed signal” of genetic variability and environmental factors, not to mention genetic by environmental factor interactions, which are unknown for most species. This issue, and the limited range of most native species, was a main reason for using cloned varieties of species in the historic USA phenology networks. However, while cloned species data are well-suited for general continental-scale phenological comparisons, they by definition cannot represent the local variations in response of native species. They also do not have full continental coverage because of limits to their growth in some regions, due to lack of chilling or lack of water. Further, native species are important for conservation purposes, or for other applied questions that are particularly relevant to native varieties (e.g. management of forest insect pests, relationships with other species, recreation, agriculture, etc.). So for application to the broadest set of questions, the USA-NPN Plant Phenology Program (PPP) is being implemented with BOTH a selection of nationally and regionally appropriate native species (almost



**Fig. 2.8** USA-NPN Plant Phenology program observers (not including project budburst participants) as of May 1, 2009

200 species protocols are available so far to facilitate observations), as well as a few wide-ranging cloned varieties of species (extension of the lilac legacy, termed the Cloned Plants Project) to allow for separation of environmental and genetic factors in phenological variability. This approach is an extension of that employed in the International Phenological Garden (IPG) program in Europe, where cloned varieties of multiple native species are used at all sites.

In support of these initiatives, initial testing of a new web page started in May 2008, with launching of a completely revised data entry module occurring in March 2009. By May 2009, over 1800 individuals had registered as USA-NPN plant phenology observers (Fig. 2.8). Project Budburst, a USA-NPN Citizen Science field campaign started in 2007, has also been highly successful in recruiting many participants. Our next technical goal is to develop and implement a data visualization/download module by the end of 2009. Planning is also well underway for the scheduled launch of an USA-NPN Animal Phenology Program in 2010. In order to be most effective, the USA-NPN must maximize the number and facilitate dense and geographically distributed coverage of phenological observation stations across the country. We continue to pursue co-location and cooperation agreements with existing observation networks, such as National Weather Service COOP, AmeriFlux, NPS Inventory & Monitoring, and LTER sites. USA-NPN is also preparing to take a leading role in the process of developing and implementing an approach for coordinated global phenological monitoring. Schwartz, Weltzin (Executive Director of USA-NPN), and Elisabeth Koch (COST 725 European phenology program leader) are moving forward with this initiative through a Group on Earth Observations (GEO) sub-Task, and possibly a World Meteorological Organization Expert Team, facilitated through the Phenology Commission of the International Society of Biometeorology.

Additional details on the progress of the USA-NPN and programs can be found in the USA-NPN web pages (<http://www.usanpn.org>), and at the Citizen Science field campaign page (<http://www.budburst.org>).

### ***2.3.8 Current Network for the Collection of Phenological Data in Russia: Data Bases, Suitability of Data, Future Networks, On-Line Databases***

**Svetlana Vidyakina and Alexander Andreevich Minin**

Currently, there is no national phenological network in Russia, but there are regional coordinators of a network of voluntary correspondents (observers) of a phenological network of the Russian Geographical Society (RGS). The RGS commenced taking phenological observations in 1848 (Filonov and Nukhimovskaya 1985 in Ostergren and Hollenhorst 2000). Most of the data from Russia and the former USSR (Ukraine, Belarus, Kazakhstan, the European part of Russia, the Urals and Siberia (see Fig. 2.9) are collected in the Moscow and St.-Petersburg centres of the RGS. Currently, the network of voluntary supervisions is maintained by the

**Fig. 2.9** Location of phenological observation stations. Including the territory of the former USSR (Ukraine, Belarus, Kazakhstan, European part of Russia, the Urals, Siberia)



regional coordinators at their own expense and depends on the enthusiasm of the correspondents.

In addition to the locations of the RGS network, monitoring is carried out in nature reserves, at meteorological and agro-meteorological stations. These data are forwarded to the Ministry of Natural Resources, regional administrations of the Hydro-meteorological Service and the Agro-meteorological Service. Part of this information forms the base of RGS and general work is carried out for the Institute of Global Climate and Ecology of the Russian Hydro-meteorological Service and Environmental Monitoring and the Russian Academy of Sciences, Moscow.

The work organising the phenological observations was carried out within the framework of the project “Nature of the European North in a changing climate”, which was funded by the Federal Special Program “Integration” N 10842, 2002–2006. The holding of lectures at teachers’ professional development courses and the running of school excursions have made it possible to increase the number of observers in the European North of Russia. Results of the work carried out are presented in a chapter of the book “Changes of climate in the European North” by Vidyakina (2004).

The coordinators of the phenological commission of RGS are: in Moscow – Alexander Andreevich Minin (aminin@pochta.ru), in St.-Petersburg – Violetta Georgievna Fedotova. Most of the data are stored in hand-written form as “Nature



Chronicles”. Over the last years the data has been systematised and organised in a form suitable for analysis. The data forms a long timeseries with 40–60 or more years. However, it represents only 15–20 locations of observations. The electronic database is in the Moscow Centre, presented with dates of the phenomena occurring. These data are available in the form of maps and graphs at the site <http://www.wwf.ru>. Results of the “Climatic documents of ecological regions” are also published in a number of publications.

Publications of the series “Ecoregional Climate Change and Biodiversity Decline” are available on the web and in printed form, for example for the Kola Peninsula (World Wildlife Fund 2003) and for the Chukotka region (Kokorin et al. 2002)

The phenological observation program corresponds to natural vegetation zones. These are lists of events recommended to be observed, with the aim being to have the widest possible distribution of the location of the phenomena observed, and to observe its precise occurrence in nature. The selection criteria also include trying to have a range of organism types and the full range of seasons. The list of the events recommended for observation include the phenomena of birds’, insects’, plants’ lives, as well as abiotic environmental conditions (commencement of frost, commencement of drifting of ice, icing over, etc.). Further details on phenological observations in Russia are provided in Minin (1991, 2000).

### 2.3.9 *International Initiatives*

#### **Frank-M. Chmielewski and Elisabeth Koch**

The Phenology Study Group of the International Society of Biometeorology started a global phenological monitoring (GPM) initiative in 1993. The main objectives of GPM are to form a global phenological backbone with a “standard observation program”, to link “local” phenological networks and to encourage the establishment and expansion of phenological networks throughout the world (Bruns et al. 2003). As GPM focuses mainly on temperature impacts on seasonal plant development, the network is restricted to mid latitudes. The first phenological monitoring garden of the network opened in Germany in 1995. In 2007 the network has expanded to more than 20 sites as shown in Table 2.5 plus some International Phenological Gardens (IPG), which have adopted *Corylus avellana*, *Forsythia suspensa* and *Syringa vulgaris* in their monitoring program. The standard program comprises eight fruit trees (see details below), whilst the extended program includes eight more flowering plants, among them Lilac (*Syringa x chinensis* “Red Rothomagensis”), *Forsythia* (*Forsythia suspense* “Fortunei”) and Hazel (*Hamamelis x Intermedia*). The IPGs are further described in the following paragraphs or for more details see <http://www.agrar.hu-berlin.de/struktur/institute/pfb/struktur/agrarmet/phaenologie/ipg>.

The International Phenological Gardens is a unique phenological network which was originally founded in 1957 by Fritz Schnelle and Ernst Volkert. Based on

**Table 2.5** Stations of GPM, as of 2007

GPM-No.	Country	GPM-Station	Lat.	Long.	Alt. (m)	Beg. of Obs.	End of obs.
1	D	Deuselbach	49°45'	07°03'	480	2000	2003
2	D	Blumberg	52°36'	13°37'	76	2001	
3	D	Braunschweig	52°17'	10°27'	81	2001	
4	D	Zingst	54°25'	12°33'	1	2001	
5	D	Moorende	53°32'	09°41'	4	2002	
6	D	Schleswig	54°32'	09°33'	36	2002	
7	D	Tharandt	50°59'	13°32'	365	2002	
8	D	Geisenheim	49°59'	07°59'	118	2003	
9	D	Linden	50°32'	08°41'	172	2004	
10	CN	Peking	40°00'	116°11'	100	2003	
11	NL	Wageningen					
12	NL	Amsterdam					
13	EST	Jögeva	58°45'	26°25'	70	2005	
14	USA	Milwaukee	43°23'	88°01'	265	2002	
15	SK	Banska Bystrica	48°44'	19°07'	427	2003	
16	CZ	Prag	50°08'	14°22'	284	2004	
17	D	Berlin-Adlershof	52°26'	13°31'	35	2005	
19	D	Offenbach	50°06'	08°47'	99	2006	
20	D	Leipzig-Holzhausen	51°19'	12°27'	138	2006	
21	D	Knüllwald	51°03'	09°31'	260	2006	

the recommendation of the Commission for Agricultural Meteorology (CAGM) they developed the idea for an international European plant phenological network called IPG in order to obtain comparable and standardized large-scale phenological observations across Europe (Schnelle and Volkert 1957). To eliminate the hereditary variability only cloned specimens of trees and shrubs were planted; microclimate effects are widely excluded as the gardens are situated in similar surroundings (mainly plain surface with meadows and some trees) and a detailed observation-guide helps to minimize subjective observation errors. The gardens are professionally looked after by the staff of University institutes, botanical gardens etc. who make the observations on a voluntary basis.

After several years of preparation, the first phenological observations started in 1959 at the Deutscher Wetterdienst in Offenbach. In the following years, the number of IPGs increased all over Europe up to 66 IPG in 1978. The IPGs were established on the grounds of different institutions and scientific agencies (e.g. agricultural, forestry, botanical and meteorological institutes), located in the vicinity of an official meteorological station. The network runs on a voluntary basis.

The coordination of the network has changed several times. For instance, from 1973 to 1977 the network was organized by the Institute of Biometeorology of the University in Munich. Between 1978 and 1995 the German Weather Service was responsible for the gardens. When in 1996 the Humboldt-University of Berlin took on the co-ordination and management there were still 50 IPGs. Unfortunately, after 1978 when 66 gardens were counted the number of IPG decreased slightly, because

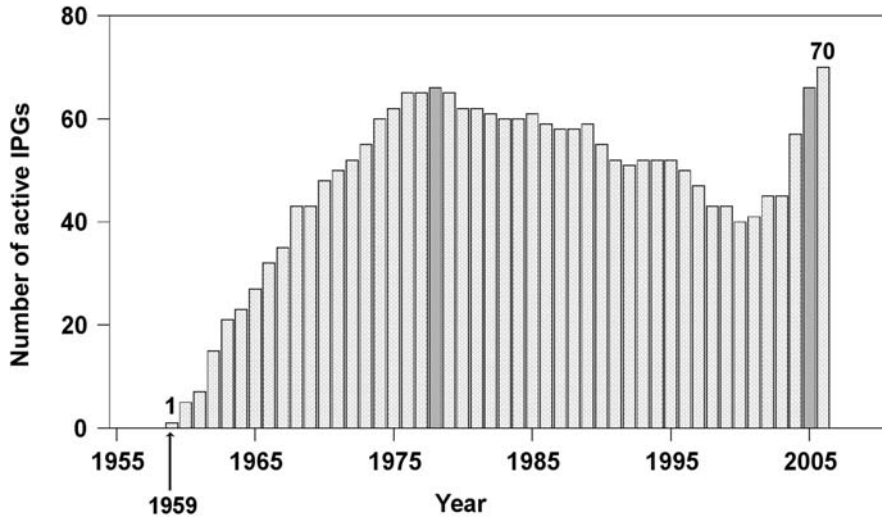


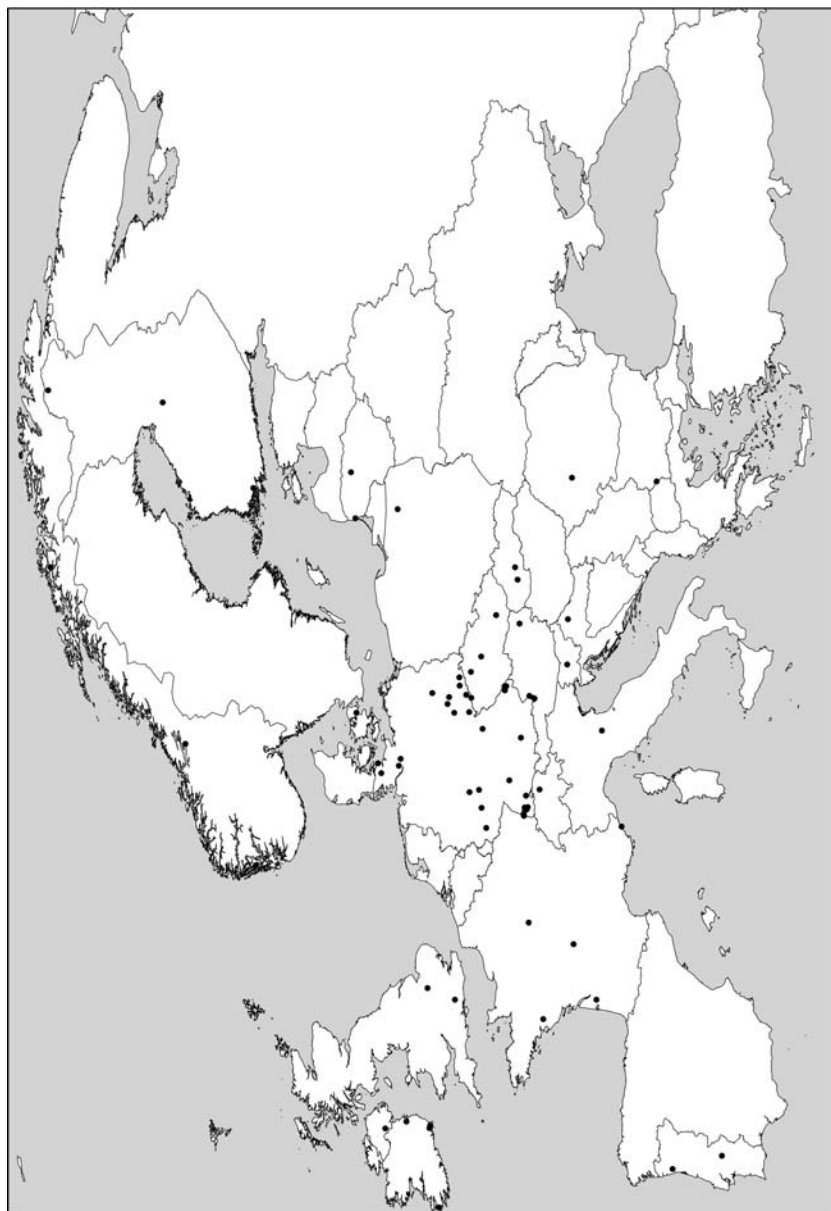
Fig. 2.10 The development of the number of IPG stations from 1959 to 2006

not enough plant material was available to establish new gardens (Fig. 2.10). However, since 2000 the number of IPGs has been increasing again.

One of the first challenges of the new management was to find a new parent garden, because the old one in Hamburg-Großhansdorf (Federal Research Centre for Forestry and Forest Products) was no longer able to continue the very important plant propagation. At first the remaining plant material from the old parent-nursery was moved to a new site at the JORDSAND association near Hamburg, where there was enough space to grow the plants. During the first years the plant-dispatch was also organized from Hamburg. Unfortunately, at this site the propagation of the IPG plants failed and it was therefore necessary to find a new institution. Since 2001 the Experimental Station of the Bavarian State Institute of Forestry at Grafrath (nearby Munich) has been undertaking the successful reproduction of the plants. Additionally, in the last two years some trees were propagated in Saxony, so that now the network is growing rapidly and we are also able to replace some older species in the gardens by young plants.

The network of the International Phenological Gardens ranges across 28° latitudes from Scandinavia to Macedonia and across 37 longitudes from Ireland to Finland in the north and from Portugal to Romania and Macedonia in the south. At present there are 70 stations (as of 2006). Thus, the network covers different climate regions from the cold to the warm climate and from the maritime to the more continental areas of Europe (Fig. 2.11).

The original IPG observation program was fixed in 1959. It was divided into a standard and in an extended program including 23 plant species (*Larix decidua*, *Picea abies*, *P. omorika*, *Pinus sylvestris*, *Betula pubescens*, *B. pendula*, *Fagus*



**Fig. 2.11** IPG sites across Europe in 2007

*sylvatica*, *F. orientalis*, *Populus canescens*, *P. tremula*, *Prunus avium*, *Quercus petraea*, *Q. robur*; *Robinia pseudoacacia*, *Sorbus aucuparia*, *Tilia cordata*, *Ribes alpinum*, *Salix aurita*, *S. acutifolia*, *S. smithiana*, *S. glauca*, *S. viminalis*, *Sambucus nigra*). The standard program included one provenance of each species. Some gardens observed additionally a few provenances of species from climatically different areas (expanded program). Since some plant species are very difficult to propagate and are not well distributed across the network, it was decided to concentrate on a subset of plants which will be planted at all new IPGs. Additionally, in 2001 three new species Hazel, Forsythia and Lilac were included in the observation program, so that now the new standard observation program consists of altogether 21 plant species (Table 2.6).

The data are published in *Arboreta Phenologica* (1960–2006) and garden owners can download their own data to the digital database via the IPG webpage (<http://www.agrar.hu-berlin.de/struktur/institute/pfb/struktur/agrarmet/phaenologie/ipg>). Selected data are also incorporated in the COST725 database and are available download <http://www.zamg.ac.at/cost725>.

The phenological observations of the IPG have been used in many studies. The data were used for modeling purposes (Kramer 1996, Menzel 1997, Chuine 2001),

**Table 2.6** IPG standard observation program since 2001

Plant species		Phenological Phases								
Botanical name	English name	BO	M	B	AB	J	F	LV	BF	
<i>Larix decidua</i>	European larch	x		x	x			x	x	
<i>Picea abies</i> (early)	Norway spruce		x	x	x					
<i>Picea abies</i> (late)	Norway spruce		x	x	x					
<i>Pinus silvestris</i>	Scotch pine, Fir		x	x	x					
<i>Betula pubescens</i>	White birch	x		x	x			x	x	
<i>Fagus sylvatica</i> 'H', 'D'	Common beech	x		x	x		x	x	x	
<i>Populus tremula</i>	Trembling poplar									
<i>Prunus avium</i> 'B'	Wild cherry	x		x	x		x	x	x	
<i>Quercus robur</i> 'W'	Common oak	x		x	x	x	x	x	x	
<i>Robinia pseudoacacia</i>	Common robinia	x		x	x		x	x	x	
<i>Sorbus aucuparia</i>	Mountain ash	x		x	x	x	x	x	x	
<i>Tilia cordata</i>	Small-leaved lime	x		x	x		x	x	x	
<i>Ribes alpinum</i>	Alpine currant	x		x	x	x	x	x	x	
<i>Salix aurita</i>	Roundear willow	x		x	x			x	x	
<i>Salix acutifolia</i>	Pussy willow	x		x	x			x	x	
<i>Salix smithiana</i>	Smith's willow	x		x	x			x	x	
<i>Salix viminalis</i>	Basket willow	x		x	x			x	x	
<i>Sambucus nigra</i>	Common elder	x		x	x		x	x	x	
<i>Corylus avellana</i>	Common Hazel	x		x	x		x	x	x	
<i>Forsythia suspensa</i>	Forsythia	x		x	x			x	x	
<i>Syringa vulgaris</i>	Common lilac	x		x	x			x	x	

BO Beginning of leaf unfolding; M May shoot; B Beginning of flowering; AB General Flowering; J St. John's sprouts; F First ripe fruits; LV Autumn colouring; BF Leaf fall.

the study of phenological trends (Menzel 1997, 1998), the investigation of relationships between climate change and plant development in Europe (Chmielewski and Rötzer 2001, 2002) and the impact of climate change on individual regions and stations (Atkinson 2002, Donnelly 2002, Köstner et al. 2005). Finally, the observations provided a fundamental basis for the COST725 action in which a phenological reference data set has been established.

Recently the value of phenology as an instrument to raise the awareness of children for environmental issues was re-discovered (in the 1950s for instance many Austrian schools took part in the observation program of the ZAMG, the Austrian national weather service). The Global Learning and Observations to Benefit the Environment (GLOBE; see <http://www.globe.gov>) was probably the first program that initiated worldwide phenological observations in schools. One of the aims of GLOBE is to encourage students to take scientifically valid measurements in the fields of atmosphere, hydrology, soils, and land cover/phenology, combining scientific research with education. GLOBE was announced in 1994 and began operations in 1995, involving schools and students with a special phenological observation program. Phenology of the North Calotte <http://sustain.no/projects/northcalotte/> is another initiative aimed at stimulating schools to actively take part in nature observations and registrations foremost addressing pupils of schools in the border area between Norway and Russia.

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# Chapter 3

## Seasonality as a Core Business of Phenology

François Jeanneret and This Rutishauser

**Abstract** The best characteristics of phenological observations are their description of seasons and seasonal patterns. Specific phenological phases are used to define the beginning and the end of seasons that form phenological calendars. Phenological observations more closely capture the integrated seasonal rhythm than statistically derived means or thresholds from climate elements. They only provide approximate indicators of seasonal changes and cannot replace visible or directly measurable phenomena. Including abiotic observations such as the timing of frost, thawing, icing, snow and fog even provides seasonality descriptions beyond the vegetation period. The length and position of seasons within the year is a foundation for an integrated description of seasonality presented as a phenological season diagram. Phenological observations are the indispensable basis for an integral description of a seasonal classification and seasonality. A well designed phenological diagram could offer a comprehensive picture of the rhythm and amplitude of seasons.

**Keywords** Biotic and abiotic phenology · Environmental monitoring · Mountain climate · Phenological diagram · Topoclimatology

### 3.1 Seasons as Genuine Phenological Units

The science of phenology contributes to the assessment of regional climate change by the use of observations of plant or animal behavior like many other geo- and biosciences (van Vliet et al. 2003). However, phenology also offers definitions of seasons, an overview of the succession of seasons and the assessment of seasonal patterns, especially in middle latitudes, but also in sub-tropical (e.g. Sanchez-Azofeifa et al. 2003) and sub-arctic conditions (e.g. Wielgolaski and Inouye 2003).

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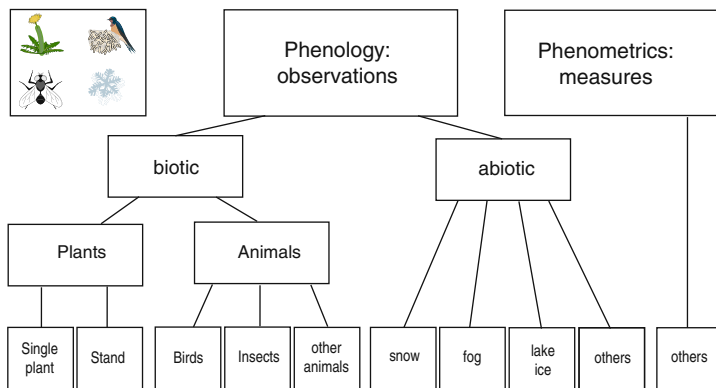
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These are unique contributions to the knowledge of seasonality. Essentially, this is the core business of phenology, whereas in climatology, means, thresholds or calculated values such as temperature sums have to be used.

Phenological observations define the seasonal rhythm of nature as visible from plant and animal phases such as budburst, flowering or first appearance. Abiotic phenologies including the timing of frost, snow and ice also describe seasonal changes and variability. Phenology is a highly economical method for bio- and geomonitoring that has been recognized by the operators of national or special phenological networks in many countries (Koch in Chapter 2, Nekovář 2008). Furthermore many nature lovers (closet observers) scattered all over the planet record and collect phenological events. Historical data, including information contained within herbarium records (Primack et al. 2004, Lavoie and Lachance 2006, Miller-Rushing et al. 2006), can be used for reconstructions of centennial-scale phenological variability (Sparks and Carey 1995, Rutishauser 2007, Aono and Kazui 2008).

The classical definition of phenology is “the art of observing the phases of the life cycle or the activities of plants and animals as they occur throughout the year” (Lieth 1971). Lieth (1974) quotes the technical definition by the US IBP Phenology Committee that described ‘[...] the causes of their timing with regard to biotic and abiotic forces [...]’. Also in this book he specifically separates out seasonality “Seasonality is the occurrence of certain obvious biotic and abiotic events or groups of events within a definite limited period or periods of the astronomic (solar, calendar) year. Van Vliet and De Groot (2003) explicitly related phenology to the physical environment and defined it as “the study of the times of recurring natural phenomena especially in relation to climate and weather”. As a consequence, phenology not only includes observations of plant and animals, but also other natural phenomena with seasonal character. Data collection is no longer bound to traditional observations, but can also include all sorts of documents and evidence such as pictures (e.g. Sparks 2007). Thus a broader definition should not replace traditional aspects but specifically address the diversity of possible documents such as proposed by (Jeanneret 2005, Jeanneret and Brügger 2005): “Phenology deals with patterns and evolution of seasonality in the biotic and abiotic environment recorded by in situ observations and data obtained from pictures, photographs and historical documents” (Ahrends et al. 2008, Rutishauser 2007).

Traditionally, phenology is based on observations rather than instrumental measurements (Fig. 3.1). Living organisms such as plants and animals are the most important object. Abiotic elements are also included as they provide seasonal information beyond the vegetation period. Phenometry, meteorology and climatology operate with instruments producing measurements of the biotic and abiotic environment. Observations include the description of environmental changes in an integrated way as opposed to measurements that only record one specific parameter. Phenology occupies therefore a relatively small but optimal position in the specific field of topoclimatic spatial scales (Jeanneret and Rutishauser, Chapter 8). The timing can be detected in the terrain on single organisms or species-specific populations, but also as integrated measurements from terrestrial or remotely sensed pictures and photographs.



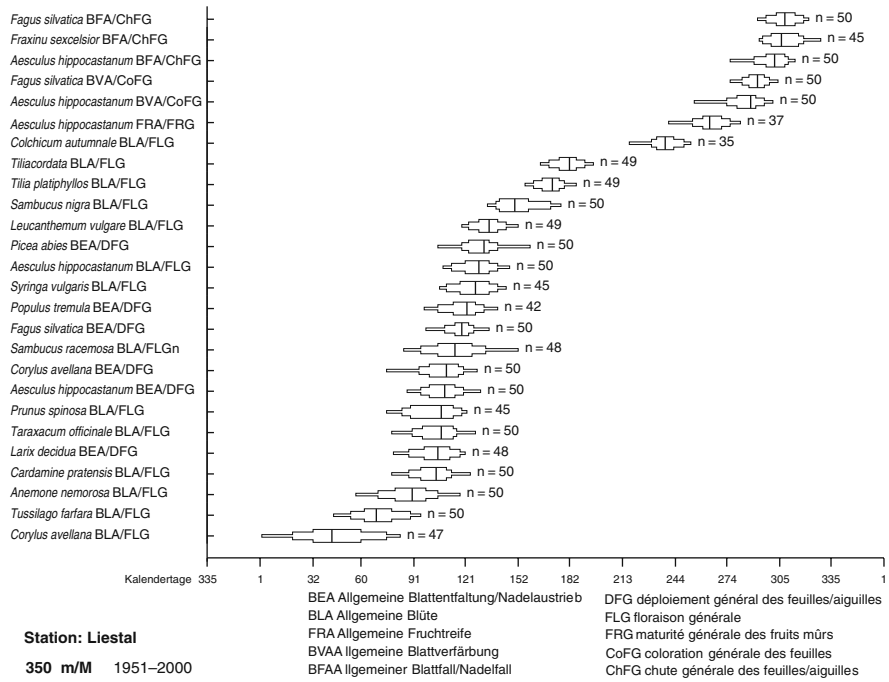
**Fig. 3.1** Phenology includes direct and indirect observations of biotic and abiotic phenomena in nature in order to describe seasonality

### 3.2 Seasonal Patterns Describe the Annual Rhythm

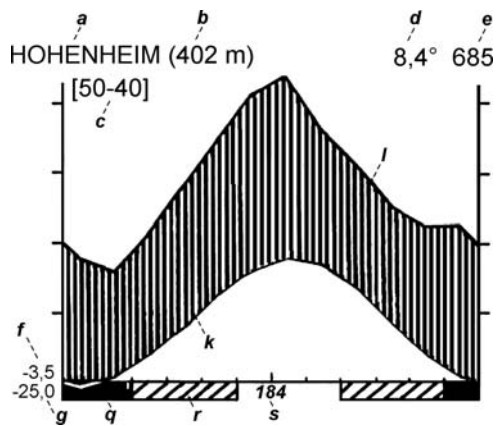
For Central Europe, Ihne defined specific phenological seasons in 1895 (Schnelle 1955) which became a classic set of denominations: for early, full and late spring, summer and autumn he selected phenological phases which announced and defined the beginning of each season. But in order to appropriately present phenological observations there is a need for specific illustration of seasonality which graphically reflect the rhythm and patterns of seasons. For mid-latitude climates, phenological calendars (e.g. Defila 1992, Fig. 3.2) show the range of phases from spring to autumn. Ahas and Aasa (2003) present and discuss a range of phenological calendars that are a characteristic way of depicting the phenological year.

These calendars statistically order plant phenological phases according to median starting date of the record length. Quartiles and whiskers depict the spread and extremes of the phases (Fig. 3.2). However, the upward succession of the boxes or curves does not make reference to the continuity of the annual seasonal cycles, nor to the inverse trend in autumn. In a different approach, the phenological clock is a continuous representation of phases and seasons, which also allows combining two periods (Henniges et al. 2005). The comparison and visual interpretation of more than one clock is difficult. Usually, phenological calendars and clocks offer no differentiation of the winter, as often no plant phenophases can be recorded in mid- to high-latitude climates.

In climate research, the well-known climate diagrams or climagrams after Walter and Lieth (1960–1967, Fig. 3.3, Lieth et al. 1999) combine temperature and precipitation as key elements to illustrate climate characteristics and patterns. They provide a simple graphical representation of key climatic parameters of a measuring site. Flat temperature curves reveal relatively oceanic and moderate climates whereas uneven curves describe rather continental climates with a distinct annual cycle. The position of the curves gives information on thermal conditions, precipitation bars on

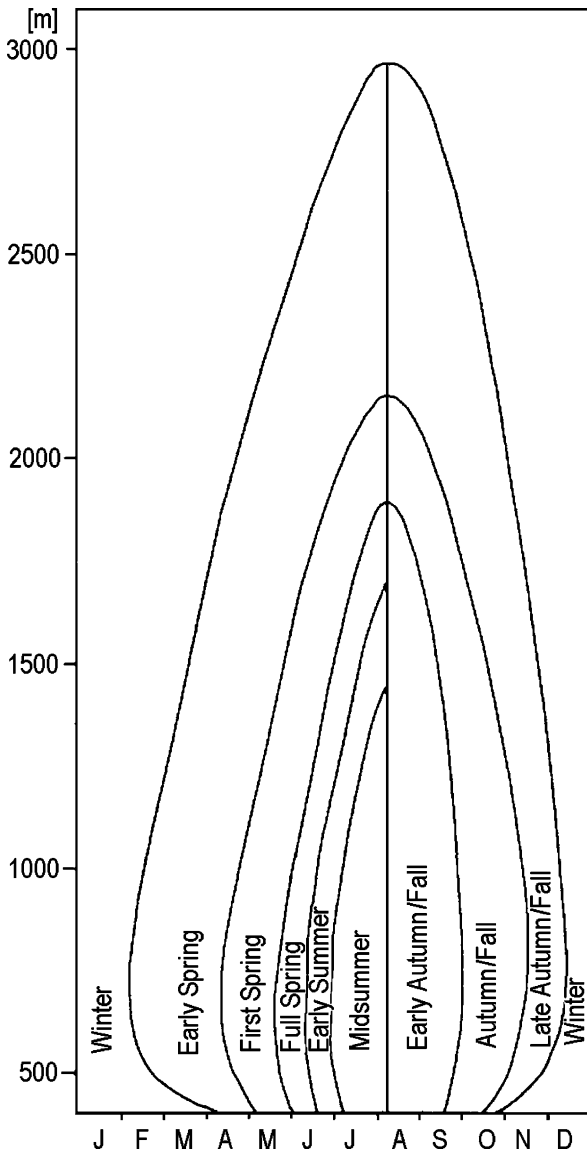


**Fig. 3.2** Phenological calendar of the station Liestal, Jura mountains, Switzerland, 350 m above sea level. Observations from 1951 to 2000 (from Jeanneret and Defila 2007, BBCH-Codes after Brügger and Vassella 2003). BEA Leaf unfolding (BBCH 13)/ unfolding of needles, BLA Full flowering (BBCH 65), FRA Full ripeness (BBCH 87), BVA Colouring of leaves (BBCH 94), BFA needles fallen (BBCH 95)



**Fig. 3.3** Example of a climatic diagram after Walter and Lieth (1960) with explanations (temperature in °C; rainfall in mm)

**Fig. 3.4** Variation of mean phenological seasons in mountain areas relative to altitude (example from the Austrian Alps, after Gams 1961, also reprinted in Lauer and Rafiqpoor 2003). Only the lower altitudes offer the full range of seasons, and winter rest becomes more important in higher areas. However, thermal inversions in larger valleys reduce the length of vegetation period



the quantity and monthly distribution of rainfall. The new ecophysiological climate typology and classification elaborated by Lauer and Rafiqpoor (2003) is based on humidity, aridity, growth activity and nivality (snow fall and cover).

As plant phenology does only rarely give evidence during the dormant season in mid-latitude climates, like eucalypts flowering in Australia in winter, abiotic elements have to be used if required as a gap-filling, graphical element, especially where winter rest increases with altitude (Gams 1961, Fig. 3.4). Plant phenological

observations describe the various stages of the growing season whereas abiotic elements characterize winter. Seasons differ according to their intensity, their length and their position within the year. The pattern of early or late, short or long defines and demonstrates a typology. A combination of biotic and abiotic observations represents the entire year.

A phenological season diagram should comprise data for all seasons. A graphical representation for year-round phenological seasons based on climagrams could be a great help to improve climatic and environmental interpretations and to reveal fields and potential of applications. Therefore, a phenological season diagram should meet the following basic requirements (Jeanneret 2008):

- represent the rhythm of all seasons, including an equivalent graphical element for winter (where there is dormancy),
- show different phenological phases during the whole growing season,
- combine the different representations to an annual image,
- adapt to different observation methods and programs (different phenophases),
- be simple to read and to interpret.

### 3.3 The Phenological Season Diagram

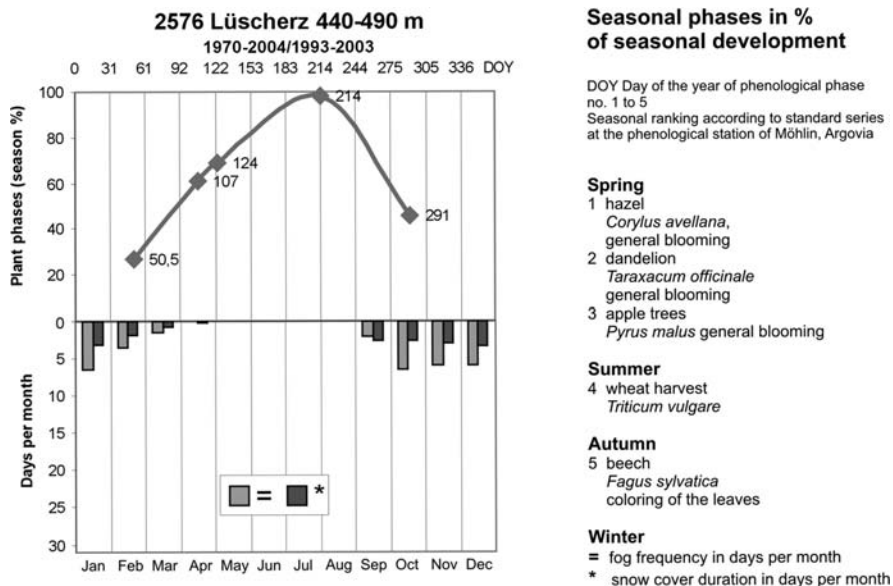
We demonstrate a phenological season diagram with data from the special topoclimatic network BERNCLIM (Jeanneret 1972, 1997, Messerli et al. 1978, Bucher and Jeanneret 1994, see also Jeanneret and Rutishauser in Chapter 8). It was founded in 1970 as a low-cost topoclimatic monitoring survey. In the Canton of Berne (7000 km<sup>2</sup>) and adjacent areas in Switzerland, data of plant phenological phases covering the entire growing season, fog frequency and snow cover duration in winter have been collected for more than three decades. The combination of a set of phenological phases from spring (blooming of the hazel *Corylus avellana*, dandelion *Taraxacum officinale* and apple trees *Pyrus malus*) to summer (wheat harvest *Triticum vulgare*), and autumn (coloring of the leaves of beeches *Fagus sylvatica*) followed by winter (snow cover and fog duration) characterizes the seasonal pattern of various topoclimates.

The observation area stretches from the Northern Jura Mountains across the central hill country to the Alps, offering a wide variety of climatic conditions over a cross-section of 120 km and from 400 to 4000 m of elevation. Observation series of up to 35 years are precious for research on recent climatic variations as well as for different applications, such as forestry and bioclimatology.

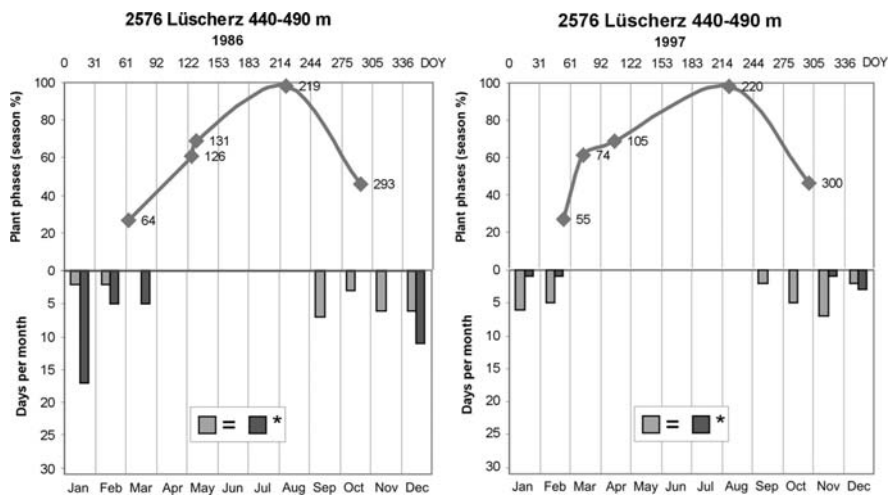
With data from two selected stations, phenological season diagram is presented (Figs. 3.5 and 3.7). The phenological season diagram combines a curve for the growth period, derived from the dates of a number of phenophases, to monthly column of duration of snow layer and frequency of fog in days.

The plant phenology curve is plotted against days of the year (DOY) and displays a ranking of the phenophases according to a reference series in percents. The

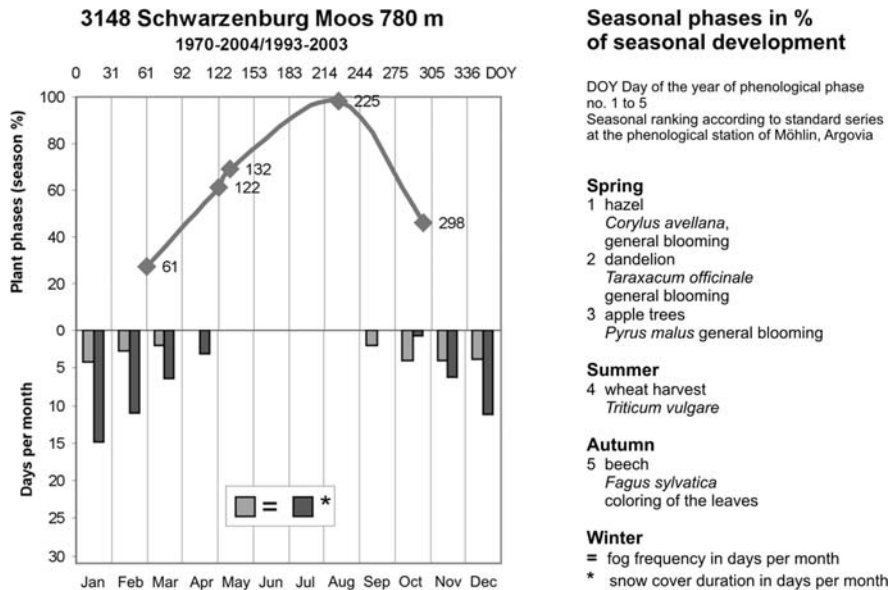




**Fig. 3.5** Combined phenological season diagram of the lower Swiss Plateau (Lüscherz at the South shore of the lake of Biemme): above the biotic phenological phases in the summer term (1970–2004) in days of the year, below the abiotic winter phases (1993–2003) in days per month. The vegetation period starts early, is relatively long, and in winter fog is rather frequent, but the snow cover is not lasting very long



**Fig. 3.6** Phenological season diagram of two distinct years at the same location of Lüscherz. 1997 was an early phenological year with a quickly advancing spring following a short winter with little fog and not much snow. 1986 shows a late pattern for spring following a winter with longer snow duration, autumn was earlier with more fog

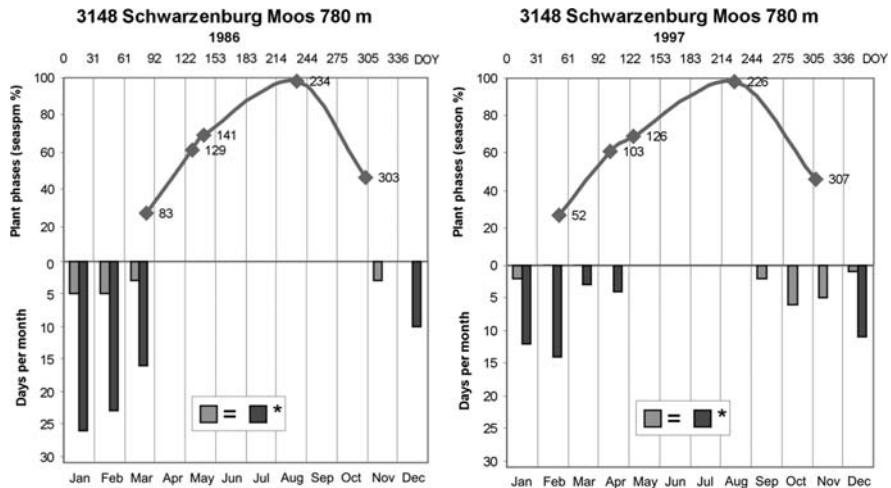


**Fig. 3.7** Combined phenological season diagram of the higher Swiss Plateau (hills of the Schwarzenburg area adjacent to the Alps): above the biotic phenological phases in the summer term (1970–2004) in days of the year, below the abiotic winter phases (1993–2003) in days per month. The vegetation period is relatively late and shorter, and in winter fog is rare, but snow cover is lasting longer

phenological reference station is a low-lying place on the Rhine River with usually rather early dates. It belongs to the national observation network of MeteoSwiss at Möhlin AG (Canton of Argovia, 305 m, 1956–1990, Defila 1992). The ranking is expressed in percent of the dates of the first 6 months of the year (181 days) and inverted for the following months (184 days). The columns of the winter data are hanging, in order to not disturb the biotic curve.

Diagrams based on long observation periods show the mean values and, thus, reflect general patterns (Figs. 3.5, 3.6, 3.7 and 3.8). Diagrams of single years illustrate particularly early (e.g. 1997, Figs. 3.6 and 3.8, left) or a late years (1986, Figs. 3.6 and 3.8, right). The climate in the low-lying village of Lüscherz on the shore of Lake of Bienne, (Figs. 3.5 and 3.6) is characterized by a relatively early beginning of spring and a long vegetation period. Winter is mild with little snow. Numerous fog days reflect the long lasting thermal inversions during high pressure periods in winter. In the Schwarzenburg area hills, culminating well above 1000 m and represented by the station of Schwarzenburg (Figs. 3.7 and 3.8), the vegetation period starts later, snow is lasting during a longer period, and the area lies often above typical thermal inversions. The two stations stand for contrasting conditions with different seasonality patterns.

The phenological season diagrams show a regular, normal season pattern when it is averaged over longer periods, and simultaneously allows a comparative analysis



**Fig. 3.8** Phenological season diagram of two distinct years at the same location of Schwarzenburg. In 1997 spring and summer were earlier after a late winter with less snow. 1986 shows a late pattern for spring following a winter with long snow duration, but autumn was normal and snow arrived late

of single years. The form and position of the curves reveal seasonal anomalies. Steep slopes show quickly advancing seasons, curves to the left represent earlier, to the right later seasons.

More examples linking plant with abiotic phenology offer the opportunity of a year-round, combined topoclimatic typology. Well-designed and normalized diagrams could be used in many publications and make phenology and seasonality more popular. An improved graph should combine various plant phenological metrics into a single curve, showing both rhythm and amplitude of seasonal patterns. Further improvements could yield to a standard graph which could be widely applied. Development should include the application of the diagram to networks with different observation programs.

### 3.4 Seasons at a Glance

It is challenging to combine plant phenology data with the frequency of fog days and snow cover duration. Each element reacts to climate variability in a complex way. The increasing length of the vegetation period is a chance for agriculture and summer tourism. On the other hand, the higher altitude and duration of winter fog causes not only more traffic problems, but also health risks due to smog situations in densely populated areas that are often located in basins with frequent thermal inversions. The reduced duration of snow cover due to winter warming has well-known economic consequences on winter tourism. All these variations are typical for topoclimatic scales, highly depending on the relief situation and reflected by

biotic and abiotic phenological data. Clear graphical illustrations will contribute to a better understanding and application of phenological observation data.

Compared to climate diagrams (Fig. 3.3), the phenological season diagram includes various climate-sensitive impact factors revealing a complex set of information on the driving climate conditions. Plants, animals, snow, ice or fog reflect the global environmental conditions and are therefore a valuable indicator of pattern and changes. It can be monitored at places far from meteorological stations, and phenological networks do not require heavy and expensive infrastructure. Phenological season diagrams are a potent and cheap tool for extracting typologies of seasonal patterns based on an analysis of single years or different stations.

The big advantage of phenological season diagrams is in fact the potential of their universal application: This is an important step to improve the use of phenological data. Phenology has not yet achieved international or global standardization (Bruns and van Vliet 2003). However, ideas such as the Global Phenological Monitoring (GPM, initiated by the International Society of Biometeorology) and research programs like the European Phenology Network EPN (5th European Program, van Vliet et al. 2003) or COST Action 725 (“Establishing a European Phenological Data Platform for Climatological Applications”) are important and most valuable steps toward a standardized method with a comprehensive graphical presentation such as the phenological seasons diagram.

**Acknowledgments** Without the year- or often decade-long observation work in past and present of numerous persons in different networks and as closet observers, phenology is unthinkable. Thanks to their nature loving engagement, masses of data are available to scientists. The invaluable assistance of Dr Reto Stöckli (Federal Office of Meteorology and Climatology MeteoSwiss, Zurich, and Department of Atmospheric Science Colorado State University, Fort Collins Colorado, USA) is gratefully acknowledged.

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# Chapter 4

## Societal Adaptation Options to Changes in Phenology

Arnold J.H. van Vliet

**Abstract** In this chapter I provided a qualitative overview of how phenological changes will strongly influence human well-being through changes in primary production sectors depending on natural productivity, including agriculture, forestry and fisheries, and the public health sector. Farmers, commercial enterprises, patients, doctors and policy makers have to adapt pro-actively to cope with, prevent or reduce potential negative impacts. Adaptation should be relatively easy in most cases because people have to ‘only’ change the timing of their activities. However, pro-active adaptation is currently often unfeasible because stakeholders do not know what phenological changes will happen where and when. They also are not aware of the ecological and socio-economic consequences of such phenological changes. They seem to miss a sense of urgency to act. Furthermore, they miss an understanding on whether, how and when to respond in order to prevent (further) negative impacts or to benefit from the emerging changes.

To adequately respond to phenological change and to improve the adaptation potential, there is a need to (1) continue and improve monitoring of phenological changes; (2) advance the analysis of phenological changes and its socio-economic and environmental impact; (3) improve the projections of phenological changes and their impacts; and (4) improve the communication on observations, knowledge, tools and techniques. Phenological networks should take the lead in all these four activities. They should, however, closely work together with major stakeholders.

**Keywords** Adaptation · Phenological networks · Primary production · Public health

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## 4.1 Introduction

Phenology is the study of the timing of annual recurring life-cycle events. Examples of phenological events include the start of flowering, leaf unfolding, insect appearance, bird migration, fruit ripening or autumn colouring. The timing of many phenological events strongly varies from year to year. This is illustrated by Fig. 4.1, which shows the variation in timing of various phenological events in The Netherlands in the period 2001–2007 for several species.

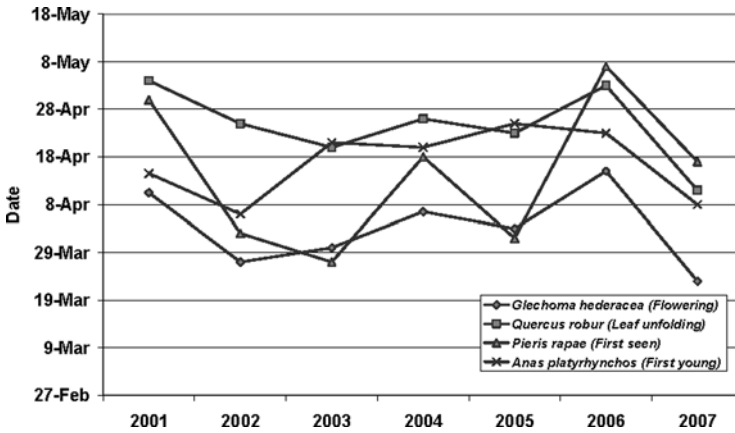
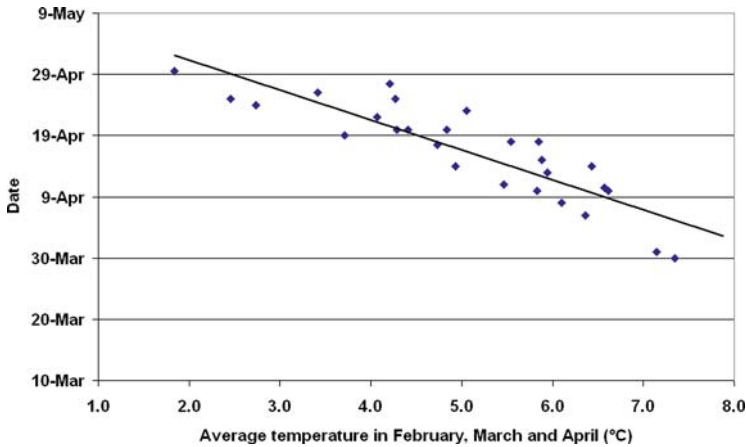


Fig. 4.1 Variation in timing of phenological events in The Netherlands between years and species

Phenological variability of plants and animals influences many societal sectors, such as public health, fisheries, hunting, forestry, nature management, gardening, tourism and recreation, transportation and water management (van Vliet et al. 2003b). All these sectors continuously adapt to phenological variability and changes, usually in a re-active or autonomous manner. In the past, the adaptation process was largely based on trial and error and less on understanding the underlying ecological and meteorological processes.

To observe and better understand the causes of phenological variability many phenological networks have been set up in the last centuries. These networks monitor, analyse, predict and communicate the timing of life cycle events in a structured and organised manner. Phenological networks exist or have existed in many countries (Schwartz 2003, van Vliet et al. 2003a). Several have been operational for decades (for example the networks in Germany and Slovakia) and some even for centuries (for example Japan and Finland). Analyses of the millions of observations made in the past have demonstrated that the inter-annual variation is largely determined by climate variables (Menzel 2000, Sparks et al. 2000, Scheifinger et al. 2002). This is clearly illustrated by Fig. 4.2, which shows the relationship between temperature and flowering of Ground-ivy (*Glechoma hederacea*).





**Fig. 4.2** Relationship between spring temperature and flowering of Ground-ivy (*Glechoma hederacea*) in The Netherlands between 1940 and 1968 (Based on data from [www.natuurkalender.nl](http://www.natuurkalender.nl))

All these analyses also show that the recently observed climatic changes have already had considerable impact on the timing of phenological events (Rosenzweig et al. 2007). Menzel et al. (2006), for example, analysed a large phenological data set of more than 125 000 observational series of 542 plant and 19 animal species in 21 European countries (1971–2000) and showed that 78% of all leafing, flowering and fruiting records advanced (30% significantly) and only 3% were significantly delayed. In contrast, the signal of leaf coloring and leaf-fall is ambiguous. Phenological changes in response to changes in weather and climate have been observed in all species groups (e.g. plants, birds, butterflies, fish, amphibians, plankton, dragonflies and mammals). Table 4.1 gives a number of examples of observed phenological changes in response to recent changes in climate.

Phenological changes thus are a good indicator for climate change impacts. However, a lot of information is still missing and cooperation between phenological networks is needed to fill these gaps. Therefore, the International Society of Biometeorology (ISB) established the Phenology Commission. This commission aims to:

- Increase our understanding of the role of climate variables in vegetation dynamics;
- Develop a combined observational program configured to be sensitive to modifications in plant/animal phenology and biodiversity changes which is able to form an effective system for early detection and warning of impending global-scale changes in ecosystems;
- Strategically deploy new and augment existing observational networks, initially in the mid latitudes;
- Contribute to the combined objectives of the Framework Convention on Climate Change (FCCC), especially with regard to adaptation, and the Convention on Biological Diversity (CBD).

**Table 4.1** A selection of observed phenological changes within different species groups

Species group	Phenophase	Observed change	Time period	Location	Reference
Meroplankton	Timing of seasonal peak	-27 days	1958–2002	North sea	Edwards and Richardson (2004)
Dinoflagellates		-23 days			
Copepods		-10 days			
Non-copepod Holozooplankton		-10 days			
Trees	Start of season	-8 days	1969–1998	Europe	Chmielewski and Rötzer (2001)
Butterflies	Mean first appearance 35 butterflies	-8.6 days	1976–1998	UK	Roy and Sparks (2000)
Migratory birds	Arrival date Departure date Average of 20 species	-8 days -8 days	1971–2000	UK	Cotton (2003)
Migratory birds	Arrival date	-14 days	1981–2000	USA, Colorado	Inouye et al. (2000)
Mammals	Emergence from winter sleep	-38 days	1977–2000	USA, Colorado	Inouye et al. (2000)
Amphibians	First spawning	0 to -21 days	1978–1994	UK	Beebee (1995)
Amphibians	Frog calling	0 to -13 days	1900–1999	USA, New York	Gibbs and Breisch (2001)

The ISB provides scientists a platform to exchange ideas and methods. The cooperation and contacts created within the ISB strongly facilitated the set up of the European Phenology Network (van Vliet et al. 2003b), the European COST 725 network (Koch et al. 2005), and the set-up of national phenological networks such as the ‘Natuurkalender’ network in The Netherlands<sup>1</sup> and the National Phenology Network in the USA<sup>2</sup>.

The recent changes in climate and the resulting phenological changes have increased the demand for phenological information. This demand will further increase over the coming decades as the Intergovernmental Panel on Climate Change (IPCC) concluded in its Fourth Assessment Report that the global mean temperature will increase between 1.8 and 4.0°C in the twenty first Century (IPCC 2007). Increases in the amount of precipitation are very likely in maritime regions,

<sup>1</sup>Dutch phenology network: <http://www.natuurkalender.nl>.

<sup>2</sup>USA phenology network: <http://www.usanpn.org>.

while decreases are likely in most Mediterranean and subtropical land regions, continuing the observed recent trends and patterns (IPCC 2007). It is very likely that the already ongoing changes in the timing of phenological events will continue in response to these climate changes. As a result phenological events are likely to occur at times of the year never previously recorded before.

It is currently largely unknown how these ongoing and the expected future phenological changes will impact society. It is also unknown whether society is able to adapt pro-actively to these phenological changes. In this chapter I aim to address the following four questions:

1. How will climate-induced phenological changes impact various sectors in society?
2. Which actors in society will be affected by phenological changes?
3. How can these actors adapt?
4. How can phenologists and other scientists facilitate the adaptation process?

The first three questions are addressed in Section 4.2. In Section 4.2.1 I focus on the primary production sectors (agriculture, forestry and fisheries) and in Section 4.2.2 on public health. I base my analysis on literature and on my own experiences gained during the coordination of the ‘Natuurkalender’ network, and the European Phenology Network. In Section 4.3 I identify questions that need to be answered to facilitate successful adaptation of these sectors. In Section 4.4 I describe how phenological networks can facilitate the adaptation process.

## **4.2 Phenological Changes: Impact and Required Adaptation**

### ***4.2.1 Primary Production Sectors***

Agriculture, forestry and fishery strongly depend on the growth and development of plants and animals. The quantity and quality of the crops, grasslands, trees or fish vary from year to year due to variation in environmental, biological, socio-economic and climatological factors. These factors are both directly and indirectly influenced by climate change causing significant impact on quantity and quality of productivity of these sectors. With the expected 55% increase in global crop production by 2030 and an 80% increase by 2050 (FAO 2005) and the significant increases in demand for forest products and fish, climate change will have significant impact on these sectors. The IPCC (Easterling et al. 2007) concludes that the potential for global food production will increase with rises in local average temperature over the range of 1–3°C. Above this range production will decrease. Crop yields in the mid to high latitudes are likely to increase but decrease in low latitudes. Projected changes in the frequency and severity of extreme climate events will also have significant consequences for food production and security, and for the forestry sector. For example, regional changes in the distribution and productivity of particular fish species are expected, due to continued warming and subsequent local extinctions at

the edges of ranges. This is particularly likely to occur in freshwater and diadromous species (e.g. salmon, sturgeon). In some cases, ranges and productivity will increase (Easterling et al. 2007).

#### 4.2.1.1 Expected and Observed Phenological Impacts

It is not possible to quantify how much climate-induced phenological changes will contribute to the expected changes in global productivity mentioned above. However, it is likely that the occurrence of climate conditions that never occurred in the past centuries will structurally change the timing of phenological processes and influence production of agriculture, forestry and fisheries. This is supported by the increasing evidence that phenological changes in crops, trees and fish are already taking place in response to the observed changes in climate. Estrella et al. (2007), for example, have studied the phenology of seventy-eight agricultural and horticultural events from a national survey in Germany spanning the years 1951–2004. They conclude that the majority of events are significantly earlier now than 53 years ago, with a mean advancement of 1.1–1.3 days per decade. Williams and Abberton (2004) found a significant earlier flowering of 7.5 days per decade since 1978 in agricultural varieties of white clover. Sparks et al. (2005) showed that 25 of the 29 agricultural and phenological events observed by a farmer in the UK were earlier in 1990–2000 than in 1980–1989. The average advancement of all twenty-nine events was 5.5 days at a time when January–March mean temperature increased by 1.4°C. Hu et al. (2005) showed that winter wheat heading or flowering dates in the U.S. Great Plains occurred 6–10 days earlier in 2004 than in 1948.

Climate-induced phenological changes of fish species are less known. Marine commercial fish stocks have changed considerably in the past few decades but it is often difficult to determine the exact role of climate change and anthropogenic influences (Frid et al. 2003, Reid et al. 2006). It is, however, clear that climate has significantly changed recruitment success, population sizes, geographic distribution and migration patterns of fish (Walther et al. 2002, Genner et al. 2004, Perry et al. 2005, Grebmeier et al. 2006, Hemery et al. 2008). Climate change is also having many impacts on forests (Robledo and Forner 2005). Modelling activities of Kramer et al. (2000) show that phenological changes will significantly influence net primary production of forests (both positively and negatively). These findings are also supported by various remote sensing studies that show the lengthening of the growing season and increases in productivity due to higher temperatures and increases in CO<sub>2</sub> concentration in the past years (Myneni et al. 1997, Zhou et al. 2001). The signals picked up by satellites over large regions were supported by analysis of long-term observations on start of leaf unfolding and leaf colouring (Menzel et al. 2006).

Climate change affects not only the timing of phenological processes of harvestable species and hence the timing of harvesting activities but also the timing of those species that, negatively or positively, influence the growth of these species will change. Examples are organisms lower in the food chain such as plankton and algae (Beaugrand et al. 2003, Platt et al. 2003, Edwards and Richardson 2004, Winder

and Schindler 2004), pests and diseases (Zhou et al. 1995, Rosenzweig et al. 2001, Harrington et al. 2007, Logan et al. 2007) and predators of food sources (Manca et al. 2007). All these changes significantly alter the growing conditions and increase the risk of environmental and climate extremes that impact productivity.

#### 4.2.1.2 Adaptation Options

How can the primary production sectors adapt to the phenological changes and who should adapt? First of all, it is important to recognize that the different stakeholders in these sectors are used to accounting for inter-annual and decadal variability in climate and phenology. Based on their experiences in the past, scientific research and the available technologies, farmers, foresters and fishers continuously select crops, trees or fishes that provide the highest profit under the average regional climatological and biological conditions. In addition, they continuously try to improve growing conditions by taking measures to control pest and diseases, by using fertilizers, and irrigation. In the timing of all these management activities, including the timing of sowing, planting and harvesting, producers try to make optimal use of the beneficial climatological conditions and to limit the damage caused by climate extremes such as cold snaps, storms and drought. Consequently, the planning of these activities significantly determines the quantity and quality of production (Bednarz et al. 2002, Schwarte et al. 2005). With the expected changes in climate, the optimal timing of their production activities is likely to change (Mackenzie et al. 2007). Therefore, farmers, foresters and fishers should consider changing the timing of sowing, planting, nutrient supply, irrigation and the control of pests and diseases. If the changes become too large they have to select different varieties of crops and trees or even different species that are better suited to the new climatological, environmental and biological conditions. According to Easterling et al. (2007), adaptations such as changing varieties and planting times should avoid a 10–15% reduction in yield in cereal cropping systems worldwide. This corresponds to a 1–2°C local temperature increase. However, according to Reidsma (2007) farmers in different European regions adapt differently to climate change and variability (e.g. varying crop types and farm size) making it difficult to estimate the success of adaptation. Furthermore, there is likely to be a gap between the potential adaptations and the realised actions. There will be large differences in adaptive capacity between regions and changes in policies and institutions will be needed to facilitate adaptation to climate change (Easterling et al. 2007).

There are many interactions and dependencies between actors that are difficult to account for the assessment of potential future impacts of climate change. Changes in the timing of the management activities will have a whole range of socio-economic consequences. It will, for example, change the timing of the amount of personnel needed throughout the year. After the very warm summer in 2003 in Europe the harvest date advanced significantly (Chuine et al. 2004). This resulted in problems for farmers as most of their seasonal employees were still on their summer holiday. In 2006, in The Netherlands, the extreme warm temperatures in July (4.9°C above average) meant fruit growers needed more personnel during a shorter period of time

to pick the fruit (Mol 2006). The warmest autumn and winter ever recorded followed; resulting in minimal time and not enough personnel, to prune the fruit trees before the start of flowering (van Brandenburg, Personal Communication).

Changes in the timing of production activities also influence the whole supply chain. Producers of seeds, nutrients, pesticides, herbicides, materials and equipment have to change their planning of production, marketing and distribution. The whole chain of activities post harvest will also change including storage in warehouses and the processing and selling of products. Wholesalers and retail businesses continuously have to decide which products to buy and sell and where they want to buy them. These decisions are based on a whole range of factors including the costs, location of production, availability and quality of products. All these factors are influenced directly or indirectly by the phenological changes and the resulting changes in quantity and quality of the products.

In addition to a large number of actors within the commercial sector, national and international governments have to respond to phenological changes. Their involvement will increase if the primary production sectors do not succeed in adapting to the expected phenological changes in time and if significant economic losses and shortages of food supply occur. The agricultural, forestry and fishery sectors are already strongly regulated by regional, national and international governments. They try to control their national production and the international competition through taxes, subsidies and quotas. Governments are also involved because these sectors have large impacts on ecosystems and biodiversity through over-production, land cover and land use changes, the use of pesticides and herbicides, and the disturbance of natural areas. In order to protect biodiversity and ecosystems, farmers, foresters and fishers are confronted with restrictions and regulations to reduce ecological damage. There are numerous examples of these regulations and in many cases phenological changes and the timely adaptation to these changes will influence the effectiveness of these regulations. In The Netherlands, farmers were requested to delay the start of mowing to increase the survival success of meadow birds. Their populations declined with 10–60% below the level of 1990 (Teunissen and Soldaat 2005, CBS/MNC 2007). The decline is partly caused by the advancement of mowing dates in response to warmer springs (Sanders et al. 2003) but not in the breeding of the birds. Another example is the regulation that restricts fishing to certain periods of the year at particular locations to allow fish to safely reproduce (CEC 2001). Policy makers, scientists, conservation organisations and fishers, are involved in determining fish quota whereby a continuous balance is sought between production and preservation. The changes in timing, distribution and population sizes of fish will intensify the many (inter)national debates about these quotas. Modelling results of Link et al. (2004) show that fish stocks are significantly influenced by changes in population dynamics, changes in fishing strategies as well as policy instruments. They conclude that without the inclusion of policy instruments, the stocks would collapse under the immense pressure of the fisheries in many scenarios of climate change induced altered population dynamics, highlighting the necessity of actively managing the anthropogenic exploitation of important marine resources. However, Rijnsdorp et al. (2002) show that there is a risk that decisions on protection of

biodiversity and on the implementation of measures that reduce impact of (in this case) fishery are currently based on outdated or non-existing knowledge. For example, both the location and time of protection measures to protect Cod populations in the North Sea were wrongly selected. The selection was based on knowledge from the 1970s. As a result, the protection measures did not have the expected benefits for Cod populations. These wrong decisions can have large implications for the ecological systems and the people that depend on these ecosystems for their food supply or their income.

Phenological changes also influence the species monitoring and evaluation programs that determine the ecological impact of agriculture, forestry, and fisheries. These programs analyse the status and development of populations of the (endangered) species in the area. These monitoring activities often take place during a limited amount of time and within a defined area. Phenological changes might require a change in the timing of monitoring activities to prevent drawing wrong conclusions on, for example, the impact of production activities. Especially rare species that have a migratory or dormant behaviour might be more difficult to find if they appear earlier or later than they usually did. Therefore, the many stakeholders involved should recognize that natural ecosystems as well as agriculture, forestry and fisheries undergo large-scale changes. Decisions on regulations and restrictions should take these (potential) changes into account.

### ***4.2.2 Public Health***

Patz et al. (2005) concluded that there is growing evidence that climate – health relationships pose increasing health risks under future projections of climate change. The warming trend over recent decades has already contributed to increased morbidity and mortality in many regions of the world ranging from cardiovascular mortality and respiratory illnesses due to heat waves, to altered transmission of infectious diseases and malnutrition from crop failures. These conclusions were supported by the Fourth Assessment Report of the IPCC. The IPCC concluded, with very high confidence, that climate change currently contributes to the global burden of disease and premature deaths (Confalonieri et al. 2007). There are numerous ways in which climate change influences public health ranging from the direct impact of extreme events such as heat waves and drought, increases in malnutrition by impacts on agriculture and fisheries, to changes in vector-borne disease. In this section I focus only on public health impacts via phenological changes of plants and insects.

Phenological changes of species that cause morbidity and mortality or of species that determine the survival of the harmful species will change the start and duration of the period during which people are exposed to these health risks. A change in geographic distribution of the harmful species due to these phenological changes will change the area where people are exposed to the risks. Furthermore, the amount of exposure of people to health risks is likely to change due to phenological changes. As Confalonieri et al. (2007) concluded the emerging evidence of climate change

effects on public health shows that climate change has altered the distribution of some infectious disease vectors (medium confidence) and altered the seasonal distribution of some allergenic pollen species (high confidence), I focus on these two subjects.

#### 4.2.2.1 Hay Fever

Hay fever or Seasonal Allergic Rhinitis (SAR) is caused by allergens that are attached to pollen of certain plants that have airborne pollen (e.g. grasses, Birch, Alder and Hazel). Contact with pollen by hay fever patients results in a diversity of allergic reactions. The prevalence of allergy has strongly increased in the last decades and constitutes a major cause of hospitalization (Strachan 1989, Aberg et al. 1995, Wuthrich et al. 1995, Gupta et al. 2003). Hay fever is associated with considerable direct and indirect costs that result from medical treatment and the loss of school and working days. In Europe alone, the total annual cost for allergic rhinitis is estimated at 3 billion Euro (UCB Institute of Allergy 2004), while the estimates for the USA amount to 4.9 billion dollars (Schoenwetter et al. 2004).

##### Expected and Observed Phenological Impacts

In Section 4.1 I showed that the timing of flowering is changing in response to changes in climate. Consequently, climate change alters the timing of the start of pollen release and thus the start of hay fever complaints. An increasing number of studies has shown that recent increases in temperature have advanced the start of the pollen season (D'Amato et al. 2002, D'Odorico et al. 2002, Emberlin et al. 2002, van Vliet et al. 2002, Huynen et al. 2003, Beggs 2004, Ziska et al. 2007). It is still unclear what the impact of climate change will be on the length and the intensity of the pollen season but it is likely that future changes in climate will change the start, duration and intensity of the pollen season.

##### Adaptation Options

Hay fever patients are obvious stakeholders that need to adapt to shifts in the start and duration of the pollen season. Adaptation is relatively simple, for most, as they 'only' need to adjust the timing of their medicine intake. This is especially the case for patients that use medicines like topical steroids have to be aware of the phenological changes. These medicines only have a maximum effect if medicine use starts several days to several weeks before the complaints are expected (van Cauwenberge et al. 2000). However, patients that use medicines as soon as the pollen season start have to have their medicines available in time.

Diagnosing hay fever by family doctors and medical specialists becomes more complex if the hay fever season occurs at times that the doctors have not experienced before. In general, hay fever symptoms are difficult to interpret and can be confused with symptoms caused by other diseases. The changing flowering times might increase the improper diagnosis and may result in higher costs for health care, especially in cases when hay fever triggers the development of allergic asthma (Bousquet et al. 2003, Schramm et al. 2003). Therefore, doctors need to be aware of the changes



in start of the pollen season. Furthermore, they have to adapt their planning of when they can expect hay fever patients to consult them about their symptoms. As many people suffer from hay fever, the number of consultations might increase, as patients are experiencing symptoms outside the period they would normally associate with hay fever.

A change in the timing of hay fever symptoms and doctor consultations will also influence the planning of the pharmaceutical and diagnostic industry. They will have to adjust the timing of the production, distribution and promotion of medicines and diagnostic tests. Analysis of the sales of medicines illustrates the relevance of this process. In the week of the start of the Birch pollen season in The Netherlands in the period 2001–2005 an average of 2.1 million Euro worth of hay fever medicines were sold by pharmacies (Based on data obtained from Stichting Farmaceutische Kengetallen in 2006).

Adaptation to the changes in timing of the hay fever season is possible if all stakeholders are informed in time by the pollen information service providers. The start and duration of this communication period will have to change according to the changes in the timing of the pollen season. Furthermore, the pollen monitoring stations that monitor pollen only during a selected period of the year have to change their counting schedule in order to cover the total pollen period. To improve the hay fever forecasts scientists have to improve their knowledge on when and where pollen are produced under changed climatic conditions, how the pollen are transported through the atmosphere and how patients respond to the pollen.

#### **4.2.2.2 Vector-Borne Diseases**

Vector-borne diseases like malaria, Lyme disease, dengue and yellow fever are infections transmitted by the bite of infected arthropod species such as mosquitoes, ticks, and blackflies. Vector-borne diseases are very important health issues globally, affecting billions of people (McMichael and Githeko 2001). Although vector-borne diseases are considered to be a large health problem, still a lot is unknown about the very complex ecological processes, the interaction with all kinds of global changes (including climate change, land use/cover change) and the proper response strategies (Sutherst 2004).

#### **Expected and Observed Phenological Impacts**

According to Dobson and Carper (1993) many factors relevant to the transmission of vector-borne pathogens are highly temperature-dependent. For the invertebrate vector, these include: spatial distribution, development and survivorship rates, and length of the gonotrophic cycle (time between blood meals). For the pathogen itself, temperature affects both the extrinsic incubation period (time from infection of vector to transmission of pathogen) and transmission rates. Phenological changes of the vectors that transmit the diseases are likely to have a large influence on the occurrence of vectors (like mosquitoes) and the parasites/pathogens in time and space (Kovats et al. 2001, Harvell et al. 2002, Hunter 2003, Sutherst 2004, Kutz et al. 2005, Patz et al. 2005). Most direct evidence of observed climate change impacts come from observed changes in geographic distribution of the vectors (Epstein et al.

1998, Epstein 2001, Confalonieri et al. 2007). Evidence for observed phenological changes of vectors is scarce. However, many studies have shown that higher temperatures increase the development speed of the vectors as well as the parasites (Rueda et al. 1990, Dobson and Carper 1993, Cox et al. 1999, Epstein 2000).

### Adaptation Options

Because of the very large socio-economic impacts of vector-borne diseases, many organisations try to reduce the problem. Addressing the problems requires actions at many different levels including improving surveillance and response capability, drug and vaccine development, and greater provision of clinical care and public health services and an improved prediction (Epstein 2001).

Most work has been done on malaria. The World Health Organisation is coordinating the Global Malaria Program (GMP). GMP is responsible for malaria surveillance, monitoring and evaluation, policy and strategy formulation, technical assistance, and coordination of WHO's global efforts to fight malaria (WHO 2008). Several components of the response strategies deal with a proper timing of activities and thus with the phenology of the vectors. The World Malaria Report (WHO/UNICEF 2005) states that improved early warning, detection and response to malaria epidemics are necessary to avert catastrophe. The likelihood of an individual becoming infected with malaria is dependent on exposure of the individual to infective mosquitoes and the number of available infective mosquitoes to bite individuals (Thomson and Connor 2001). As the development of mosquitoes and their activity depend on weather conditions, there is a seasonality in the infection risk with distinctive peaks (Cox et al. 1999, Abeku et al. 2003). Furthermore, the survival from malaria is determined by the patient's personal vulnerability (e.g. low immunity and malnutrition) and early diagnosis and prompt treatment with effective anti-malarial drugs (Thomson and Connor 2001). Therefore, the medical sector as well as the public should be informed and prepare themselves in time in order to respond to increased risks and increased demands for health care. Several countries in the Southern African Development Community (SADC) aim to improve their epidemic detection and response, that is 60% of epidemics should be detected within two weeks of onset, and 60% of epidemics should be responded to within two weeks of detection. The SADC countries recognize that to achieve these targets they need improved information on where and when to look for epidemics (DaSilva et al. 2004). They use the Malaria Early Warning System (MEWS) framework as set out by WHO (WHO 2004). The MEWS consists of four components: (1) vulnerability monitoring, (2) seasonal climate forecasting, (3) environmental monitoring, and (4) sentinel case surveillance. According to Epstein (2001) integrating health surveillance into long-term terrestrial and marine monitoring programs, 'ecological epidemiology', can benefit from advances in satellite imaging and climate forecasts that complement fieldwork. Health early warning systems based on the integrated mapping of conditions, consequences and costs can facilitate timely, environmentally friendly public health interventions and inform policies (Epstein 2001). Thomson et al. (2006) have demonstrated that probabilistic seasonal climate

forecasts with the use of multi-model ensemble climate predictions can be used to predict malaria incidence at least five months before the peak malaria season. However, although the potential benefits of these models in terms of improved management of epidemics are clear, several technical and practical hurdles still need to be overcome before the models can be widely integrated into routine malaria-control strategies (Cox and Abeku 2007).

The magnitude of the challenge that the global community is facing is enormous as hundreds of millions of people that live in or travel to areas where vector-borne diseases occur have to be aware of the temporal and spatial changes in the occurrence of vector-borne diseases. Even without climate-induced changes in phenology and distribution this is already a challenge. The public has to take measures to recognise the disease in time and take correct medication or protection measures to reduce the risk of being infected. Family doctors, medical experts and Area Health Authorities should improve the early diagnoses and treatment of the vector-borne diseases to prevent or reduce health problems. They can also educate the public on how to recognize symptoms of the disease and on prevention measures. Governmental organisations from the local to the national level play a role in informing the public and experts. Governments should set up monitoring and research programs and organise disease control. Often cooperation is needed with land owners, nature conservation organisations, natural resource managers and water managers to control the vectors. Travel agencies and tourist offices have the responsibility to inform millions of people that travel to areas where there is a risk for vector-borne diseases. Scientists have to be aware of the phenological changes that (will) take place and include those processes in their models. Proper analyses and prediction of the phenological changes and the associated health risks, requires the involvement of many different scientific disciplines ranging from biologists, meteorologists, sociologists and economists. Furthermore, monitoring of changes in timing and population sizes of both the vectors and the diseases is important for improving research and communication activities.

### **4.3 Successful Adaptation Requires Answers to Four Questions**

The previous two sections illustrated that phenological changes can have very large socio-economic consequences by impacting the quantity and quality of primary productivity and by influencing public health. However, estimates of the total cost or estimates of the amount of morbidity and mortality are not available. This lack of knowledge hampers the creation of a sense of urgency to adapt. It causes a lack of awareness of the problems and of the need for adaptive response strategies. The previous sections also made clear that within each sector a large number of stakeholders have to deal with the consequences of phenological changes. Within agriculture, for example, it is not only the farmers that (have to) respond to an earlier start of the growing season but also many organisations that supply farmers, the organisations that process the agricultural products, and (non-)

governmental organisations that issue restrictions and regulations to control the agricultural production processes. Because phenological dynamics are fundamental processes of ecosystems, all individuals within the various stakeholder groups are confronted with the changes counting up to hundreds of millions of people world-wide.

As adaptation to phenological changes mainly consists of changing the timing of activities and changing crop varieties, many stakeholders should be able to adapt in time if they can find answers to the following questions:

1. What phenological events will happen when and where under different climate change scenarios in the short and long term?
2. What will be the socio-economic and environmental impact of these changes (with and without adaptation) under different climate change scenarios?
3. Who should do what and when to reduce impacts or to benefit from the phenological changes in the short and long term?
4. What tools, technologies, knowledge, data and institutions are available to assist in the adaptation process?

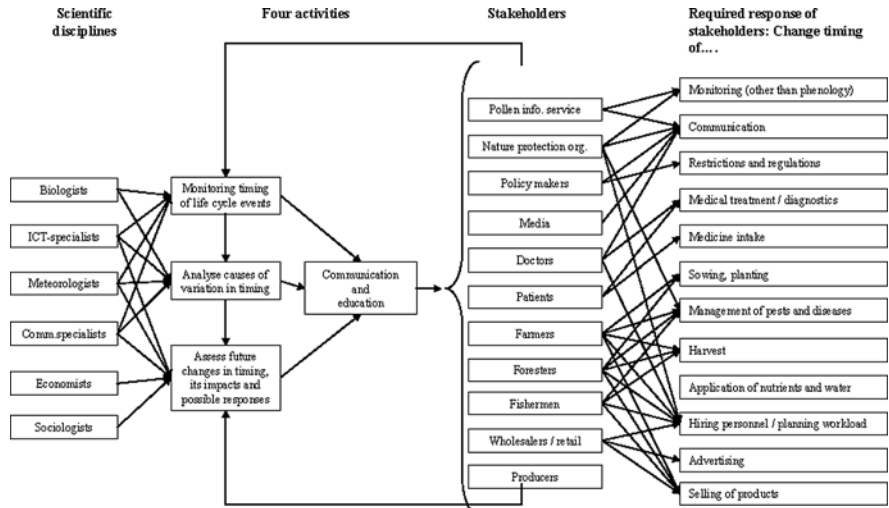
Unfortunately, the ability of stakeholders to adapt to phenological changes is still very limited because the answers to these four questions are often unknown. Consequently, to pro-actively adapt, stakeholders require a lot of information that is often not available or not available at the right time at the right place. Therefore, unless the information is provided, society continues to adapt autonomously to the ongoing phenological changes and is likely to do so in response to the expected future changes.

#### **4.4 Contribution of Phenological Networks to the Adaptation Process**

Based on my analyses I conclude that four types of activities are required to allow adaptation to climate-induced phenological changes:

1. Monitoring the timing of life cycle events;
2. Analysing the causes of phenological changes and the socio-economic and environmental impacts;
3. Assessing the potential future phenological changes and the socio-economic and environmental consequences;
4. Communicating the knowledge, tools and methodologies to the stakeholders.

Phenological networks should take the lead in organising these activities as they are most aware of the ongoing phenological changes. Figure 4.3 gives a schematic overview of the required four activities, the scientific disciplines to involve, the stakeholders and the required response of the various stakeholders in the whole adaptation process. However, to really help stakeholders or society to adapt, phenological networks will have to develop and improve their methodologies and



**Fig. 4.3** Schematic overview of the required activities, the scientific disciplines involved, the stakeholders and the required response of these stakeholders in the adaptation process. The arrows indicate the direction of the flow of knowledge and data

techniques and have to broaden their scope. The following sections present a number of required developments that can facilitate the adaptation process.

### 4.4.1 Phenological Monitoring

Many phenological networks have already monitored for decades and even centuries (Schwartz 2003). These long-term series are crucial for showing the variability and changes in timing of life cycle events in the past. To improve the adaptive capacity of society, phenological monitoring networks need to:

(a) *Continue existing monitoring programs*: The expected future large changes in climate will result in phenological responses that have not been seen before. Therefore, phenological networks should continue existing long-term phenological monitoring programs. With these data the phenological models can continuously be validated, calibrated and updated.

(b) *Expand and create networks*: In those areas where no phenological observations are carried out networks should be established. This can be done by expansion of neighbouring networks or by the creation of new ones. With the new ICT-technologies the costs for setting up and for management of the networks, like submission, storage and visualization of phenological observations, could be kept relatively low.

(c) *Increase socio-economic relevance*: Phenological networks should include more species and phenophases that have a clear socio-economic relevance. Examples are plants that cause hay fever or animals that are vectors for diseases

(e.g. ticks). The inclusion of these species will increase the socio-economic relevance of phenological networks, the interest of public and media in the results of the network, and will increase the support the funding of these networks. Sector representatives and phenologists should select the relevant species together.

*(d) Increase the spatial detail:* The level of spatial detail of phenological observations and information required for successful adaptation varies between stakeholders. In many cases the more observations the better as this decreases the uncertainty and provides more spatial detail and a better overview of the variability between individuals within a species. In addition to broadening the scope of the analysis to society, the various actors in society will improve their adaptive capacity if the science of phenology focuses more on improving the spatial analysis and detail; for example by realizing a better integration between remote sensing and in situ observations or by implementing new technologies concerning Geographic Information Systems.

*(e) Increase the number of species and species groups monitored:* Many phenological networks only focus on one or a few species groups. As different species groups have different responses to climate changes, having information of as many groups as possible improves our understanding of possible climate change induced changes in ecosystems.

*(f) Standardise and link networks:* In order to better interpret the observations and internationally compare phenological changes, the ongoing efforts to standardise and link existing phenological networks as in the context of the European Phenology Network (van Vliet et al. 2003b), the COST725 program (Koch et al. 2005, Menzel et al. 2006), and the National Phenology Network of the United States (Betancourt et al. 2007) should be intensified. In this standardisation process the integration of field observations and remote sensing data should be stimulated (Fisher and Mustard 2007).

#### **4.4.2 Phenological Analysis**

Phenological observations have provided the basis for the analysis of how climate variability and climate change influence the timing of life cycle events at various spatial and temporal scales. The number of published phenological studies has increased rapidly over the last years as it became clear that phenological changes could be used as climate change impact indicators. Although our knowledge on the relation between climate and timing of phenological events has increased, a lot is still unknown. Therefore, phenological networks need to:

*(a) Assess the relationship between timing and climatological and environmental variables:* Most phenological studies focus on describing trends in the timing of life cycle events in response to climate change. They try to determine which climate variables can explain the variation in timing. These studies have demonstrated that the timing of life cycle events is strongly determined by climate variables (see Section 4.1). Future studies should continue and expand these analyses. Important

issues to address are the impact of climate extremes as the climate extremes are expected to become larger. Also the role of changes in nutrients and carbon dioxide levels on the timing of life cycle events may be of interest. For models which determine the timing of phenological events to remain valid then need to be refined as new information becomes available.

(b) *Assess socio-economic consequences of phenological changes:* To increase the awareness and the sense of urgency of stakeholders to adapt it is important to quantify the consequences of phenological variability and change on ecosystems and society. These analyses should include the (required) response of the various stakeholders within each sector such as patients, family doctors and the private sector. These analyses will increase the socio-economic relevance of phenological networks and require the involvement of scientific disciplines in the sociological, economical and technological domains.

### 4.4.3 Assess Future Changes

Knowing what will happen when and where is crucial in any adaptation strategy. To answer these questions phenological networks need to:

(a) *Assess the timing of life cycle events in the future:* There is a growing need for studies that focus on assessing or predicting when phenological events will take place. These studies require the combination of phenological models developed with weather forecasts and climate change scenarios. The various stakeholders will likely have different wishes concerning the temporal and spatial resolution of the predictions. Hay fever patients are interested in knowing what will happen in the coming days in the area where they work and live. Governments and farmers that want to protect meadow birds require assessments for the coming weeks and months at regional or national level while ecosystem modellers require assessments for the coming decades at various spatial levels. For the short-term, phenological forecasts and phenological models should be combined with (seasonal) weather forecasts. For long-term assessments a variety of climate change scenarios are available. In these assessments it is important to not only consider the projected changes in average temperature but also to look at the weather and climate extremes. These assessments should also have uncertainty analyses undertaken so stakeholders can be informed on the range and risk for certain events.

(b) *Set up field and laboratory experiments:* Making projections for the future based on historic observations can cause uncertainties as it is unknown how species respond to climate conditions that they have never experienced before. To obtain better insight in the potential phenological response and the biological consequences of the response, it is essential to carry out field and/or laboratory experiments in which several climatological and environmental characteristics can be manipulated.

(c) *Assess future socio-economic and environmental impacts:* The willingness to take adaptive actions depends on the magnitude of the socio-economic and environmental impacts that are likely to take place. Phenological networks should

try to quantify these impacts by integrating phenological models with socio-economic and environmental models in combination with short-term and long-term scenarios.

#### **4.4.4 Communication**

Monitoring, analysis and assessment of phenological changes, as well as active adaptation to the observed or expected future phenological changes, requires the involvement of a wide variety of stakeholders in many sectors (See Fig. 4.3). The willingness to support, participate and/or invest in these activities increases if people are aware of the importance of the issue, if they know what they can do, what tools, data and techniques they can use and if they know what people or organisations they should or could cooperate with. Realizing all this requires successful communication to and with the stakeholders. Phenological networks can improve communication if they:

(a) *Develop online information systems to gather and visualize phenological observations, analyses and forecasts:* A core business of phenological networks is the monitoring of the timing of life cycle events. Each observation contains the date and location of the observation, the species and the phenophase. Observations are brought together for analysis. To keep the observers motivated to continue the observations they need to be regularly informed about the results. Gathering, digitizing and communicating the observations used to be a labour intensive work. However, since the late twentieth century many new ICT-technologies became widely available. Several phenological networks started to build interactive websites via which volunteers could upload their observations directly into a database. With Geographic Information Systems and tools such as Google Maps it became easier for observers to add the coordinates of observations. As the observations are directly available in a database the same information systems could directly visualize all observations (see e.g. the UK network at [www.phenology.uk.org](http://www.phenology.uk.org) and the Dutch network at [www.natuurkalender.nl](http://www.natuurkalender.nl)). Many improvements are foreseen in the development of these systems in combination with mobile communication tools.

(b) *Focus on the socio-economic and environmental relevance of phenological changes and cooperate with stakeholders:* Increasing the sense of urgency and raising awareness is only effective if the public knows how phenological changes impact their own environment and preferably their own life. Therefore, it is important to increase the socio-economic and environmental relevance of phenological changes and try to quantify the impacts as much as possible. Including information on where (geographically) and when the impacts will occur will increase the success of communication. Therefore, involving stakeholders in the monitoring, research, communication and adaptation activities is crucial. This, however, implies that cooperation is needed between many people from different sectors, disciplines and regions. Cooperation is a challenge as each group has its own ‘language’, network and way of working. Phenological networks like the Nature’s Calendar network in the Netherlands demonstrate that cooperation between scientists, the media, the private sector, the general public, NGOs, (ICT-) technicians and sector



representatives such as medical specialists, farmers and foresters is possible. The cooperation in The Netherlands has provided a lot of data, tools and methods, facilitating adaptation in public health, agriculture, natural resource management and gardening. However, successful cooperation requires time, an open attitude to other tools, methods and habits that people are not familiar with.

(c) *Involve media in the communication:* As phenological information is relevant for millions of people it is a challenge how to reach all these people with the available resources. Building an interesting and interactive website alone is not enough. The only option is to involve (mass) media in the communication. The recent phenological changes have attracted a lot of attention especially from the media in countries all over the world. The media were and remained interested because they wanted to visualize climate change impacts. In the past years phenological changes have become one of the best indicators of ecological effects of climate change. They are good indicators as there is a clear link between the variation in timing and climate. Furthermore, long-term phenological monitoring networks exist which enable the quantification of the changes. Finally, phenological changes are easily visible in everyone's 'backyard'. With all the attention, phenological networks have been able to drive home the messages about climate change (Whitfield 2001, Marris 2007). The experiences of the Dutch phenological network Nature's Calendar show that there is a large potential to communicate via the media. The activities of the Nature's Calendar network have resulted in hundreds of newspaper articles and numerous interviews for radio and television programs. Journalists were mainly triggered by the visible phenological changes caused by the many climate extremes in The Netherlands. Secondly, by involving farmers and medical specialists in their consortium The Nature's Calendar network was better able to quantify and visualize how public health and agricultural production were impacted by phenological changes. With the media attention the consortium was able to significantly increase society's awareness on the phenological changes that were (and continue) to take place and its impacts. Furthermore, the publicity resulted in thousands of volunteer observers and many new contacts with sector representatives. These contacts provide a whole range of new ideas, funds, and opportunities for active adaptation in the future.

In the future, phenological networks have to broaden their scope of communication and target it towards specific groups in society for which the information on impacts is relevant. The way of communication should be comparable to the way weather forecasts are made and communicated. Weather forecasts are everywhere and their focus ranges from the general public to specific target groups. The main questions addressed in these weather forecasts are: what were, are, and will be the weather conditions at different locations? In a similar way phenological reports can be made and communicated. Because of the clear dependence of the timing of phenological processes on weather conditions, a direct link with the weather forecasts should be considered. If phenological networks are able to communicate like the weather forecasts they will have the ability to continuously inform the public and specific stakeholders. With this information society will be better able to pro-actively adapt to climatic change induced phenological changes.

## 4.5 Conclusions

The IPCC (Schneider et al. 2007) concludes that market and social systems have a considerable adaptation potential but that the economic costs are potentially large, largely unknown and unequally distributed, as is the adaptation potential itself. In this chapter I showed that the timing of phenological events, such as the start of flowering, immediately follows changes in climate. These changes are evident in all species groups throughout the whole year and in all parts of the world. The phenological conditions that society will be confronted with over the coming decades will be unprecedented. Society has not experienced such a rapid change during the last centuries.

In this chapter I provided a qualitative overview of how phenological changes will strongly influence human well-being through changes in primary production sectors depending on natural productivity and the public health sector. Farmers, foresters, fishers, commercial enterprises, patients, doctors and policy makers have to adapt pro-actively to cope with, prevent or reduce potential negative impacts. Adaptation should be relatively easy in most cases because people have to ‘only’ change the timing of their activities. However, pro-active adaptation is currently often unfeasible because stakeholders do not know what phenological changes will happen where and when. They also are not aware of the ecological and socio-economic consequences of such phenological changes. They seem to miss a sense of urgency to act. Furthermore, they miss an understanding on whether, how and when to respond in order to prevent (further) negative impacts or to benefit from the emerging changes.

To adequately respond to phenological change and to improve the adaptation potential, there is a need to (1) continue and improve monitoring of phenological changes; (2) advance the analysis of phenological changes and its socio-economic and environmental impact; (3) improve the projections of phenological changes and their impacts; and (4) improve the communication on observations, knowledge, tools and techniques. Successful adaptation can only take place if all four activities are addressed simultaneously. Phenological networks should take the lead in all these four activities. They should, however, work closely together with major stakeholders, including scientists and medical specialists, the media, the private sector, the general public, NGOs, farmers, foresters, fishers and physicians (and their patients).

As phenological events are a fundamental characteristic of biological systems everywhere, tools and methods developed for monitoring, analyses, assessment and communication by one phenological network can be relatively easily transferred to other regions and countries. International organisations such as the International Society of Biometeorology have enabled this exchange of information and the cooperation between phenologists and stakeholders from all over the world. The need for adaptation to phenological changes requires the continuous efforts and support of these international networks to stimulate the required cooperation.

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## Chapter 5

# The Influence of Sampling Method, Sample Size, and Frequency of Observations on Plant Phenological Patterns and Interpretation in Tropical Forest Trees

L. Patricia C. Morellato, Maria Gabriela G. Camargo, Fernanda F. D'Eça Neves, Bruno G. Luize, Adelar Mantovani, and Irene L. Hudson

**Abstract** The research field of plant phenology, which often involves the monitoring of several to hundreds of species of different life forms and/or different vegetation types, has increased exponentially over the last three decades. This has occurred in general, without consideration of the comparability of data and patterns across areas, and its influence on the interpretation of resultant patterns. In this chapter we address the influence of sampling method, sample size and the frequency of observations on the analysis of tropical tree phenology. Our approach is to compare the results of direct observations on transects with those obtained from litter traps. Transects and litter traps are the two most common methods used to sample and monitor plant phenology. Data from 3 locations were used to simulate different sample sizes and frequencies, and results were then compared with the original data. We conclude that sample size influences the patterns observed and there is a clear trade off between sample size and the frequency of observations. We show that direct observations were more accurate in defining both the beginning and the peak of phenological phases, and there was a significant difference between the peaks and seasonal patterns detected by both sampling methods. For tropical tree forest applications we recommend a minimum sample size of 15 trees and that a fortnightly frequency of observation be used especially if the sample size is small. We advocate the combination of presence/absence data and a quantification method to estimate plant phenology, a careful application of indices and a cautious generalization of pattern.

**Keywords** Frequency of observations · Phenological methods · Sample size · Tree phenology · Tropical trees

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## 5.1 Introduction

Phenological studies address the timing of recurring biological events. For plants, these involve reproductive events such as bud formation and flowering, fruiting, and seed germination, along with vegetative processes like leaf flushing and shedding. The influence of sampling method, sample size and the frequency of observations on the analysis and interpretation of plant phenology has been addressed only occasionally in the phenological literature (Fournier and Carpentier 1975, Chapman et al. 1992, 1994, Hemingway and Overdorff 1999, D'Eça Neves and Morellato 2004). Most of the efforts towards a common position on plant phenology have considered better definition of phenophases, provision of greater precision and accuracy for data collected across phenological networks and phenological stations (Brügger et al. 2003, Meier 2003, COST 725 (2008) and see Schwartz 2003 for additional references). When we consider tropical phenology, which is less traditional and deals with a high diversity of species and complex ecosystems (Frankie et al. 1974, Newstrom 1994a, Sakai 2001, Morellato 2003) the lack of a coherent set of sampling rules and methods, if not analytic methods and procedures, is even more evident. Among the few studies dealing with methods for data collection and observation are the papers by Fournier and collaborator, suggesting an observation method to quantify plant phenology (Fournier 1974), and discussing the sample size and frequency of observations for tropical trees (Fournier and Charpentier 1975). Alternatively, Newstrom et al. (1994b) proposed a classification system to describe phenological patterns for tropical forest tree flowering, considering variables such as timing, frequency and amplitude. Newstrom's et al. (1994b) system however could be applied to recurrent events in plants and animals from any part of the world (Newstrom et al. 1994a, 1994b).

Field research on plant phenology, which may involve the monitoring of several to hundreds of species from different life forms and vegetation types, has increased exponentially over the last three decades (Morellato 2003, Schwartz 2003). This has occurred without consideration of the comparability of data and patterns across areas, and often based upon the given study's research objectives only, not taking into account the influence of methodology on the interpretations of the resultant patterns (Schirone et al. 1990, Chapman et al. 1994, Newstrom et al. 1994a, 1994b, Mac Dade and Morellato 1998). The best discussion in the recent literature dealing with comparisons among methods focus on the estimation of fruit production (e.g. Chapman et al. 1994, Greene and Johnson 1994, Zhang and Wang 1995, Stevenson et al. 1998). Of particular relevance is the study of D'Eça-Neves and Morellato (2004) who performed a survey of studies on tropical forest phenology, compiling information about sampling and estimation methods of tropical forest phenology, discussing their proportion of occurrence and applicability. Methods surveyed were grouped by type and time (decade), and the authors discussed their proportion of occurrence and applicability. D'Eça-Neves and Morellato (2004) state that the lack of standardized procedures or the use of some common techniques for sampling and estimation in plant phenology persists, and suggest the application of transects as a sampling technique and the combination of qualitative or presence/absence and quantitative or semi-quantitative methods to estimate plant phenology.



Although the choice of methods is closely linked to the study's goals and questions (Galetti et al. 2003), the increasing importance of plant phenology in monitoring and detecting climate change demands a more general and comparable collection of methods to be applied to plant phenology studies. The use of different methods has made it difficult to make comparisons across the different phenological studies, especially in the tropics. We note, however, that analytic methodological differences have been less problematic in various meta analytic studies seeking to find so-called phenological fingerprints of global climate change for temperate systems (Parmesan and Yohe 2003, Root et al. 2003, Root et al. 2005, Menzel et al. 2006, Parmesan 2007, Rosenzweig et al. 2008, Chapter 21). What has, however, been recently discussed is the need for the phenological community to reach a consensus on inclusion criterion for studies selected for these meta analytic studies. Criteria which also pertain to sampling and observation frequency, that is length of observations (length of the time series) and also selection criteria of studies to be included in the synthetic analysis, based on whether a reported neutral, negative or positive result was exhibited in regard to climate change impact on phenology (see Chapter 21). Indeed, Hemingway and Overdorff (1999) also recognize that whilst the method used to collect phenological data can affect the resultant pattern, these underlying influences and potential methodological biases have not been formally examined to date. There are some similar approaches between this chapter and Hemingway and Overdorff's (1999) study, in which they also investigated the effects of phenological method (selected tree observations and systematic transect monitoring), sample size and species composition on phenological patterns, however using data collected to estimate food availability for three of primate species in Ranomafana National Park, Madagascar. They found an effect just of species composition.

While not wishing to constrain creativity or to promote so-called formulaic research, the discussion of phenological measurements and data recording may allow us to improve data accuracy and help us achieve some comparability among data sets across sites. In this chapter we address the influence of sampling method, sample size and the frequency of observations on the analyses of tropical tree phenology. We tackle this question using three different approaches. Firstly, we examine the sample size and frequency of observations based on the monitoring of a set of trees planted in gardens, thereby we can control for age and environmental heterogeneity. Secondly, we evaluate the effect of sample size using trees sampled in the field, under natural conditions, where we cannot control for age and environmental heterogeneity. Lastly, we address the influence of sampling and estimation methods, comparing direct observations on transects with litter traps. These are the two most common methods used to sample and monitor plant phenology, especially in highly diverse tropical forests (D'Eça Neves and Morellato 2004). We conclude that sample size influences the patterns observed and that there is a trade-off between sample size and the frequency of observations. The direct observations were more accurate in defining the commencement and the peak of phenological phases than traps, and there was a significant difference between the peaks and seasonal patterns detected by both methods. We make this proviso, however, that, traps can be a reliable way to quantify plant phenology, an important feature when

resource availability is the main concern, even if some information is missing for those species dispersed by animals.

## 5.2 Methods

### 5.2.1 Frequency of Observations

We analyzed the phenology of trees from the campus of UNESP – Universidade Estadual Paulista, at Rio Claro, São Paulo State, Brazil (22° 24'36'' S 47° 33' 36''), hereafter referred to just as Campus. The trees were planted from seedlings of known origin, at the same time, were evenly spaced, in square plots along the main entrance of the University campus, under plain light. Under these conditions we minimize the influence of age, size, climate, soil and competition with different species, on the trees' phenology, making our assumptions more precise. When the observations began, in 2001, they were all mature, reproductive trees, at least 15 years old. We present data for three species, representative of the larger number of trees *Tabebuia roseoalba* (Ridl.) Sandw. – Bignoniaceae (n = 21 individuals), *Tecoma stans* (L.) Jussieu ex. Kunth – Bignoniaceae (n = 17) and *Erythrina speciosa* Andrews – Fabaceae (n = 18), observed weekly from August 2002 to August 2004.

### 5.2.2 Sample Size

To verify the influence of sample size we analyzed the phenology of trees from the Campus (described above) and of trees under natural conditions, from two native vegetation types: a semi deciduous altitudinal forest at Serra do Japi, Jundiá, São Paulo State (23° 13' S 46° 52' W), and from the savanna cerrado vegetation at Itirapina, São Paulo State (22°13'S 47°53'W), hereafter referred to as Forest and Cerrado, respectively, Southeastern Brazil. The two sites are around 130 and 60 km from the Campus site, respectively. All Forest and Cerrado trees were sampled using transects (D'Eça Neves and Morellato 2004) and were observed at monthly intervals. The study sites (Campus, Forest and Cerrado) are under a seasonal climate, with a dry and cold season from April to September and a wet and warm season from October to March (Morellato et al. 1989, Camargo et al. unpubl. data). Detailed information on site description and phenological sampling are found elsewhere (D'Eça Neves and Morellato 2004, Reys 2008, Morellato et al. 1989). We analyzed the phenology of the four most abundant Forest species: *Callisthene minor* Mart. – Vochysyaceae (n = 48 individuals); *Cupania vernalis* Cambess. – Sapindaceae (n = 17); *Lapacea semiserrata* Cambess. – Theaceae (n = 18); *Pera glabrata* (Schott) Poepp. ex Baill. – Euphorbiaceae (n = 23) and *Matayba juglandifolia* (Camb.) Radlk. – Sapindaceae (n = 25), observed monthly from January 1999 to May 2000. The Cerrado trees selected for analyses presented the largest number of individuals (n = 90) per species, and were observed monthly from September

**Table 5.1** Place of occurrence, frequency of observations and sample size (n) of analysed species

Place	Frequency	Family	Species	n
Campus	Weekly	Bignoniaceae	<i>Tabebuia roseoalba</i> (Ridl.) Sandw.	21
			<i>Tecoma stans</i> (L.) Jussieu ex. Kunth	17
Forest	Monthly	Fabaceae	<i>Erythrina speciosa</i> Andrews	18
		Euphorbiaceae	<i>Pera glabrata</i> (Schott) Poepp. ex Baill.	23
		Sapindaceae	<i>Cupania vernalis</i> Cambess.	17
			<i>Matayba juglandifolia</i> (Camb.) Radlk.	25
			<i>Laplacea semiserrata</i> Cambess.	18
Cerrado	Monthly	Vochysiaceae	<i>Callisthene minor</i> Mart.	48
		Annonaceae	<i>Xylopia aromatica</i> Mart.	90
		Melastomataceae	<i>Miconia rubiginosa</i> (Bonpl.) DC.	90
			Myrtaceae	<i>Myrcia guianensis</i> (Aubl.) DC.

2004 to January 2007: *Miconia rubiginosa* (Bonpl.) DC. –Melastomataceae, *Myrcia guianensis* (Aubl.) DC. – Myrtaceae, and *Xylopia aromatica* Mart. – Annonaceae (Table 5.1).

### 5.2.3 Comparison of Sampling And Estimation Methods

The study was carried out in the semi deciduous altitudinal forest of Serra do Japi, the Forest site described above. We compared the two most common sampling methods used in the study of tropical forest tree phenology: transects and traps (D’Eça Neves and Morellato 2004). We sampled the trees on five transects of 100 × 2 m each, randomly plotted parallel to the 3.5–4.5 m trail crossing the forest, at 15 m from the edge. All trees with diameter at breast height >5 cm (reproductive trees, Morellato et al. 1989) were sampled, measured and marked with aluminum tags. Along each transect six square traps of 0.5 × 0.5 m were randomly set, in such a way that two or more litter traps could not fall below the canopy of the same trees species (Morellato 1992). The material from the litter traps were collected at the same time that the phenological observations were performed, dried to 80°C, and sorted out into flower buds, flowers, unripe fruits and ripe fruits (plus seeds), identified to species level and weighed (see D’Eça Neves and Morellato 2004, for detailed site and method descriptions). The phenological observations and the trap collections were both carried out monthly, from January 1999 to May 2001.

### 5.2.4 Phenological Observations

For all three sites, to estimate the intensity of each phenological event, we attributed a score from 0 to 4, as follows: 0 = 0 or no activity, 1 = 1–25%, 2 = 26–50%, 3 = 51–75% and 4 = 76–100% of tree branches were in any phenophase, according to

the method proposed by Fournier (1974). This approach allows us to estimate the Fournier Index (FI) of intensity described below, as well as the proportion of trees presenting each observed phase or estimate the Activity Index (AI) (Bencke and Morellato 2002). We observed six reproductive phases: (i) flower buds, (ii) open flowers, anthesis or flowering itself, (iii) unripe fruits, (iv) ripe fruits or fruiting itself, and the vegetative phases of (v) leaf fall and (vi) leaf flush or new leaves, as defined in Morellato et al. (2000).

All data presented here were collected by the authors and are part of the long-term phenological studies developed by the Phenology Laboratory, at the Botany Department, UNESP – Rio Claro. They are stored in the Phenology Laboratory Data Bank and are available upon request to the corresponding author.

### 5.2.5 Data Analyses

The scores attributed to each tree according to the semi-quantitative scale of Fournier were transformed into the species percentage Intensity of Fournier Index or %FI, calculated for each date of observation, according to the formula (Fournier 1974):

$$\%FI = \left[ \sum_{i=1}^n x_i / (n * 4) \right] * 100 \quad (5.1)$$

where  $n$  is the number of individuals sampled in a population and  $x_i$  is the value of the semi quantitative scale attributed to the individual  $i$ .

We also calculated the proportion of trees per species manifesting each phenophase during the entire observation period or the species percent of Activity Index (AI) (Bencke and Morellato 2002). The use of both methods is recommended to describe both the intensity and the synchrony of phenological events for a given species, or for a given group of species (Bencke and Morellato 2002).

The frequency of observations (weekly, fortnightly or monthly), was evaluated based on the graphical analysis of the percentage of Fournier and Activity indices. We considered the number of peaks, amplitude and the duration of each event, according to Newstrom's et al. (1994a) terminology, so as to describe and compare the patterns.

We performed 50 random population simulations or re-samplings (Good 2006) for each defined sample size  $N$  smaller than that from original population sample. Each simulated population represents a random combination of trees selected from the original population sampled in the field, without repetition, but allowing for the repositioning of individuals. The simulations were performed with the Resampling statistics routine in Excel. As an example, the species *Callisthene minor* has 48 individuals which are sampled/monitored and, hereafter, could generate 1,712,304 different re-samples of five individuals or 6,540,715,896 samples of 10 individuals; we set up a data bank for *C. minor* with 50 simulated populations of 5, 10, 15, 20, 25, 30, 35 and 40 individuals.

For all 50 simulations of each one of the simulated population sizes, we calculated the Intensity of Fournier Index (FI) and the Activity Index (AI) for a specific and defined date, i.e. when most of the trees were manifesting phenological activity. Then, we calculated the standard deviation (SD) amongst the simulated samples according to the formula:

$$SD = \sqrt{\frac{1}{n-1} \sum_{i=1}^n (X_i - \bar{X})^2} \quad (5.2)$$

where  $X_i$  is the index of FI or AI calculated for the simulated population  $i$ ;  $\bar{X}$  is the mean, calculated for all simulated samples;  $n$  is the number of simulations (always = 50). The standard deviation estimates the variation or dispersion among values, in our case, the FI and AI, calculated for each simulated sample at that same time.

We performed graphical analyses of the phenological patterns to compare the sampled and simulated populations; these comparisons were based on AI and FI indices, according to Newstrom et al. (1994b) terminology. We analyzed the frequency distribution of the AI and FI indices calculated for each of the 50 simulated populations and compared these to the AI and FI of the sampled population.

To compare floristic diversity sampled by transects and traps we calculated Jacquard's coefficient of similarity (CC<sub>j</sub>) according to Müller-Dumbois and ElleMBERG (1974). To perform a comparison of the phenological patterns, generated by the different sampling and estimation methods, we calculated six phenological variables, based on each estimation method (direct estimation: AI and FI, and indirect estimation: traps); following Morellato et al. (2000): (a) date of first flowering, (b) date of first fruiting, (c) date of peak flowering, (d) date of peak fruiting, (e) date of peak leaf flushing, and (f) date of peak leaf fall. For the trap data we calculated also the peak flower and fruit dates.

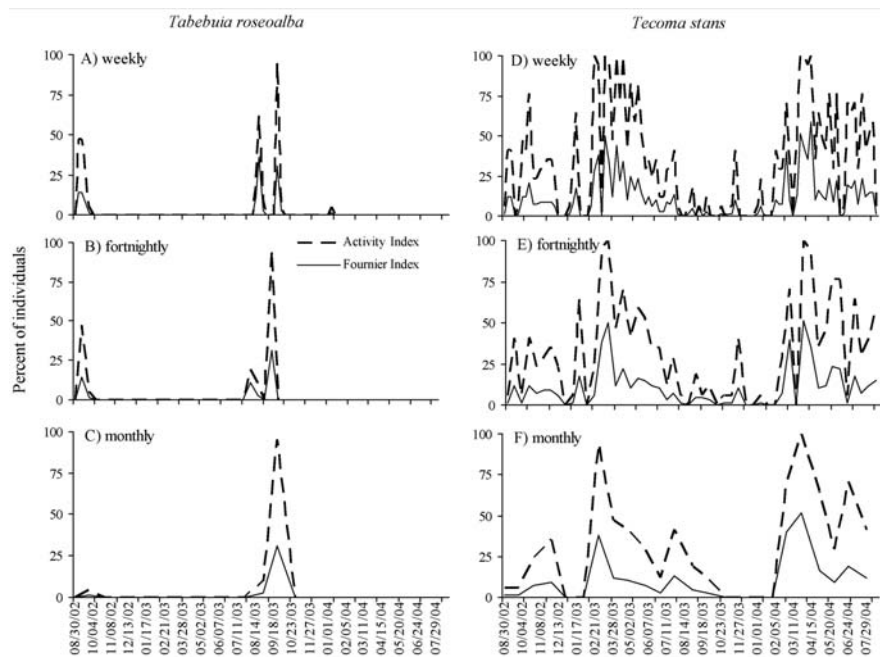
We then applied the circular statistical analytic methods as proposed by Morellato et al. (2000), and described on Chapter 16. The Spearman rank correlation test was used to establish similarity between the number of species on each phenophase observed using the transects and traps methods. Note that the number of species per month is one of the most available results in community level phenology papers (e.g. Morellato et al. 2000, Bawa et al. 2003, Morellato 2003, Bollen and Donati 2005, Boulter et al. 2006, Selwin and Parthasarathy 2006).

We performed graphical analyses of the phenological patterns to compare the sampled and simulated populations; these comparisons were based on the AI and FI indices, according to Newstrom's et al. (1994b) terminology. We analyzed the frequency distribution of the AI and FI indices (calculated for each of the 50 simulated populations) and compared these to the AI and FI of the sampled population.

## 5.3 Results

### 5.3.1 Frequency of Observations

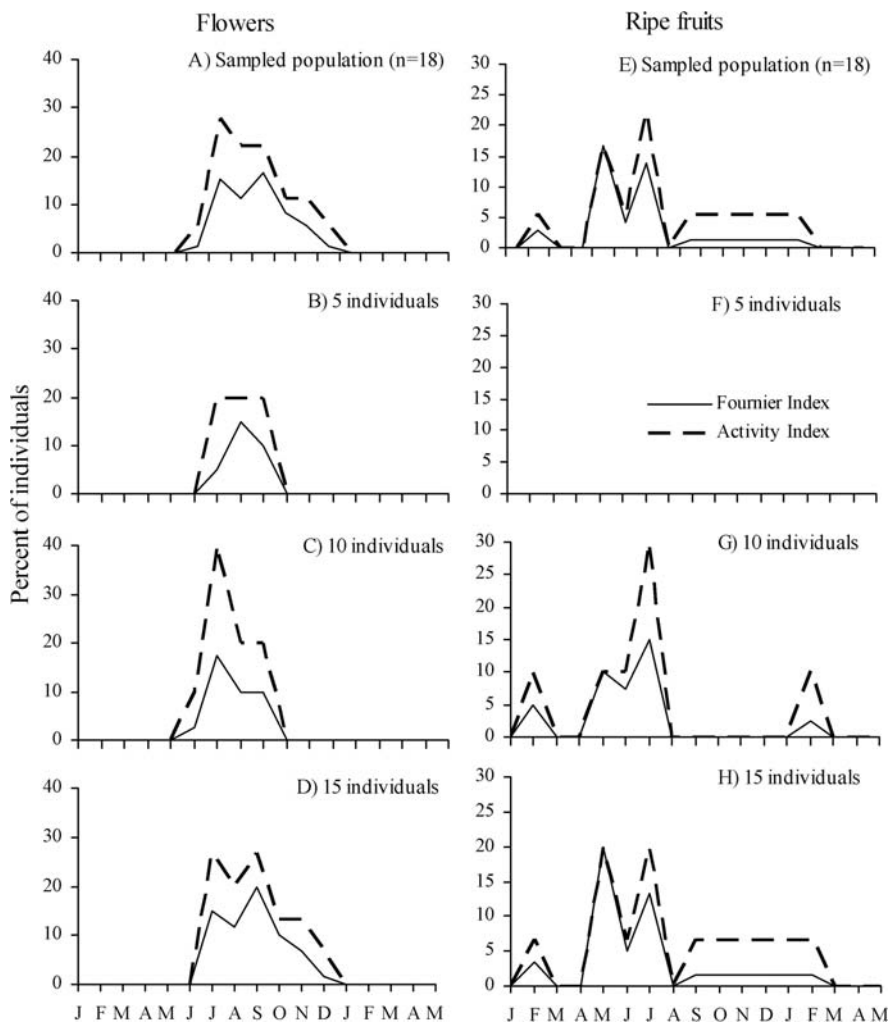
Flowering was chosen to evaluate the frequency of observations (weekly, fortnightly or monthly) as the terminology was developed based on this phase (Newstrom et al. 1994b). The other phases had similar results and can be classified using this same terminology. The results showed that the fortnightly and, predominantly, the monthly observations reduce the number of peaks observed in relation to the weekly pattern (Fig. 5.1). Weekly observations depicted the better defined peaks and were more precise in estimating the flowering duration (Fig. 5.1). However, the curves were similar between weekly and fortnightly observations, while monthly observation changed the pattern observed, by losing some flowering events, reducing the number of peaks and/or increasing the total duration (Figs. 5.1c and f). Most importantly, the definition of start and end of flowering changed according to the frequency of observation. For instance, monthly observations showed the longest flowering duration, since small fluctuations were not detected by this interval choice (Figs. 5.1a–c).



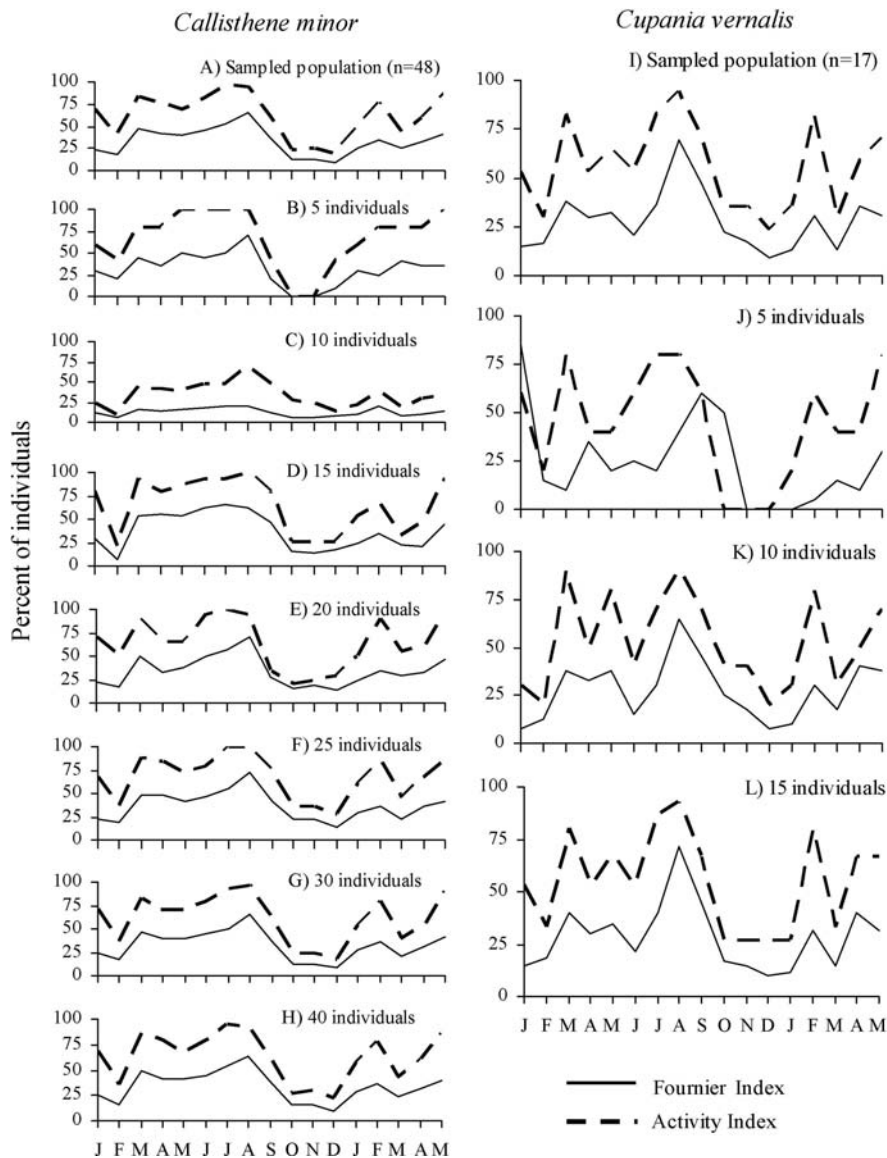
**Fig. 5.1** Flowering patterns of percent of Fournier and of Activity indices according to the frequency of observations for *Tabebuia roseoalba* (left column) and *Tecoma stans* (right column)

### 5.3.2 Sample Size

We show the selected results of *Laplacea semicerrata* for reproductive patterns (Fig. 5.2) and *Cupania vernalis* and *Callisthene minor* for leaf fall (Fig. 5.3), to represent the general patterns and trends found for differing sample size. When we compared the monthly phenological patterns of sampled and simulated populations we detected important variations in the amplitude, duration, and timing of occurrence with sample size, and even lost of information regarding low intensity events (Figs. 5.2 and 5.3). The smaller simulated samples ( $n = 5$ ) lost information for almost all phases and species analysed (Figs. 5.2f, 5.3b and j). A sample size



**Fig. 5.2** Flowering (left column) and fruiting (right column) patterns for sampled and simulated populations of *Laplacea semiserrata*



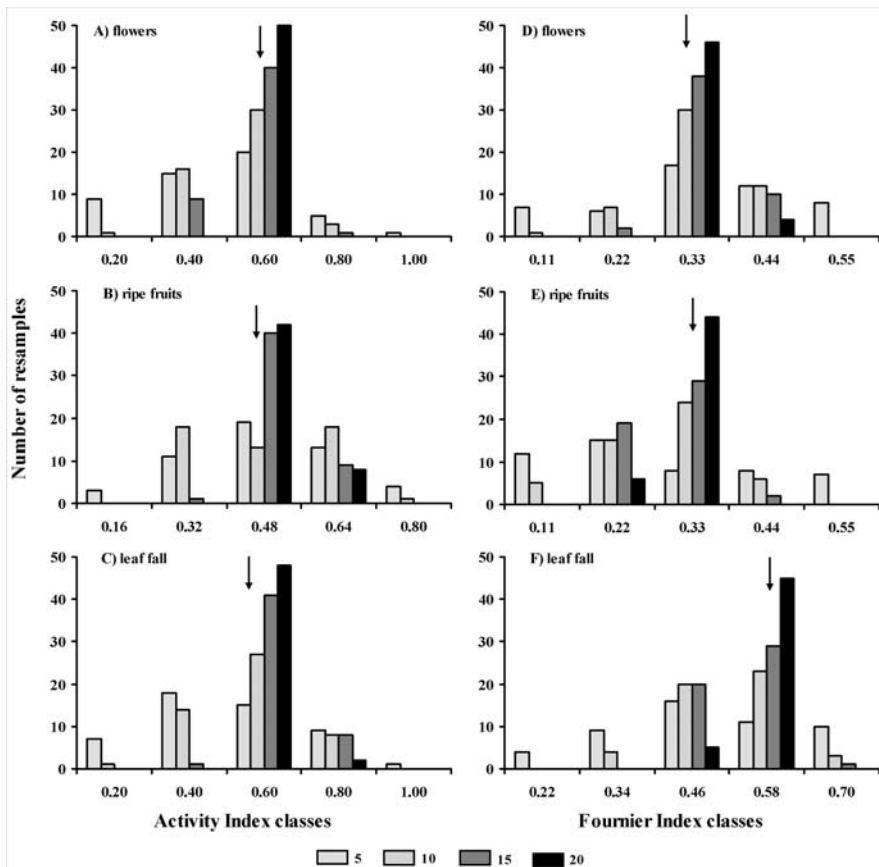
**Fig. 5.3** Leaf fall patterns for sampled and simulated populations of *Callisthene minor* (left column) and *Cupania vernalis* (right column)

of 10, the most used in phenological field work (D’Eça Neves and Morellato 2004, Morellato, pers. observ.), since the work of Fournier and Charpatier (1975), still loses information, this due to the lack of occurrence of a fruiting event (Fig. 5.2f), the reduction in the Fournier and Activity indices (Fig. 5.3c) or the reduction in duration (Fig. 5.2g). When using 15 individuals or more the patterns observed for

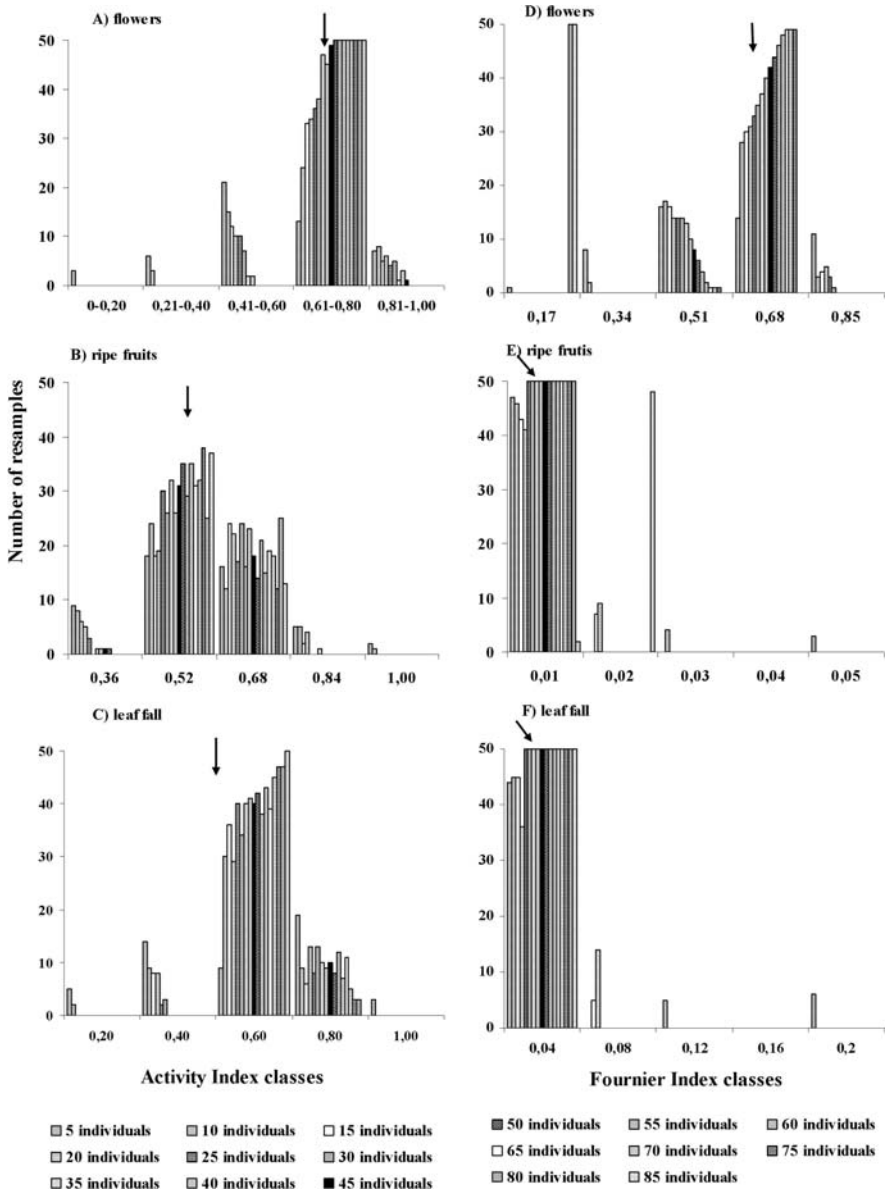


the simulated populations were quite similar to the pattern obtained from the sampled population (Fig. 5.3, sampled population and simulated populations of 15 or more trees).

The histograms of the number of resamples, by classes of Fournier and Activity indices, according to the size of the simulated population, confirm the evaluation of best recommended sample size (Figs. 5.4 and 5.5). As the sample size decreases, the variation increases, in that the indices calculated for the simulated populations deviate more than the indices calculated for the sampled population (Fig. 5.5). Again, from a sample size 15 or more, the simulated population indices were closer to the sampled population indices (Fig. 5.5). Significant variation was found among the smaller simulated populations of 5 or 10 trees up to 35 trees, where the indices were spread out over a large range of classes (Fig. 5.4). For species with an elevated number of individuals, such as *Miconia rubiginosa*, we observed a high concentration



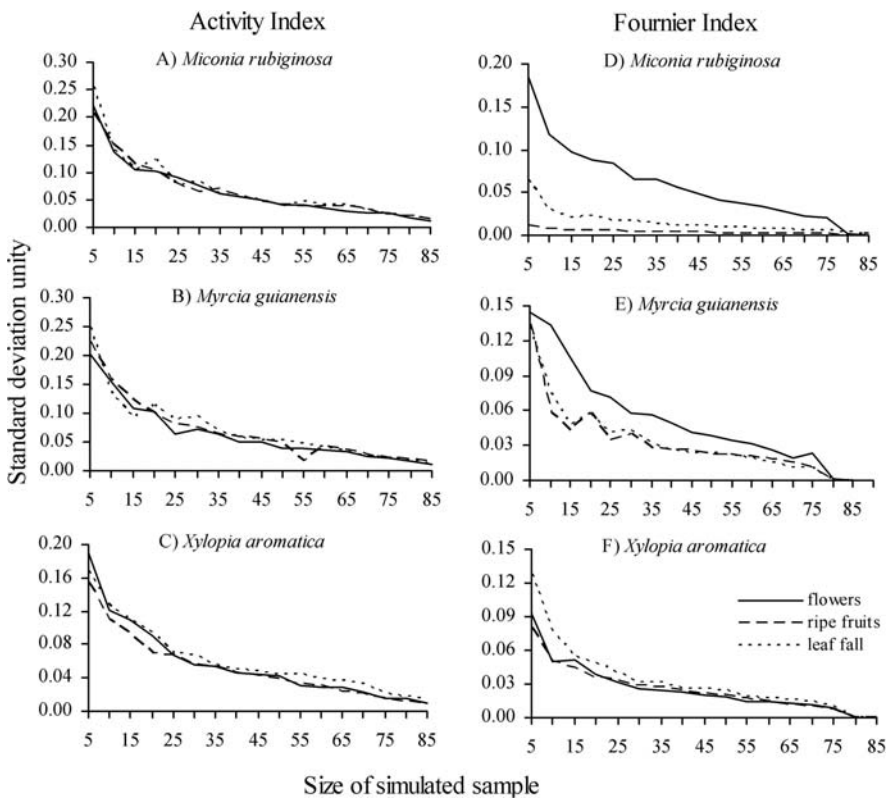
**Fig. 5.4** Frequency histograms of the number of resamples by classes of Activity Index (*left column*) and of Fournier Index (*right column*) according to the size of the simulated population (5–20 trees) of *Pera glabrata*. The arrow indicates the class of the index for the sampled population ( $n = 23$ ). Legend indicates size of the simulated sample



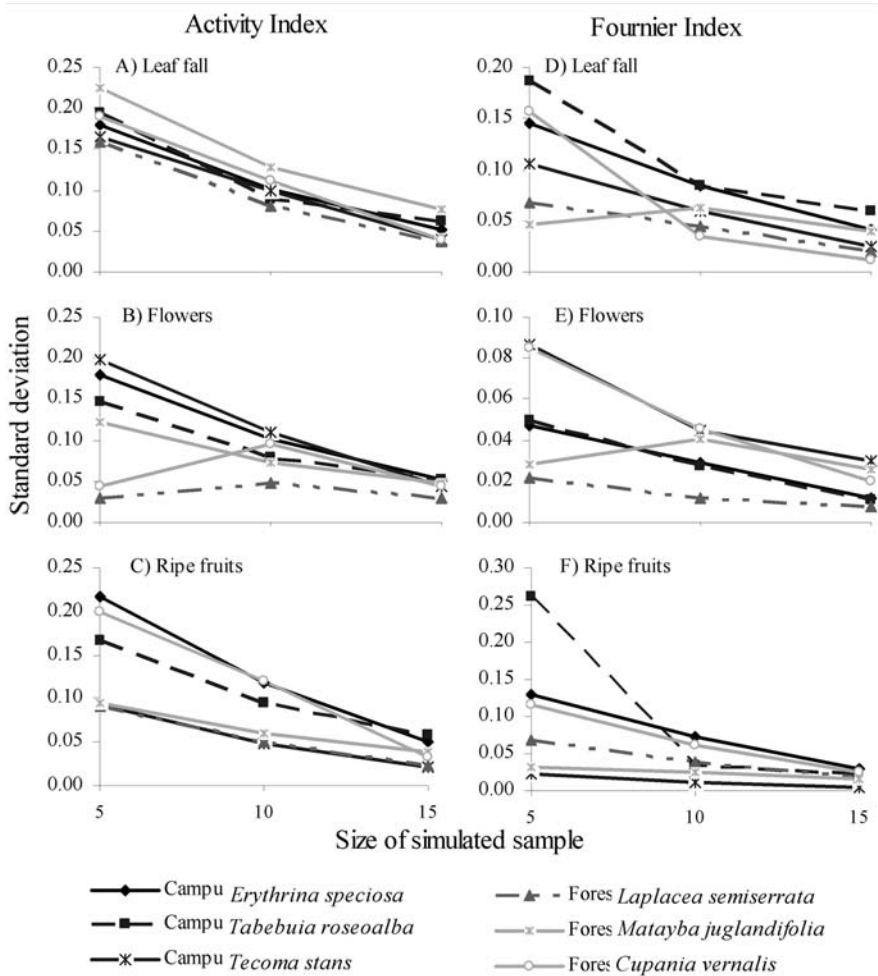
**Fig. 5.5** Frequency histograms of the number of resamples by classes of Activity Index (*left column*) and Fournier Index (*right column*) according to the size of the simulated population (5–85 trees) of *Miconia rubiginosa*. The arrow indicates the sampled population (n = 90) the class of the index for the sampled population. Legend indicates size of the simulated sample

of the simulated population indices falling within the same class of the sampled population indices (Fig. 5.5).

In spite of the certainty that standard deviation (SD) decreases as the sample size increases, the simulated populations of 10 trees presented a standard deviation of the order of magnitude around 0.1, while for the simulated samples of 15 trees, the SD's order of magnitude dropped to 0.01. An analysis of the tendency of the standard deviation curves for the species with largest sample sizes, shows that after 25–30 samples there is proportionally much less of a decrease in the SD for the number of samples (Fig. 5.6), indicating the ideal sample size to reduce uncertainty. Finally, the anticipated higher variability in standard deviation was not observed when we compared Campus versus natural (Forest and Cerrado) vegetation trees (Fig. 5.7). Instead, the trends diverged among phenophases and the Campus trees where shown to be more variable than forest trees, although the SDs were equally reduced in the larger sample sizes.



**Fig. 5.6** Standard deviation of the Activity Index (left column) and Fournier Index (right column) by simulated population size for three savanna cerrado species



**Fig. 5.7** Comparison of the standard deviation for simulated samples of 5, 10 and 15 trees species from Campus and Forest. Activity Index (left column) and Fournier Index (right column)

### 5.3.3 Comparison of Sampling Methods

The reproductive phenological patterns were significantly seasonal (Table 5.2), regardless of whether they were described using the Fournier or the Activity indices, all peaking in July, during the dry season (Figs. 5.8a–d). The traps showed a divergent pattern, with one peak for flower and fruit production in March, occurring at the end of the wet season (Figs. 5.8a–d). The mean data or angle of occurrence was significant for all phenological variables collected by the transect method, confirming the significant seasonal pattern, except for leaf flush (Table 5.2 and see

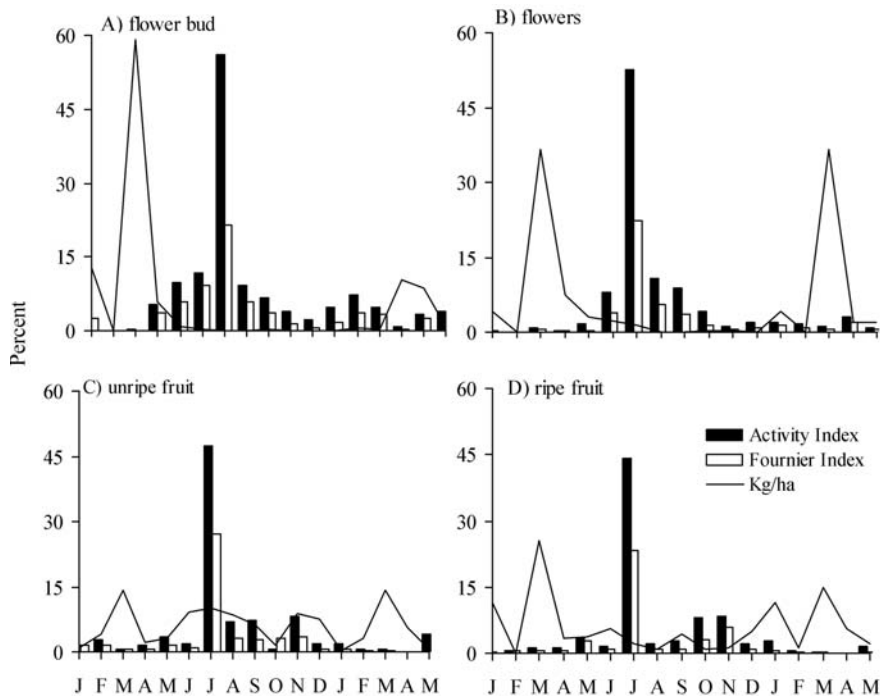
**Table 5.2** Results of the circular statistical analysis and Rayleigh test of the mean angle (mean date) or test for the occurrence of seasonality on phenological pattern, for the phenology transect – Index of Activity and Index of Fournier (in brackets), and traps – dry weight, in the semideciduous altitudinal forest of Serra do Japi, Southeastern Brazil

	Phenological variables – transects					
	First flower	Flower peak	First fruit	Peak fruit	Leaf flush peak	Leaf fall peak
Observations ( <i>N</i> )	24 (24)	27 (28)	17 (17)	20 (24)	29 (29)	28 (28)
Mean angle ( <i>a</i> )	175.51° (175.51°)	195° (197.67°)	187.67° (178.81°)	201.34° (203.44°)	254.44° (254.44°)	219.05° (215.64°)
Mean date	25/Jun (25/Jun)	15/Jul (17/Jul)	08/Jul (28/Jun)	21/Jul (23/Jul)	– (–)	09/Jul (05/Jul)
Circular standard deviation	46.04° (46.04°)	31.27° (40.78°)	30.25° (49.37°)	24.01° (43.90°)	82.77° (82.77°)	48.66° (51.64°)
Vector ( <i>r</i> )	0.72 (0.72)	0.86 (0.78)	0.87 (0.69)	0.92 (0.75)	0.35 (0.35)	0.70 (0.67)
Rayleigh test ( <i>P</i> )	0.00 (0.00)	0.00 (0.00)	0.00 (0.00)	0.00 (0.00)	0.03* (0.04*)	0.00 (0.00)
	Phenological variables – traps					
Observations ( <i>N</i> )	–	14	–	13	–	–
Mean angle ( <i>a</i> )	–	117.84°	–	113.79°	–	–
Mean date	–	27/Apr	–	–	–	–
Circular standard deviation	–	45.87°	–	86.18°	–	–
Vector ( <i>r</i> )	–	0.73	–	0.32	–	–
Rayleigh test ( <i>P</i> )	–	0.00	–	0.26 NS	–	–

\*value may be unreliable because of low concentration (uniform distribution)

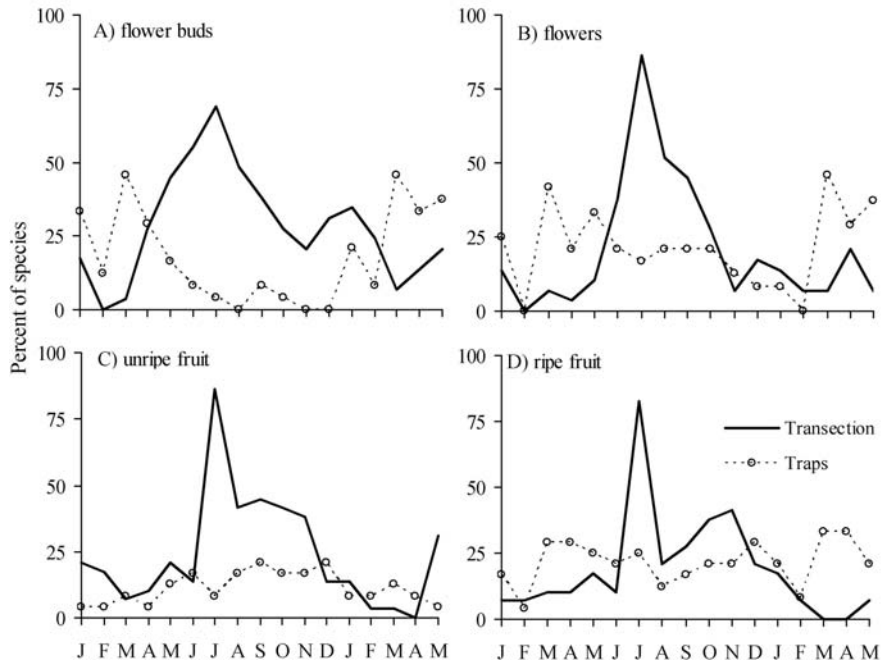
NS = non significant values

comments on Chapter 16). The high degree of seasonality was confirmed also by the elevated values of *r*, ranging from 0.65 to 0.88 (leaf fall – Fournier Index and fruiting – Activity Index, respectively), and were higher for the Activity Index than for the Fournier Index (Table 5.2). Conversely, the mean dates of all reproductive variables did not differ significantly between the Fournier and Activity estimation methods (F test (Watson-Williams, Zar 1999)), confirming the similarity between the patterns irrespective of the index. However, the trap method showed a significant seasonal pattern just for peak flowering (Table 5.2). The flower peak mean angle was significantly different between trap (April 9th) and both the direct observations: Activity Index (July 1st;  $F = 27.54$ ,  $p < 0.001$ ) and the Fournier Index (July 4th;  $F = 22.67$ ,  $p < 0.001$ ).



**Fig. 5.8** Phenological patterns of trees sampled by transects (direct observation percent Activity and Fournier indices) and by traps (indirect observation – percent of weight in kg/ha), in a semi deciduous altitudinal forest from Southeastern Brazil

A similar number of tree species were sampled using transects ( $n=29$ ) and traps ( $n=24$ ), with a similarity coefficient ( $CC_j$ ) of 45% (Müller-Dumbois and Elleberg 1974). The proportion of species reproducing per month observed by the transects and trap methods did not show a significant correlation, except for the opposite trend on flower buds ( $r_s = -0.59$ ;  $P = 0.013$ ; Fig. 5.9). The most outstanding difference, in fact, was between the patterns generated by traps in kg/ha (Fig. 5.8) and the one generated for percent of species (Fig. 5.9). While direct observation produced generally the same pattern in percent of trees (AI), percent of intensity (FI) or percent of species, traps showed a more divergent pattern (Figs. 5.8 and 5.9). The strong peaks of flower production (Figs. 5.8a and b) were not detected in the proportion of species profiles (Figs. 5.9a and b). Production was higher when the lowest number of species and trees were reproducing. This occurred because one, or a few species, were responsible for the traps' peak – for instance, the large buds and flowers of *Inga sessilis* Mart. (Fabaceae), contributed the most material to the traps.



**Fig. 5.9** Percent of tree species flowering by sample method of transects ( $n = 29$ ) and traps ( $n = 24$ ), in a semi deciduous altitudinal forest from Southeastern Brazil

## 5.4 Discussion and Concluding Remarks

Our results indicate that the frequency of observation (weekly, fortnightly or monthly), affect phenological patterns, and that a fortnightly frequency would provide reasonable accuracy for tropical trees, irrespective of the sample size. Fournier and Charpentier (1975) proposed that monthly observations gave a fair indication of tree phenology but recommended that fortnightly observations should be taken when possible. There is a tradeoff between frequency of observations and sample size (Lohr 1999; Camargo et al., unpubl. data), larger sample sizes describe phenological patterns with increasing accuracy as the frequency of observations increases, while small samples lose information and precision. When working with complex and highly diverse ecosystems, such as tropical forests, the sample sizes can be extremely variable and it is advisable to take into account these two factors when both sampling and interpreting the data.

Sample size is a complex issue, and our results point to a sample size of at least 15 trees to best approximate the pattern described for a sampled population. For population studies, a sample size of 25 trees or larger is the best to reduce uncertainty and increase the accuracy for monthly observations. We disagree with Fournier and Charpentier (1975), who recommended a sample of 10 trees for studies aiming to analyze in detail the phenology of one forest tree species in particular. However,

we concur with their suggestion to include, for tropical community studies, even species with smaller sample sizes, since the species abundance reflects the community structure; and a given species may be important, irrespective to its density and frequency.

Most phenological studies represent phenological patterns as the number of species per observation interval. This can be deceiving when one wants to consider the amount of flowers and fruits produced. Our results demonstrate the similarity between patterns, irrespective of whether patterns are based on the Activity Index, Fournier Index or the number of species. However the trap method showed significantly different seasonal patterns from those obtained from phenology transects, either in regards to production (kg/ha) or in the number of species. Our results agree with Chapman's et al. (1994) findings in the Kinbaule forest, Uganda, who found a significant correlation between the estimates of fruit abundance, derived from fruit traps and from phenological transects. On the other hand, Stevenson et al. (1998) found similar temporal fruiting patterns between fruit traps and fruiting trees in Colombia lowland tropical forest; and Zhang and Wang (1995) observed comparable fruiting patterns between fruit traps and platform observations in French Guiana tropical rain forest. The inconsistencies observed between phenological transects and traps in our study may be related to chance events that overestimate flower and fruit production (see below). Such chance events were identified in this study as well as in previous studies carried out at Serra do Japi forests (Morellato 1992).

However, the differences we observed in the number of species flowering or fruiting (over time) between transects and traps are more difficult to explain. Since the Serra do Japi altitudinal forest is very dense and seasonal, and is suitable for the sampling methods applied (see comments on Stevenson et al. 1998); transects and traps showed around 50% similarity in species composition, which is considered a high level of similarity for tropical, highly diverse vegetation, we expected similar patterns in the number of species. Stevenson et al. (1998) found a comparable number of species fruiting over time for both methods and suggested that, as the methods share half of the species, they work similarly at the floristic level. The phenological pattern generated here by the transect data did not differ from the general phenological patterns detected in previous studies of our site (Morellato et al. 1989), and also from studies of other seasonal forests (Morellato 1995, Rubim 2006).

A number of authors have pointed out the bias inherent in the application of traps when estimating fruit production or fruit fall (Terborgh 1983, Chapman et al. 1992, 1994, Stevenson et al. 1998). We detected bias, as follows, when estimating phenology from traps:

1. The time lag between the direct observation of a phase in the tree (flower or fruit) and the appearance of the species in the traps;
2. The difference in the species sampled by transects and traps in the same studied area;
3. The sensitivity to local effects or "the chance concentration effect" (Stevenson et al. 1998), as the presence in the traps of large amounts of one species (flower or fruit), or the presence of heavy flowers or fruits overestimating production.



While the change in the starting date of a phenophase can be misleading, when correlating trap data to actual climatic data, it may however be important complementary information if the goal of the study is to understand local resource availability. One final consideration is the effort or time spent for each method. Phenological transects needed one quarter of the time of fruit traps (Stevenson et al. 1998, D'Eça Neves and Morellato 2004), which in general can be applicable for estimating flower production as well (Morellato et al. personal obs.). It is also worth considering Hemingway and Overdorff's (1999) study; here two phenological methods were compared: selected tree observations and systematic transect monitoring. By generating bootstrapped subsamples (Efron and Tibshirani (1993)) derived from the transect tree data set, Hemingway and Overdorff's (1999) simulated two selected tree data sets and subsequently compared the observed and bootstrapped values. Whilst we adopt a resampling approach here, we did not calculate bootstrap confidence intervals, a possible topic for future work.

Hemingway and Overdorff (1999) noted also that although the observed values fell within their bootstrapped confidence intervals, suggesting no significant effects of sampling protocol nor of sample size, additional lines of evidence suggest otherwise. It is of value to follow their considerations. Hemingway and Overdorff (1999) showed that observed samples composed of different plant species, whether based on species attributes such as life-form or categories such as food versus non-food plants, consistently produced different phenological patterns. Wide confidence intervals of the bootstrapped samples possibly indicated high individual variation in reproductive activity within the species sampled. This points out to the importance of variation on plant species diversity. Hemingway and Overdorff (1999) compared how well the selected tree and the transect methods represented food items used by all three primate species studied and found that the transect methods sampled a wider diversity of food items, including rare foods, and a higher percentage of main primate food items than selected tree methods.

Methods to study plant phenology described in the literature vary widely and the choice and comparability of methods remains an issue in phenological studies. Castro-Diez et al. (2003) compared phenological information gathered from two different methods on the same population of *Halimium atriplicifolium* (LAM.) SPACH (Cistaceae), a Mediterranean evergreen shrub. Interestingly they adopted, as we recommend, monthly observations and monitoring of ten whole plants (five less than we recommend). Specifically their first method, the so-called semi-quantitative (SQT), was based on a monthly estimation of each phenophase's incidence, assessed via a visual inspection of ten whole plants. The second, called quantitative (QT) was based on a monthly monitoring of all the leaves, buds, flowers and fruits borne on five tagged branches throughout an annual cycle. Both methods allowed a calendar of leaf production and shedding, development of inflorescence and flower buds, flowering, fruit setting and seed dispersal to be drawn up. In addition, leaf shedding was also studied using ten litter collectors, placed below the SQT-sampling plants (LC method). The mean dates of each phenophase's beginning, maximum incidence, ending and the duration obtained from the different methods were calculated for both methods. The 95% confidence limits of the variable means were

calculated, together with the minimum sampling size necessary to get a '30 days 95% confidence limit' for each variable. It has been estimated that, to get similar confidence limits, the QT method requires 4–5 hours of field work per sampling date, versus only one hour for SQT. Hemingway and Overdorff (1999) found a good agreement between the methods for most of the phenophases studied. The main inter-method differences appeared in phenophase duration, which tended to be longer via the SQT method.

Clearly methods may vary depending on the phenophase investigated. This was noted in Hemingway and Overdorff's (1999) study, where while direct observations of reproductive phenology were more accurate than traps, the observation of leaf change, especially leaf fall were more subjective, making the traps a more reliable way to quantify and estimate that specific phenophase for a community. However, it is important to note that the species or individual information, for instance, degree of deciduousness or "evergreenness" is missing in trap collection.

Our suggestions and recommendations in this chapter represent an idealized study for tropical vegetation. As field biologists we are acutely aware of the difficulties in conducting frequent observations on a large number of trees in remote tropical forest sites. Monthly observations with a few repetitions per species are much better than no phenological study, but we must always consider our conclusions with some caution, especially when the final goal of the study is the management of natural resources. We however, recommend a minimum sample size of 15 trees, a fortnightly frequency of observation, especially if the sample size is small, combined with a quantitative or semi-quantitative method and qualitative method to estimate and quantify plant phenology, and a careful application of indices and cautious generalization of patterns.

There is now a huge impetus to marry ground-based phenological records with satellite imagery of vegetation (Tarpley et al. 1984, Duchemin et al. 1999, White et al. 2003, Morissette et al. 2008). Part of the ground based initiative is to use school children through the GLOBE Plant Phenology Observations initiative (Almeida et al. 2006), see also <http://www.lter.uaf.edu/~dverbyla/globe>. Our suggested recommendations for sampling (number and frequency of observation) do not pertain in general to these efforts. However, it is worth noting that in the GLOBE initiative students are asked to visit their pre-selected trees twice weekly or daily during the week(s) (Brombaugh et al. 2003). Plant phenology protocols are now currently being developed by the USA National Phenological network for consistent monitoring of phenology across the north east region and the nation (USA NPN) (McNeil et al. 2008). See also the USA-NPN website and (<http://www.nerpn.org/protocols/protocols.shtml>). Generally these protocols recommend the selection at the site of 3–5 individuals of each plant species and those observations be made at least weekly. Again, they do not pertain to the realm of the present study, since those are temperate networks of observation by amateurs mostly, over large areas. However, we believe local observation studies may benefit greatly from our considerations in general.

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# Chapter 6

## Regression and Causality

Tim Sparks and Piotr Tryjanowski

**Abstract** Regression is a long established statistical tool that is widely used in phenological research for two main purposes i) to detect changes in the timing of phenological events and ii) to relate the timings of phenological events to one or more environmental conditions, typically temperature. Regression provides a flexible and robust method for the analysis of phenological data but can be influenced by start and end years and the length of the data series being analysed. In addition, spurious relationships can arise by trawling through large numbers of environmental variables without consideration of the likely mechanisms driving phenology. This chapter is illustrated using examples of flowering phenology from the United Kingdom.

**Keywords** First flowering date · Phenology · Responses · Temperature trends

### 6.1 Introduction

Regression analysis has a long history. Its principal purpose is to relate one variable, typically known as the response variable, to one or more explanatory variables. In phenological research regression has two main purposes; to detect changes through time in the timing of phenological events and to relate the timings of phenological events to one or more environmental conditions, typically temperature but potentially including other variables such as rainfall, large pressure systems (such as the North Atlantic Oscillation), latitude, longitude and altitude.

Regression techniques can be quite elaborate (Draper and Smith 1998), but those typically used in the analysis of phenological data are relatively simple involving a small number of explanatory variables. We would recommend that careful thought is given to the selection of these explanatory variables since spurious relationships can arise by trawling through large numbers of environmental variables without

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consideration of the likely mechanisms driving phenology. Furthermore there is a danger in attempting to find relationships with a limited number of years of data. Such regressions will have limited statistical power (the ability to detect real effects) and claims that these are “long-term” studies are hardly justifiable.

In this chapter we illustrated regression in phenological studies using examples of flowering phenology from the United Kingdom (UK).

## 6.2 An Example Dataset

Throughout this chapter we will make use of some examples of phenology. The first of these is a record collected by Mary Manning in Norwich, UK of the date of first flowering dates (FFD) of Hazel (*Corylus avellana*) between 1976 and 2004. As is typical in phenological analysis, the dates of flowering have been converted to days since December 31, so that January 1 is day 1, April 1 is day 91 (92 in a leap year) and so on. Analysis has been carried out, and graphs created, in the Minitab package (versions 13–15). A graph of the observations is shown in Fig. 6.1.

**Fig. 6.1** The flowering date of Hazel in Norwich from 1976 to 2004

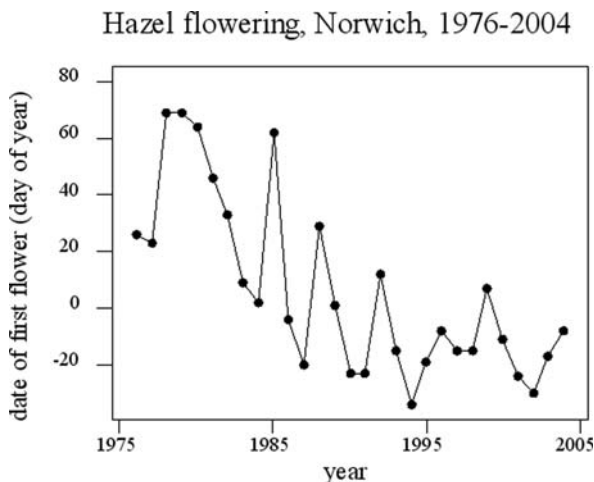


Figure 6.1 visually suggests change in flowering date; possibly an advance from 1978 to 1994 and relative stability thereafter. There is also some suggestion that the year-to-year variability is smaller in recent time. A description of the graph might suggest that flowering has advanced from occurring in January or February, to December. It is not unreasonable to ask whether there has been a statistically significant advance in flowering and to quantify the change. As is typically the case with statistical analysis, there are a number of ways that this could be achieved. We could, for example, divide the data into two halves, say 1976–1990 and 1991–2004 and compare the mean dates.

This would suggest a 40 day change between the two periods. A two-sample t-test would reveal this to be highly significant ( $t_{27} = 4.44$ ,  $P < 0.001$ ), that is the

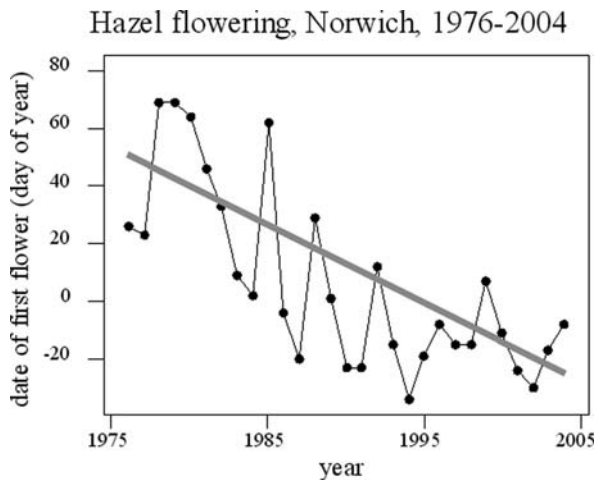
Variable	period	N	Mean	Median	StDev
Hazel FFD	76-90	15	25.73	26	31.41
	91-04	14	-14.29	-15	12.62

difference is very unlikely to occur by chance alone. We may be worried that the variability in the first period seems nearly three times greater than for the second period; indeed a formal test would show them to be significantly different. Is the assumption of equal variances in a standard two sample t-test invalidated? If so, we could undertake a two sample t-test based on unequal variances, a computer intensive resampling test (e.g. Sparks and Rothery1996), or a nonparametric test. An example of the latter would be to reanalyse using a Mann Whitney test. This still reveals a difference in median dates (of 41 days) and is also highly significant ( $P < 0.001$ ).

However, a more typical analysis of these data would be to use linear regression, (i.e. to fit a straight line to the data), and to test if the slope, or gradient of the line, is significantly different from zero (i.e. horizontal). The standard approach to this is to fit the line using the method of least squares that minimises the sums of the squares of the deviations of the real values from the fitted line, (i.e. the sums-of-squares of the residuals). The fitted line in these simple cases will always pass through the point that represents the mean of the y-values (the response variable) and the mean of the x-values (the explanatory variable). In our example the mean year is 1990.0 and the mean day number is 6.41. Therefore, the fitted line will pass through the point (1990, 6.41). Linear regression is widely available in computer packages.

### 6.3 Linear Regression

In our example the fitted line is shown in Fig. 6.2



**Fig. 6.2** The flowering date of Hazel in Norwich from 1976 to 2004 with linear regression line superimposed



A summary of the analysis is as follows:

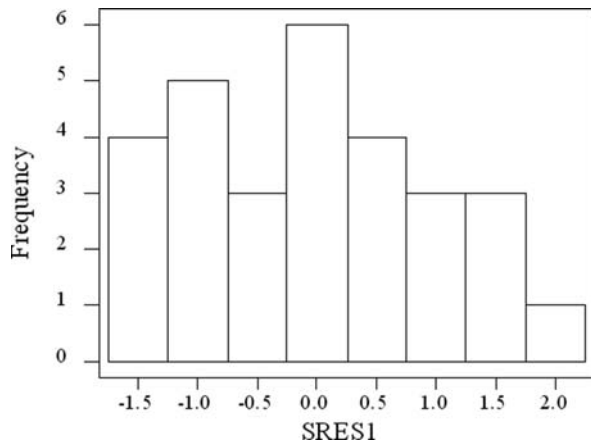
<b>Regression Analysis: Hazel FFD versus year</b>					
The regression equation is					
Hazel FFD = 5386 - 2.70 year					
Predictor	Coef	SE Coef	T	P	
Constant	5386.3	955.7	5.64	0.000	
year	-2.7034	0.4803	-5.63	0.000	
S = 21.64		R-Sq = 54.0%		R-Sq(adj) = 52.3%	
Analysis of Variance					
Source	DF	SS	MS	F	P
Regression	1	14837	14837	31.69	0.000
Residual Error	27	12643	468		
Total	28	27479			

What does this all mean? The equation of the line is  $FFD = 5386 - 2.70 \times \text{year}$ . 5386 is known as the intercept, where the line crosses the y-axis (i.e. the theoretical day of first flowering in year zero). The value  $-2.70$  represents the slope or gradient and tells us that the average change in flowering date per year increase is  $-2.70$ , i.e. an advance of 2.7 days per year. As we have 29 years of data, the estimate of advance between the first and last years is  $29 \times 2.70$  or 78 days. This is much bigger than when we just compared the two time periods. However, that approach took the means of the two periods, and represents the difference between the two mid points of 1983.0 and 1997.5. If we convert the 40 days difference to a 29 year period we need to double it to 80 days (i.e. very similar to the figure above).

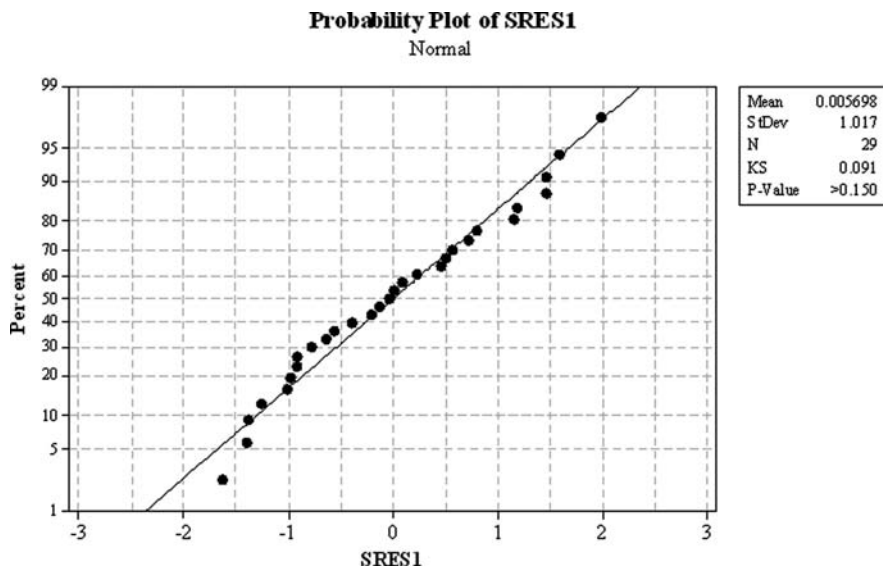
But let us return to the output from the regression output. The slope has a standard error (SE) associated with it that reflects how accurately the slope is estimated. In this example the slope ( $-2.70$ ) is much bigger than its standard error (0.48). The ratio of the two forms a t-statistic ( $-5.63$ ) which we can test for significance. In our example it is highly significant (given as 0.000 but more normally written as  $P < 0.001$ ) and we can conclude that there is very strong evidence for a change in first flowering date. The differences on the y-scale between the points in Fig. 6.2 and the fitted line are known as residuals. When these are squared and summed they form the residual sums-of-squares (here 12643). This represents the bit of the relationship between first flowering date and year that cannot be explained by the

regression. The total variation in first flowering dates is given as the total sums-of-squares (27479), and the bit that *can* be explained by regression is obtained by subtraction (27479–12643 = 14837). The mean squares here are sums-of-squares divided by their degrees of freedom and their ratio is an F statistic that tests whether there is a significant relationship between the response variable and the explanatory variable(s). In this simple case, with a single explanatory variable (i.e. just year), the F statistic is simply the square of the t-statistic for the slope and they are effectively testing the same thing. One other important term here is  $R^2$  (or R-sq) which is the proportion of the total sums of squares explained by the regression. It is expressed either as a proportion (taking values between 0.00 and 1.00) or as a percentage, as here, between 0 and 100%. Our example has an  $R^2$  of 54% calculated as the ratio of 14837 to 27479. Larger values of  $R^2$  mean that points are very much closer to the fitted line, (i.e. there is much less scatter about the line). The reader should be warned that it is easier to get high values of  $R^2$  in analyses based on a small number of data points, and that this should be borne in mind when considering the magnitude of  $R^2$ .

Is the straight line fit adequate for our data? Predictions in the future would continue to show the same rate of advanced flowering, is that feasible? After all, we originally suggested that the flowering date had levelled off. Is the fitted line rather too high above the points in the middle of the graph? The type of regression we used makes a number of assumptions about the data. These include that the residuals are Normally distributed and that they are random. The latter point implies that they will not be correlated with each other in time (autocorrelated) and there will be no discernable pattern when plotted against the explanatory variable. It is common practice to standardise the residuals (this involves subtracting the mean from each residual and dividing by their standard deviation) which reduces them to having a mean of zero and standard deviation of one. We can then use our knowledge of the Normal distribution, for example we expect approximately 95% of values to lie between  $-2$  and  $+2$ , to check for anomalies. Let's look at these for our example data.



**Fig. 6.3** A histogram of the standardised residuals from the regression of Hazel first flowering date on year



**Fig. 6.4** A Normal probability plot of the residuals from the regression of Hazel first flowering date on year

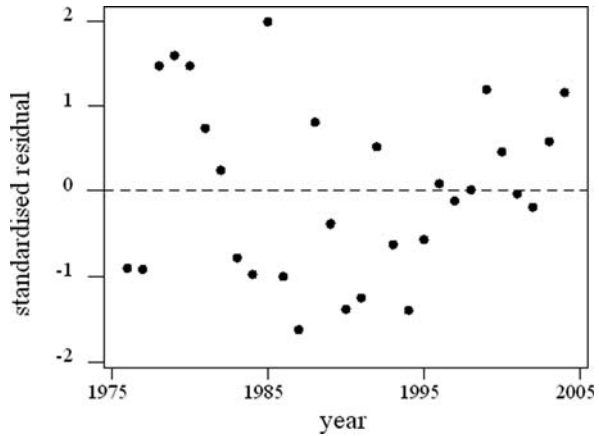
A histogram of the standardised residuals is shown in Fig. 6.3. This doesn't appear to be the typical bell-shaped curve we expect from the Normal distribution, but this may be because of the relatively small sample size ( $n = 29$ ). Let us do a formal Normality test (Fig. 6.4). If Normally distributed, points will lie along the straight line. Here the P-value ( $> 0.150$ ) is high enough that we don't have enough evidence to reject the idea that the residuals are Normally distributed.

There is no significant autocorrelation in the residuals, for example the first order correlation is only 0.21. Our experience would suggest that autocorrelation is rarely an issue in phenology, despite the time-series nature of the records.

A plot of the residuals against the explanatory variable (Fig. 6.5) should be a random horizontal scatter around  $y = 0$ . In our example there is some evidence that points tend to be above the horizontal at the beginning and end of the series and below in the middle area. We will investigate this further in Section 6.4.

In other scientific applications transformation of data to satisfy the requirements of regression is sometimes carried out. We suggest that is less likely to be necessary in phenological analysis, and has the undesirable feature of creating units on an unfamiliar scale compared to the readily identified days of the year, or degrees centigrade. Advances in computing also mean we no longer need to try to achieve Normality since Generalized Linear Models offer much more flexibility. However, our experience would suggest that the typical variables encountered in phenological analysis can usually be considered to be approximately Normal.

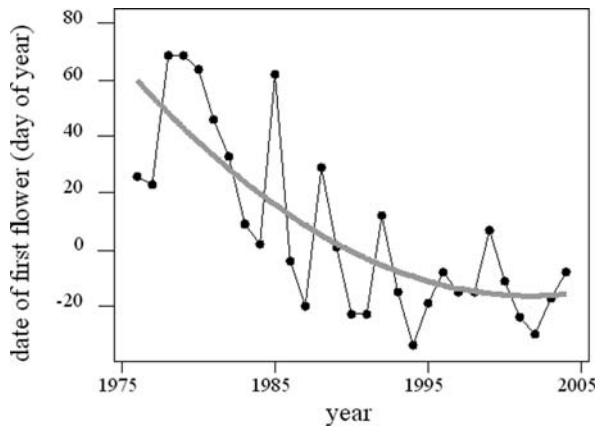
**Fig. 6.5** A plot of the standardised residuals against year. We want this to be a random scatter around the horizontal (i.e. around  $y = 0$  (dotted line))



### 6.4 Polynomial Regression

Traditional ways in regression of fitting curves are to expand linear regression into polynomial regression. Thus, instead of a single explanatory variable (the linear part), quadratic regression has two explanatory “variables” (the linear and the quadratic components), cubic regression has three (linear plus quadratic plus cubic components) and so on. It is unlikely to be sensible to go above cubic regression. In these higher order models the additional explanatory “variables” are tested to see if they improve the fit of the line (e.g. is a quadratic curve a better fit than a linear one?). The quadratic regression to the Hazel flowering date is shown in Fig. 6.6.

Figure 6.6 and the analysis below suggest that a quadratic fit may be an improvement. Visually the line looks a better fit (Fig. 6.6). However the addition of a quadratic term to the linear term isn’t quite significant ( $P = 0.071$ ) at traditional



**Fig. 6.6** The flowering date of Hazel in Norwich with quadratic regression line superimposed

**Polynomial Regression Analysis: Hazel FFD versus year**

The regression equation is  
Hazel FFD = 463778 - 463.407 year  
+ 0.115755 year\*\*2

S = 20.6851      R-Sq = 59.5 %      R-Sq(adj) = 56.4 %

Analysis of Variance

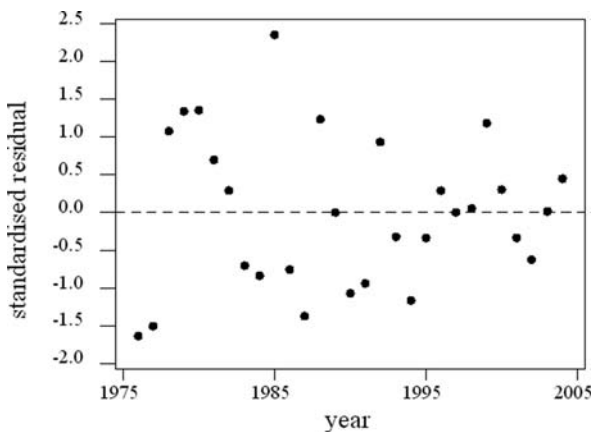
Source	DF	SS	MS	F	P
Regression	2	16354.3	8177.15	19.11	0.000
Error	26	11124.7	427.87		
Total	28	27479.0			

Source	DF	Seq SS	F	P
Linear	1	14836.5	31.6856	0.000
Quadratic	1	1517.8	3.5472	0.071

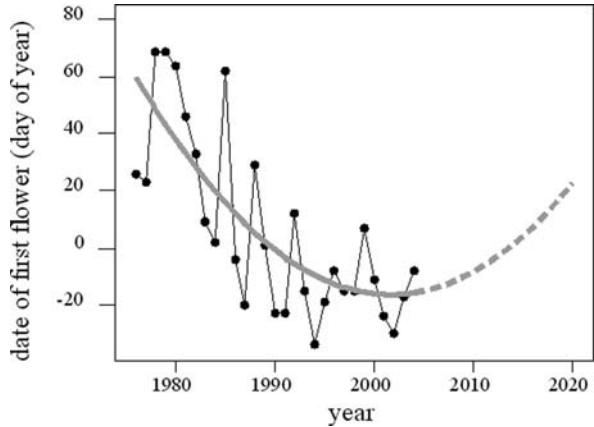
levels. However, it would be a foolish person who ignored results this close to the arbitrary 5% threshold. The standardised residuals from the quadratic look more Normal, the test of Normality suggests greater agreement with a Normal, autocorrelation is lower and the residuals look more random (Fig. 6.7, although one might argue they look more variable in the early years).

As with the linear fit, prediction beyond current time may be biologically meaningless. Because the quadratic is a mathematical equation producing a symmetric



**Fig. 6.7** A plot of the standardised residuals from the quadratic regression against year

**Fig. 6.8** Prediction into the future with a quadratic regression may not be satisfactory because of the symmetrical nature of the curve

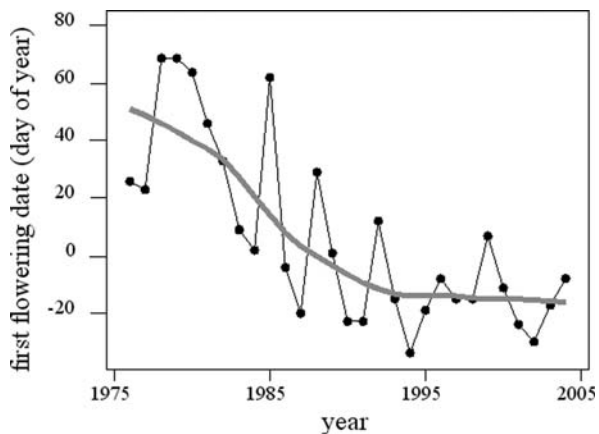


curve, predictions in the future have to mirror changes in the past (Fig. 6.8). In a period of projected continued warming, this is a very unlikely case.

### 6.5 Some Alternative Ways of Identifying Trends

We believe that it is clear that flowering date has advanced. How do we quantify that change? We could examine the average change from one year to the next. The 28 values have a mean of  $-1.21$  suggesting an average advance of 1.21 days per year. An alternative is to look at all 406 pairs of years and calculate the per annum change between them: this yields  $-2.52$  days/year with a standard error of 0.45, very similar to that found by linear regression.

A very good exploratory tool is using lowess (locally weighted scatterplot smoother) lines on a graph. Figure 6.9 shows the underlying trend in first flowering,



**Fig. 6.9** The flowering date of Hazel with a lowess line superimposed



largely agreeing with our initial visual assessment and later quadratic regression. More recently, Bayesian methods have been investigated (see Chapter 11 in this book).

## 6.6 Effects of Starting Year, End Year and Duration

Table 6.1 summarises all slopes of linear regressions of all permutations of 9–29 contiguous years. The estimated slopes vary considerably depending on start and end years; those starting in 1977–1980 up to 1991 producing slopes as large as  $-6$  days/year while those starting from 1990 onwards rarely exceed  $-1$  day/year and are even occasionally positive. A re-examination of the original plot (Fig. 6.1) would anticipate these broad findings; 1976 and 1977 seem slightly peculiar then there is rapid advancement in flowering followed by relative stability. Emboldened slopes in Table 6.1 are statistically significant; showing that significant change is more likely to be detected in the longer series, but less likely in the more recent period. Sparks and Menzel (2002) recommended 20 years as the minimum for phenological series; in practice that is not always possible, for example where a data series terminated prematurely on the death of the observer. However, there are dangers in using short series, not least of which is a reduced chance of detecting statistically significant change.

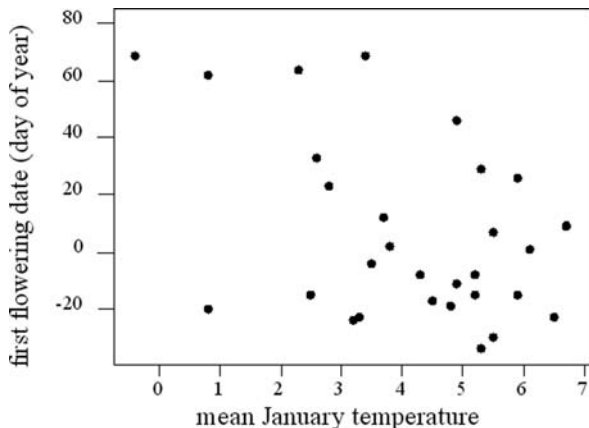
## 6.7 Multiple Regression: Relations with Temperature

What drives the phenology in our example? We have correlated the first flowering dates with mean monthly temperatures from September of the previous year to March of the current year. The table of correlation coefficients suggest that there are relatively few significant correlations between flowering date and monthly temperatures, and even between temperatures of adjacent months. The only significant correlation with first flowering date is for January temperature, and the relationship whilst statistically significant isn't very impressive visually (Fig. 6.10).

The  $R^2$  is much lower than in the regression against year, and this can be seen by the much greater spread around the fitted regression line (Fig. 6.10). The slope suggests a  $1^\circ\text{C}$  increase in temperature was associated with 7.9 day advancement in flowering. Now, January temperatures over this time period may have increased by  $2^\circ\text{C}$  which could account for a 16 day advancement in Hazel flowering, but not the c.80 day advancement that has been recorded. Is monthly data inappropriate for a phenological variable that is changing this rapidly? For example, January temperatures are the month *after* recent flowering so cannot be causative. There may be extra factors to consider, such as sunshine, rainfall, soil temperature and the incidence of frosts. Are the scales of measurement, (i.e. monthly), too crude? Certainly, year is still an important variable if we fit it in addition to January temperature, see below. In this example the P-values associated with each term (January, year) are the significances *after* fitting the other terms, and January temperature looks far less important than year in explaining changes in the phenology



**Fig. 6.10** A plot of Hazel first flowering dates against January mean temperature (°C) with the fitted regression line superimposed



	Hazel FFD	ps	po	pn	pd	j	f
Ps	0.120 0.536						
Po	0.031 0.875	-0.060 0.756					
Pn	0.050 0.795	-0.015 0.938	0.086 0.658				
Pd	-0.045 0.818	-0.140 0.470	-0.049 0.801	-0.140 0.468			
J	<b>-0.447</b> <b>0.015</b>	0.204 0.290	-0.302 0.112	-0.190 0.323	0.191 0.322		
F	-0.290 0.127	0.058 0.767	-0.050 0.796	0.161 0.405	-0.046 0.814	0.360 0.055	
M	-0.345 0.067	0.271 0.155	-0.117 0.544	-0.226 0.238	-0.064 0.741	<b>0.500</b> <b>0.006</b>	<b>0.463</b> <b>0.011</b>
Cell Contents: Pearson correlation P-Value							
Correlations between Hazel FFD and mean monthly temperatures from the previous September (ps) to March of the current year (m). Figures in bold are significant at P<0.05.							

**Regression Analysis: Hazel FFD versus j**

The regression equation is  
 Hazel FFD = 38.7 - 7.88 j

Predictor	Coef	SE Coef	T	P
Constant	38.70	13.51	2.87	0.008
j	-7.881	3.033	-2.60	0.015

S = 28.53      R-Sq = 20.0%      R-Sq(adj) = 17.0%

Analysis of Variance

Source	DF	SS	MS	F	P
Regression	1	5497.6	5497.6	6.75	0.015
Residual Error	27	21981.5	814.1		
Total	28	27479.0			

**Regression Analysis: hazel ffd versus j, year**

The regression equation is  
 hazel ffd = 4848 - 4.06 j - 2.42 year

Predictor	Coef	SE Coef	T	P
Constant	4847.7	973.6	4.98	0.000
j	-4.063	2.351	-1.73	0.096
year	-2.4245	0.4908	-4.94	0.000

S = 20.88      R-Sq = 58.7%      R-Sq(adj) = 55.6%

Analysis of Variance

Source	DF	SS	MS	F	P
Regression	2	16139.4	8069.7	18.50	0.000
Residual Error	26	11339.6	436.1		
Total	28	27479.0			

Source	DF	Seq SS
j	1	5497.6
year	1	10641.9

We can examine if a better model might be achieved by including temperature of other months in addition to January. Stepwise regression may be the chosen method. The basic approach is to first fit the single explanatory variable that best

explains the response variable. Further explanatory variables are either added (if they improve the model) or discarded (if they become redundant once other variables are included). These steps are done automatically within a computer package; typical options allow a specification of the significance threshold for adding or removing explanatory variables, forcing some variables to be always included etc. Variants of this method include forwards selection (starting from no variables and expanding the model) and backwards elimination (including all variables initially and then excluding redundant variables). Unfortunately our example data doesn't get further than using January temperature because the addition of other candidate explanatory variables does not substantially improve the model.

### Stepwise Regression: hazel ffd versus ps, po, pn, pd, j, f, m

Alpha-to-Enter: 0.15 Alpha-to-Remove: 0.15

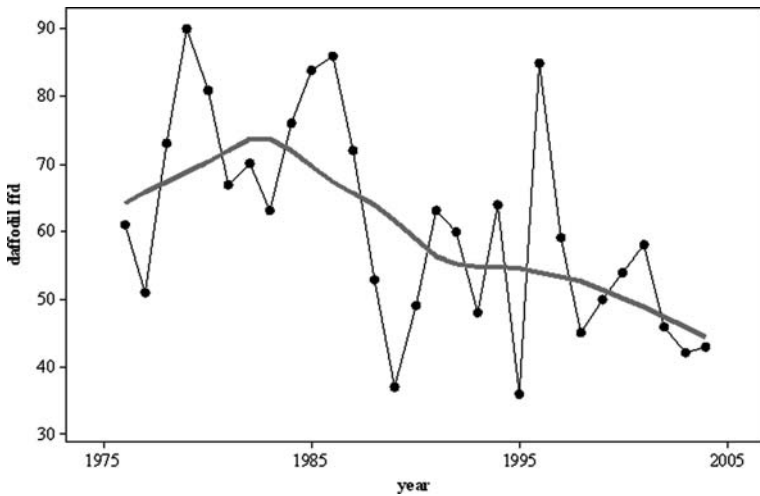
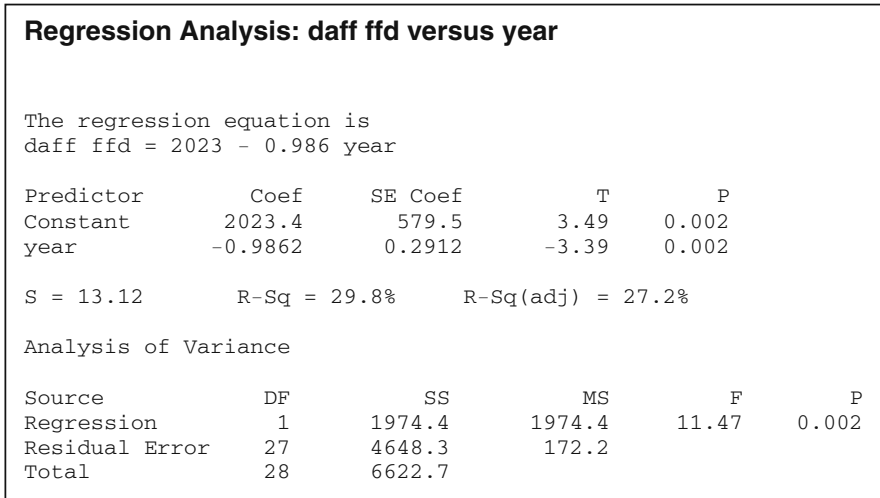
Response is hazel ff on 7 predictors, with N = 29

Step	1
Constant	38.70
j	-7.9
T-Value	-2.60
P-Value	0.015
S	28.5
R-Sq	20.01
R-Sq (adj)	17.04
C-p	-1.0

Consequently we will make use of another phenological event, observed by the same recorder in the same years: the first flowering date of Daffodil (*Narcissus pseudo-narcissus*). There also seems to have been an advance in flowering in this species, but not as marked as for Hazel. A graph of the observations is shown in Fig. 6.11, with a lowess line (a distance weighted smoothed line) to show the underlying pattern.

A regression of first flowering date on year suggests a very significant advance of just under 1 day/year, equating to 29 days over the entire recording period (i.e. considerably less than that for Hazel).

We will use stepwise regression on monthly temperatures from the preceding November (pn) to March to see which explanatory variables (monthly temperatures) most influence flowering date. The output below shows that February temperature appears to be the most important month with a slope of  $-5.3$  days/ $^{\circ}$ C. Step 2 adds January temperature as the second variable and the slopes for February and January are, respectively,  $-4.1$  and  $-3.9$  days/ $^{\circ}$ C. These combine to suggest a  $1^{\circ}$ C increase



**Fig. 6.11** The flowering date of Daffodil in Norwich 1976–2004 with a lowess line superimposed

in these two months would advance flowering by 8.0 days.  $R^2$  has increased from the single variable model of 50.6%, to 68.5%. The third, fourth and fifth steps all add variables, rather than removing them, with the  $R^2$  in the five variable model being 77.1%. Which model should we chose? There are many criteria for this, but we suggest the highest step in which all variables are significant (at  $P < 0.05$ ) and which is significant overall (as assessed by the F-ratio from the analysis, not shown in the stepwise output). Others will suggest other criteria, for example based on Mallows' C-p statistic or Akaike's Information criterion (AIC statistics), but there is no universally held opinion on which is best. Both C-p and AIC are discussed

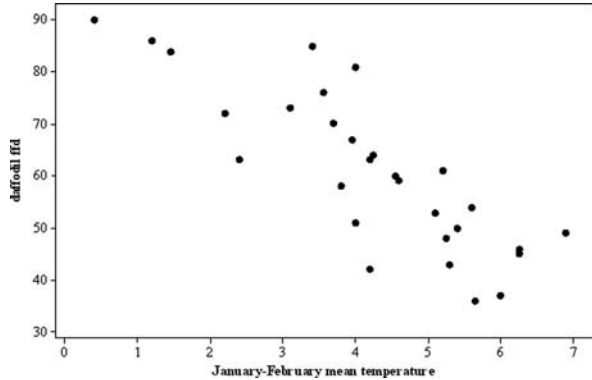
by von Storch and Zwiers (2001) and there are even whole books devoted to model selection (Burnham and Anderson 2002).

<b>Stepwise Regression: daff ffd versus pn, pd, j, f, m</b>					
Alpha-to-Enter: 0.15    Alpha-to-Remove: 0.15					
Response is daff ffd on 5 predictors, with N = 29					
Step	1	2	3	4	5
Constant	83.88	94.67	105.47	125.22	136.24
f	-5.34	-4.11	-3.57	-3.02	-3.04
T-Value	-5.26	-4.64	-3.91	-3.22	-3.33
P-Value	0.000	0.000	0.001	0.004	0.003
j		-3.9	-3.2	-3.4	-3.0
T-Value		-3.84	-2.96	-3.26	-2.86
P-Value		0.001	0.007	0.003	0.009
m			-2.5	-3.2	-3.6
T-Value			-1.68	-2.15	-2.46
P-Value			0.106	0.042	0.022
pn				-2.3	-2.6
T-Value				-1.71	-1.95
P-Value				0.101	0.064
pd					-1.6
T-Value					-1.53
P-Value					0.140
S	11.0	8.96	8.66	8.35	8.13
R-Sq	50.59	68.49	71.67	74.74	77.07
R-Sq(adj)	48.76	66.06	68.27	70.53	72.09
C-p	24.6	8.6	7.4	6.3	6.0

Using our, admittedly simple, approach we would select the model including January and February temperatures. A graph of Daffodil flowering date against the mean of the two months is shown as Fig. 6.12, and is much more impressive than the temperature model we saw earlier for Hazel (Fig. 6.10).

The output from the regression for the two variable model is given below which confirms both variables are significant, and that the overall model is significant.

**Fig. 6.12** A plot of Daffodil flowering date plotted against the mean temperature of January–February ( $^{\circ}\text{C}$ )



In this case, but is by no means always true, a very similar regression is obtained by taking the average of the two months as a single variable. Over the recording period the mean of January–February temperature increased by  $2.4^{\circ}\text{C}$ , suggesting that this may have caused 19 days of flowering advancement, still 10 days short of the observed change. Adding year as a third variable confirms the significance of January and February temperature, and hints there may an additional trend in time although this doesn't quite achieve significance ( $P = 0.073$ ). Once again, some other climate variables, or those recorded at a different scale may explain the discrepancy. Alternatively, other non-recorded environmental factors, such as increased light pollution, may have contributed to the advance in flowering. However, it must be emphasised that the importance of temperature is very strong. Our experience suggests that, in temperate zones which are not water limited, temperature of up to three months prior to the phenophase seem to be the main drivers of spring phenological change.

We did not check the residuals from these models, and would probably not routinely do this unless we suspected problems. Like Analysis of Variance, regression is a procedure that is very robust to departures from Normality. Departures from Normality will not affect the estimates of the slope, but they may inflate the significance. When significance is borderline, it may be more important to check assumptions, but in highly significant examples like this, and when we have no prior suspicions of breaking the assumptions required for regression, we suggest it is not necessary.

As we mentioned earlier, there are many ways to select the variables in a multiple regression model. One method to explore the various permutations is to use best subsets regression. The example below lists the best two single variable models, the best two-variables models and so on. The selected model of January and February temperatures can be seen in the context of alternative models, for example February and March temperatures which is inferior.

### Regression Analysis: daff ffd versus j, f

The regression equation is  
 $\text{daff ffd} = 94.7 - 3.92 j - 4.11 f$

Predictor	Coef	SE Coef	T	P
Constant	94.673	4.828	19.61	0.000
j	-3.923	1.021	-3.84	0.001
f	-4.1109	0.8855	-4.64	0.000

S = 8.959      R-Sq = 68.5%      R-Sq(adj) = 66.1%

#### Analysis of Variance

Source	DF	SS	MS	F	P
Regression	2	4535.7	2267.8	28.25	0.000
Residual Error	26	2087.0	80.3		
Total	28	6622.7			

Source	DF	Seq SS
j	1	2805.5
f	1	1730.2

### Regression Analysis: daff ffd versus jf

The regression equation is  
 $\text{daff ffd} = 94.7 - 8.05 jf$

Predictor	Coef	SE Coef	T	P
Constant	94.735	4.711	20.11	0.000
jf	-8.054	1.052	-7.66	0.000

S = 8.794      R-Sq = 68.5%      R-Sq(adj) = 67.3%

#### Analysis of Variance

Source	DF	SS	MS	F	P
Regression	1	4534.5	4534.5	58.63	0.000
Residual Error	27	2088.2	77.3		
Total	28	6622.7			

## 6.8 Comparing Slopes

It may be useful to compare two regression lines to see if they differ. The interest may lie in whether the two lines are parallel but separated (i.e. one higher than the other), or whether the two lines have substantially different gradients. To illustrate

**Regression Analysis: daff ffd versus j, f, year**

The regression equation is  
 $daff\ ffd = 883 - 3.52\ j - 3.57\ f - 0.398\ year$

Predictor	Coef	SE Coef	T	P
Constant	882.7	420.8	2.10	0.046
j	-3.5208	0.9983	-3.53	0.002
f	-3.5701	0.8936	-4.00	0.001
year	-0.3980	0.2125	-1.87	0.073

S = 8.556      R-Sq = 72.4%      R-Sq(adj) = 69.0%

Analysis of Variance

Source	DF	SS	MS	F	P
Regression	3	4792.5	1597.5	21.82	0.000
Residual Error	25	1830.2	73.2		

**Best Subsets Regression: daff ffd versus pn, pd, j, f, m**

Response is daff ffd

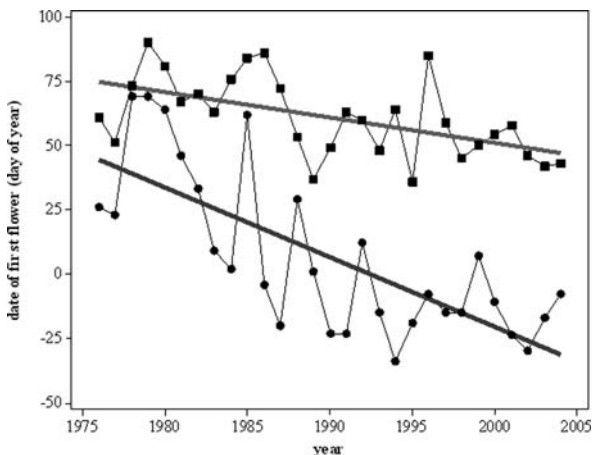
Vars	R-Sq	R-Sq(adj)	C-p	S	p	p	j	f	m
					n	d			
1	50.6	48.8	24.6	11.009					X
1	42.4	40.2	32.8	11.890					X
2	68.5	66.1	8.6	8.9594					X X
2	61.7	58.8	15.4	9.8719					X X
3	71.7	68.3	7.4	8.6625					X X X
3	69.9	66.3	9.2	8.9328	X				X X
4	74.7	70.5	6.3	8.3488	X				X X X
4	73.3	68.8	7.8	8.5840		X			X X X X
5	77.1	72.1	6.0	8.1250	X	X			X X X X

this feature we will use the Hazel and Daffodil flowering dates and examine if their regression lines on year are different from one another. The dates and regression lines are shown in Fig. 6.13.

The two lines appear to be separate and possibly of different gradient (i.e. changing differently over time). To examine whether this is the case we need to consider a hierarchy of three models and see whether each stage is a significant improvement over the previous stage (i.e. that the model better fits the data). The three models are:



**Fig. 6.13** A plot of Daffodil flowering date (*upper line*) and Hazel (*lower line*) flowering date on year in Norwich 1976–2004 with linear regression lines superimposed



1. a common line fitted to all data
2. two parallel lines (i.e. with common slope)
3. two non-parallel lines

These are tested by an analysis of the pooled Hazel and Daffodil data, with two explanatory variables being year and an indication of the species (here coded zero for Hazel and one for Daffodil).

The first model is a linear regression of first flowering date on year for all data.

Analysis of Variance for ffd (both spp), using Sequential SS for Tests						
Source	DF	Seq SS	Adj SS	Seq MS	F	P
Year(both spp)	1	13818	13818	13818	12.22	0.001
Error	56	63325	63325	1131		
Total	57	77143				
S = 33.6275    R-Sq = 17.91%    R-Sq(adj) = 16.45%						
Term	Coef	SE Coef	T	P		
Constant	3705	1050	3.53	0.001		
Year(both sp)	-1.8448	0.5278	-3.50	0.001		

This shows that the model is highly significant meaning that the pooled data shows a trend towards earliness over time (of  $-1.84$  days/year).

The second model is obtained by adding a second explanatory variable (the species indicator variable). We are using sequential tests in this analysis so the second of the F-statistics checks whether a model with two parallel lines is significantly better than just a single line. In the above example this is highly significant ( $P < 0.001$ ), the  $R^2$  has risen from 18 to 74%, and the two parallel lines are about 56 days apart.

```

Analysis of Variance for ffd (both spp), using Sequential SS for Tests

Source           DF  Seq SS  Adj SS  Seq MS      F      P
Year(both spp)   1   13818   13818   13818    37.47  0.000
spp (0=h, 1=d)   1  43041   43041   43041   116.71  0.000
Error            55  20284   20284     369
Total           57  77143

S = 19.2041  R-Sq = 73.71%  R-Sq(adj) = 72.75%

Term            Coef  SE Coef   T      P
Constant        3704.9  599.8    6.18  0.000
Year(both sp   -1.8448  0.3014  -6.12  0.000

Least Squares Means for ffd (both spp)

spp
(0=h,
1=
  Mean  SE Mean
0      6.414  3.566
1     60.897  3.566
    
```

```

Analysis of Variance for ffd (both spp), using Sequential SS for Tests

Source           DF  Seq SS  Adj SS  Seq MS      F      P
Year(both spp)   1   13818   13818   13818    43.15  0.000
spp (0=h, 1=d)   1  43041   2898    43041   134.42  0.000
spp (0=h, 1=d)*Year(both spp)  1   2993   2993    2993    9.35  0.003
Error            54  17291   17291     320
Total           57  77143

S = 17.8941  R-Sq = 77.59%  R-Sq(adj) = 76.34%

Term            Coef  SE Coef   T      P
Constant        3704.9  558.9    6.63  0.000
Year(both sp   -1.8448  0.2808  -6.57  0.000
Year(both sp*spp (0=h, 1=
0              -0.8586  0.2808  -3.06  0.003
    
```

The third model checks whether any improvement can be obtained by considering two non-parallel lines, one for each species. For this we need to include an interaction between our year and species variables.

The third term in the analysis tests whether having two non-parallel lines is a significant improvement on two parallel lines. Since the significance level is  $P = 0.003$  we can conclude that this is a significantly better fit.  $R^2$  has risen modestly from 74 to 78%. Slopes for the two lines can be estimated as  $-2.70$  ( $= -1.84$  to  $-0.86$ ) for Hazel and  $0.98$  ( $-1.84 + 0.86$ ) for Daffodil.

With care this approach can be extended to comparing more than two slopes and in comparing non-linear relationships.

## 6.9 Final Thoughts

We have only touched the surface of the potential of regression methods in phenology. Other applications are described elsewhere in this book, smoothing methods were previously discussed by Roberts (2008) and Chapter 12, and Hudson et al. (2005) have reviewed statistical methods in phenology. We would thoroughly recommend Draper and Smith (1998) to anyone that wishes to learn more. For the analysis of phenological data, analysis is typically simple. It would normally include one or both of: regression of phenological data on year to examine for trends, and regression of phenological data on temperature (or other climate variables) to look for evidence of, and to quantify, a climate response. Having described it as simple, in our experience this is usually sufficient and adequate. For spring plant phenology in temperate zones that are not water limited, temperature is the predominant driving force for leafing, flowering and ripening phenology. Not only this, but it would also seem that the temperatures of the immediately preceding months are the important ones (e.g. Menzel 2003, Estrella et al. 2007). Rarely, and even then less importantly, do temperatures from the previous autumn appear to influence spring phenology.

Whilst linear regression is very popular, it is unlikely that relationships in phenology are actually linear. They may be approximately linear within a given or an observed range, but caution needs to be used if extrapolating linear relationships into the future for predicting the effects of future climate warming on phenology. The same is true for temperature responses, since it is highly likely that a phenological event has extreme dates beyond which it cannot stray (e.g. see Sparks et al. 2000). For estimating trends, linear regression should rather be used to estimate the average trend within a period, rather than assuming that the trend is actually linear (i.e. constant). There is a large literature on curve fitting methods (e.g. Welham et al. 2007).

The examining of phenological data for trends is affected by start and end years. Data which end, for example, in 2005–2007 will have a decade of extremely warm years at the end of the series, while those ending in the mid 1980s may well terminate with a cooler period. These will give an impression of major advance and slight delay respectively. The detection of trends and temperature responses is much more reliable in series of 20 or more years.

It is now relatively easy to access large amounts of climate and other environmental data from databases and/or the internet. This allows the researcher to examine for relationships with a large number of potential explanatory variables. As the number of variables goes up the chances of spurious significant relationships also increases. Regression (and correlation) will detect relationships, but, in most circumstances, will not prove causality (see Sparks and Tryjanowski (2005) for some examples). Causality can only be proved when undertaking designed, controlled experiments; which are uncommon in the phenological literature. The researcher must exercise prudence and common sense in the selection of variables as potential explanatory variables. Preferably they should have some biological reason for inclusion. They must also be time relevant, for example there is no point in considering May temperature if flowering occurs in March.

In summary, regression can provide a relatively simple means to examine phenological data for trends and for temperature responses. Whilst being simple and straightforward, it still requires care and the application of that rarest of commodities – common sense.

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# Chapter 7

## Combining Messy Phenological Time Series

Jörg Schaber, Franz Badeck, Daniel Doktor, and Werner von Bloh

**Abstract** We describe a method for combining phenological time series and outlier detection based on linear models as presented in Schaber and Badeck (*Tree Physiol*, 22, 973–982, 2002). We extend the outlier detection method based on Gaussian Mixture Models as proposed by Doktor et al. (*Geostatistics for environmental applications*, Springer, Berlin, 2005) in order to take into account year-location interactions. We quantify the effect of the extension of the outlier detection algorithm using Gaussian Mixture Models. The proposed methods are adequate for the analysis of messy time series with heterogeneous distribution in time and space as well as frequent gaps in the time series. We illustrate the use of combined time series for the generation of geographical maps of phenological phases using station effects. The algorithms discussed in the current paper are publicly available in the updated R – package “pheno”.

**Keywords** Linear models · Gaussian mixtures · Outliers · Robust estimation · Station effects

### 7.1 Introduction

Phenology, the science of “the timing of recurrent biological events, the causes of their timing with regard to biotic and abiotic forces, and the interrelation among phases of the same or different species” (Lieth 1974) has a long tradition embedded in biological sciences. Réaumur (1735) already proposed a temperature sum model as explanation for the variation in the onset of phenological phases, such as leaf bud break or initiation of flowering in the spring in temperate ecosystems. Linné described the purpose and methods of phenological observations as early as 1751. Phenological studies played a prominent role in the discovery of mechanisms

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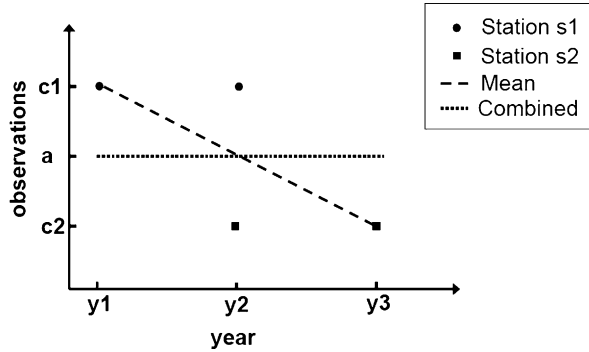
with which organisms synchronise their development and behaviour with the environmental conditions. Spectacular changes in nature that are associated with the advancement of the seasons (greening of the vegetation, colourful flowering, Indian summer or seasonal migration of animals) as well as their usefulness for the timing of human activities are at the origin of observational time series that date back as far as several centuries (see several chapters in Schwartz 2003 on the history of phenology in different countries). In recent years these data have been discovered and explored for studies in the context of climate change research. Since 1991, publications on phenology as one of the easily detectable biotic responses to climate change have experienced a rapid growth (for review see Parmesan 2006, Rosenzweig et al. 2007 and papers cited therein). The growth rate of papers was higher than in other rapidly growing research domains against a background of a slowly growing number of publications on phenology in general.

Phenological data have specific limitations that have to be considered, when inferences are to be made from their analysis. It must be realized that phenological data origin from observations rather than from exact measurements. To obtain the data phenological observers use instructions that leave room for interpretation. Additionally, the exact location of the observation and therefore the environmental conditions as well as the genotype of plant individuals are usually unknown. These various sources of uncertainty introduce an intrinsic variability to phenological observations that is difficult to quantify (Schaber 2002). Moreover, phenological time series are often incomplete and reveal large data gaps, further complicating their analysis. The problem of the uncertainty of individual time series and gaps is often reduced by averaging a set of phenological time series over a geographical area of interest or a time period of interest (e.g. Estrella and Menzel 2006, Menzel et al. 2006, 2008). This way the resulting time series has less gaps and noise of individual time series is reduced at the cost of local information.

The principal problem associated with the use of average time series is often neglected, but can be demonstrated by a very simple consideration (Figure 7.1): assume we have two phenological stations  $s_1$  and  $s_2$ , and  $s_1$  has observations in years  $y_1$  and  $y_2$ , whereas  $s_2$  has observations in years  $y_2$  and  $y_3$ . Further assume that observations at  $s_1$  are equal, say,  $c_1$  and at  $s_2$  we observe  $c_2$  in both years and  $c_1 > c_2$ . Obviously, by averaging we obtain a monotonically decreasing time series  $\{c_1, (c_1+c_2)/2, c_2\}$ . Subsequent trend analysis, which is especially popular for phenological time series (see Schaber 2002 and references therein), would show a negative trend. However, neither station actually shows a trend and thus, the resulting combined time series should also not exhibit a trend. In this simple example the resulting trend is clearly due to the fact that the stations have different observation years and that phenology at one station happens to be earlier than the other.

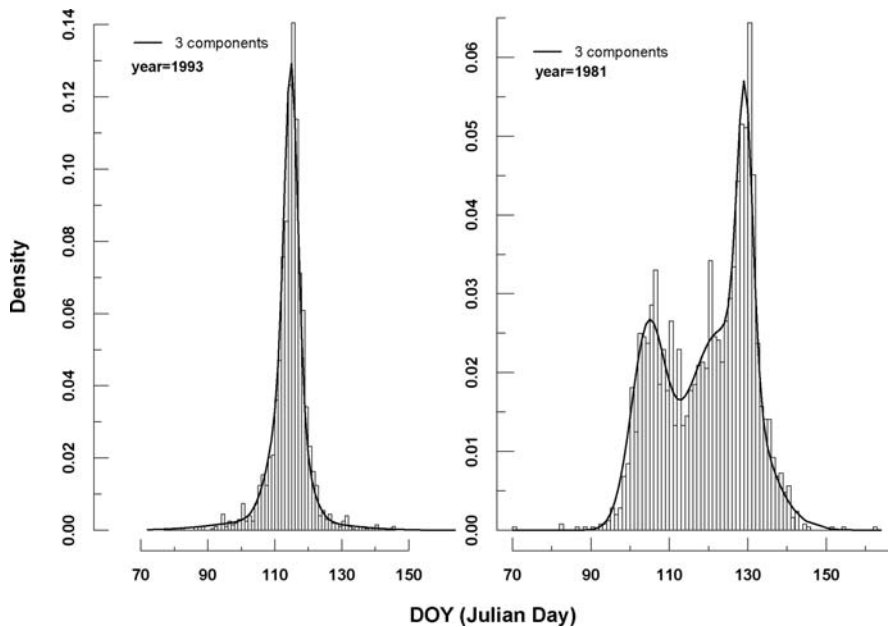
In general terms, phenological time series are unequally distributed in time and space and simple averaging in order to obtain less noisy and longer time series can lead to artifacts as demonstrated in Schaber (2002) for trends of time series of the International Phenological Gardens as published in Chmielewski and Roetzer (2001). In the above example, a solution is simple; first, we take a general mean  $a$ ,  $a=(c_1 + c_2)/2$  and correct the time series' observations according to their deviations

**Fig. 7.1** Illustration how averaging time series for station s1 and s2 can lead to undesired results because of their unequal distribution of observations in time (arbitrary units)



from the general mean (i.e.  $c_1 - (c_1 - a)$  and  $c_2 - (c_2 - a)$ ), and then take the average. Obviously, the resulting time series is now  $\{a, a, a\}$ , which shows no trend, as we expect from inspection of the single time series (Figure 1).

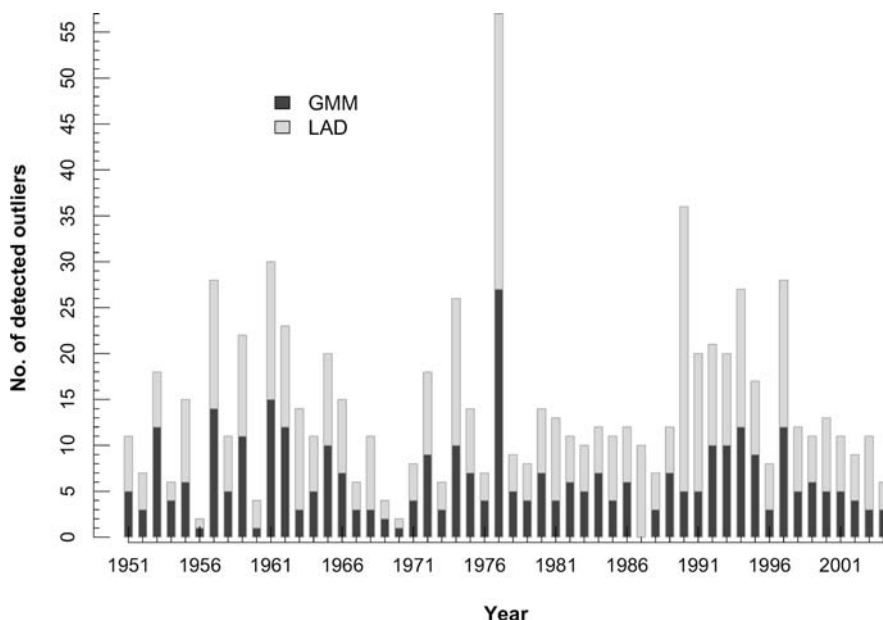
In general, this process is called combination of time series and has been introduced to phenology by Häkkinen et al. (1995) and was put into the general framework of linear models by Schaber and Badeck (2002).



**Fig. 7.2** The density function of observed budburst dates of Beech (grey bars) modelled for 1993 and for 1981 each with 3 components (curves). A large scale and consistent warming up in spring time usually produces unimodal distributions, as in 1993. In contrast, strong changes in temperature regimes as experienced in 1981 result in multimodal distributions. Still, even unimodal distributions might not be normally distributed but can be more accurately be described by a Gaussian mixture

There are several areas of application where methods for combining phenological time series can be useful and where they have already been applied. One application is to obtain a reliable series out of several messy time series. In this application the focus would be on noise reduction (Häkkinen et al. 1995, Linkosalo et al. 1996, 2000, Linkosalo 1999, 2000, Schaber 2002). Another main application is to construct a long time series for trend analysis. In this application data gap filling is of primary interest (Schaber and Badeck 2005). Additionally, combined time series can also be used to find outliers in individual time series (Linkosalo et al. 2000, Schaber 2002, Schaber and Badeck 2002, Doktor et al. 2005). However, applying combined time series for outlier detection might lead to removal of correct observations, if the between station differences vary strongly at inter-annual time scales due to differences in the temperature trajectories, as already hypothesized by Schaber and Badeck (2002). Doktor et al. (2005) discussed some empirical evidence of cold spells that delay the transition to subsequent phenophases cause systematic deviations of the frequency distribution of dates of phase onset. They also introduced Gaussian mixtures as a tool for the quantification of the inter-annual variation in between station differences. This approach can potentially be integrated into the use of combined time series for outlier detection in order to avoid assignment of false outliers.

In the following, we will shortly introduce the method of combination of phenological times series by different types of linear models and discuss some practical



**Fig. 7.3** Number of detected outliers per year for Beech using the outlier detection algorithm of Schaber and Badeck (2002) (LAD) and using Gaussian Mixture Models (GMM). The mixture components are determined and parameterised by an optimisation algorithm



issues. Moreover, we will discuss outlier analyses and show applications. We present the algorithms for integration of Gaussian normals (Figure 7.2) into the outlier detection with combined time series and illustrate the effect of this model improvement (Figure 7.3).

One useful result of the construction of combined time series is the extraction of station effects, (i.e. the characteristic deviation of the date of phase onset at a given observational station relative to the population of all stations). This result is less sensitive to gaps in the data series and different length of observation periods than the deviation from average values. It can be applied to producing maps of average geographical variation in the onset of a phenological phase. We illustrate this application for the bud break of beech in Germany (Plates 1, 2 and 3).

## 7.2 Linear Models of Phenological Time Series

### 7.2.1 Linear Models

It is reasonable to assume that over a climatologically sufficiently homogeneous region, (e.g. middle Europe or Central North America), the phenological development of certain phases is consistent concerning years and stations. This means that a year, which is particularly late, should be late for all stations, and a station that is particularly late, because for example, it is situated on a top of a mountain, should be late in all years. Putting this in mathematical terms, we say that the effect of year  $y_i$ ,  $i=1, \dots, n$  and the effect of station  $s_j$ ,  $j=1, \dots, m$  are independent and additive, such that

$$o_{ij} = a + y_i + s_j + \varepsilon_{ij}, \quad i = 1, \dots, n \text{ and } j = 1, \dots, m. \quad (7.1)$$

where  $o_{ij}$  is the observation in year  $i$  at station  $j$  and  $a$  is the general mean.  $\varepsilon_{ij}$  is an error term that is usually assumed to be homoscedastically normally distributed around zero with some variance  $\sigma^2$ , that is

$$\varepsilon_{ij} \propto N(0, \sigma^2) \quad (7.2)$$

In statistics, (7.1) is called a linear two-way crossed classification model. Usually, additional conditions are imposed that assure that a unique solution exists, such as setting

$$\tilde{y}_i = a + y_i \text{ and } \sum_{j=1}^m s_j = 0. \quad (7.3)$$

We call  $\tilde{y}_i$ ,  $i = 1, \dots, n$  the combined time series.

Given observations  $o_{ij}$ , that may have missing data, (7.1) and the conditions (7.3), it is essentially straightforward to estimate the  $\tilde{y}_i$  and  $s_j$  using least-square optimisation (i.e. minimizing the sum of squared residuals SSR),

$$SSR = \sum_{i,j} \varepsilon_{ij}^2. \quad (7.4)$$

### 7.2.2 Fixed and Mixed Effects Models

Depending on the type of analysis we are interested in, we can treat the year and station effects differently, which has consequences for the type of estimation procedure we apply. For instance, when we are mainly interested in the combined time series  $\tilde{y}_i$ , we can refrain from estimating the specific station effects but rather consider the stations to be randomly distributed. Thus, we treat the  $s_j$  as a random variable

$$s_j \propto N(0, \sigma_s^2) \quad (7.5)$$

and estimate the variance component  $\sigma_s^2$ , rather than station effects  $s_j$ . This is called the mixed model, because we have one fixed and one random effect. For this type of analysis special estimation and analysis procedures exist (Searle 1987, Milliken and Johnson 1992, Pinheiro and Bates 2000). Examples of the application of mixed models to obtain reliable phenological time series can be found in Schaber and Badeck (2002, 2005).

On other occasions, we might be interested in the year effects as well as in the specific station effects in order to identify stations that are particularly late, for instance. In this case, we would treat both effects as fixed. In Section 7.3.2 we will give an example. For details on linear models and the large theoretical body that comes with it, please refer to Rencher (2000), Searle (1971, 1987) and Milliken and Johnson (1992) and the literature cited therein.

### 7.2.3 Practical Issues and the R Pheno-Package

As already indicated, linear models constitute an entire field in statistics and calculations are far from being as easy as just calculating an average. The large theoretical body that comes with the theory of linear models can even be an obstacle rather than being helpful for phenological applications. Therefore, the authors wrote the software package “pheno: auxiliary functions for phenological data analysis” (Schaber 2007) that was designed to make calculations of combined phenological time series and station effects as easy as possible. This software is freely available as a package for the free statistical computing environment R (R Development Core Team 2007). The user has just to provide a table with three columns (observation, year, station) to a function corresponding to the analysis of interest, without having to worry about the calculations. All subsequent examples were calculated using the pheno-package.

One especially useful feature of the pheno-package is that it automatically handles large data sets. To illustrate the problem, we refer to the example in the following Section 7.2.4. In order to calculate the average time series of beech and

the station effects for Germany over the years 1951–2004, we considered 74,996 single data points from 2,318 stations. For calculation of the fixed year and station effects, this involves the inversion of a  $74,996 \times (2,319 + 53 + 1)$  matrix. With the usual 8-byte number coding the matrix itself occupies around 1.4 GB. With the extra storage needed for matrix inversion, even nowadays most personal computers would exceed their working storage capacity with this operation. Fortunately, the matrices involved mainly consist of zero-entries, such that the application of sparse matrix algorithms saves a great deal of computational and storage resources. Sparse matrix algorithms are provided in other R-packages such as *SparseM* and *quantreg* (Koenker and Ng, Koenker 2006) and are already integrated in the R-*pheno* package. This way, combined time series for whole Germany can be computed on a regular personal computer.

Another prerequisite for the application of linear models is that the time series be connected or overlapping. For many stations this is usually not a problem, but for few data (stations or years) it is recommendable to check (Schaber 2002). There are procedures within the R *pheno*-package that test for connectivity and automatically extract connected sets of time series.

## 7.2.4 Outlier Detection

As already mentioned in the introduction, obtaining phenological data is often an error-prone process (Schaber 2002, Schaber and Badeck 2002). Therefore, a proper outlier detection method is indispensable. One of the few types of errors that can be detected is the so-called month mistake. Schaber and Badeck (2002) developed a method to detect month mistakes with combined time series. The usual least-square estimation of combined time series is sensitive to outliers. Therefore, Schaber and Badeck (2002) recommended applying a robust estimation procedure that minimizes least absolute deviations (LAD) (7.6),

$$\text{LAD} = \sum_{ij} |\varepsilon_{ij}|, \quad (7.6)$$

before applying the classical least-square estimation. Residuals  $\varepsilon_{ij}$ , (i.e. the difference between observed and predicted values), that are estimated to be larger than 30 days are considered as month mistakes and are removed. The details of the procedure are described in Schaber and Badeck (2002) and are also implemented in the R *pheno*-package.

## 7.2.5 Gaussian Normals

The assumption that year effects and station effects are independent may not always hold true. This is the case when the inter-station differences vary due to the annual

weather trajectories. Years with retarded phase onset in a subset of phenological observation stations due to a cold spell as compared to years without intermittent cold spells are an example of this class of interactions. As an extension to the outlier detection with LAD estimation, frequency distributions of observed budburst dates can be characterised and modelled using Gaussian Mixtures Models (*GMM*) (Figure 7.2). In many years, observations of a single species can be approximated by a probability density function (*pdf*), which consists of one, two or more underlying distributions. These can be mainly attributed to changing weather situations within spring, which alter the phenological pace. *GMM* quantify the number and type of the underlying distributions and thereby allow distinguishing years with different temporal evolution of budburst dates in a quantitative manner. The models can describe distributions with unknown underlying patterns and have the property of being able to represent any distribution of natural observations (Gilardi et al. 2002). A mixture distribution with continuous components has a density of the form (Poland and Shachter 1994):

$$f(x) = p_1 f_1(x) + \dots + p_n f_n(x) \quad (7.7)$$

Where  $x$  is the probability to have an observation at a certain day,  $p_1, \dots, p_n$  are positive numbers summing up to one and  $f_1(x), \dots, f_n(x)$  are the component densities (7.7). To determine potential outliers one has firstly to analyse the uni- or multi-modal frequency distribution to identify the main underlying components (mixtures) and their describing parameters mean, standard deviation and weight ( $\mu_k, \sigma_k, p_k$ ).

For each year  $i$ , all observations  $o_{ij}$  are related to a component's mean  $\mu_k$ . The component  $k_a$  an observation  $o_{ij}$  is most related to is determined based on the frequencies  $f_{ijk}$  of component  $k$  at the observation day  $o_{ij}$ :

$$f_{ijk} = \frac{np_k}{\sigma_k \sqrt{2\pi}} e^{-\frac{(o_{ij} - \mu_k)^2}{2\sigma_k^2}}, \quad (7.8)$$

where  $n$  is the total number of observations of the analysed year  $i$ . Then,

$$k_a = \arg \max_k f_{ijk} \quad (7.9)$$

An observation is declared to be an outlier if

$$|o_{ij} - \mu_{k_a}| \geq 30 \quad (7.10)$$

An optimisation algorithm is applied on the minimisation of several (here maximum four) Gaussian Mixture functions. Due to the authors' experience from phenological data analysis it is very unlikely that changes in temperature regimes with a sustained impact on the phenological evolution happen more than three times within the period the plant population is experiencing budburst, at least in Central Europe. Akaike's Information criterion (Akaike 1974) is applied to choose the most appropriate model, balancing between model complexity (number of components)

and model fit. The parameterised mixture components are used for outlier detection in order to reduce the number of falsely detected outliers in years showing bi- or multi-modal distributions (i.e. in years with a high variability of observed phenological events).

Obviously, this method is more conservative as the one based on LAD estimates. LAD estimation assumes that each year the observations are distributed around one general mean (the year effect) whereas applying Gaussian mixtures we assume that there might be several means. We detect only outliers at the margins of the whole Gaussian mixture and consequently less than before (Figure 7.3).

Interestingly, even a unimodal distribution could be more accurately defined by a Gaussian mixture (Figure 7.2). In fact, there was not a single year between 1951 and 2004 where the distribution of observations could be described by a single normal distribution ( $P < 0.01$ , Shapiro-Wilk test).

## 7.3 Applications

### 7.3.1 *Gaussian Normals*

The two outlier detection methods are compared with respect to the number of observations declared as outliers in each year, respectively. As expected *GMM* identifies, in general, fewer outliers (Figure 7.3). This, however, comes at a cost of false negatives (declaring an observation not to be an outlier when it actually is).

### 7.3.2 Station Effects

We calculated the fixed effect model (1) with constraints (2) for whole Germany for the years 1951–2004 for beech budburst without month-mistakes. We considered only stations that had at least 20 observations. After the removal of 433 outliers according to the robust estimation method we considered 74562 observations from 2318 stations. In Plate 1 we present a map of the calculated station effects plus the general mean  $m=120$  (30th of April in non-leap years) in day of the year (DOY). To our knowledge, this is the first time that a consistent map for the characteristic timing of a specific phenological phase for such a large region is presented. Note that for this application the underlying trends (see Schaber and Badeck 2005) have not been removed.

The underlying assumption that the observations within the relatively large geographic space of Germany (357,092 km<sup>2</sup>) are elements of a unimodal population is illustrated with Figure 7.2 (curve for year 1993). In many cases a station net well distributed over a geographical space with continuous gradients of environmental conditions will result in such a distribution. However, the distribution may be different from unimodal, if a geographical domain is made up by two sub-domains with very different environmental conditions (Figure 7.2, year 1981).

The maps of the station effects (Plate 1) and the interpolated station effects by external drift krigging (EDK) (Plate 2) illustrate phenological responses to

1. climatological differences between regions at similar elevation (e.g. 50–100 [m] asl): the northern lowlands of Saxony are phenologically later than the Muensteraner Becken and the Northern Upper Rhine valley. The average March and April temperatures (1951–2003) are 3.94 and 8.27 °C, respectively in Saxony at 15 stations at 12.4–13.9 longitude and 51.4–51.9 latitude. They are 5.19 and 8.62 °C, respectively in the vicinity of Muenster at 11 stations at 7.0–7.9 longitude and 51.7–52.2 latitude. They are 6.26 and 9.91 °C, respectively in the Northern Upper Rhine valley at 7 stations at 8.3–8.45 longitude and 49.3–49.9 latitude,
2. the lapse rate across elevational gradients (the higher, the later),
3. the combined influence of the inverse lapse rate of early spring (see Table 1 and Figure 2 in Doktor et al. (2005)) and general climatological gradients between east and west Germany (northern lowlands: the closer to the sea the later at similar elevation).

The difference map (Plate 3) between station effects and station averages shows a slight general bias towards later combined station effects especially in the eastern part of Germany. These differences might be due to gaps in the time series, which are particularly common in this part of Germany. An indication that this is indeed the case is the fact there is a slight negative tendency between difference and number of observations per station ( $P < 0.07$ ).

## 7.4 Summary

Phenological data are messy data. Their analysis calls for appropriate methods that can deal with their inherent uncertainties as well as correct for effects due to their heterogeneous distribution in time and space. Simple averaging as a method to accommodate noise and gaps is likely to lead to erroneous results especially when the ratio of gaps to total number of observations is high or when a low number of observation series is averaged. The application of linear models to obtain combined time series constitutes an adequate method to handle gaps and noise in individual time series.

The application of Bayes statistics is an alternative way of analysing messy phenological datasets (see e.g. Dose and Menzel 2004). Future work should compare Bayes statistics to the methods discussed in the current paper and address the respective sensitivity to assumptions about priors and underlying distributions as well as to the types of errors and data gaps.

The approach of Gaussian mixtures to consider station  $x$  year effects can be further developed by assigning stations to tentative mixture components before checking for outliers or including mixed terms in the linear model (1).

With ongoing efforts to expand the databases of phenological observations by data mining it is very likely that more data sets with sparse data and data gaps will become available in the near future. For example, see the instructive account of the spatial and temporal coverage of the Japanese cherry flowering time series and the step-wise expansion of the data base (Aono and Kazui 2007). The methods described with the current paper are available as an R-package. The routines within this R pheno-package allow for the construction of combined time series that can serve for time series analyses. They can be applied for outlier detection. The calculation of station and year effects facilitates geo-statistical analyses of geographic patterns in the onset of phenological phases as well as their relation to weather pattern in specific years.

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# Chapter 8

## Phenology for Topoclimatological Surveys and Large-Scale Mapping

François Jeanneret and This Rutishauser

**Abstract** Biotic and abiotic phenological observations can be collected from continental to local spatial scale. Plant phenological observations may only be recorded wherever there is vegetation. Fog, snow and ice are available as phenological parameters wherever they appear. The singularity of phenological observations is the possibility of spatial intensification to a microclimatic scale where the equipment of meteorological measurements is too expensive for intensive campaigning. The omnipresence of region-specific phenological parameters allows monitoring for a spatially much more detailed assessment of climate change than with weather data. We demonstrate this concept with phenological observations with the use of a special network in the Canton of Berne, Switzerland, with up to 600 observations sites (more than 1 to 10 km<sup>2</sup> of the inhabited area). Classic cartography, gridding, the integration into a Geographic Information System GIS and large-scale analysis are the steps to a detailed knowledge of topoclimatic conditions of a mountainous area. Examples of urban phenology provide other types of spatially detailed applications. Large potential in phenological mapping in future analyses lies in combining traditionally observed species-specific phenology with remotely sensed and modelled phenology that provide strong spatial information. This is a long history from cartographic intuition to algorithm-based representations of phenology.

**Keywords** Downscaling · GIS · Mapping · Spatial modelling · Topoclimate

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## 8.1 Phenology in Space and Time

### *8.1.1 At the Crossroad of Interdisciplinarity*

Many scientific disciplines make use of phenology, each one having its own motivation and its own approach (Jeanneret 1996). Biologists are interested in the behaviour of single species and plant communities (Visser and Holleman 2001, Newstrom et al. 1994), doctors in pollen release (Confalonieri et al. 2007), agronomists in plant growth and environmental risk (Rosenzweig et al. 2007), and remote sensing specialists in the annual green-up in midlatitude climate regions called the “green wave” or spring green-up. The green wave is equivalent to phenological events representing the onset of plant photosynthetic activity in the spring or of the start of the growing season (SOS) (Schwartz 1994, Reed et al. 2003).

Geographers discovered the spatial dimension of phenology that is the role of geographical factors like latitude, altitude, distance to the coast, landforms and others (Schnelle 1955, Jeanneret 1972, Messerli et al. 1978). Plants are present in both natural and urban landscapes, hence representing the possibility of increasing the observation density by raising the number of observation sites. Meteorological point measurements are limited to costly instruments at single sites. However, for weather forecasts and long-term climatological studies, methods have been developed to overcome the difficulty of spatial interpolation of point measurements (e.g. WMO 1996, Szalai et al. 2006).

Geographers traditionally address questions of spatial dimensions or representations of specific phenomena and their interplay in space. The science of geography has also discovered the importance of time and temporal development (e.g. Hägerstrand 1967) and established landscape history. Phenology within geography seems to have followed a similar development. In recent years, the importance of environmental questions put forward the spectacular impact of climate change phenology (e.g. White et al. 2003, Koch et al. 2006). Temporal changes, either with a natural or anthropogenic origin, have significantly altered phenological rhythms (e.g. Parmesan 2006) and seasonal development (see Chapter 3). The changes were attributed to an anthropogenically induced temperature increase (Rosenzweig et al. 2008). As a consequence, the focus of research has also changed towards temporal analyses of phenological time series (see Chapter 7 and Chapter 11). Spatial applications were initiated as early as the 1700s by Carl Linné (“so as to show how areas differ” Menzel 2002, Freer 2003) and successfully implemented (e.g. Friedrich Schnelle (1955)) and they remain a core application of phenology. The wide distribution of the International Phenological Gardens (IPG) network has also led to an awareness of spatial patterns at a continental scale (Rötzer and Chmielewski 2001).

### *8.1.2 Sources of Data Acquisition*

Even if the planet is widely vegetated, there are limits to the idea of a universal presence of observable plants: First, plants are limited in their spatial distribution

as plant species only occur in specific locations. Species ranges are changing under different climate conditions (Parmesan 2005), which means that it might not be possible to observe one species at one location over a long time. Second, much of the Earth's surface is covered with cultivated or at least very much modified vegetation. As a consequence, we have to account for both human-induced and natural variability. Third, observers are not everywhere. This is especially true when a high spatial coverage of an observation network is required. In addition, networks have to deal with a changing number of observers and tend to lose observers as they grow older (e.g. Studer et al. 2005).

Different methods of data gathering for phenological mapping have been employed. The first one is based on observations from a number of stations where observers note the phenological data of specific species. As a consequence, the maps represent species-specific onset dates such as the flowering of the apple tree or grain harvest in Europe (Schnelle 1955). The maps contain uncertainties induced by different interpolation methods.

The second method – itinerating phenological surveys – consists of a survey along selected routes that allow observation of the vegetation's phenological state (Ellenberg 1956, Schreiber 1977, Ahas and Aasa 2001, Crimmins et al. 2008). This approach is also called relative phenology, because it is based on comparative observations of different surveys (Plate 4). Observations are made on one or only very few defined days. The analysis stresses relative differences of phenological stages and their spatial distribution along the way. This method, set up by Ellenberg in Germany (1956, 1974), has been widely applied, for example, by Schreiber et al. (1977), Schreiber (1983) and Chytrý and Tichý (1998) in central Europe and by Böhling (1994) and Bergmeier (1998) in the Mediterranean area.

Another method is phenological site assessments or relative phenology which means mapping by comparing the seasonal development of plant communities at different sites (Ellenberg 1956, Schreiber et al. 1977). Transects are surveyed several times in relation to a calibration run of standardized phenological observations. Afterwards the observations are compiled to create a generally large-scale map (e.g. for agricultural applications). As this method is mainly applied in spring, the result has sometimes been called growth-climate or thermal mapping. This name is somewhat controversial as some critics have the opinion that a phenological product is more than a thermal issue, related to the short period of observation (Primault 1977). The use of the phrase 'relative phenology', however, would suggest that it is the result of a comparison of vegetative development within a short time.

More recently, remote sensing techniques have been used for spatial upscaling and a representation of ground-observed phenological events in space (e.g. Stöckli and Vidale 2004, Reed et al. 2003). However, technical and analytical challenges still remain such as the comparability of different data sources and/or frequent temporal gaps.

Remote sensing is the third approach to record the annual changes of the Earth's surface greenness or green wave (e.g. Reed et al. 2003). Land surface phenology (LSP) measures foliage development over an area defined by the size of the satellite resolution as opposed to the phenology of organisms. We define LSP as the study of

the spatio-temporal patterns of the vegetated land surface observable with synoptic sensors at spatial resolutions and extents relevant to meteorological processes in the atmospheric boundary layer according to de Beurs and Henebry (2005 and in Chapter 9).

Remote sensing deals mainly with green-up, maturity, senescence and dormancy at the spatial scale of the canopy (Zhang et al. 2003) and can be most successfully applied to relatively homogeneous surfaces such as forests, meadows and crop fields.

For tracking LSP in temperate climates, the onset of green-up (or start of season: SOS), senescence (or end of season: EOS), the timing of the maximum (peak) of the growing season and the duration of greenness are the metrics most frequently calculated from image time series (Stöckli and Vidale 2004, Reed et al. 2003). Station observations are used to ground truth the satellite data (e.g. Studer et al. 2007).

On the other side, LSP is limited in spatial resolution and cannot pick up specific species and other phases. Thus, remote sensing is not suitable for specific aspects of phenology – assessment of single phases or species – but can contribute to small scale mapping (Table 8.1).

**Table 8.1** Types of phenological infrastructure: network operators, data user and life expectation

	Operator	Users	Duration
National and official networks	state agencies	Research	decades
Special networks	research agencies, universities	Research	years
Site assessment/relative mappings	research agencies, universities	Planning authorities	one or several seasons
Public networks	Private, media	Media, public	unknown

### 8.1.3 Available Phenology Data for Survey

In order to understand the available data for spatial analyses, some classification of the acquisition infrastructure is required (Table 8.1). This is also important if new infrastructure is planned. And it is also necessary to consider the actual and potential use as well as the users for making decisions on maintaining existing infrastructure.

The most common infrastructure is a network organisation with fixed stations. This setting offers continuity over time at a constant point in space. Short-term observation campaigns allow an intensive assessment usually without a long-time monitoring goal. Internet-based public networks have characteristics similar to intensive short-term campaigns lacking continued observation from a defined site (Koch et al. 2006). Image-based assessments – terrestrial and remote sensing – produce real-time information, but require intensive handling and interpretation of the data. They comprise the potential for long-term observation in space.

Schnelle (1955) noted that with a station density in a network of 1–2 per 100 km<sup>2</sup>, mapping is possible up to a scale of 1:500,000. More detailed surveys require a significantly higher station density. Here, camera-equipped stations could supplement observers and allow revising and checking of phenological data (Ahrends et al. 2008).

Sparks and Collinson (2008) reported that there are over 40,000 registered recorders in the UK Phenology Network throughout Britain. Unlike in other European schemes, there are no fixed locations observed every year. The observations are presented in a website that permits the examination of summary records and a dot map showing the progression of the seasons ([www.phenology.org.uk](http://www.phenology.org.uk)). The Netherlands runs a comparable public network ([www.natuurkalender.nl](http://www.natuurkalender.nl)).

Basically, official or private network operators are possible, some infrastructures are designed for a specific use and some for general monitoring – the latter is most important in periods with intensive changes in the environment (Tables 8.1 and 8.2).

**Table 8.2** Phenological data collection methods and their characteristics

Data source	Typical data density [stations/km <sup>2</sup> ]	Typical spatial resolution [km <sup>2</sup> ]	Time resolution	Observation duration [years]	Goal and motivation
Network observation	100–500	1–10	Weekly	decades	representative monitoring
Site assessment	linear transects (e.g. 0.3 km/km <sup>2</sup> )	0.1–1	short missions	one to several seasons	detailed survey
Remote sensing	any	1	Weekly	spring	real-time monitoring
Special networks	Ca. 100	0.1–1	varying	one to several seasons	specific research
Photo-phenology	isolated stations	any	any (real time)	years to decades	methodological research
Public networks	dependent on participation	dependent on participation	real time	dependent on funding policy	Individual, public or commercial interest
Closet observers	individual	individual	Daily to yearly	years to decades	Individual interest

## 8.2 Network and Survey Data for Mapping

### 8.2.1 *The Space: Phenology for Survey*

Different methods of data gathering for phenological mapping have been applied such as phenological networks, the itinerating phenology survey and remote sensing methods. The first one is based on observations from a number of stations where

observers note the phenological data of specific species. As a consequence, the maps represent species-specific onset dates such as the flowering of the apple tree or grain harvest in Europe (Schnelle 1955, Rötzer and Chmielewski 2001). The maps contain uncertainties induced by different interpolation methods, based on different interpolation bases like gradients or subjective appreciation and pondering of factors.

For very detailed spatial analyses of environmental change, phenology can be considered a “monitoring zoom”. Phenology is predisposed for surface surveys as plants grow in most locations. The cartographer Eduard Imhof (1972) considered phenological maps as the most continuous representation of the land surface, despite the fact that no species is omnipresent, however, plants are so numerous that a phenological map can be considered as a continuum.

**Table 8.3** Climatic/meteorological vs phenological topoclimatic assessment

	Meteorological measuring station	Phenological observation
Time sequence	As often as measurements are made (up to nearly continuous, e.g. 10 minutes)	As often as an observer or a camera records phenological phases or development
Scale	Meso to topo	Topo
Data acquisition	Instrumental measurements	Subjective observations or image interpretation
Standard	Highly standardized	Standards within one network

### 8.2.2 Classical Phenological Maps at Medium And Large Scale

Phenological maps have been drawn since the late 19th century (Hoffmann 1881, Ihne 1895 in Schnelle 1949, Schnelle 1965, 1979, Mäde 1952). Classical manual cartography produced maps with intuitive interpolation, generally making use of the extensive personal experience and knowledge of the terrain conditions of the cartographer. The first computer-drawn maps appeared in the 1960s (Lieth and Radford 1968, Caprio et al. 1974, Jeanneret 1974, Puppi-Branzi et al. 1985).

The phenological maps first published in the Climate Atlas of Switzerland (Plate 5, Primault 1984) resulted from isophane curves based on the personal experience of the author. Primault harmonized phenological events according to different climate areas based on a regional standard altitudinal gradient and the slope orientation. He drew four nation-wide maps of Switzerland for the flowering of dandelion (*Taraxacum officinale*, the beginning of spring), the start of hay mowing (the beginning of early summer), the blooming of lime trees (*Tilia platyphyllos*, the beginning of summer), and beech leaves changing colour (*Fagus sylvatica*, the beginning of autumn). The four selected phases represent four seasonal development stages during the vegetation period.

In 2002, these four maps were integrated into the digital version of the Atlas of Switzerland version 2.0 (Hurni and Raber 2004, their Figure 2). This is a conclusive demonstration of digital phenological mapping but it cannot be considered a modelled map. However, a main feature of this atlas is the zooming possibility between approximately 1:1 million and 1:100,000. Furthermore, thematic maps of the same atlas can be activated and shown as additional overlays (Plate 5, Sieber and Huber 2007).

## 8.3 Mapping in Detail: Topoclimatic Scale

### 8.3.1 A Special Network in Mountainous Areas

At the end of the 1960s, regional planners needed detailed climatic maps that could be produced quickly at low cost. For this reason, meteorological measurements requiring expensive equipment such as weather stations, high spatial resolution at topoclimatic scales and long temperature series were not suitable. Furthermore, the maps needed to be easily produced, interpreted and show a detailed coverage of the Canton or state of Bern, Switzerland. Thus, the Geographical Institute of the University of Bern set up a mesoclimatological network in the Canton of Bern (5,961 km<sup>2</sup>), and adjacent areas covering a total of 7,000 km<sup>2</sup>. The Canton is oriented North-South, representing a cross-section through the main geographical regions of Switzerland: the chains of the Jura mountains in the North, the plains and hills of the Midland (or Plateau) in the centre and the high mountain environment of the Alps in the South.

The network started in 1970 with 200 stations, with over 500 observed sites. Therefore, the station density was one station per 30 km<sup>2</sup>. In subsequent years, the station density dropped to one to 150 km<sup>2</sup>. The network has continued operating since, even though many more stations have closed. In 2008, ten stations were still in operation. The average length of the time series is about 7 years, ranging from 2 to 40 years for one observer.

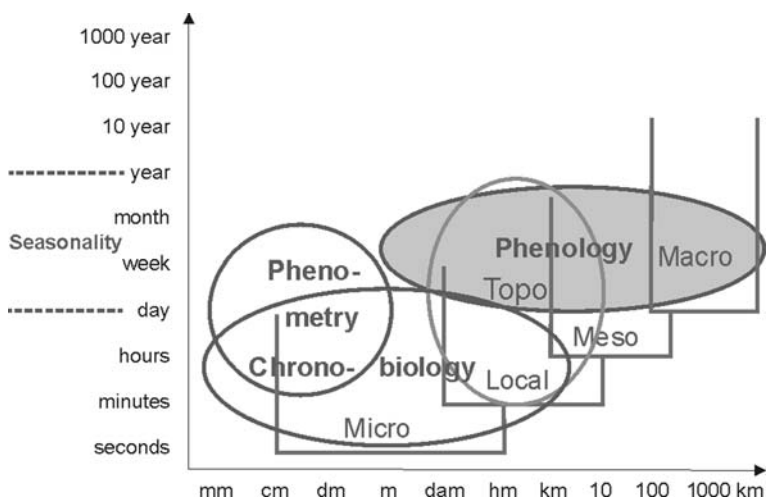
The phenological observations were collected throughout the year, mainly by former students and geography teachers (Jeanneret 1970, 1972). The instruction book of the national network of the Swiss Meteorological Institute is used to obtain compatible results with their existing longer series and phenological calendars (Defila 1991, 1992). In addition to the metadata for the observation site being recorded the local observers were also asked to record details from several sites. This information included different slopes, aspects and altitude (Jeanneret 1971). Based on their local expertise, observers watch out for typical topoclimatic differences within their area, undertake observations on plant phenology in summer and on fog and snow in winter. These data allowed analyses on regional topoclimatic patterns. Emphasis was put more on spatial rather than seasonal differentiation. The phenological program is limited to five phases, each representing the beginning of one season: the blooming of hazel (*Coryllus avellana*) for early spring, dandelion (*Taraxacum officinale*)

for full spring, apple trees (*Pyrus malus*) for late spring, wheat harvest (*Triticum vulgare*) for summer, colouring of the beech leaves (*Fagus silvatica*) for autumn. Work undertaken for the planning authorities established during the 1970s comprise several research programs on phenology, fog and snow (Messerli et al. 1978, Jeanneret 1996).

### 8.3.2 *Topo Scale Maps – A Genuine and Unique Product of Phenology*

Topoclimatic-scale phenological mapping focuses on terrain characteristics (Figure 8.1). The goal is the representation of a phenological survey that is interpolated accordingly to independent factors (i.e. altitude, slope angle and orientation, relative topography). This means that factors controlling the interannual variability of phenology are not taken into consideration (i.e. temperature or moisture). The survey of plant phenology is then another step independent of the observed and surveyed data (Plate 6).

Phenological maps reflect the spatial pattern of plant phenological development stages as an independent representation of climatic factors. As a consequence, the remaining driving factors include climate. Topoclimatic phenological maps as a tool for bio-monitoring allows independent comparisons with many other factors (e.g. slope, latitude, altitude, continentality) that also influence the plants. The total of all independent factors eventually leads to integrated spatial modelling.



**Fig. 8.1** Phenology and seasonality studies represent a specific range in temporal and spatial scales of climates (adapted after Oke 1987, from Jeanneret et al. 2008). Phenology offers an original and genuine contribution at topo-scale



## 8.4 Interpolation, Extrapolation and Spatial Modeling

### 8.4.1 Phenology Mapped at Mesoscale

As soon as phenological observations are recorded in a network, maps for visualisation become an interesting product. Differences in phenological rhythms occur in diverse regional patterns and are in turn explained by growth factors. Thus, they reflect the spatial distribution of environmental conditions.

If plant phenological data are available, different phenological behaviour can be assessed. And if the patterns are dependent on the growth condition of the location, phenological data are suited for a survey. Hence the idea of mapping phenological data, which has a long tradition (Schnelle 1955), with modern examples of small-scale mapping (Roetzer and Chmielewsky 2001), sometime based on remote sensing techniques (Karlsen et al. 2007).

Motivations to map phenology are numerous, often driven by requirements for example: regional planning (Jeanneret 1974, Volz in Messerli et al. 1978), aerobiology (pollen emission, Branzi and Zanotti 1989, García-Mozo et al. 2006), and agronomy (Mariani et al. 2007).

### 8.4.2 Modelled Phenological Maps in GIS

In an early attempt, Klante (1986) produced what was called a synthetic phenological map of the bloom of lilac, surveyed at 223 stations between 1951 and 1980. It was based on a raster system of 1 km extending 156 by 145 km. Altitudes and continentality gave the gradients for interpolation (i.e. 3.9 days per 100 m, -0.97 days per 100 km North-South, -1.88 days per 100 km East -West). Branzi and Zanotti (1989) presented a method for an empirical model using phenological and topographical data to develop a phenological delay matrix. The matrix could be used to produce chronological, synoptical and differential phenological maps.

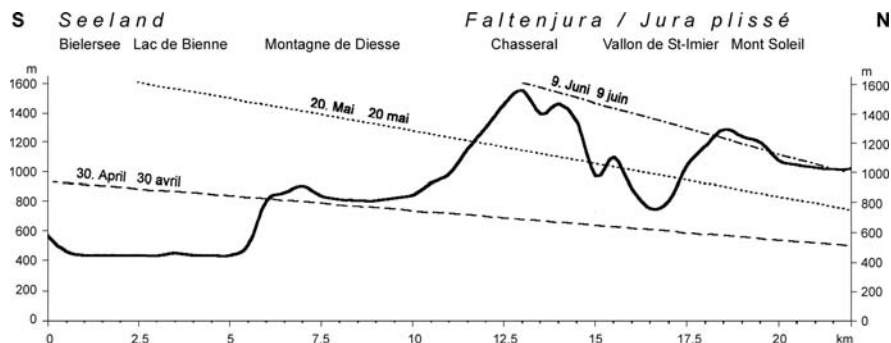
Régnière and Logan (2003) introduced methods designed for interpolation of climatic variables that can also be applied to phenological point data.

$$Y = a + mE \cdot E + mN \cdot N + mW \cdot W \quad (8.1)$$

Where Y is a climate value, E is elevation, N is latitude and W the longitude, a is an intercept constant and mE, mN and mW are regional thermal gradients for elevation, latitude and longitude.

Rötzer and Chmielewski (2001) is an example of the widely used method designed for interpolation of phenological values for small-scale mapping:

$$pp(x,y,z) = c + ax \cdot x + ay \cdot y + az \cdot z \quad (8.2)$$



**Fig. 8.2** Cross-sections through the Jura Mountains with the dates of blooming of hazel and dandelion, showing the average day number and date (day and month). The gradients vary from one area to the other: the influence of thermal inversions might interfere in the South of the Jura, the plateau situation in the North. This phenological phase reveals particularly great gradients (after Bucher and Jeanneret 1993)

where  $pp(x, y, z)$  is the starting date of the phenological phase at altitude  $z$ , longitude  $x$  and latitude  $y$ ,  $c$  is a constant and  $ax$ ,  $ay$  and  $az$  are regression coefficients.

Based on a similar method, maps of every observation year and mean maps can be produced with a Geographic Information System (GIS), using correlations of grid points with elevation (days per m for each phenological phase). An example of this is the phenological maps for Germany produced by Müller-Westermeier (2006).

In a complex topography and at bigger scales, more factors must be taken into consideration in order to perform a genuine downscaling. A cross-section reveals that there are more factors involved than altitude (Figure 8.2). Other environmental variables which should also be applied to phenological surveys are (Carrega 2006):

- Position: negative altitude difference within 100 m from a point (m)
- Slope above a point (°)
- Orientation from 0° North to 180° South
- Distance from the sea (km)
- Vegetation cover,
- Albedo, soil conductivity, etc. at micro-scale.

This includes what could be called a relative topography, that is not only the altitude of a point, but also taking in account the topographical situation such as valley bottom, slope, the elevation of surrounding heights, terrace, summit, ridges, pass which requires a complex algorithm for classification of the surrounding values of the Digital Elevation Model (DEM). This method is much more reliable than the ones based on spatial autocorrelation. Chytrý and Tichý (1998) include solar radiation as an additional factor for interpolation ( $PDSI = \text{Potential direct solar irradiation}$ ). Their method was developed for interpolation of phenological observations by weighted regression of phenology on the irradiation model, thus introducing an

independent terrain variable. Among spatial methods, kriging seems to be the best one (Carrega 2006, Patriche 2006, Helminen 2006). Closely related to regression analysis, kriging belongs to a group of geostatistical interpolation techniques. It computes a best linear unbiased estimator and according weights that estimated under different assumptions such as known and unknown trends or a general linear model (Stein 1999). Patriche (2006) suggests the use of slope and orientation for interpolation and Helminen (2006) recommends Gandin kriging rather than residual kriging

### ***8.4.3 Toposcale Maps in Switzerland***

The network survey in the Canton of Berne from 1971 to 1974 reveals some similarities with relative phenology (Ellenberg 1956, Schreiber 1977). Observations aggregate to an overall density of three sites to 100 km<sup>2</sup>. A specific density of 10 observations per 100 km<sup>2</sup> is possible in relation to the possible observation due to the species' occurrence. Different statistical and cartographical experiences show the possibilities of analysis of phenological observations for mesoclimatic purposes (Jeanneret 1974, Plate 6 and Figure 8.3). Proportionality between dates and altitudes was found in areas with large differences of altitude. One example shows the possibility of the description of a continuous time surface for the phenological event. For each point the regression equation is applied to grid-based data of different variables (e.g. altitude, exposition, slope angle) to compute the phenological date (Jeanneret 1974, Figure 8.3). This experience shows the possibilities of extrapolation of observations made at points to a continuous surface. Grid-based data bases will allow the application of such methods (Plate 7).

### ***8.4.4 Urban Phenology – Surveys in a Special Type of Space***

Basically, plant phenology provides similar advantages for surveys in urban areas (Rötzer et al. 2000, Henniges and Chmielewski 2006). However, urbanized surfaces offer special conditions, as the vegetation is very much defined by humans. Wild plants are relatively rare, but the vegetation bears a high percentage of what can be called a cosmopolitan flora, allowing comparison between different urban areas.

Urban phenology very often represents a specially detailed aspect, a special case of a large-scale survey. A major question is the mapping of urban influence on climate, the heat island effect, and the difference with the cooler outskirts (Rötzer et al. 2000, Henniges and Chmielewski 2006).

The produced phenological maps are often meso-scale and obviously allow a detailed overview of special climatic and ecological conditions within the urban areas. In many cities, such maps have been presented and are available to all sorts of applications, such as premises and causes of the urban climate, the conversion of natural ground cover into sealed surfaces, anthropogenic heat release and emissions of air pollutants, the behaviour of thermal and hydrological properties of urban surfaces which influence urban climate and human-biometeorological effects of the

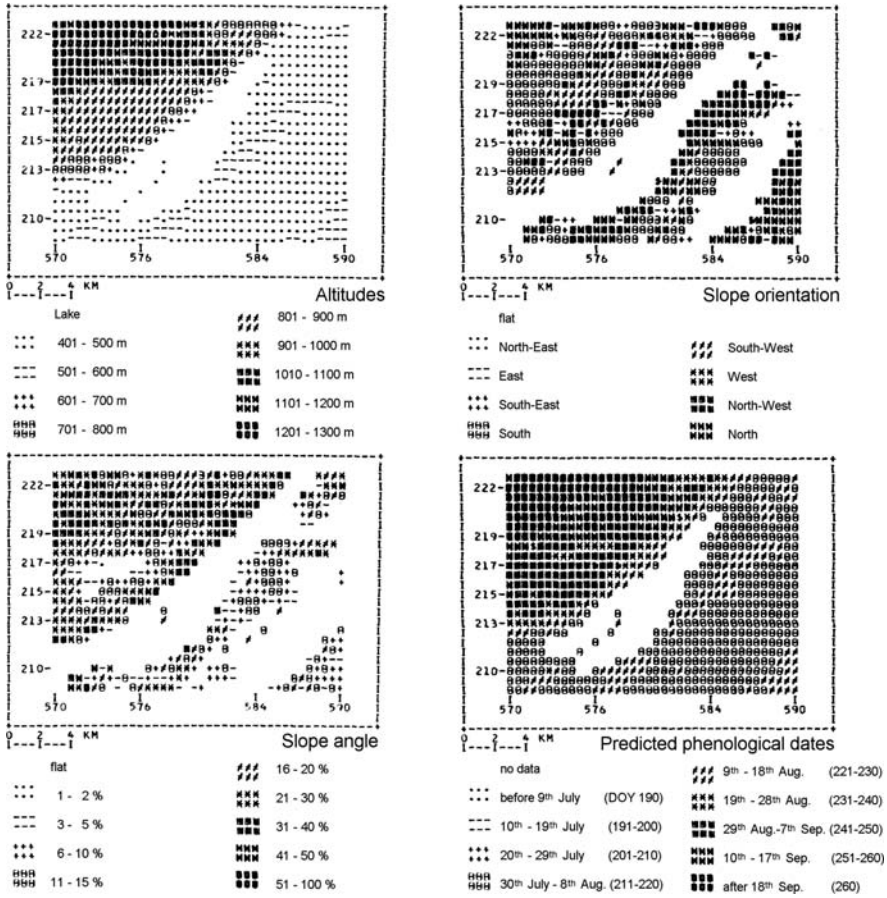


Fig. 8.3 Choroplethes map modelled from phenological dates of wheat harvest in the Lake of Biene area in 1970 (see Plate 6) and environmental factors (altitude, slope orientation and slope angle) and predicted phenological dates. Reproduced by permission of swisstopo (BA081114)

urban climate (e.g. Roller 1966 in Linz, Karsten 1986 in Mannheim, Kuttler 2000 in Vienna, Henniges and Chmielewski 2006 in Berlin).

### 8.5 Future Phenological Mapping

A wide variety of methods is available for phenological mapping. Satellite data provide a broad survey of the seasonal green-up and green-down waves, offer real-time information and are a very valuable approach to small-scale or continental-scale mapping. Small-scale phenological mapping based on observations is useful, but not unique, rather an additional or surrogate to climate mapping (e.g. Schnelle 1965, Schwartz 2003). Internet-based dot maps (Sparks and Collinson 2008,

www.phenology.org.uk) are not cartographic products but rather a spatial view of phenological observations. Remote-sensing studies provide consistently generated estimates of growing season indicators (Reed et al. 2003) and could potentially replace traditional small-scale mapping from ground observations. Reed et al. (2003) list “confounding issues” and refer to regions with no clear growing season, evergreen types and regions with multiple growing seasons. Furthermore, they discuss the caveats of methods when extracting growing season indicators from remotely sensed measurements. Bradley and Mustard (2008) presented a regional-scale phenological analysis based on satellite observations. This study accounts for changes in relation to land cover classes focusing on larger-scale phenological phenomena.

Large-scale phenological maps are unequalled and irreplaceable in providing a maximum amount of topoclimatic information. They can be produced with data from special networks as absolute phenology (Kottmann 2008) or from the application of the site assessment method (Ellenberg 1956, Schreiber 1977) by means of relative phenology. Future applications in small-scale phenological mapping should combine increasing reliable products from remotely sensed phenology as well as very detailed and verified ground-observed phenology. The synthesis will provide downscaled and very detailed maps for applications in ecological and climate impact applications and modelling studies. Verification of vegetation models (e.g. Delbart et al. 2008, Stöckli et al. 2008) will not be limited to local point-verification but can make use of reliable phenological information in space. In a transition from cartographic intuition to algorithm it is important to make use and to link together every available source of data assessment, terrain information, knowledge and experience.

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# Chapter 9

## Spatio-Temporal Statistical Methods for Modelling Land Surface Phenology

Kirsten M. de Beurs and Geoffrey M. Henebry

**Abstract** This chapter surveys 12 different spatio-temporal statistical methods to determine the start and end of the growing season using a time series of satellite images. In the first section of the chapter, we divided the methods into four categories: thresholds, derivatives, smoothing functions, and fitted models. The general use, advantages, and potential limitations of each method are discussed. In the second section of the chapter, a case study is presented to highlight one method from each category. The four study areas range from the Northwest Territories in Canada to the winter wheat areas in south-central Kansas. We concluded the case study with a discussion of the differences in results for the four methods. The chapter is finished with a synopsis discussing the use of nomenclature, the problems with a lack of statistical error structure from most methods, and the perennial issue of oversmoothing.

**Keywords** Derivatives · Model fit · Smoothing functions · Thermal time · Thresholds

### 9.1 Introduction

We have previously defined the phrase “land surface phenology” (LSP) to refer to the spatio-temporal development of the vegetated land surface as revealed by satellite sensors (de Beurs and Henebry 2004a). Due to the spatial resolution of satellite sensors, LSP deals with mixtures of land covers and thus is distinct from the traditional notion of a species-centric phenology (Friedl et al. 2006). LSP metrics are primarily based on image time series of vegetation indices (VI) from optical sensors.

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Data from the AVHRR, SPOT Vegetation, and MODIS sensors are the most commonly used in applications of land surface phenology. To overcome problems associated with the stability of measurements from the AVHRR sensors over time, a large set of corrections have been developed and applied. Among the most widely known datasets created based on the AVHRR sensors are the NASA/NOAA Pathfinder AVHRR Land (PAL) NDVI dataset (James and Kalluri 1994) and the data from the NASA Global Inventory Monitoring and Modeling Systems (GIMMS) group at the Laboratory for Terrestrial Physics (Tucker et al. 2005). The latest dataset released, the Long Term Data Record (LTDR), is designed to produce a consistent long term record from the AVHRR and MODIS sensors (Pedelty et al. 2007, <http://ltdr.nascom.nasa.gov/ltdr/>). While most of the other datasets (PAL, GIMMS, and also SPOT Vegetation) exist as series of periodically composited data, the LTDR data are provided as a daily series without compositing.

The aim of compositing methods is to select the best observation available for each pixel over the duration of the compositing period. Several algorithms have been developed for this selection process and they do not necessarily deliver identical results (Dennison et al. 2007). The most common method is maximum value compositing (MVC) in which each pixel is assigned the maximum value across all observations for that pixel acquired during the compositing period. Other recent techniques include using a bidirectional reflectance distribution function (BRDF-C) to select observations and the constraint – view angle – maximum value composite (CV-MVC) (MODIS user guide 2008).

Land surface phenology metrics typically aim to retrieve:

1. onset of greening,
2. onset of senescence,
3. timing of the maximum of the growing season, and
4. growing season length based on analysis of the VI curve (Reed et al. 1994, 2003, Zhang et al. 2003, 2004).

If a VI derived from satellite observations is to be used to monitor the duration of vegetation activity, it is desirable to compare the satellite retrieved phenological estimates with data observed at ground level. However, a principal disadvantage of phenological observation by satellite imagery is the complexity of validation of the data by ground observations that usually measure something quite different (Schwartz et al. 2002, Fisher et al. 2006). As a result, it is often unclear what the LSP metrics actually track. For example, in high latitude biomes, the greatest temporal increase in the Normalized Difference Vegetation Index (NDVI), which some methods use to indicate “start of the season” (SOS), is often due to snow melt (Reed et al. 1994, Delbart et al. 2005). The end of the greenness (EOS) metric, on the other hand, can be fooled by an extended period of cloudiness that yields low NDVI, instead of actual senescence. Since the relationship between satellite measures of LSP and phenological events of particular species or lifeforms is ambiguous, a diversity of

satellite measures and methods has arisen. Some authors present a whole range of phenological measures such as, rate of green-up, rate of senescence, growing season modality, range of NDVI, time-integrated NDVI, and more (e.g. Reed et al. 1994, Jönsson and Eklundh 2004). Most authors (see Table 9.1), however, limit themselves to four primary measures: time of onset of greenness (SOS), time of end of greenness (EOS), duration of greenness, and time of maximum (peak) VI. This chapter surveys the currently available and often applied methods, but the survey is not exhaustive. The range of methods can be divided into four main categories: threshold, derivative, smoothing algorithms, and model fit (Table 9.1).

**Table 9.1** Detection methods for phenological events ordered by publication year

Method	Classification	Reference
Inflection points on fitted, bell-shaped curve	Model fit	Badhwar (1984), Tucker et al. (2001)
0.099 NDVI threshold	Threshold	Lloyd (1990)
0.17 NDVI threshold	Threshold	Fischer (1994)
Divergence of smoothed curve from moving average	Threshold	Reed et al. (1994)
Time derivative	Derivative	Moulin et al. (1997)
Six thresholds in 0.05 increments from 0.1 to 0.35	Threshold	Myneni et al. (1997)
50% point	Threshold	White et al. (1997)
Fourier analysis	Transformation	Moody and Johnson (2001), Jakubauskas et al. (2001), Wagenseil and Samimi (2006), Hermance (2007)
NDVI threshold on day 120 and day 270	Threshold	Shabanov et al. (2002)
0.3 NDVI threshold	Threshold	Zhou et al. (2003)
Locally fit Gaussian-type functions	Model fit	Jönsson and Eklundh (2002, 2004), Verbesselt et al. (2006), Huemann et al. (2007)
Principal component analysis	Transformation	Hall-Beyer (2003)
Largest derivative	Derivative	Tateishi and Ebata (2004)
Logistic model of vegetation growth fit to increasing and decreasing section of EVI time series.	Model fit	Zhang et al. (2003, 2004)
Phenology models based on AGDD	Model fit	de Beurs and Henebry (2004a, 2005a, 2005b)
Normalized Difference Water Index threshold analysis	Threshold	Delbart et al. (2005)
Thresholds based on long-term mean VI	Threshold	Karlsen et al. (2006), Piao et al. (2006), Philippon et al. (2007)
Camelback phenology algorithm	Derivative	Baltzer et al. (2007)

## 9.2 Thresholds

The simplest and most frequently applied method determines SOS and EOS based on threshold values.

### 9.2.1 *Vegetation Indices (VI) Thresholds*

Some authors (Lloyd 1990, Fischer 1994, Myneni et al. 1997, Zhou et al. 2003) arbitrarily set a threshold value at a certain level or amplitude, (e.g. 0.09, 0.099, 0.17 or the range of values from 0.1 to 0.35). The SOS is then determined as the day of the year (DOY) that the NDVI crosses the threshold in upward direction; likewise, the EOS is determined as the DOY that the NDVI crosses the same threshold in downward direction. To determine at which DOY the threshold is reached, the time series is filtered to eliminate remaining cloud cover and interpolated to a daily dataset. Within the Northern Hemisphere, pixels in the south generally have an earlier SOS than pixels more northern. Across the conterminous United States of America, the NDVI threshold for the SOS can vary from 0.08 to 0.40 (Reed et al. 2003). Thus, in the case of one fixed threshold for a larger study area, the thresholds may not measure the same phenological event and the approach becomes inconsistent. There is also an implicit simplifying assumption that crossing the threshold in one direction is functionally equivalent to crossing it in the other. Yet, there is little reason to assume that these systems do not exhibit hysteresis: the timing and rate of greening across the landscape is independent of and different from the timing and rate of senescence across the same landscape.

#### 9.2.1.1 **Thresholds Based on Long-Term Mean VI**

A variation of the VI threshold method is presented by Karlsen et al. (2006, 2007). In this case the authors calculated a 21-year mean value for each pixel, for Fennoscandia only incorporating pixels with positive values of NDVI. The SOS, for each year, was then considered to be the date when the NDVI value passed the long-term mean value. This threshold was chosen because it showed the highest correlation with the onset of leafing in birch as observed at ground level. The EOS was determined by the date when NDVI passed below 70% of the 21-year mean. Peak timing was determined as the date with maximum NDVI (Karlsen et al. 2006, 2007). A similar method was developed for Africa where the SOS and the EOS were determined as the date of the 10-day period right before the one where NDVI passes the annual mean level upward (SOS) or downward (EOS) (Philippon et al. 2007). Piao et al. (2006) apply a similar method in China. First, the rate of change is determined for the 18-year average NDVI as follows:

$$\text{NDVI}_{\text{ratio}}(t) = \frac{[\text{NDVI}(t+1) - \text{NDVI}(t)]}{\text{NDVI}(t)} \quad (9.1)$$

Based on the  $\text{NDVI}_{\text{ratio}}$  the timings of the greatest increase and decrease are determined as well as their corresponding NDVI values. In the last step, the SOS is determined for each year as the day that a smoothed curve passes the NDVI threshold (Piao et al. 2006). Smoothing is performed with a sixth-degree polynomial curve.

### 9.2.1.2 Thresholds Based on a Baseline Year

Shabanov et al. (2002) determined the SOS and the EOS by comparing years among each other. First, they designated the NDVI values on DOY 120 and DOY 270 as determining the SOS and the EOS thresholds for a baseline year. The median year in the time series was selected as the baseline year (Shabanov et al. 2002). The DOYs at which the NDVI thresholds were reached in each other year determined the SOS and the EOS for that year.

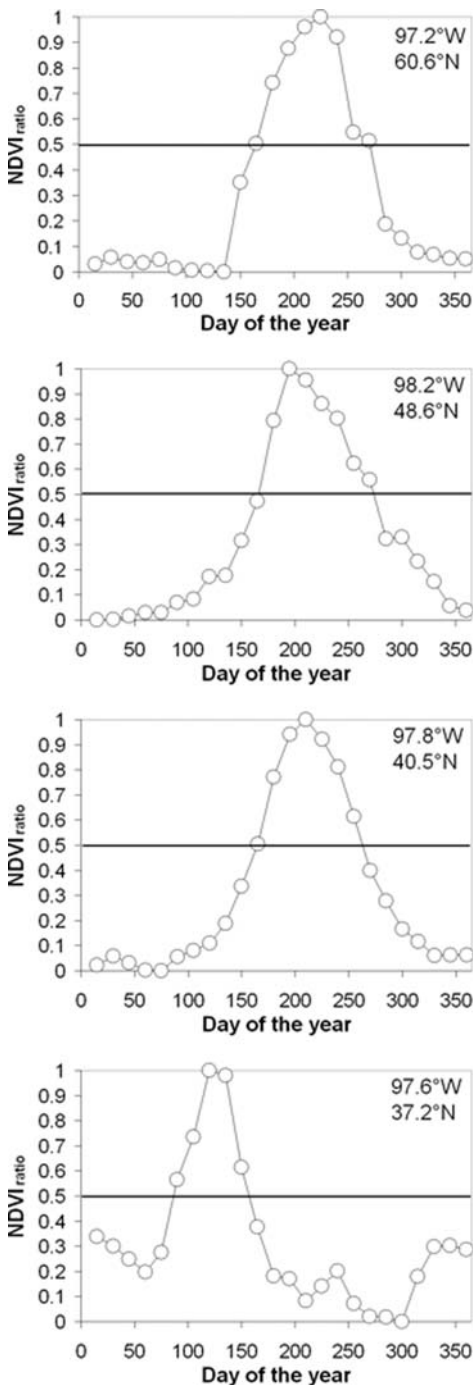
### 9.2.1.3 Thresholds Based on NDVI Ratios

White et al. (1997) determined the SOS threshold as the 50% point of the NDVI curve. The state of the ecosystem is indexed by transforming of the NDVI to an  $\text{NDVI}_{\text{ratio}}$  as follows (White et al. 1997):

$$\text{NDVI}_{\text{ratio}} = \frac{\text{NDVI} - \text{NDVI}_{\text{min}}}{\text{NDVI}_{\text{max}} - \text{NDVI}_{\text{min}}} \quad (9.2)$$

The  $\text{NDVI}_{\text{ratio}}$  ranges from 0 to 1. NDVI is the daily NDVI,  $\text{NDVI}_{\text{max}}$  and  $\text{NDVI}_{\text{min}}$  are the annual maximum and minimum of the NDVI curve. This ratio method is similar to the Vegetation Condition Index (Kogan 1995). However, in White's et al. case the minimum and maximum NDVI are determined annually, while Kogan (1995) used long-term minima and maxima in NDVI maximum value composites. The SOS was determined as the day that the  $\text{NDVI}_{\text{ratio}}$  reached 50% in upward direction. The EOS was determined as the day that the  $\text{NDVI}_{\text{ratio}}$  reached 50% in downward direction (see Fig. 9.1). The justification offered for the choice of the 50% threshold is that the increase in greenness is believed to be most rapid at this threshold and if only one phenological date is to be used, then the period of most rapid growth is more important than the first leaf occurrence or budburst. Furthermore, lower vegetation signals are more easily confounded with soil reflectance. A 50% point states that a certain pixel (or study region) has attained 50% of its maximum greenness. The transformation to  $\text{NDVI}_{\text{ratio}}$  is attractive because it allows for a consistent determination of the 50% point of the

**Fig. 9.1** Threshold method based on NDVI ratios for four different 64 km<sup>2</sup> pixels ranging from 60.6 to 37.2°N. The profiles are extracted from GIMMS 2002 data. SOS is determined as the day that the curve crosses the 50% threshold in upwards direction. (See Table 9.2 for the SOS and EOS results.)



vegetation, independent of the geographic location and land cover of the observed study area. Furthermore, the  $NDVI_{ratio}$  retains high frequency vegetation changes that can be lost if data are first smoothed.

In a later application of this method, White and Nemani (2006) opted for the transformation of NDVI to  $NDVI_{ratio}$  based on long-term minimum and maximum values. The advantage of long-term average minimum and maximum NDVI values is that they are usually not strongly influenced by outliers (White and Nemani 2006). The disadvantage is that the minimum and maximum NDVI might not be stable through time and could change significantly, for example due to disturbance processes, or other changes in the landscape (White et al. 1997, Rich et al. 2008). An inadequately calibrated data record can exhibit changes in the NDVI that are artifactual (de Beurs and Henebry 2004b).

#### 9.2.1.4 Threshold Based on NDWI

Delbart et al. (2005) argued that the NDVI is not the optimal index when measuring the SOS and the EOS in areas experiencing snow cover, because the onset of the NDVI increase corresponds with the beginning of snowmelt. Thus, trends in the SOS might not be due to actual earlier vegetation onset but rather due to reduction in the snow cover extent. The Normalized Difference Water Index (NDWI), which is based on reflectances in the Near Infra-Red (NIR) and Short Wave Infra-Red (SWIR) regions, may be more efficient in estimating the start of season for areas where extensive snow cover might be expected (Delbart et al. 2005). Using NDWI they defined the onset of greening (SOS) as:

$$t_{greening} = \max(t \in [0,200]) | (NDWI(t) < NDWI_{min} + \epsilon) \quad (9.3)$$

This equation gives the SOS for a particular year as the last day ( $t$ ) where NDWI is smaller than the minimum NDWI plus a small empirically identified threshold ( $\epsilon$ ). The last day has to be chosen before day 200. Time ( $t$ ) is time in days,  $NDWI_{min}$  is the minimal observed value of NDWI over one year.

Thus, the SOS is chosen as the last record, before an increase in the NDWI associated with vegetation green-up. The increase in the NDWI needs to fulfill the following constraints: (1)  $\epsilon$  should be larger than the noise affecting the NDWI profile, and (2)  $\epsilon$  must be smaller than the first NDWI increase due to vegetation growth. They found the most accurate results with  $\epsilon$  set at 20% of the spring amplitude in the NDWI.

For snow covered areas, the method based on the NDWI has been shown to provide a definite advantage in discriminating green-up from snow melt. However, there are some limitations. Firstly, the threshold value,  $\epsilon$ , is chosen arbitrarily and likely not optimally for all land cover types that may experience snow cover. Secondly, the low spring NDWI amplitudes can result in extremely small  $\epsilon$  values that come very close to background variability or noise. Lower spring amplitudes could be expected in the tundra due to small amount of vegetation and the extended period



of concomitant snow melt and vegetation green-up. Areas with higher proportions of evergreen vegetation also tend to exhibit lower spring amplitudes (Delbart et al. 2005).

### Principal Limitations of Threshold Methods

Threshold methods do not provide an analytical solution to the error structure of the statistic. Thus, the only way to determine the significance of observed differences is through reference to a baseline determined through many years of observation, which is difficult given the short duration of the satellite era. Some authors (White and Nemani 2006) have used spatial neighborhoods in an attempt to estimate the interannual variation of the SOS or EOS. Unless the dynamical system under investigation exhibits the property of ergodicity (a spatio-temporal average represents the ensemble average), this kind of “space for time” substitution does not work. Spatial variation does not capture temporal variation. The positive autocorrelation typically encountered in geospatial data will diminish the residual variability thereby inflating significance levels and increasing the risk of a Type I inferential error. Thus, it is very difficult to understand whether any observed changes in the SOS and/or the EOS are significantly different or simply fall within the expected range of interannual variability.

## 9.3 Derivatives

Authors (e.g. Tateishi and Ebata 2004, White et al. 1997, Baltzer et al. 2007) who study derivatives of NDVI curves generally accept the maximal increase and decrease in NDVI as the SOS and the EOS.

### 9.3.1 *Greatest Increase/Decrease in VI*

Tateishi and Ebata (2004) defined the SOS as the time of the greatest increase in the NDVI. They assumed, like White et al. (1997), that the SOS is characterized by the greatest leaf expansion or the fastest green-up during the growing season. To smooth the derivative series, they determined the derivative based on three consecutive ten-day composites (Tateishi and Ebata 2004). The timing of the highest positive derivative reveals the fast increase in the NDVI and is thus designated as the SOS. In a similar way the lowest negative derivative is considered the EOS. The method is very simple and easily determines the fastest increase and decrease in NDVI.

Moulin et al. (1997) determined the derivative separately for SOS and EOS. For the start date vector they used the following equation:

$$b_i = |x_i - x_0| - \lambda [(x_{i+2} - x_i) - |x_{i-2} - x_i|] \quad (9.4)$$

where,  $x_0$  is determined as a NDVI value close to the soil background and  $x_i$  is the NDVI at day  $i$ . The  $\lambda$  factor weights the derivative term. They proposed 3 as a reasonable value for  $\lambda$ .

The end date vector is determined as:

$$e_i = |x_i - x_0| - \gamma [|x_{i+2} - x_i| - (x_{i-2} - x_i)] \quad (9.5)$$

The terms are the same as defined for Equation 9.4. For the end date,  $\gamma$  is set at a value of 5.

The final start date is determined using three rules (Moulin et al. 1997):

1. the NDVI value is close to a value of bare soil;
2. the time derivative before the start date based on  $b_i$  can be either positive or negative, but it should be close to zero; and
3. the time derivative after the start date based on  $b_i$  should be positive.

For the end date comparable criteria were established.

### 9.3.2 Camelback Phenology Algorithm

Baltzer et al. (2007) presented an algorithm motivated by the derivatives method that was originated by Moulin et al. (1997). A moving window consisting of five composites is passed over the time series for every pixel. Within every window the slope of the regression of the NDVI against time is calculated. In the second step, with the same moving window, the second order derivative is calculated. The SOS is determined as the time point when the second derivative of the moving window regression reaches a local maximum within a 13-composite window and the slope is positive (Baltzer et al. 2007). The EOS is determined at the time where the second order derivative reaches a local maximum and the slope is negative.

#### 9.3.2.1 Limitations of Derivative Methods

As with the threshold methods, the phenological estimates from the derivative methods do not have an analytical error structure. Thus, it is extremely difficult to understand whether observed changes fall within the natural variability of the data or result from a significant change. These methods have problems determining the SOS and the EOS when the NDVI signal fails to follow an abrupt and rapid increase or decrease. They can be especially problematic in the determination of the EOS, because the maximum value compositing used to suppress cloud contamination in VI time series also defers the appearance of senescence to the next compositing period.

## 9.4 Smoothing Function and Model Fits

### 9.4.1 Autoregressive Moving Average

Reed et al. (1994) determined the SOS and the EOS as the dates that a smoothed time series crosses a curve established from moving average models. The moving average has an introduced time lag which is arbitrarily chosen. Based on 14-day composites, Reed et al. (1994) found that a moving average curve based on nine composite periods gave the best results. This method was adjusted for and applied to semi-arid Africa by Archibald and Scholes (2007). The savannas in semi-arid Africa retain their leaves until late in the growing season and there is a relatively short time period (~2 months) for which the NDVI is at its lowest value. As a result, the moving average curve was shortened to two months (or four composites) (Archibald and Scholes 2007).

#### 9.4.1.1 Limitations of the Moving Average Method

The method assumes that the phenology can be well captured by a moving average model, which might not be appropriate in case of disturbances or other changes on the land surface. In addition, the method does not work well in rain-green systems that respond strongly and rapidly to rainfall events and exhibit a more erratic and even multi-modal growing season. Further, clear criteria regarding the selection (and adjustment) of the delay time are lacking.

### 9.4.2 Fourier Analysis

Fourier analysis approximates complicated curves with a sum of sinusoidal waves at multiple frequencies. As the number of component sinusoidal waves increases, the sum becomes able to approximate a LSP signal more closely. For a given pixel, the Fourier function is given by:

$$f(t) = \overline{f(t)} + \sum_{n=1}^{L/2} \left( A_n \cos \frac{2\pi nt}{L} - \phi_n \right) \quad (9.6)$$

where,  $f(t)$  gives the NDVI for a given composite and  $\overline{f(t)}$  is the mean of the of  $f(t)$ ;  $A_n$  gives the amplitude  $A$  of harmonic term  $n$ ;  $\phi_n$  gives the phase of the  $n$ th harmonic; and  $L$  is the number of observations within the study period (Jakubauskas et al. 2001, Wagenseil and Samimi 2006). Thus, 10-day composites and a year of data yields  $L = 36$ , and for 14-day composites,  $L = 26$ .

Moody and Johnson (2001) applied the discrete Fourier analysis to the temporal signature of vegetation as recorded by image time series. Fourier analysis is shown to be sensitive to systematic changes, but relatively insensitive to nonsystematic data noise. The strength of the Fourier analysis is the frequency decomposition. By

discarding higher order harmonics while retaining the first-order and second-order harmonics, it is possible to retrieve lower noise signals that characterize the basic temporal behavior of the vegetated surface. Inspection of the higher order dynamics can give information about higher temporal variability phenomena (Moody and Johnson 2001).

The first Fourier harmonic is often interpreted as representing mean NDVI, which in its turn is inferred to indicate the overall productivity of the region for that time period. Comparisons of the mean NDVI allow for the distinction between more and less productive sites. The amplitude of the first harmonic indicates the variability of the productivity over the year, while the phase measures the timing of the peak; there is no direct measure for the timing of onset. The second harmonic is interpreted as the strength and timing of any bimodal signal resulting from secondary cover types (Moody and Johnson 2001).

#### 9.4.2.1 Limitations of Fourier Analysis

The analysis decomposes the signal into an arbitrary number of sinusoid functions that do not necessarily have an ecological interpretation. In most cases the observed component signals are interpreted in terms of ecological behavior of the land surface. While this approach might provide useful information for a well-characterized region, its efficacy depends on a prior ecological understanding and thus limits its utility in areas less well known. Furthermore, Fourier analysis operates in the frequency domain and thus requires a long time series of equally spaced observations. The longer the time series, the finer the resolution of the frequency decomposition. The Nyquist frequency is the highest frequency that can be resolved by Fourier decomposition and is given as the highest frequency within the data divided by two (Moody and Johnson 2001). In other words, the sampling rate of the data must be at least double the rate of the frequency of the highest Fourier harmonic that is sought (Moody and Johnson 2001). Missing or irregularly spaced observations require gap filling and/or padding of the series.

As the shapes of the NDVI signals are usually not exactly sinusoidal or strictly periodic, it is necessary to fit several higher frequency terms to yield a suitable approximation (Wagenseil and Samimi 2006).

The second harmonics from different years can be contrary to each other, which presents a significant problem for interpretation. Moody and Johnson (2001) also warned for the degree and consistency with which the second- and higher-order harmonics relate to secondary vegetation, climate anomalies, or other land cover changes. In addition to these problems, the influence of data quality and noise on the Fourier decomposition is poorly understood.

Even though observations in the power spectrum can have confidence intervals (Bloomfield 1976), we are not familiar with an application of these uncertainty measures in the LSP literature. Since the uncertainty levels of Fourier measures are often not provided, comparison of the means is complicated, and it is unclear whether there has been a real change or that the difference falls within the expected range of interannual variability.

To overcome some of the main limitations for “classical” discrete Fourier analysis, Hermance (2007) presented a new stabilizing high-order, non-classical harmonic analysis. This novel method allows the user to incorporate some of the higher-order Fourier oscillations without introducing artifacts, through dampening oscillatory behavior by minimizing model roughness (Hermance 2007). This Fourier smoothing function was used by Bradley et al. (2007) to determine the SOS in the Great Basin (USA). The Fourier smoothing function was applied to the noisy satellite data to smooth the data and provide a cleaner signal (Bradley et al. 2007). However, the Fourier curves were not used to estimate timing or amplitude, but merely applied as an advanced smoothing function. Bradley et al. (2007) resorted to the half-maximum threshold method (White et al. 1997) to extract phenological metrics from the smoothed curve.

### ***9.4.3 Principal Component Analysis***

Principal component analysis (PCA) is another transformation that is sometimes applied to multi-year image series (Townshend et al. 1985, Eastman and Fulk 1993, Hall-Beyer 2003). The objective of PCA is to account for a maximum portion of variance present in the entire dataset through a linear combination of the original observations. Principal component analysis of the NDVI time series provides an alternative to phenological metrics for tracking the response of the vegetated land surface to variability resulting from climate and other land surface changes (Hall-Beyer 2003). It is important to note that the eigenvectors by themselves do not have a particular ecological meaning. It is therefore necessary, as with Fourier analysis, to interpret the eigenvectors in combination with ancillary data and prior information about the study region (Hall-Beyer 2003). In general, as with Fourier analysis, the first principal component is accepted as the integrated VI value that closely resembles the dataset average, while the second is usually interpreted as an indication of the VI seasonality (Townshend et al. 1985). Higher principal components are sometimes interpreted as regional seasonalities, artifacts from different sensors, or the influence of climate modes (Eastman and Fulk 1993).

#### **9.4.3.1 Limitations of the Principal Component Analysis**

As with the Fourier analysis, the eigenvectors as retrieved by the PCA are derived exclusively from the input data. As a result, the components are not stable and may not be able to be interpreted in the same way from year to year (Hall-Beyer 2003). This instability presents a problem for comparisons of phenologies between periods or across regions. Since the components can vary year to year, it is difficult to do quantitative comparisons based on the components. The problem does not just occur from year to year, but could also result when one or more images are added to the original time series (Henebry 1997). This indicates that PCA may result in fairly different loading structures when the temporal resolution of the image time series changes from 10-day to 7- or 14-day composites. In other words, the weights

assigned to each composite to create the principal components can be very different depending on the temporal resolution of the image time series.

## 9.5 Model Fit

The last category for the description of vegetation phenology based on satellite imagery is model fitting. To allow for the variable nature of the NDVI curves, authors have developed several models that can easily be adjusted to the available satellite data.

### 9.5.1 Logistic Models

Badhwar (1984) developed the first method to parameterize NDVI temporal profiles that was later used by Tucker et al. (2001). The temporal profile is divided at the peak NDVI into two time series. The following curve is fitted to the first part of the time series (Badhwar 1984):

$$\log(\text{NDVI}) = \log P_1 + P_3 (\log t - \log P_2) + P_4 (P_2^2 - t^2) \quad (9.7)$$

There are four parameters that need to be estimated for each part of the curve.  $P_1$  provides the displacement of the NDVI versus time.  $P_2$  provides an approximation of SOS.  $P_3$  relates to the peak value and  $P_4$  is the rate of growth of the vegetation (Tucker et al. 2001). For the second half of the growing season,  $P_2$  provides an approximation of the EOS and  $P_4$  provides an approximation for the rate of vegetation senescence.

Zhang et al. (2004) fitted a logistic model of vegetation growth to the Enhanced Vegetation Index (EVI). Like Tucker et al. (2001), the authors divided the annual EVI curve in two parts, vegetation growth and senescence, and fit the models separately. The logistic model is expressed as:

$$\text{EVI}(t) = \frac{c}{1 + e^{a+bt}} + d \quad (9.8)$$

This is a very straightforward model with  $a$  and  $b$  as empirical coefficients that are associated with the timing and rate of change in EVI. The parameter  $c+d$  combined give the potential maximum value and  $d$  presents the minimum value (the background EVI value). This model can be approximated with numerical methods such as Levenberg-Marquardt (Zhang et al. 2003, Fig. 9.6). To fit both growth and senescence, a total of eight parameters must be estimated. Based on the fitted models, the phenological transition dates are determined by the derivative of the curvature of the function. The curvature of the function is as follows (Zhang et al. 2004):

$$C_{CR} = b^3 cz \left\{ \frac{3z(1-z)(1+z)^3 [2(1+z)^3 + b^2 c^2 z]}{[(1+z)^4 + (bcz)^2]^{5/2}} - \frac{(1+z)^2 (1+2z-5z^2)}{[(1+z)^4 + (bcz)^2]^{3/2}} \right\} \quad (9.9)$$

With,  $z = e^{a+bt}$  and a, b, c and d as defined above.

The curvature shows local maxima and minima. During green-up there are two local maxima that Zhang et al. (2004) designated as the onset of green-up and the onset of maturity. Both Fisher et al. (2006) and Fisher and Mustard (2007) also applied this curve fitting method and determine the start of season as the half-maximum or the time point where  $c+d/2$  is reached. This approach delivered results similar to those using the local minimum of the curvature function (Fisher et al. 2006, Fisher and Mustard 2007). Beck et al. (2006) proposed the fit of a double logistic function similar to Zhang et al. (2004) but adjusted especially for areas in the far northern latitudes that experience snow-cover (Beck et al. 2006).

### 9.5.2 Gaussian Local Functions

Jönsson and Eklundh (2002) developed a model fit existing of a number of local model functions that are merged in a global function. This merging of multiple local functions increases the flexibility of the fittings and allows the fitted function to follow the complex behavior of the time series that is not possible with a simple Gaussian model or lower order Fourier estimates (Jönsson and Eklundh 2002). The Gaussian-type local functions are as follows:

$$NDVI = c_1 + c_2 \begin{cases} \exp \left[ - \left( \frac{t - a_1}{a_2} \right)^{a_3} \right], & \text{if } t > a_1 \\ \exp \left[ - \left( \frac{a_1 - t}{a_4} \right)^{a_5} \right], & \text{if } t < a_1 \end{cases} \quad (9.10)$$

The base parameters  $c_1$  and  $c_2$  determine the intercept and the amplitude of the curves, respectively. The parameter  $a_1$  determines the timing of the maximum (measured in time units). The upper part of the equation is fitted to the right half of the time series (time is after the peak  $a_1$  is reached). While, the lower part of the equation fits to the left half of the time series. The parameters  $a_2$  and  $a_4$  determine the width of the curves on the right and left side, respectively. The parameters  $a_3$  and  $a_5$  determine the flatness (or kurtosis) of the curves on the right and left side respectively. The fit of this local function alone already requires the estimation of seven parameters. The authors provided the option of fitting a centre piece to the model, in case of a flat plateau for a peak, introducing even more parameters. After this rather complicated function has been fitted to the NDVI time series, the SOS is determined from the global model as the point in time for which the value has increased 10% above the base level. So, the authors have returned to a threshold method to determine the SOS.

This function fitting routine was added to a software package called TIMESAT. TIMESAT fits smooth continuous curves using the Savitzky-Golay filtering, asymmetrical Gaussian, or double logistic functions (Jönsson and Eklundh 2002, Jönsson and Eklundh 2004). The package allows for upper envelope filtering to account for negatively biased noise. The package has since been used in several other studies, but mainly as a smoothing algorithm after which a threshold system is applied (Verbesselt et al. 2006, Huemann et al. 2007, Gao et al. 2008, the new MODIS North American phenology product: <http://accweb.nascom.nasa.gov>).

### 9.5.2.1 General Limitations of Complex Models

When both curves are fitted, at least four and sometimes as many as eight parameters must be estimated, this is substantial, especially considering the limited number of observations per year. Furthermore, it remains unclear how the parameter estimation is influenced by the temporal resolution of the data (Ahl et al. 2006).

### 9.5.3 Models Based on Growing Degree-Days

Plant phenology models relate thermal regimes of the growing season with events in plant development (Schwartz 2003). The thermal regime of the growing season can be measured as accumulated growing degree-days (AGDDs) by summing growing degree – days from some consistent start date until a specific subsequent date. Degree-days can be interpreted as measures of accumulated heat (or insolation) above a specified base temperature. Base temperatures differ depending on plant life form, (e.g. annual versus perennial, C<sub>3</sub> versus C<sub>4</sub> photosynthetic pathway, herbaceous versus woody). A variety of base temperatures have been developed for crops, crop pests, and other vegetation. A common base temperature often used for cereal crops and woody plants is 5°C (Wielgolaski 1999). Higher base temperatures are sometimes used for plants native to warmer regions, such as 10°C for maize. A base temperature of 0°C is used for most spring wheat varieties that grow mainly in colder regions (Rickman et al. 1991) as well as for temperate grasslands (Goodin and Henebry 1997). Thermal-based regression models using AGDDs as the explanatory variable have been regularly used in crop phenology studies to describe and predict the green-up, flowering, fruiting, and senescence stages of crops and grasslands and to compare multiple crop varieties (Goodin and Henebry 1997, Mitchell et al. 2001, Smart et al. 2001, Davidson and Csillag 2003).

We have proposed this method to analyze changes in long image time series using AGDDs instead of compositing periods or days of the year. This approach enabled us to align the imagery using a temporal metric that is more relevant to vegetation than an anthropocentric calendar. We calculated the 15-day average growing degree-days (GDD) for a base 0°C and the seasonal accumulated growing degree-days (AGDD) using the daily minimum and maximum 2-metre air temperatures available from the NCEP Reanalysis project (Kalnay et al. 1996).



To detect and assess the significance of changes in LSP, we proceeded in two steps: (1) we fitted a statistical model for each period of interest; and (2) we tested the estimated parameter coefficients of the models for significant differences. We have sought for parsimonious statistical models with few parameters that could have clear biogeophysical or ecological interpretations. Quadratic regression models have proven to work well for fitting phenology of herbaceous vegetation (e.g. croplands and grasslands) in temperate climates (de Beurs and Henebry 2004a, 2005a). Woody vegetation in northern latitudes, however, follows a more rapid green-up and forests and tundra stay green for a relatively long period prior to a rapid senescence. Quadratic regression does not capture the NDVI plateau. We have found that a non-linear spherical model offers a much better fit for the first part of the growing season (de Beurs and Henebry 2005a). While we acknowledge that in the latter portion of the temperate growing season, daylength and water stress can become important factors affecting vegetation growth and the onset of senescence (Henebry 2003), we have restricted our focus here to the first part of the growing season.

### 9.5.3.1 Quadratic Model

The quadratic regression models have only three parameters to estimate and these yield straightforward ecological interpretations. Furthermore, these models can be applied directly to the data without the need of applying filters to attenuate noisy data. The basic quadratic regression model is in this form:

$$\text{NDVI} = \alpha + \beta\text{AGDD} + \gamma\text{AGDD}^2 \quad (9.11)$$

where AGDD are the accumulated growing degree-days in °C. The intercept ( $\alpha$ ) gives NDVI at the start of the observed growing season. The slope parameter ( $\beta$ ) and the quadratic parameter ( $\gamma$ ) together determine the green-up period, defined as the amount of AGDD (°C) necessary to reach the peak NDVI as follows:

$$\text{AGDD to NDVI}_{\text{peak}} = -\beta/2\gamma \quad (9.12)$$

The height of the peak NDVI is determined by using AGDD at the peak position (Eq 9.12) in Equation 9.11 and calculating the corresponding NDVI value. We have developed an exhaustive search algorithm that fits candidate quadratic models at multiple seasonal windows of differing lengths and starting periods (de Beurs and Henebry 2008). Thus, we fitted the quadratic model multiple times for every pixel time series while varying the number of sequential composites included and the beginning time of the composite sequence. The quadratic model generally fitted better if only the growing season dynamic is taken into account by excluding early composites that exhibit low VI values with little change through time. The models were thus able to detect the SOS by searching for the best fitting model. We determined the SOS as the first composite of the best fitting model selected for each pixel independently. In addition, we determined the peak height in NDVI and the peak position both as AGDD and as day of the year.

### 9.5.3.2 Spherical Models

Nonlinear spherical models can describe the green-up dynamics in taiga and tundra ecoregions parsimoniously (de Beurs and Henebry, 2005a). The spherical model is popular in geostatistics where it is mainly used for the spatial interpolation of variables. The spherical model with AGDD as independent variable and the NDVI as dependent variable follows this form:

$$\text{NDVI} = \begin{cases} \alpha + \sigma \left( 1.5 \frac{\text{AGDD}}{\phi} - 0.5 \left( \frac{\text{AGDD}}{\phi} \right)^3 \right) & \text{if } \text{AGDD} < \phi \\ \alpha + \sigma & \text{if } \text{AGDD} > \phi \end{cases} \quad (9.13)$$

where, the intercept ( $\alpha$ ) gives the NDVI value for low AGDD; the peak ( $\alpha + \sigma$ ) gives the maximum NDVI; and the third parameter coefficient ( $\phi$ ) is the quantity of AGDD required to reach the peak value, which corresponds to the duration of the observed green-up phase.

LSP regression models can reveal changes in phenological pattern between periods only if the model explains a significant proportion of the NDVI variation. The fraction of all variance in NDVI that is explained by multiple regression models can be expressed by the coefficient of determination adjusted for model complexity ( $r^2_{\text{adj}}$ ). Once a model with a good statistical fit has been identified, values of the parameter coefficients can give insight into the processes that drive LSP.

To evaluate the significance of differing values of the parameter coefficients, there is a particular testing sequence and stopping criterion for the quadratic model: testing begins with the highest order parameter and stops when a pair of coefficients is assessed as significantly different. The testing sequence begins with a standard F-test for equality of the highest order parameters in two periods. The test procedure ends when a significant difference between the parameter coefficient estimates for two periods is found. If a pair of parameter coefficient estimates is found to be not significantly different, the two parameter coefficients are weighted by the sum of squares of the observations from both periods and this new single coefficient is used to re-estimate the lower order parameter coefficients in each period. The test procedure is followed until the lowest order parameter coefficient, typically the intercept, is tested. If no significant change is found for any parameter coefficient, it can be concluded that the estimated phenology models for both periods are statistically equivalent, even if the parameter coefficients have different values. For the spherical model, there is no testing order or stopping criterion, because the parameters shape the curve independently; thus, every parameter coefficient pair is tested.

## 9.6 Case Study

In this case study we compared several methods for the analysis of land surface phenology. Figures 9.1, 9.2, 9.3, 9.4, 9.5 and 9.6 show the land surface phenology trajectories at four sites along a latitudinal transect in the middle of North America. These time series were extracted from the 2002 GIMMS data, which has 24 15-day composites per year. The top panel shows the northernmost pixel (97.2°W, 60.6°N), which is located in the Northwest Territories of Canada. The second pixel (98.2°W, 48.6°N) is located in the spring wheat belt of North Dakota. The third pixel (97.8°W, 40.5°N) is located in an extensive area of irrigated corn in south-central Nebraska. The bottom panel shows the southernmost pixel (97.6°W, 37.2°N), which is located in a winter wheat region of south-central Kansas.

The most northerly pixel is covered with natural vegetation which greens up as soon as the environmental conditions permit growth, while the rest of pixels are dominated by agriculture. The green-up trajectories of the pixels in North Dakota and Nebraska are strongly dependent on the time of sowing. The pixel located in the winter wheat belt of south-central Kansas reveals a much earlier growing season, as the crop is sown in the autumn, overwinters, and matures in early summer. These particular pixels were chosen at random within well-defined ecoregions, but the results are only valid for these particular pixels observed during 2002. A colour plate (Plate 8) maps the entire study area with results from a subset of the methods.

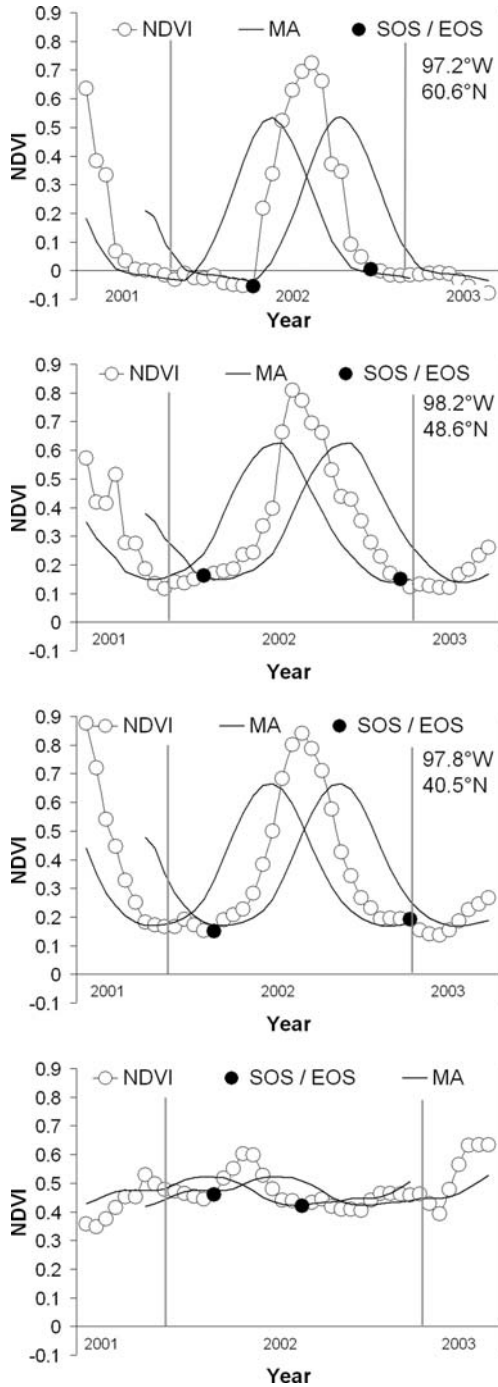
### 9.6.1 Thresholds

Figure 9.1 gives the results of the 50% threshold method, which identifies the SOS and the EOS as the 50% point between the winter NDVI and the peak NDVI (White et al. 1997). The SOS dates for three of the four selected pixels were similar to each other varying between DOY 164 and 167 for Canada, North Dakota and Nebraska. The only site with a substantially earlier SOS is Kansas, due to the dominance of winter wheat in this pixel. For natural vegetation we would expect a north-south gradient of the SOS and the EOS with the SOS starting later in the north than in the south due to latitudinal differences in insolation and temperature (Schwartz and Reiter 2000, Schwartz et al. 2006). However, as we have focused on agricultural areas, there is a strong direct human influence on phenology (de Beurs and Henebry 2004a, 2005a). We found that the apparent growing season length is shortest in Kansas (71 days) followed by Nebraska, Canada, and North Dakota.

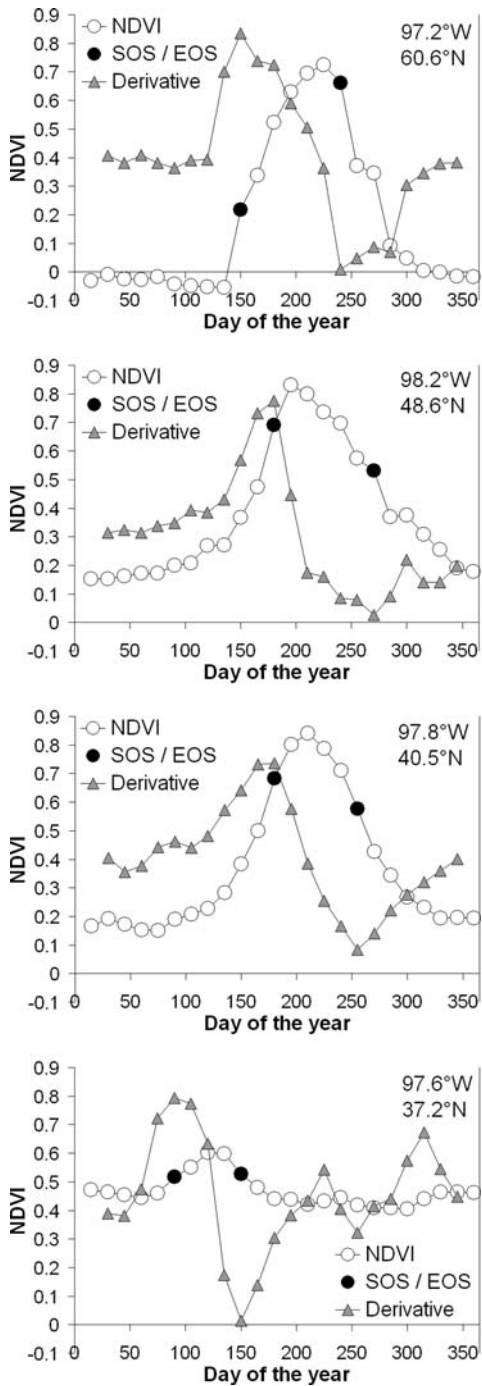
### 9.6.2 Moving Average

Figure 9.2 gives the results for the moving average method (Reed et al. 1994). In this case the SOS for the pixels varied more widely (Table 9.2) and the SOS was clearly

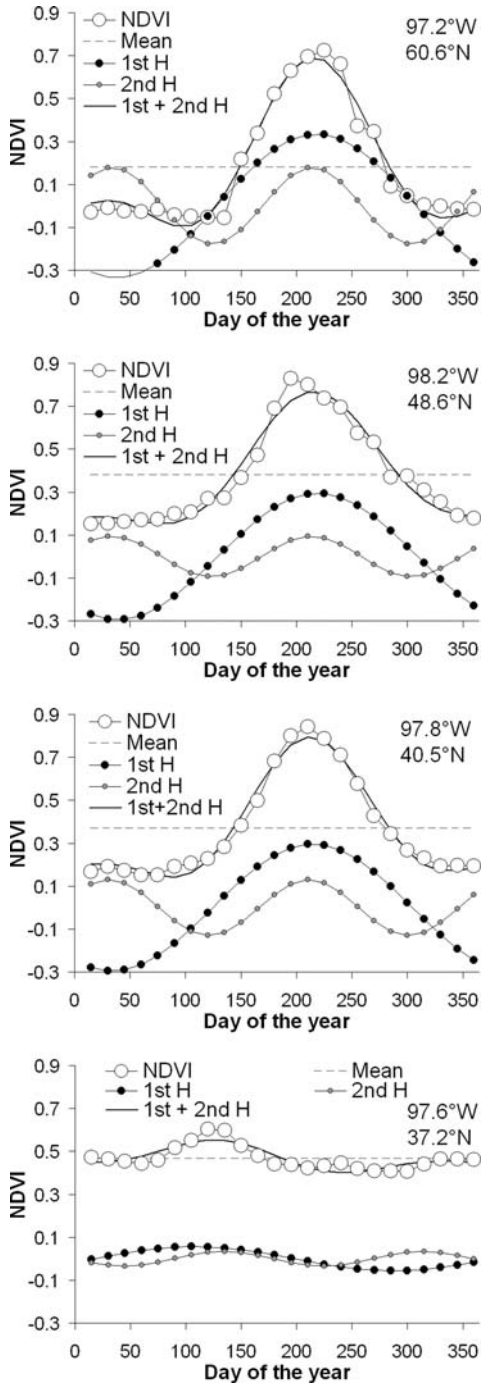
**Fig. 9.2** Moving average method applied to detect the onset of greenness and senescence (See Table 9.2 for the SOS and EOS results.)



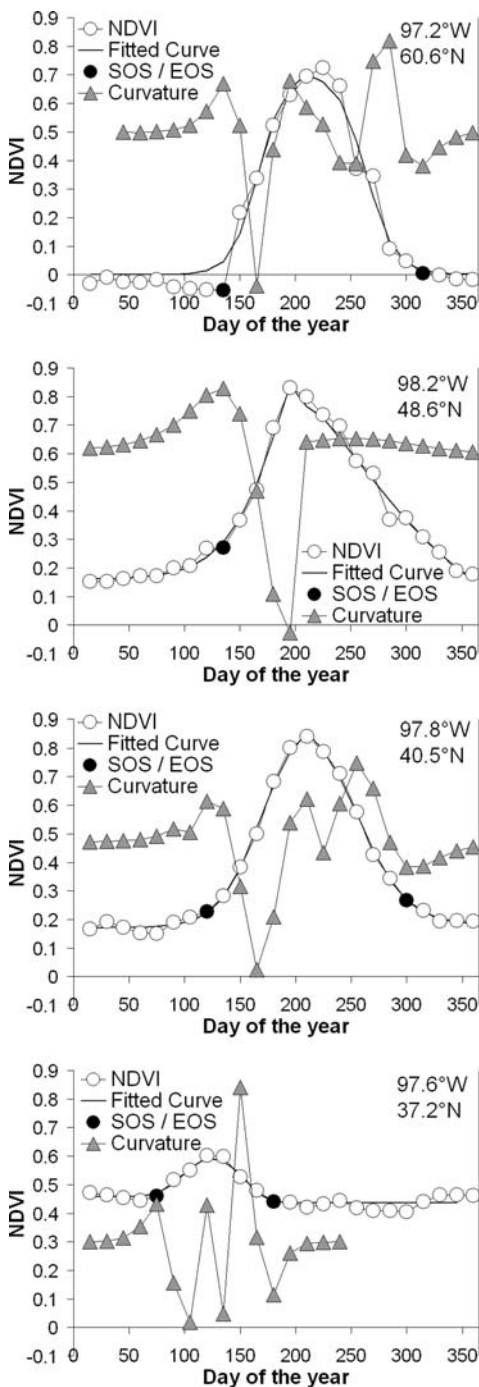
**Fig. 9.3** The start of season as determined by the largest derivative. The SOS and the EOS are indicated by the black circles in the time series of NDVI. The derivative itself is plotted on the second y-axis; however, the values are omitted. (See Table 9.2 for the SOS and EOS results.)



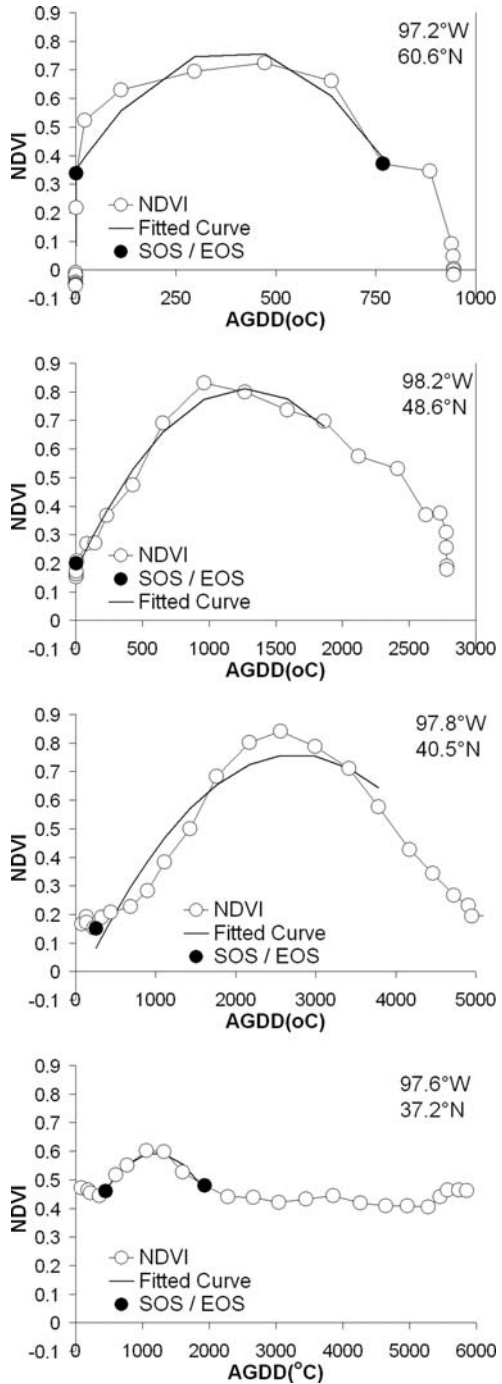
**Fig. 9.4** Fourier decomposition of the 2002 GIMMS data. The mean of the data is stable over the growing season. The first harmonic tends to give the seasonality of the data. The sum of the mean and the first two harmonics results in a good approximation of the actual NDVI curve



**Fig. 9.5** Application of the logistical model as proposed by Zhang et al. (2003, 2004). The grey triangles give the curvature function which is used to determine SOS and EOS (See Table 9.2 for the SOS and EOS results.)



**Fig. 9.6** Application of the quadratic model based on AGDD by de Beurs and Henebry (2004a, 2005a, 2005b). The model does not confuse snow melt with the actual start of season due to the incorporation of AGDD. The model fits well in Canada and North Dakota and Kansas, but does not fit as well in Nebraska





**Table 9.2** Phenological metrics evaluated using five different methods at four sites across North America. SOS (Start of Season) and EOS (End of Season) are day of the year; GSL (growing season length=EOS-SOS) is in days. NA indicates that the method did not identify the EOS date and thus the GSL calculation is not possible. The corresponding methods can be found in Figs. 9.1, 9.2, 9.3, 9.5 and 9.6

	Canada			North Dakota			Nebraska			Kansas		
	SOS	EOS	GSL	SOS	EOS	GSL	SOS	EOS	GSL	SOS	EOS	GSL
Threshold 50%	165	271	106	167	289	122	164	264	100	87	158	71
Moving Average	135	315	180	60	345	285	75	365	290	75	210	135
Derivative	150	240	90	180	270	90	180	255	75	90	150	60
Logistic model	135	315	180	135	NA	NA	120	300	180ag	75	180	105
Quadratic model	150	255	105	90	NA	NA	75	NA	NA	75	165	90

latest in Canada. The EOS was earliest in Kansas as a result of the harvesting of winter wheat which typically commences in early June. Compared to the threshold method, the estimated SOS was earlier by as much as 100 days (North Dakota). This discrepancy is mainly due to the fact that the moving average method determines the point that the NDVI value starts to increase as opposed to the most rapid increase. In addition, the growing season length is between 64 and 190 days longer when observed with the moving average method.

### 9.6.3 Derivatives

Figure 9.3 gives the results of the derivative method which also determines the period of fastest increase. In this case we have applied the method of Tateishi and Ebata (2004). The results for the SOS and the EOS were comparable to the results from the 50% threshold method, which was expected since both methods investigate the period of most rapid increase. On average the difference between the two methods is about 12 days, where the derivative generally has a little later SOS (except for Canada). Again earliest SOS was found in Kansas and latest in North Dakota and Nebraska. The EOS was earlier in Canada than in North Dakota and Nebraska, but the EOS arrived earliest in Kansas due to the timing of crop harvest. The growing season length varied between 60 and 90 days with the longest growing seasons in Canada and North Dakota and the shortest growing season in Kansas.

### 9.6.4 Model Fitting

Figure 9.5 gives the results of the model fit for the logistic model as presented by Zhang et al. (2003). The model fitted the data extremely well in all cases. The grey triangles give the curvature of the model as calculated with Equation 9.9. The SOS and the EOS are determined as the first peak and the last trough of the curvature, respectively. These results were somewhat similar to the results of the moving average method (Reed et al. 1994); however, the figure demonstrates that for the pixel in North Dakota, the curvature function is too flat to determine the EOS. From Fig. 9.5 it can be seen that SOS as determined in Canada might be too early and most likely resulted from snow melt as opposed to vegetation green-up. The same effect was visible for the moving average method. In later versions of Zhang's model, a correction is provided for snow covered areas (Zhang et al. 2004). The SOS was reached at day 135 in both Canada and North Dakota. The SOS was reached earlier (day 120) in Nebraska and even earlier in Kansas (day 75, see Table 9.2). The procedure failed to estimate a growing season length in North Dakota, and it was estimated as 180 days both in Canada and in Nebraska. As expected, the growing season was a lot shorter in Kansas. These SOS results were somewhat comparable to the results based on the moving average method, but the growing season was shorter for both Nebraska and Kansas (Table 9.2).

Figure 9.6 gives the results of the model fit for the quadratic models based on accumulated growing degree-days (de Beurs and Henebry 2004a, 2005a, 2005b). This method was not developed for optimal detection of the SOS or EOS, but rather for the analysis of interannual variability and change in land surface phenology. Yet, to facilitate comparisons among the methods, we have applied the method here to detect SOS. The curves in Fig. 9.6 show which sequence of data points were used to fit the model. Again the results were somewhat similar to the moving average method as well as the logistic models (Table 9.2). In two sites the quadratic model could not determine the EOS, due to an early end of the model. The quadratic model incorporates AGDD which results in a later SOS in Canada compared to the logistic model and the moving average method, which are based only on calendar dates. Since AGDD is still zero when there is a significant amount of snow cover, SOS was not sensitive to snow melt in this case.

The colour plate (Plate 8) provides a spatial comparison of the four methods: the logistic model fits, the quadratic model fits, the threshold method, and the derivative method. It clearly demonstrates that the SOS is much later for the derivative and threshold methods than for the model fitting methods in most of the study areas. The largest differences could be found in the agricultural regions of the Midwest. Towards the south, the differences became smaller (but in the drier areas of Texas, the methods failed). In the north the differences were small as well, most likely due to the shorter growing season in those areas which does not allow for long delays between emergence and the period of most rapid green-up.

When we compared the two methods that look at the period of most rapid green-up (derivative and threshold), we saw that the results were very similar with most observations within two weeks of each other. In southern Texas, the differences were much larger due to diminished variability in the data within a year, which can readily lead to method failure. It is interesting to note that, across most of the study region, the derivative method resulted in slightly later SOS, while in the north the derivative resulted in slightly earlier SOS.

When we compared the results for the two model fitting routines, we found much more spatial heterogeneity compared to the threshold and derivative methods. First, there were large differences in the southern part of the study region. These differences were a result of a failing of the logistic regression models. The fitted logistic curve was relatively flat which results in the lack of peaks and troughs in the curvature function. When peaks or troughs cannot be detected, there is no means to identify the SOS or the EOS. The quadratic models did provide SOS estimates for these sites and were able to find relatively well-fitting curves. However, the vegetation in these areas most likely responded more strongly to precipitation differences as opposed to temperature differences that are tracked by AGDD. The second area of interesting differences can be found in a band extending from Iowa to North Dakota and Saskatchewan. In these areas the pixels followed a fairly clean green-up period, and accumulated growing degree-days were above zero early in the season. Based on the visible model estimates it appeared that the quadratic models fit very well, but started too early. The last discrepancy is in the far northern part of the study

region, where the logistic regression model appeared to detect snow melt and thus estimated SOS too early.

## 9.7 Synopsis

Having surveyed representative methods for the characterization and change analysis of land surface phenology, we conclude with observations and remarks on the wide range of methods and results.

### 9.7.1 *A Nomenclature is Needed*

Most of the methods focus on a derived metric called the onset of season or the start of season (SOS). However, use of the same term masks a disparity about which phenomenon constitutes the SOS. This ambiguity generates a wide discrepancy among the evaluated metrics. To move toward global terrestrial land surface phenology products and their analysis, it is vital to conduct quantitative evaluations of competing methods and their predictions. A coherent nomenclature is critically needed, but it is currently lacking.

### 9.7.2 *Uncertain Error Structures*

We have discussed only briefly some key limitations of the methods. While each has its particular strengths and weaknesses, the most pressing and common problem is the lack of error measures for the observations that give an indication of the expected natural variability around the observed value. The error structures of observed SOS and EOS are seldom articulated; thus, it is impossible to determine whether apparently unusual points or years are significantly different or just rare extremes of the usual variability. As a result, most methods fail to move beyond the descriptive phase and observed changes cannot be tested for significance.

Without an error structure that allows for statistical comparisons between phenologies recorded over different time periods, we cannot test whether the detected trends are significant. White and Nemani (2006) suggested that individual pixels should not be analyzed independently, but rather simultaneously to form an empirical distribution. Although this aggregation can minimize the influence of a few pixels with erratic behavior, an empirical distribution as formed by a group of pixels in space is not the same as the standard errors of a method over time (unless the dynamical system exhibits ergodicity, which is not only unlikely but very difficult to test given the paucity of image time series currently available). On the one hand, the standard error is estimated from a spatial distribution; thus, it gives an indication of the expected spatial variability of the observations. On the other hand, the standard

error is estimated from a temporal distribution across many years. It is this latter standard error that gives an indication of how well a particular method is capable of estimating a particular phenological metric such as start of season, or duration of green-up period.

### ***9.7.3 Limits of Fitted Models***

Model fitting is a frequently applied method for the description of land surface phenology based on satellite imagery. To allow for the variable nature of the NDVI curves, several authors have developed flexible models that can easily be adjusted to the available data (Badhwar 1984, Tucker et al. 2001, Jönsson and Eklundh 2002, Zhang et al. 2004). While all the models are based on different theory, they have several aspects in common:

1. they are very general and can be easily adapted to a wide range of situations;
2. time is the independent variable;
3. they require that at least four parameter coefficients be estimated; and
4. these parameter coefficients are not readily interpreted in ecological or biogeophysical terms.

Higher model complexity often inhibits straightforward interpretation of the estimated parameter coefficients. In addition, while the large number of variables in models might increase the coefficients of determination ( $r^2$ ), fitting many variables to sparse data can substantially reduce the statistical power of the resulting model.

The models have become increasingly better at mimicking observed NDVI curves. Methods such as the high-order, non-classical harmonic analysis of NDVI data with damping model roughness or the Gaussian local functions as incorporated in TIMESAT can do extremely well in approximation of the NDVI trajectories. However, there are at least two general limitations. Firstly, the mathematical model is assumed only to approximate the true phenological curve. This assumption will break down quickly in case of disturbance on the landscape that might subsequently be missed due to the smoothing action (White and Nemani 2006). Secondly, the fitting routines have become so complicated that they are mainly applied as advanced smoothing filters. As a result, to determine the SOS based on these models, most authors (Jönsson and Eklundh 2002, Verbesselt et al. 2006, Bradley et al. 2007) fall back on accepting a certain percentage increase in the NDVI, similar to the basic 50% threshold method.

### ***9.7.4 Parochial Perspectives***

Few authors take an approach that compares model estimates based on two or more periods or regions. In other words, most procedures offer only statistical fits of the data without an analysis of the significance or robustness of the model. The phenological models based on AGDD are the only models presented here that allow for the statistical comparison of results from different growing seasons or regions.

An extension of this model for rain-green systems (i.e. vegetation communities in which development is triggered by sporadic precipitation events) in Africa has recently been developed (Brown and de Beurs 2008). While the method does a poorer job for the testing and determining of the SOS and the EOS, it excels in measuring the significance of temporal changes in phenology models by looking at the peak position and peak height. Such ecologically meaningful models not only describe the observed phenology, but can also be used to test for statistically significant differences between time periods or study regions.

### ***9.7.5 The Challenge of Water-Limited Systems***

Most of the methods presented here are focused on the analysis of land surface phenology in temperature and light limited systems. Few methods currently deal directly with rain-green systems (e.g. Brown and de Beurs 2008). Rain-green systems are often more difficult to deal with because of the concomitant occurrence of precipitation (and thus reflectance obscuring clouds) and vegetation green-up resulting in noisier observations. In addition, rain-green systems often reveal larger interannual variability, lagged responses, “false” starts of the season as well as areas where the “season” does not arrive some years.

### ***9.7.6 Challenges Ahead***

Characterization and analysis of land surface phenologies has advanced rapidly in recent years with the advent of more and richer data sources and a widening realisation of the centrality of phenology to integrating diverse biogeophysical processes. We have restricted our attention in this chapter to a technical discussion of the methods commonly employed with land surface phenology. However, we would be remiss to conclude without pointing to the principal outstanding challenge; namely, linking remotely sensed observations of the land surface phenologies with ground level and in situ observations of the specific phenologies of plants and animals. Reconciling the mixture of signals from the land surface with the discrete life events of multiple species will remain an active area of research. Finally, the forecasting of land surface phenologies is not the same task as modelling phenologies retrospectively, but it is an important area for future work to provide much needed feedback to modellers of weather and biogeochemistry as well as to natural resource managers (White and Nemani 2006, Kathuroju et al. 2007).

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# Chapter 10

## Climatic Influences on the Flowering Phenology of Four Eucalypts: A GAMLSS Approach

Irene L. Hudson, Susan W. Kim, and Marie R. Keatley

**Abstract** This chapter represents one of the first attempts to utilize phenological data to detect non-linear responses of flowering to climate change using GAMLSS. We use the flowering of four species (*Eucalyptus leucoxylon*, *E. microcarpa*, *E. polyanthemos* and *E. tricarpa*) as a case study. Regardless of cyclicity of flowering over time, this study shows that each species flowering is significantly influenced by temperature and this effect is non-linear. Stepwise GAMLSS showed that the main temperature driver of *E. leucoxylon* is minimum temperature ( $P < 0.0001$ ), maximum temperature for *E. polyanthemos* ( $P < 0.0001$ ), both minimum and maximum temperature ( $P < 0.0001$ ) for *E. tricarpa*, and mean temperature for *E. microcarpa* ( $P < 0.0001$ ). Rainfall was not a significant predictor of flowering. GAMLSS allowed for identification of upper/lower thresholds of temperature for flowering commencement/cessation; for the estimation of long and short-term non-linear effects of climate, and the identification of lagged cyclic effects of previous flowering.

Flowering intensity of all species was positively and significantly correlated with last month's flowering ( $P < 0.0001$ ); and with flowering 12 months earlier for *E. polyanthemos* and *E. microcarpa*. Flowering of *E. polyanthemos* was negatively and significantly correlated with flowering intensity 2 and 4 months prior; in the case of *E. microcarpa* with flowering 6 and 8 months earlier. Overall, *E. microcarpa* and *E. polyanthemos* flower more intensely in response to predicted increases in mean and maximum temperature, respectively. *E. leucoxylon* flowers less intensely with predicted increases in minimum temperature; *E. tricarpa* flowers less intensely with increased maximum temperature, but more intensely with increased minimum temperature (after accounting for maximum temperature).

**Keywords** Climate change · Cubic smoothing splines · Generalised additive model for location · Scale and shape (GAMLSS) · Multiple time series · Thresholds

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## 10.1 Introduction

Phenology involves the recording of recurring natural events such as the commencement of flowering (Fitter et al. 1995) or the arrival of migratory birds (Sparks 1999), and the influence on such events by edaphic and climatic factors (Leith 1974). Analyses of phenological data have been used to examine the impacts of climate change (Menzel 2002, Chambers 2006, Rosenzweig et al. 2007). These studies, however, remain concentrated in the Northern Hemisphere. Indications are that long-term phenological studies, within any discipline, are extremely limited in Australia (IPCC 2007). Datasets spanning a century or more such as are found in Europe (Sparks and Carey 1995) are unlikely in Australia, given the short period of European settlement (e.g. since 1788 for Sydney, 1835 for Melbourne).

As eucalypts are a dominant genus, both in a botanical and economic sense, they have been the focus of most Australian plant phenological studies (Ashton 1975, Cremer 1975, Law et al. 2000, Keatley et al. 2002; Bassett et al. 2006; Keatley and Hudson 2007). The flowering pattern of plant species, may fluctuate haphazardly. Numerous explanations are given in the literature to explain that pattern, including: genetics, reproduction costs, herbivory effects, climate, inflorescence architecture, phylogenetic constraints, competition, etc (Primack 1980, Waser 1983, Eldridge et al. 1993, McKittrick 1993, Keatley and Hudson 1998, Pfeifer et al. 2006).

GAMLSS (Generalised additive model for location, scale and shape) are part of the Generalized Linear Models (GLM) (Nelder and Wedderburn 1972) and Generalized Additive Models (GAM) “family” (Hastie and Tibshirani 1999, Hastie 2008), were introduced by Rigby and Stasinopoulos (2001) and Akantziliotou et al. (2002); and further developed in 2005 (Rigby and Stasinopoulos 2005) to overcome various limitations of the popular GLM and GAMs. For example, GAMLSS can deal with non normally distributed data (e.g. highly skewed, or kurtotic continuous and discrete distributions). Current updates of GAMLSS can deal with up to 50 different types of distributions (Stasinopoulos and Rigby 2007).

GAMLSS thus extend linear regression to a non-linear form by allowing each regression variable to have a non-linear relationship with the dependent variable. The type of non-linearity is not pre-specified a priori, but calculated and tested in the modelling process. GAMLSS are thereby a general framework for univariate regression analysis which allows for testing of semi-parametric models. By this we mean, they need a parametric distribution for the response variable, however, they can cope with a wide range of distributions such as the (Poisson, negative binomial, log normal, Weibull etc). They are “semi” in the sense that the modelling of the actual parameters, such as the mean or location (as functions of the explanatory variables) may involve using non parametric smoothing functions (for example cubic smoothing splines; for a discussion on this see Chapter 12).

Recent applications of GAMLSS have involved modelling climate with Sudden Infant Death Syndrome (Hudson et al. 2008) and in the establishment of the world standard child growth curves by the World Health Organisation (Borghini et al. 2006) (see also examples in Rigby and Stasinopoulos 2005). As far as the authors are aware, GAMLSS have not been applied to phenological research to date. It

should be noted, however, that Hudson et al. (2003) used GAMs (the precursor to GAMLSS) and Bayesian methods to model *E. leucoxylon* flowering, and found that the estimated effects of mean temperature were smoothly non-linear on flowering intensity. The work of Roberts (Chapter 12) on penalized splines or *P*-splines is a method that also has some inter-relatedness with GAMLSS in that spline functionals (the term “spline” is used to refer to a wide class of functions that are used in applications requiring data interpolation and/or smoothing) are used in the modelling procedures. Penalized splines were introduced by Eilers and Marx (1996). *P*-splines are piecewise polynomials defined by *B*-spline basis functions in the explanatory variable, where the coefficients of the basis functions are penalized to guarantee sufficient smoothness (see Eilers and Marx 1996).

The benefits of GAMLSS for phenological data (which is a time series) are that they

- can identify the main drivers of the event of interest from a multiplicity of predictors such as climate and food sources etc,
- allow for non linear impacts of the explanatory variables or predictors,
- can statistically detect thresholds, for example, the lowest temperature for the commencement of flowering,
- can model and/or account for the auto-correlated nature of the phenological series, for example by incorporating lag effects.

This chapter presents one of the first attempts to utilize phenological data to detect non-linear responses of flowering to climate change using GAMLSS. We use the flowering of four species (*Eucalyptus leucoxylon*, *E. microcarpa*, *E. polyanthemus* and *E. tricarpa*) as a case study. The primary aim of this chapter is to investigate the relationship between flowering intensity and three temperature variants, minimum, maximum and mean temperature (since temperature is a major climatic influence on phenological events such as flowering (Menzel 2002)). In addition to studying possible non-linear impacts of rainfall (Hudson et al. 2003, 2008). In this chapter we clearly illustrate the benefit of GAMLSS in modelling and interpretation of possibly non-linear climatic impacts on eucalypt flowering.

## 10.2 Data and Methods

### 10.2.1 Phenological and Climate Data

Flowering observations were undertaken on a monthly basis at the population level by Forests Commission officers (Keatley et al. 2002). They categorised their observations of flowering according to the quantity and distribution of flowering across the population. Flowering quantity is ranked from “No flowering” to “Heavy flowering”, whilst distribution ranges from “Isolated” to “General” (Table 10.1). Flowering was quantified by assigning a rank value to these descriptions according

**Table 10.1** Terms used to describe flowering intensity and their assigned value

Observation parameter	Description	Assigned value
Quantity	No flowering	0
	Very scattered or isolated	0.5
	Light Flowering	1
	Medium Flowering	2
Distribution	Heavy Flowering	3
	Isolated	0.5
	Scattered	1
	Fairly General	1.5
	General	2

to the formulation in Keatley (1999). Flowering intensity (ranging from 0 to 5) was calculated, based on the sum of the quantity and distribution of the rank values, where a score of 0 indicates that no flowering occurred whilst a score of 5 indicated that flowering was heavy and distributed throughout the observation area. The flowering intensity score assumes an equal weighting (importance) of its components (quantity and distribution). Whilst it is possible that the importance of one component is greater than the other, there are no data available to support such weighting.

These flowering records are the basis of this study, which focuses on the flowering of four species: *Eucalyptus leucoxylo*n, *E. tricarpa*, *E. microcarpa* and *E. polyanthemos*. Monthly flower counts for flowering intensity and mean monthly readings of climate (minimum and maximum temperature (°C), mean diurnal temperature (°C) and rainfall (mm)). For example *E. leucoxylo*n flower counts (which ranged from 0.0 to 5.0) for the study period (1940–1971) constituted 409 monthly time points. Table 10.2 provides the mean, median duration of flowering for the 4 species in addition to the most probable month of flowering per year as calculated by Keatley and Hudson (2007).

**Table 10.2** Mean and median flowering duration (months  $\pm$  1 SD) and most probable month of eucalypt species at Havelock

Species	Mean duration (months)	Median (months)	Month with highest probability of flowering in a month in a flowering year	Month of peak intensity
<i>E. leucoxylo</i> n	9.7 $\pm$ 4.2	9.0	October	Sept
<i>E. microcarpa</i>	4.0 $\pm$ 1.0	4.0	March	March
<i>E. polyanthemos</i>	3.6 $\pm$ 1.5	3.5	November	Nov/Dec
<i>E. tricarpa</i>	6.2 $\pm$ 2.1	6.0	July	July

## 10.2.2 GAMLSS Method

The GAMLSS framework of statistical modelling is implemented in a series of packages in R, (R Development Core Team 2007), a free software (see URL <http://www.R-project.org>). The packages can be downloaded from the R library, CRAN, or from <http://www.gamlss.com>. For this study the GAMLSS procedure was used with a cubic spline smoothing function and a forwards stepwise (stepGAIC) function in GAMLSS (Stasinopoulos and Rigby 2007). Each model tested assumed that the flowering series represented Poisson counts and the RS algorithm, a generalization of the algorithm of Rigby and Stasinopoulos (1996a, 1996b) was used to obtain the estimates of the climatic predictors as non-linear cubic spline terms. Lagged dependencies of current with past flowering (up to 12 months prior) were added as auto-regressive (AR) lags. Note that cubic smoothing splines is denoted by *cs()* in this chapter.

### 10.2.2.1 The GAMLSS Framework

We follow essentially the development of Rigby and Stasinopoulos (2005) to explicitly outline the GAMLSS model. Let  $y^T = (y_1, y_2, \dots, y_n)$  be the vector of the response variable observations. The  $p$  parameters  $\theta^T = (\theta_1, \theta_2, \dots, \theta_p)$  of a population probability (density) function (p.d.f)  $f(y|\theta)$  are then modelled by using additive models. Specifically the model assumes that, for  $i=1, 2, \dots, n$ , observations  $y_i$  are independent conditional on  $\theta_i$ , with p.d.f.  $f(y_i|\theta^i)$ , where  $\theta^{iT} = (\theta_{i1}, \theta_{i2}, \dots, \theta_{ip})$  is a vector of  $p$  parameters related to the explanatory variables and random effects.

Here  $g_k(\cdot)$  for  $k=1, 2, \dots, p$ , is a known monotonic link function relating to both explanatory variables and to random effects through an additive model given by

$$g_k(\theta_k) = \eta_k = X_k \beta_k + \sum_{j=1}^{J_k} Z_{jk} \gamma_{jk} \quad (10.1)$$

where  $\theta_k$  and  $\eta_k$  are vectors of length  $n$ . For example  $\theta_k^T = (\theta_{1k}, \theta_{2k}, \dots, \theta_{nk})$ ,  $\beta_k^T = (\beta_{1k}, \beta_{2k}, \dots, \beta_{J_k k})$  is a parameter vector of length  $J_k$ ,  $X_k$ , is a known design matrix of order  $n \times J_k$ ,  $Z_{jk}$  is a fixed known  $n \times q_{jk}$  design matrix and  $\gamma_{jk}$  is a  $q_{jk}$  dimensional random variable. Model (10.1) is called the GAMLSS.

Rigby and Stasinopoulos (2005) note that the vectors  $\gamma_{jk}$  for  $j = 1, 2, \dots, J_k$  could be combined into a single vector  $\gamma_k$  with a single design matrix  $Z_k$ . The formulation in (10.1), nevertheless is preferred as it is suited to the back fitting algorithm (which is integral to the fitting of the additive components) and also straightforwardly allows combinations of different types of additive random-effects terms to be added in the model (see also Stasinopoulos and Rigby (2007)). Model (10.1) clearly reduces to a fully parametric model when  $k=1, 2, \dots, p$ ,  $J_k=0$ . This is given by

$$g_k(\theta_k) = \eta_k = X_k \beta_k \tag{10.2}$$

If  $Z_{jk} = I_n$ , where  $I_n$  is an  $n \times n$  identity matrix, and  $\gamma_{jk} = \mathbf{h}_{jk} = h_{jk}(\mathbf{x}_{jk})$  for all combinations of  $j$  and  $k$  in model (10.1), we then have

$$g_k(\theta_k) = \eta_k = X_k \beta_k + \sum_{j=1}^{J_k} h_{jk}(\mathbf{x}_{jk}) \tag{10.3}$$

where  $\mathbf{x}_{jk}$  for  $j=1,2,\dots,j_k$ , and  $k=1,2,\dots,p$ , are vectors of length  $n$ . The function  $h_{jk}$  is an *unknown function* of the explanatory variable  $\mathbf{x}_{jk}$  (assumed to be known) and  $\mathbf{h}_{jk} = h_{jk}(\mathbf{x}_{jk})$  is the vector which evaluates the function  $h_{jk}$  at  $\mathbf{x}_{jk}$ . The model in equation (10.3) is called the semi-parametric GAMLSS. Model (10.3) is an important special case of model (10.1). It is noteworthy that if  $Z_{jk} = I_n$  and  $\gamma_{jk} = \mathbf{h}_{jk} = h_{jk}(\mathbf{x}_{jk})$  for specific combinations of  $j$  and  $k$  in model (10.1), then the resultant model includes parametric, nonparametric and also random-effects terms.

It is common place for the first two population parameters  $\theta_1$  and  $\theta_2$  in model (10.1) to be characterized as location and scale parameters, which we denote by  $\mu$  and  $\sigma$ ; whereas the remaining parameter(s), if any, are characterized as the so-called shape parameters (Rigby and Stasinopoulos 2005). Given that a maximum of two shape parameters  $\nu (= \theta_3)$  and  $\tau (= \theta_4)$  are sufficient for many families of population distributions, we can then write the following model,

$$\begin{aligned} g_1(\theta_1) &= \eta_1 = X_1 \beta_1 + \sum_{j=1}^{J_1} Z_{j1} \gamma_{j1} \\ g_2(\theta_2) &= \eta_2 = X_2 \beta_2 + \sum_{j=1}^{J_2} Z_{j2} \gamma_{j2} \\ g_3(\theta_3) &= \eta_3 = X_3 \beta_3 + \sum_{j=1}^{J_3} Z_{j3} \gamma_{j3} \\ g_4(\theta_4) &= \eta_4 = X_4 \beta_4 + \sum_{j=1}^{J_4} Z_{j4} \gamma_{j4} \end{aligned} \tag{10.4}$$

The GAMLSS model (10.1) is clearly more general than the GLM, the generalized linear mixed model (GLMM) (Fox 1997, Gelman and Hill 2006, Jiang 2007) or the generalized additive mixed model (GAMM) (Lin and Zhang 1999, Pinheiro and Bates 2000, Fahrmeir and Lang 2001) in that the distribution of the dependent variable is not limited to the exponential family and in that all parameters (not just the mean) are modelled in terms of both fixed and random effects.

It should be mentioned that the GLMM combines the GLM and linear mixed model, by introducing a random-effects term in the linear predictor for the mean of a GLM. Note that whilst the GLMM and GAMM are more flexible than the GLM and GAM respectively, they still require an exponential family conditional distribution for  $y$  and infrequently model parameters other than the mean (or location)

of the distribution of the response variable  $y$ , as functions of the explanatory variables. This is not the case for GAMLSS. Of particular importance is that unlike the GLMM and GAMM, the GAMLSS is not highly time consuming nor computationally intensive. This is particularly so in the presence of many explanatory predictors, where model selection requires testing numerous alternative models. Indeed their fitting depends on Markov chain Monte Carlo (MCMC) or integrated (marginal distribution) likelihoods (Rigby and Stasinopoulos 2005).

### 10.2.2.2 Model Estimation

GAMLSS models with non-linear terms can be examined via partial residuals, which are defined in the back fitting function (Rigby and Stasinopoulos 2005). The partial residuals, say for a given variable of interest, are plotted after removal of the effects of the other variables (see term plot in R). The model terms in GAMLSS are additive, so the effects from each of the other variables are easily removed. Residuals are examined for influential or outlying cases and non-random trends (see diagnostic plots in `gamlss()` in R).

The backfitting algorithm and the fact that quadratic penalties in the likelihood result from assuming a normally distributed random effect in the linear predictor are fundamental to the way that additive components are fitted within the GAMLSS framework. Shrinking (smoothing) matrices  $S_{jk}$  within a backfitting algorithm are used in the resultant estimation as follows.

Assume in model (10.1) that the  $\lambda_{jk}$  have independent (prior) normal distributions with  $\gamma_{jk} \sim N_{q_{jk}}(0, \bar{G}_{jk})$  where  $\bar{G}_{jk}$  is the (generalized) inverse of a  $q_{jk} \times q_{jk}$  symmetric matrix  $G_{jk} = G_{jk}(\lambda_{jk})$ , which may depend on a vector of hyperparameters<sup>1</sup>  $\lambda_{jk}$ . If  $G_{jk}$  is singular, then  $\lambda_{jk}$  is understood to have an improper prior density function proportional to  $\exp\left(-\frac{1}{2}\gamma_{jk}^T G_{jk} \gamma_{jk}\right)$ . The assumption of independence between different random-effects vectors  $\lambda_{jk}$  is essential within the GAMLSS framework. From this point onward we refer to  $G_{jk}$  rather than to  $G_{jk}(\lambda_{jk})$  for ease of notation, although the dependence of  $G_{jk}$  on hyperparameters  $\lambda_{jk}$  remains throughout.

Rigby and Stasinopoulos (2005) show via empirical Bayesian arguments, that posterior mode estimation (Berger 1993) for the parameter vectors  $\beta_k$  and the random-effect terms  $\gamma_{jk}$  (for fixed values of the smoothing or hyperparameters  $\lambda_{jk}$ ), for  $j = 1, 2, \dots, J_k$  and  $k=1, 2, \dots, p$ , is equivalent to penalized likelihood estimation. Thus for fixed  $\lambda_{jk}$ s the  $\beta_k$ s, the  $\gamma_{jk}$ s are estimated within the GAMLSS framework by maximizing a penalized likelihood function  $l_p$  given by

$$l_p = l - \frac{1}{2} \sum_{k=1}^p \sum_{j=1}^{J_k} \gamma_{jk}^T G_{jk} \gamma_{jk} \tag{10.5}$$

---

<sup>1</sup>In Bayesian statistics, parameters of prior distributions are called hyperparameters. This is to distinguish them from parameters of the model of the underlying data (Gelman et al. 2003).



where  $l = \sum_{i=1}^n \log \{f(y_i | \theta^i)\}$  is the log-likelihood function of the data given  $\theta^i$  for  $i=1,2,\dots,n$ .

Rigby and Stasinopoulos (2005) prove that maximizing  $l_p$  is achieved by the CG algorithm, wherein the maximization of  $l_p$  requires that the shrinking (smoothing) matrix  $S_{jk}$ , be applied to partial residuals  $\varepsilon_{jk}$  to iteratively update the estimate of the additive predictor  $Z_{jk}\gamma_{jk}$  within a backfitting algorithm, given by

$$S_{jk} = Z_{jk} \left( Z_{jk}^T W_{kk} Z_{jk} + G_{jk} \right)^{-1} Z_{jk}^T W_{kk} \tag{10.6}$$

for  $j=1,2,\dots,J_k$  and  $k=1,2,\dots,p$ , and where  $W_{kk}$  is a diagonal matrix of iterative weights.

One further conceptualization comes from the fact that different forms of  $Z_{jk}$  and  $G_{jk}$  correspond to diverse types of additive terms in the linear predictor  $\eta_{jk}$  for  $k=1,2,\dots,p$ . Indeed for random-effects terms  $G_{jk}$  are often a simple or low order matrix (or both), whereas for a cubic smoothing spline term we have the following equivalences  $\gamma_{jk}=h_{jk}$ ,  $Z_{jk}=\mathbf{I}_n$  and  $G_{jk} = \lambda_{jk}K_{jk}$ , where  $K_{jk}$  is a structured matrix. Moreover either case allows simple updating of  $Z_{jk}\gamma_{jk}$ . Note also that the hyperparameters  $\lambda$  can be fixed or estimated.

### 10.2.2.3 The Linear Predictor

#### Parametric Terms

Recall from the GAMLSS (10.1) that the linear predictors  $\eta_k$ , for  $k=1,2,\dots,p$ , comprise a parametric component  $X_k\beta_k$  and additive components  $Z_{jk}\gamma_{jk}$ , for  $j=1,2,\dots,J_k$  (Rigby and Stasinopoulos 2005). Noteworthy also is the following generality, that the parametric component can include linear and interaction terms for explanatory variables and factors, polynomials, fractional polynomials (Royston and Altman 1994) and also piecewise polynomials (with fixed knots) for variables (Smith 1979, Stasinopoulos and Rigby 1992). Importantly non-linear parameters can be included into the GAMLSS (10.1) and fitted by either: the profile fitting method, where estimation of non-linear parameters is achieved by maximizing their profile likelihood; or the derivative method. In the latter derivatives of a predictor  $\eta_k$  with respect to non-linear parameters are incorporated in the design matrix  $X_k$  in the fitting algorithm (Benjamin et al. 2003).

#### Additive Terms

Rigby and Stasinopoulos (2005) discuss a suite of different additive terms that can be included in the GAMLSS. The additive components  $Z_{jk}\gamma_{jk}$  in model (10.1) can fit a variety of terms such as smoothing and random-effect terms, in addition to terms that are valuable for time series analysis. For simplicity we now drop the subscripts  $j$  and  $k$  in the vectors and matrices, where appropriate.

### Cubic Smoothing Splines Terms

Let  $\mathbf{h} = h(\mathbf{x})$  be the vector of evaluations of the function  $h(t)$  at the values  $\mathbf{x}$  of the explanatory variable  $X$ , where with cubic smoothing splines terms we assume in model (10.3) that the functions  $h(t)$  are arbitrary twice continuously differentiable functions and we maximize a penalized log-likelihood, given by  $l_p$  subject to penalty terms of the form  $\lambda \int_{-\infty}^{\infty} h(t)^2 dt$ . The maximizing functions  $h(t)$  are all natural cubic splines and thus can be expressed as linear combinations of their natural cubic spline basis functions  $B_i(t)$  for  $i=1,2,\dots,n$ , that is  $[h(t) = \sum_{i=1}^n \delta_i B_i(t)]$ .

Let  $\mathbf{N}$  be an  $n \times n$  non-singular matrix containing as its columns the  $n$ -vectors of evaluations of functions  $B_i(t)$ , for  $i=1,2,\dots,n$ , at  $\mathbf{x}$ . Then  $\mathbf{h}$  can be expressed by using a coefficient vector  $\delta$  as a linear combination of the columns of  $\mathbf{N}$  by  $h=N\delta$ . Let  $\Omega$  be the  $n \times n$  matrix of inner products of the second derivatives of the natural cubic spline basis functions, with  $(r,s)$  th entry given by  $\Omega_{rs} = \int B_r''(t) B_s''(t) dt$ . The penalty is then given by the quadratic form

$$Q(h) = \lambda \int_{-\infty}^{\infty} h''(t)^2 dt = \lambda \delta^T \Omega \delta = \lambda \mathbf{h}^T \mathbf{N}^{-T} \Omega \mathbf{N}^{-1} \mathbf{h} = \lambda \mathbf{h}^T \mathbf{K} \mathbf{h}, \tag{10.7}$$

where  $\mathbf{K} = \mathbf{N}^{-T} \Omega \mathbf{N}^{-1}$  is a known penalty matrix that depends only on the values of the explanatory vector  $\mathbf{x}$ .

The exact form of the matrix  $\mathbf{K}$  is given in Green and Silverman (1994), Section 2.1.2. Note that the model can be formulated as a random-effects GAMLSS (10.1) by letting  $\gamma(h)$ ,  $\mathbf{Z}=\mathbf{I}_n$ ,  $\mathbf{K}=\mathbf{N}^{-1} \Omega \mathbf{N}^{-1}$  and  $\mathbf{G}=\lambda \mathbf{K}$ , so that  $h \sim N_n(0, \lambda^{-1} \mathbf{K}^{-1})$ , a partially improper prior (Rigby and Stasinopoulos 2005).

### The Two Algorithms

The objective of the algorithms is to maximize the penalized likelihood function  $l_p$ , given in equation (10.5), for fixed hyperparameters  $\lambda$ . Two basic algorithms are used, firstly the CG algorithm, which is a generalization of the Cole and Green (1992) algorithm (and uses the first and second and cross-derivatives of the likelihood function with respect to the parameters  $\theta$ . However, for many population p.d.f.'s  $f(y|\theta)$  the parameters  $\theta$  are information orthogonal (since the expected values of the cross-derivatives of the likelihood function are 0). This is true for location and scale models and dispersion family models (Rigby and Stasinopoulos 2005). In this latter case the second and simpler RS algorithm, a generalization of the algorithm used by Rigby and Stasinopoulos (1996a, 1996b) for fitting mean and dispersion additive models (MADAM) (and does not use the cross-derivatives), is more suitable. Note that the parameters  $\theta$  are fully information orthogonal for only the negative binomial, gamma, inverse Gaussian, logistic and normal distributions.

Rigby and Stasinopoulos (2005) provide details of the algorithms and their advantages, and demonstrate that the CG algorithm maximizes the penalized likelihood  $l_p$ , given by equation (10.5). The algorithms are implemented in the option method in the function `gamlss()` within the R package GAMLSS (<http://www>.

R-project.org). In general the algorithms have been found to be stable and fast using very simple starting values (e.g. constants) for the ( $\theta$ )-parameters (Rigby and Stasinopoulos 2005).

### 10.2.3 Model Selection

#### 10.2.3.1 Statistical Modelling: Model Selection, Inference and Diagnostics

For parametric GAMLSS models each model  $\mathbf{M}$  of the form (10.2) can be assessed by its fitted global deviance  $\mathbf{GD}$  given by  $\mathbf{GD} = -2l(\hat{\theta})$  where  $l(\hat{\theta}) = \sum_{i=1}^n l(\hat{\theta}^i)$ .

Two nested parametric GAMLSS models,  $\mathbf{M}_0$  and  $\mathbf{M}_1$ , with fitted global deviances  $\mathbf{GD}_0$  and  $\mathbf{GD}_1$  and error degrees of freedom  $\mathbf{df}_{e0}$  and  $\mathbf{df}_{e1}$  respectively may be compared by using the (generalized likelihood ratio) test statistic  $\Lambda = \mathbf{GD}_0 - \mathbf{GD}_1$  which has an asymptotic  $\chi^2$ -distribution under  $\mathbf{M}_0$ , with degrees of freedom  $d = \mathbf{df}_{e0} - \mathbf{df}_{e1}$  (given that the regularity conditions are satisfied). For each model  $\mathbf{M}$  the error degrees of freedom parameter  $\mathbf{df}_e$  is defined by  $\mathbf{df}_e = n - \sum_{k=1}^p \mathbf{df}_{\theta_k}$ , where  $\mathbf{df}_{\theta_k}$  are the degrees of freedom that are used in the predictor model for parameter  $\theta_k$  for  $k=1,2,\dots,p$ .

For comparing non-nested GAMLSSs (including models with smoothing terms), to penalize overfitting, the generalized Akaike information criterion, GAIC (Akaike 1983) can be used. This is obtained by adding to the fitted global deviance a fixed penalty  $\#$  for each effective degree of freedom that is used in a model, that is where  $\mathbf{df}$  denotes the total effective degrees of freedom used in the model and  $\mathbf{GD}$  is the fitted global deviance. The model with the smallest value of the criterion  $\mathbf{GAIC}(\#)$  is then selected. The Akaike information criterion, AIC (Akaike 1974) and the Schwarz Bayesian criterion SBC (Schwarz 1978) are special cases of the  $\mathbf{GAIC}(\#)$  criterion corresponding to  $\#=2$  and  $\#=\log(n)$ , respectively.

## 10.3 Results

Table 10.3 shows the results of a GAMLSS modelling using a forwards stepwise selection procedure via the stepGAIC function in GAMLSS (Stasinopoulos and Rigby 2007). All effects shown are non-linear effects (cubic splines (cs())) (see Fig. 10.1).

From Table 10.3 we see that the temperature variants had singly or jointly highly significant ( $P < 0.0001$ ) non-linear effects on flowering for each species. Rainfall was not a significant factor in predicting flowering intensity after the effect(s) of temperature and previous lags were accounted for (thus it was omitted from the model by the stepwise procedure). For each species flowering one month prior significantly increased ( $P < 0.0001$ ) the likelihood for current flowering (a positive though non-linear lag1 effect (Table 10.3)). Indeed for all species flowering one

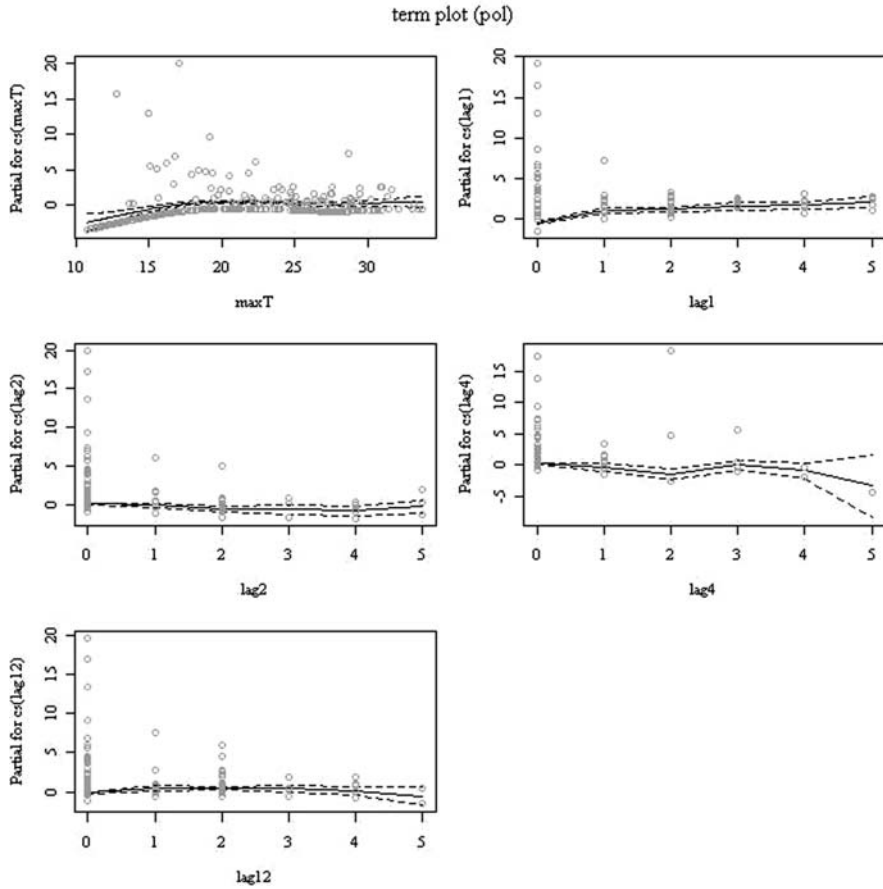
**Table 10.3** Parameter estimates and goodness of fit statistics of the GAMLSS model for the four species

Species	Predictors	$\beta$ estimate	Std error	T value	P	GD <sup>ϕ</sup>	AIC <sup>ϕ</sup>	SBC <sup>ϕ</sup>
<i>E. leucoxylon</i>	Intercept	0.42	0.14	3.07	< 0.0001	942.7	960.7	995.9
	minT	-0.10	0.01	-7.14	< 0.0001			
	lag1	0.39	0.03	11.71	< 0.0001			
<i>E. tricarpa</i>	Intercept	0.72	0.36	1.97	0.05	641.6	675.6	742.1
	maxT	-0.17	0.04	-4.65	< 0.0001			
	minT	0.21	0.06	3.71	< 0.0001			
	lag1	0.60	0.05	12.49	< 0.0001			
	lag5	-0.14	0.06	-2.35	0.02			
<i>E. microcarpa</i>	Intercept	-3.37	0.33	10.09	< 0.0001	484.4	526.4	608.5
	meanT	0.15	0.02	7.97	< 0.0001			
	lag1	0.60	0.04	13.39	< 0.0001			
	lag6	-1.29	0.60	-2.15	0.03			
	lag8	-0.45	0.16	-2.85	< 0.0001			
	lag12	0.14	0.06	2.53	0.01			
<i>E. polyanthemos</i>	Intercept	-2.47	0.40	-6.21	< 0.0001	507.1	549.1	631.1
	maxT	0.06	0.02	3.47	< 0.0001			
	lag1	0.56	0.06	9.67	< 0.0001			
	lag2	-0.28	0.07	-4.2	< 0.0001			
	lag4	-0.38	0.11	-3.52	< 0.0001			
	lag12	0.22	0.06	4.01	< 0.0001			

<sup>ϕ</sup>GD denotes the scaled deviance statistic, AIC denotes the Akaike information criterion and SBC denotes the Schwarz Bayesian Criterion goodness of fit statistics.

month prior significantly increased ( $P < 0.0001$ ) the likelihood for current flowering (a positive lag1 effect). A significant lag 12 effect was found in *E. microcarpa* and *E. polyanthemos* only. For *E. polyanthemos* there is a highly significant and non-linear (positive) effect of maximum temperature on flowering (Table 10.3) and particularly significant and non-linear (negative) lag effects of previous flowering at 2 and 4 months prior in relationship to current flowering (Table 10.3). This means that flowering 2 and 4 months earlier were highly correlated with a decreased likelihood of current flowering in *E. polyanthemos* (i.e. *E. polyanthemos* usually does not flower 2 and 4 months prior to current flowering). The 6 and 8 month lags for *E. microcarpa* had a similar negative effect on current flowering (Table 10.3). These negative lags agree with the autocorrelation (ACF) plot (not shown) for *Eucalyptus microcarpa* which shows negative lags for 6 and 8 months and positive lagged dependencies at 1 and 12 months: the ACF lags correlations are (0.67, -0.26, -0.21, 0.32) for lags (1, 6, 8, 12 months prior) in that order.

For *E. microcarpa* and *E. polyanthemos* there is a significant and non-linear effect of temperature in that they flower more intensely in response to predicted increases in mean and maximum temperature, respectively (see the positive and highly significant  $\beta$  estimates ( $P < 0.0001$ ) in Table 10.3. *Eucalyptus leucoxylon*



**Fig. 10.1** Term plot of the GAMLSS model for *E. polyanthemus*. The dotted line shows the 95% confidence band around the cubic spline curve (solid line)

flowers less intensely in response to predicted increases in minimum temperature, whereas *E. tricarpa* flowers less intensely in response to predicted increases in maximum temperature, but more intensely with increased minimum temperature (after accounting for maximum temperature); indicating for *E. tricarpa* there are two main but opposing temperature drivers. *Eucalyptus tricarpa* prefers cooler maximum temperature but warmer minimum temperature.

All the GAMLSS models fitted the original data very well (see the diagnostic plot in Fig. 10.2 for *E. polyanthemus* only and the observed and fitted time series plots in Fig. 10.3). The best fit was obtained for *E. microcarpa* as evidenced by *E. microcarpa* GAMLSS model's low value of scaled deviance statistic (GD) in Table 10.3. GAMLSS analysis found the same contemporaneous effects of climate on flowering for *Eucalyptus tricarpa* and *E. leucoxydon*, which constitutes one species pairing; and for *E. microcarpa* and *E. polyanthemus* (the other species pairing).

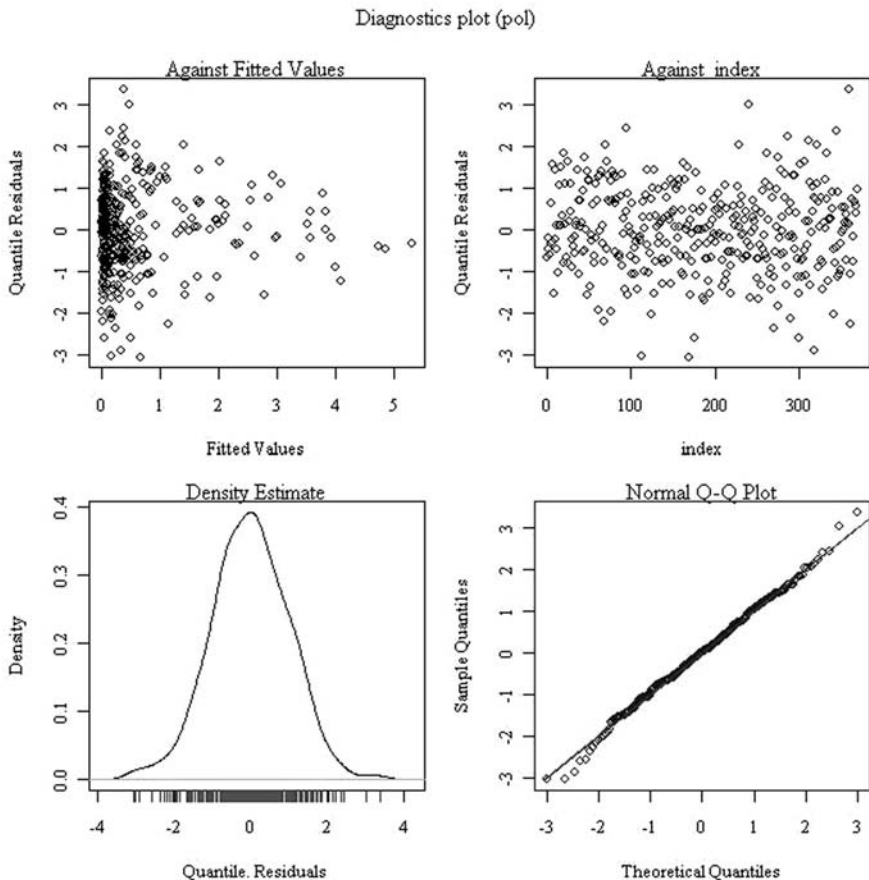
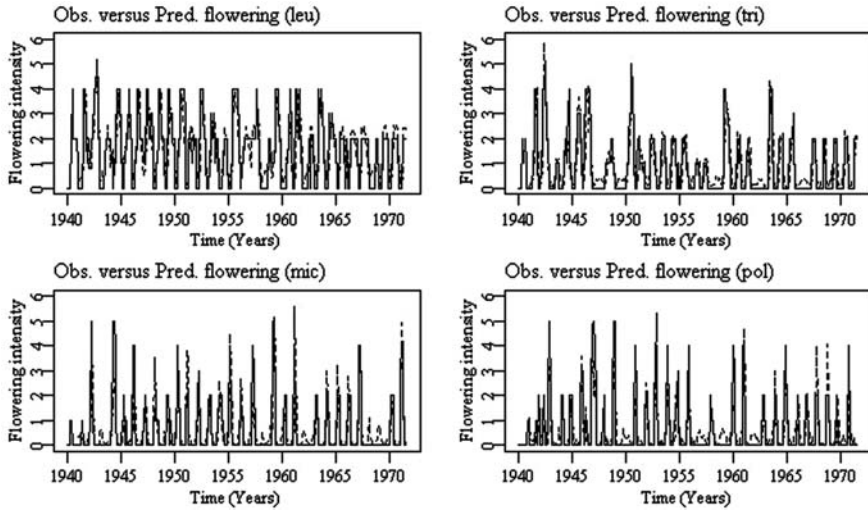


Fig. 10.2 Diagnostics plot of the GAMLSS model for *E. polyanthemus*

### 10.3.1 Thresholds for Start and Finish of Flowering

The  $\beta$  estimates in Table 10.3 and the so-called GAMLSS term plot for each model (for *E. polyanthemus* in Fig. 10.1) demonstrate the cubic spline effect of each predictor (whether climatic or lag in Table 10.3) after the other effects in the model have been accommodated for (see for example the term plot for *E. polyanthemus* in Fig. 10.1).

Reading off the exact temperature (on the horizontal axis) at which the spline line and its 95% confidence limits go above zero for the partial residuals (Fig. 10.1) gives the lower temperature threshold for flowering commencement for a given species (17.5°C maximum temperature for *E. polyanthemus*). Similarly reading off the exact temperature at which the spline curve and its 95% confidence limits go below zero for the partial residuals gives the higher temperature threshold for finish of flowering for a given species (25.9°C maximum temperature for *E. polyanthemus*), when they



**Fig. 10.3** Predicted fit (*dashed line*) of the GAMLSS model for *E. leucoxylon* (leu), *E. tricarpa* (tri), *E. microcarpa* (mic) and *E. polyanthemos* (pol) overlaid with the observed data (*solid line*)

exist from the resultant cubic spline. The resultant temperature thresholds for all four species are listed in Table 10.4.

**Table 10.4** Temperature thresholds for the start and finishing of flowering

Species	MinT (°C)		MeanT (°C)		MaxT (°C)	
	Start	Finish	Start	Finish	Start	Finish
<i>E. leucoxylon</i>	8.0	–	–	–	–	–
<i>E. tricarpa</i>	10.2	–	–	–	–	21.3
<i>E. microcarpa</i>	–	–	16.1	–	–	–
<i>E. polyanthemos</i>	–	–	–	–	17.5	25.9

### 10.4 Discussion

Phenological records are now regularly used to determine and report the impacts of global warming (Menzel et al. 2006a, IPCC 2007, Keatley and Hudson 2008, Rosenzweig et al. 2008). Inter-annual changes in spring plant phenology (typically an advance in the commencement of flowering) are one of the most sensitive and observable indicators of the biotic response to climate change (Walther et al. 2002, Menzel et al. 2006b). An understanding of past behaviour in relation to climate is needed for predictions of the response to climate change (Sparks and Carey 1995, Visser and Both 2005). The GAMLSS analysis discussed here shows that flowering in each of these eucalypt species is influenced by temperature. This is in agreement

with previous studies on these eucalypts (Porter 1978, Keatley and Hudson 2000, Keatley et al. 2002). However, this GAMLSS analysis confirms that this effect is non-linear for *E. leucoxylon* (Hudson et al. 2003) and is also non-linear for the remaining species. The non-linear effect of temperature is well recognized for crops (Loomis and Connor 1992) but less so for native species (Sparks et al. 2000).

The main driver for flowering in *E. leucoxylon* is minimum temperature with flowering intensity being less when there are warmer minimum temperatures; minimum temperatures in the region where these observations were recorded have decreased significantly by 0.1°C between 1998 and 2007 (Dept. Sustainability and Environment 2008). Hence over this period it is expected that flowering intensity has been slightly more intense. More intense flowering should have been evident in *E. microcarpa* and *E. polyanthemos* as they are positively influenced by maximum and mean temperatures, respectively: maximum daily temperature has increased by 0.6°C and mean daily temperature by 0.3°C. Flowering in *E. tricarpa* would be expected to be to less intense over this period, as it is negatively influenced by maximum temperature and positively influenced by minimum temperatures.

In this chapter we identified a lower threshold temperature of 8°C to induce flowering in *E. leucoxylon* which is lower than the base temperatures of 9.9°C previously determined by Keatley and Hudson (2000) (using the methods put forward by Yang et al. (1995)). Keatley and Hudson (2000) assumed a linear relationship between temperature and flowering which could account for some of the difference. Whilst no upper threshold temperature was identified here, Hudson et al. (2003) had previously estimated 18°C. Both *E. tricarpa* and *E. polyanthemos* were also included in the study of Keatley and Hudson (2000) therefore their base temperatures were identified, 11.7°C and 14.05°C, respectively compared to 10.2°C and 17.5°C (see Table 10.4). Keatley and Hudson (2000) concluded that further work was required in determining the base temperature of *E. polyanthemos* (14.05°C) because of the large co-efficient of variation in the calculated growing degree days; hence the 17.5°C is probably correct.

This chapter delineated for the first time that upper threshold temperatures have been determined for either of these species. *Eucalyptus microcarpa* has not previously had a lower threshold temperature identified. Its temperature of 16.1°C, along with that of *E. polyanthemos*, is quite high indicating that flowering for these species is in a heat-demanding developmental period (Wielgolaski 1999). *Eucalyptus polyanthemos* has the highest base temperature but the shortest interval, 1 month, between the pre-determined starting date (1st of September) and flowering (Keatley and Hudson 2007). *Eucalyptus leucoxylon* commences flowering the latest, in May, indicating that it has the lowest temperature requirement for development and this assumption is supported by it having the lowest threshold temperature.

GAMLSS found no significant effects of rainfall on flowering, whereas, wavelets analysis (see Chapter 17) showed that rainfall significantly ( $P < 0.05$ ) influences the flowering intensity of *E. tricarpa*; with flowering intensity increasing with increasing rainfall. This is in agreement with the results of a mixed transition distribution (MTD) analysis of the same 4 species by Kim et al. (2005 and Chapter 14) which confirmed, using two states for flowering, “on” or “off,” that the only species whose



likelihood of flowering systematically showed a significant (main effects) dependence on rainfall was *E. tricarpa*. It should, however, be noted that a novel extension of MTD analyses to allow for interactions (Kim et al. 2008), in this case to interactions between the (climatic) predictors, revealed a highly significant interactive effect between mean temperature with rainfall in *E. polyanthemos* (see Chapter 14). Kim et al. (2008) showed that flowering in *E. polyanthemos* is enhanced especially when conditions are warmer and dryer.

Knowing what the main driver for a given species is, say a particular temperature variant, may assist us in interpreting the possible changes in flowering due to climate change. Specifically *E. leucoxylo*n's flowering intensity at the study site has probably increased slightly because of the decrease in minimum temperature. However, in other parts of its range, minimum temperature has increased significantly by 0.3°C, hence flowering intensity in this region should have decreased. Additionally, these new lower threshold temperatures can be used in both the recalculation and/or calculation of growing degree days (GDD) (Wielgolaski 1999) for these species. GDD assumes that there is a relationship between the development rate and temperature for the phenological stage being examined and that this development only occurs above a base (lower) threshold temperature (Wielgolaski 1999).

Flowering intensity and flowering commencement in these species will be affected by climate change (Keatley et al. 2002). These changes can be regarded as the short-term implications of climate change (Rehfeldt et al. 2004). The longer-term consequences are changes in their individual reproductive success and distribution. For example, the flowering period of *E. leucoxylo*n and *E. tricarpa* are synchronous but their peak flowering is well separated (Keatley et al. 2004). Flower production in *E. tricarpa* at this site is positively skewed, in that flowers are produced quickly with the remaining and smaller proportion of flowers produced over an extended period of time by comparison. In *E. leucoxylo*n flower production is negatively skewed, the opposite mode of production. Rapid production of flowers, or positive skewness, is believed to quickly accustom potential pollinators to a new food source (Thomson 1980). *Eucalyptus leucoxylo*n and *E. tricarpa* are placed in the same series (Pryor and Johnson 1971) and are therefore taxonomically close, with morphologically similar flowers. *Eucalyptus leucoxylo*n flowers would thus be already familiar to potential pollinators as *E. tricarpa* had already flowered. Consequently, the production of *E. leucoxylo*n flowers possibly does not have to be rapid to attract pollinators to enable them to adjust to a new food source. However, this facilitation of pollination may occur later in the flowering period (or not at all) of *E. leucoxylo*n if there a decrease in its flowering intensity possibly resulting in less seed production; or if there is an increase in flowering intensity this switch could occur earlier, increasing not only the competition for pollinators between the species but also the possibility of hybridization.

Any change in reproductive behaviour also has implications for the pollinators and the species which depend on eucalypts as a food source: 20 percent of resident vertebrate Box-Ironbark species are nectarivorous (Traill 1991, Tzaros 2005).

Eucalypt flowers also attract invertebrates which contribute to the diet of nectarivorous birds (Tzaros 2005). Changes in phenology have led to mismatches in food abundance and breeding which has resulted in decreased reproductive success (Visser and Both 2005). These species contribute significantly to the honey industry in Victoria and therefore changes in flowering would have significant economic consequences.

## 10.5 Conclusion

In summary changes in temperature are likely to translate to changes in both the timing of flowering commencement and in terms of flowering intensity as shown here. Ultimately these changes may result in a change to species composition, as the relative reproductive success of the species changes over time. We show here that GAMLSS modelling allows for the identification of upper and lower thresholds of flowering temperature and the estimation of long and short-term non-linear effects on flowering of climate, and the lagged cyclic effects of previous flowering. GAMLSS analysis demonstrates a contemporaneous effect of climate on flowering for *Eucalyptus tricarpa* and *E. leucoxyton*, which constitutes one species pairing; and for *E. microcarpa* and *E. polyanthemus* (the other species pairing). We conclude that GAMLSS add credibility to the use of phenological records to detect phenological phases, local climatic impacts on flowering and possibly global climate change *per se*.

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# Chapter 11

## Bayesian Methods in Phenology

Christoph Schleip, Annette Menzel, and Volker Dose

**Abstract** The identification of changes in observational data relating to human induced climate change remains a topic of paramount importance. In particular, scientifically sound and rigorous methods for detecting changes are urgently needed. Analyses based on the BAYES approach here offer new possibilities to describe long-term phenological time series. The first example of this chapter will focus on the model comparison option of the Bayesian approach that was used to compare three different types of models (constant, linear, and one change point) for the analysis of three species in Germany. In addition to the functional behaviour, rates of change in terms of days per year were also calculated. The second example of this chapter illustrates the application of the Bayesian method to several phases throughout the year in two different countries. Thus we particularly investigate phenological changes of different phases and seasons.

**Keywords** BAYES · Climate change · Model comparison · Trend · Rate of change

### 11.1 Introduction

The global average surface temperature has increased over the twentieth century by about  $0.6 \pm 0.2^\circ\text{C}$  and is projected to continue to rise at a rapid rate (Trenberth et al. 2007). Many studies have revealed evidence of ecological impacts of this recent climate change. In particular, shifts in plant and animal phenology for the boreal and temperate zones of the northern hemisphere have been reported (Menzel and Estrella 2001, Sparks and Menzel 2002, Walther et al. 2002, Root et al. 2003). Reviews of phenological trend studies indicate that most of the data originate from the last four to five decades. These recent data predominantly reveal advancing of flowering and leaf unfolding in Europe and North America by 1.2–3.8 days decade<sup>-1</sup> on average

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and a strong seasonal variation with highest advances in early spring (Rosenzweig et al. 2007, 2008).

However, there are several problems involved in the commonly used methods of searching for signals in phenological time series. The detection of shifts is mostly done by classical statistical methods, such as slopes of linear regression models (e.g. Bradley et al. 1999, Menzel and Fabian 1999, Jones and Davis 2000, Schwartz and Reiter 2000, Defila and Clot 2001, Menzel et al. 2001, Ahas et al. 2002, Peñuelas et al. 2002, Menzel 2003), rarely by other curve fitting methods (e.g. Ahas 1999, Sagarin and Micheli, 2001). Trends are then reported in days per year or decade, or days of change over the study period. It is apparent that using linear regression models the length of a time series and its start and end dates are critical in detecting changes and in determining their magnitude, especially when highly variable phenological time series of a few decades are analyzed (Sparks and Tryjanowski 2005). Thus, series that include the whole of the 1990s benefit from the decade being the warmest on record. However, the observation periods vary between phenological networks and among stations in networks because phenological observations mostly depend on volunteers and thus have often discontinuous, incomplete data series. Moreover, different individuals may apply different standards in their observations. Several studies have addressed this problem (e.g. Menzel and Estrella 2001, Sparks and Menzel 2002) and illustrate the variation of resulting changes with the period of interest (e.g. Scheifinger et al. 2002). Few studies use these linear regression models for even longer time series, some covering almost one century (Beaubien and Freeland 2000, Sagarin and Micheli 2001 for lake and river ice cover). Reviews of phenological trend studies suggest that only about 40% of the reported trends have proved statistically significant. The significance is often tested by the F-test (Defila and Clot 2001), and occasionally by the Mann–Kendall trend test, which does not require a Gaussian distribution of the data (e.g. Menzel 2000). Few studies also report the standard error of the slope (e.g. Sagarin 2001). Studies analyzing long-term phenological records often reveal a heterogeneous pattern of temporal variability with sometimes alternating periods of advanced and delayed onset (e.g. Schnelle 1950, Lauscher 1978, 1983, Freitag 1987, Sparks and Carey 1995, Ahas 1999). The advance of phenological events in the last decades is compared to the timing in preceding periods, mostly only by comparing averages in distinct periods (e.g. Fitter and Fitter 2002). Another phenomenon in time domain described (Chmielewski and Rötzer 2002, Scheifinger et al. 2002) is a discontinuity in time series behaviour in the late 1980s, as in many areas almost no trend is observed before the discontinuous shift towards earlier occurrence dates after the late 1980s.

These limitations of the currently used methods render comparison and interpretation of the observed changes extremely difficult. They may partly account for the observed spatial variability among sites or the different response of species besides the inherent inhomogeneity caused by local microclimate conditions, natural variation, genetic differences or other nonclimatic factors. Thus, there is strong need to improve the recently applied method of change detection in phenological time series.

In the next Section 11.2, we introduce the Bayesian concepts as an alternative to the classical statistic methods. We shall introduce the Bayesian concepts and terminology only to the extent that is necessary to define the nomenclature in the rest of the article. In the subsequent Section 11.3, we perform a Bayesian comparison of different models to describe the functional behaviour of different phenological phases. We will focus on two examples that deal with long-term phenological observations in Germany and Switzerland. With the help of the Bayesian method, we analyse the variations of the onset of phenological phases and additionally illustrate phenological changes of different seasons in the 20th century.

Section 11.3 consists of three different examples illustrating the Bayesian use of a combined analysis of phenological and temperature time series. The recent quantification of changes in time series of phenology data with Bayesian methods has provided compelling evidence for nonlinear changes during the last 20 years. In the first selected example of the third section Dose and Menzel (2006) correlated the phenological observations with spring temperature time series. They compared two alternatives models Ma: temperature and blossom onset time series evolved independently and Mb: temperature and blossom onset time series are synchronous in their change. In the second example Schleip et al. (2008) analysed rates of change and the relationship between temperature changes and bud burst of Norway spruce in the 51 year period 1953–2003. This study does not only deliver quantitative results on the correlations between temperature and Norway spruce bud burst in Germany, but it also offers new in-sights into model improvement and to methods for the understanding of ecological responses to climate change.

## 11.2 Bayes Theory

Bayesian data analysis is based on two rules. The first is the conventional product rule for manipulating conditional probabilities. It allows a probability density function to be broken down depending on two (or more) variables  $p(\vec{\theta}, \vec{d} | M, I)$  conditional on the model  $M$  that specifies the meaning of the parameters  $\vec{\theta}$  and additional information  $I$  into simpler functions

$$p(\vec{\theta}, \vec{d} | M, I) = p(\vec{\theta} | M, I) * p(\vec{d} | \vec{\theta}, M, I) \quad (11.1)$$

where  $p(\vec{\theta} | M, I)$  and  $p(\vec{d} | \vec{\theta}, M, I)$  depend only on the single (vector-) variables  $\vec{\theta}$  and  $\vec{d}$  respectively. Equation 11.1 may be expanded in an alternative way due to symmetry in the variables  $\vec{\theta}, \vec{d}$ .

$$p(\vec{\theta}, \vec{d} | M, I) = p(\vec{d} | M, I) * p(\vec{\theta} | \vec{d}, M, I) \quad (11.2)$$

Equating the right hand sides of Equation 11.1 and Equation 11.2 yields Bayes' theorem.



$$p\left(\vec{\theta} \mid \vec{d}, M, I\right) = p\left(\vec{\theta} \mid M, I\right) * p\left(\vec{d} \mid \vec{\theta}, M, I\right) / p\left(\vec{d} \mid M, I\right) \quad (11.3)$$

The function on the left hand side is called the posterior density of the parameters  $\vec{\theta}$  given data  $\vec{d}$  and model  $M$ . It is equal to the prior density of the parameters  $\vec{\theta}$ ,  $p\left(\vec{\theta} \mid M, I\right)$  which encodes our information on  $\vec{\theta}$  prior to considering the data  $\vec{d}$  times the likelihood  $p\left(\vec{d} \mid \vec{\theta}, M, I\right)$ .

$p\left(\vec{d} \mid M, I\right)$  is formally the normalisation for the posterior density

$$p\left(\vec{d} \mid M, I\right) = \int d\vec{\theta} P\left(\vec{\theta} \mid M, I\right) * p\left(\vec{d} \mid \vec{\theta}, M, I\right) \quad (11.4)$$

By inverse application of the product rule we arrive at the Bayesian marginalisation rule, which completes Bayes' theory and has no counterpart in traditional statistics

$$p\left(\vec{d} \mid M, I\right) = \int d\vec{\theta} P\left(\vec{\theta} \mid M, I\right) * p\left(\vec{d} \mid \vec{\theta}, M, I\right) \quad (11.5)$$

Equation 11.5 allows for an important interpretation. It is obviously the likelihood of the data  $\vec{d}$  given the model  $M$  regardless of the numerical values of the parameters  $\vec{\theta}$ . Employing Bayes' theorem to invert (11.5) we obtain

$$p\left(\vec{d} \mid M, I\right) = \int d\vec{\theta} P\left(\vec{d}, \vec{\theta} \mid M, I\right) \quad (11.6)$$

Equation 11.6 is then the probability of a model  $M$  out of a possible variety given the data  $\vec{d}$ .

We shall now adapt these abstract concepts to the problems of Section 11.3. The data  $\vec{d}$  are then the phenological or temperature time series. They are modelled either by a constant, implying time independence or by a linear function in time, which associated constant rate of change or by a function consisting of two linear segments matching at a given time  $t_E$ . Apparently, the latter model, which we call the (one-) change point model, is not only the most complicated but reduces also to the other two by selecting variables. The likelihood for the change point model reads

$$p\left(\vec{d} \mid \vec{f}, t_E, M, I\right) \quad (11.7)$$

where  $\vec{f}$  is a three component vector of the support functional values at the beginning of the time series ( $f_1$ ), the change point ( $f_2$ ) and the end of the time series ( $f_3$ ). The likelihood for the linear model evolves from (11.7) by electing  $f_2$  and  $t_E$ , and for the constant model by deleting  $f_2, f_3$  and  $t_E$ . Our first task is to find the change point probability distribution  $P\left(t_E \mid \vec{d}, M, I\right)$ . By Bayes' theorem it is given by

$$p\left(t_E|\vec{d}, M, I\right) = p\left(t_E|M, I\right) * p\left(\vec{d}|t_E, M, I\right) / p\left(\vec{d}|M, I\right) \quad (11.8)$$

The marginal likelihood  $p\left(\vec{d}|t_E, M, I\right)$  is derived from (11.7).

$$p\left(\vec{d}|t_E, M, I\right) = \int d\vec{f} p\left(\vec{f}, \vec{d}|t_E, M, I\right) = \int d\vec{f} p\left(\vec{f}|t_E, M, I\right) * p\left(\vec{d}|\vec{f}, t_E, M, I\right) \quad (11.9)$$

Application of Equation 11.8 requires the specification of  $p\left(t_E|\vec{d}, M, I\right)$ , which was taken flat, independent of  $t_E$  in all subsequent applications.

Note that Equation 11.8 contains also the marginal likelihood  $p\left(\vec{d}|M, I\right)$  which is needed to infer the probability of the model  $M$  given the data  $\vec{d}$  using Equation 11.6.

One final point needs to be mentioned. Having obtained the posterior distribution of the parameters using Equations 11.3 and 11.7 we can calculate expectation values of the parameters given the data. For example the expectation value of  $\theta_k$  is given by

$$\langle\theta_k\rangle = \int d\vec{\theta} \theta_k * p(\vec{\theta}|\vec{d}, M, I) \quad (11.10)$$

It can be shown that Equation 11.10 also holds for any function  $\phi(\vec{\theta}|\vec{d}, M, I)$  and can be used in particular to derive estimates of the moments  $\mu_1$  and  $\mu_2$  of our model functions at any given time  $t$ .  $t$  is not restricted to the time interval covered by the data but can also lie in extrapolation regions. Defining  $\mu_N$  as

$$\mu_N = \sum_E \int d\vec{f} p(\vec{f}, E|\vec{d}, M, I) * \left\{\phi(\vec{f}, E|t, \vec{d}, M, I)\right\}^N \quad (11.11)$$

we find for the mean of the model functions  $\mu_1$  and for the standard deviation

$$\left\langle\Delta\phi^2\right\rangle^{1/2} = \left\{\mu_2 - \mu_1^2\right\}^{1/2} \quad (11.12)$$

This completes the formal calculations referred to in Section 11.3. For details of the algebra the reader is referred to Dose and Menzel (2006).

## 11.3 Examples of Bayes Theory in Phenological Research

### 11.3.1 Time Series Analysis by Bayesian Non Parametric Estimation

#### 11.3.1.1 Methods

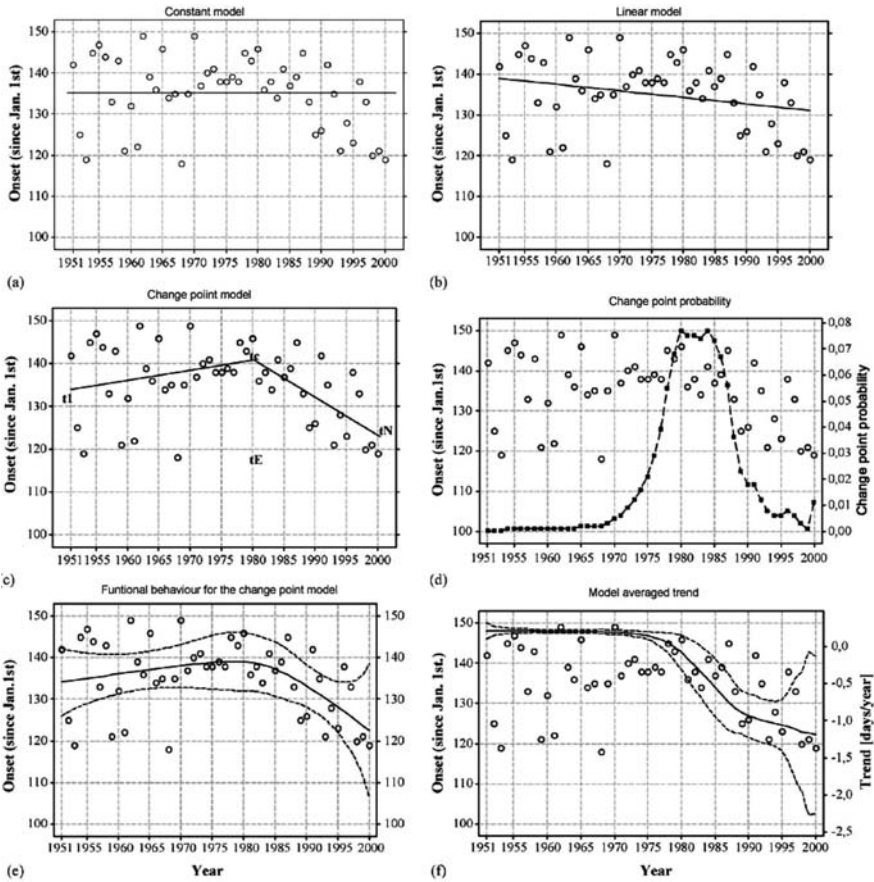
The Bayesian approach for analysing the functional behaviour of phenological time series and their trends follow the method introduced by Dose and Menzel (2004). We refer to this publication for further insight into the mathematical formulae. Here, the main features of the Bayesian approach are explained in the six graphs (Fig. 11.1a–f).

The phenological time series plotted in Fig. 11.1 can be described by different models/functions. We selected three of them:

1. a constant model with a fixed date of onset (Fig. 11.1a),
2. a model with linear change of onset dates in time (Fig. 11.1b) and
3. a change point model, which is the choice of a function that consists of two linear segments which match at a particular time  $t_E$  (Fig. 11.1c). We call the point  $t_E$  the change point.

The constant model represents the hypothesis of no change at all. It assumes a functional behaviour constant in time with associated zero rates of change/trend. The forecasting equation for the linear trend model is  $y(t) = \alpha + \beta t$ : where  $t$  is the time index. The parameters alpha ( $\alpha$ ) and beta ( $\beta$ ) (the “intercept” and “slope” of the trend line) are usually estimated via a simple regression in which  $y$  is the dependent variable and the time index  $t$  is the independent variable.

The change point model with two linear segments (Fig. 11.1c) fits our data with a residual sum of squares of 2800 compared to 3593 for the linear regression model and 3865 for the constant model. The obvious improvement in fit is penalized by a further complication as the model needs four parameters ( $t_E$ , the functional values at  $t_E$ ,  $t_c$  and a functional value for each segment). Further complications of the model (i.e. more change points) would achieve better fits – ending with an ultimate model containing as many parameters as data points. Bayesian probability theory generally calculates the probability of a given model compared to one or more alternatives. The change point model is not simply another arbitrary functional form that is likely to provide a better fit to the data due to its extra parameter. The assessment of the quality of a model is determined by the so-called odds ratio that is described in detail in Dose and Menzel (2006). The odds ratio assumes the same prior probabilities for competing models and in this case is equal to the so called “Bayes Factor”. The Bayesian approach provides a powerful way of assessing competing models at the forefront of science by automatically quantifying Occam’s razor (Garrett 1991). Occam’s razor is a principle attributed to the medieval philosopher William of Occam (or Ockham). The principle states that one should not make more



**Fig. 11.1** The Bayesian approach to phenological time series analysis (an example using the beginning of flowering of *Syringa vulgaris* at Grünenplan, Germany). (a) constant model, (b) linear model, (c) change point model, (d) change point probability distribution for the change point model, (e) the functional behaviour of the time series (continuous line) with confidence intervals (dashed lines) for the change point model and (f) the derivative of the time series, the trend, with dashed lines representing the upper and lower confidence interval

assumptions than necessary. It chooses the simplest from a set of otherwise equivalent models of a given phenomenon. In any given model, Occam’s razor helps us to “shave off” those variables that are not really needed to explain the phenomenon (Garrett 1991). The one change point model is sufficient to represent the major change in a 50 year long phenological and temperature time series.

Figure 11.1c displays only the maximum likelihood fit of a continuous function with two linear segments. In Bayesian probability, however, not only the single triangular function shown in Fig. 11.1c, but the overlay of all possible triangular functions (their number is  $N-2$  for  $N$  data points) weighted with their associated probability should be considered. The Bayesian marginalization rule is employed

to remove the change point variable by marginalization. This extremely important rule removes ‘nuisance’ parameter/s from a Bayesian calculation (Dose and Menzel 2004). The change point variable is such a ‘nuisance’ parameter because we do not consider the best solution to be that which minimises the root mean square error (RMSE), or the two or three best triangular functions, but all of them. The advantage is that the marginalisation rule overlays all possible triangular functions and then weighs them by their respective change point probability. By using the Bayesian marginalization rule the support functional values can be eliminated resulting in a probability,  $p(E)$ , for a particular change point choice. If the data exhibited an abrupt change, then this change point probability would be zero except for that particular  $E$ . In cases of more gradual change, appreciable change point probabilities are also observed for  $E \pm 1, E \pm 2 \dots$ . The associated probability of a change point position can be rigorously calculated. We do not show how these change probabilities are calculated but display the result as a curve in Fig. 11.1d. A detail explanation of the used Bayesian calculations is shown in Dose and Menzel (2004). Readers who want to know more fundamental detail about the Bayesian ideas are referred to the excellent tutorial by Sivia (2005).

In Fig. 11.1e the functional behaviour of the data, following the above procedure, is displayed, including the uncertainty of the function estimate which should not be confused with the variability of the data.

Even more interesting than the functional behaviour of a time series is the functional behaviour of its derivative, the trend. The derivative of a linear function is a constant, the derivative of a triangular function is a constant  $c_1$  in the range  $t_1 < t < t_c$  and another constant  $c_2$  in the range  $t_c < t < t_N$ . The Bayesian result for the overall trend is, as for the function estimation, the overlay of all possible step functions weighted by their respective change point probabilities. The resulting trend estimates including point-wise uncertainties are shown in Fig. 11.1f. What happens if all three model alternatives exhibit similar probabilities?

Bayesian probability theory calculates the probability of a given model (i.e. in our case the change point model compared to two alternatives) such as the constant and linear models. Unless one of the models sticks out with a very high probability, the description of the data in terms of only one model is again unsatisfactory. Instead, the rigorous application of Bayesian probability theory describes that the proper functional behaviour and the proper trend are obtained by superposition of a constant, a linear function and the change point model function again weighted with their respective model probabilities.

### 11.3.1.2 Examples

Example 1 Bayesian Analysis of Climate Change Impacts in Phenology (Dose and Menzel 2004)

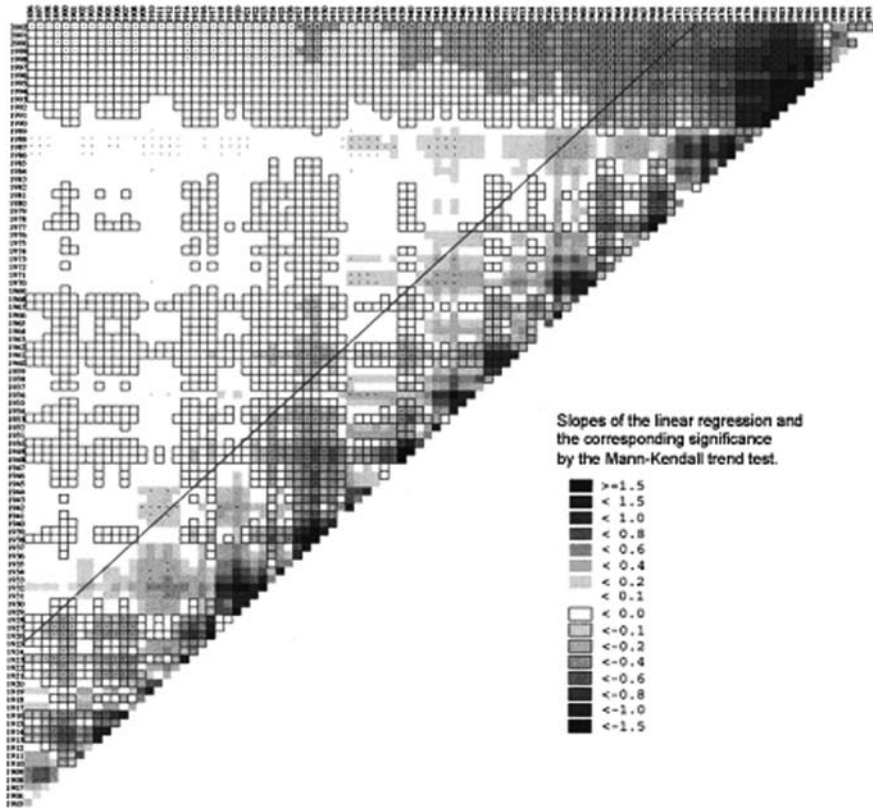
Dose and Menzel (2004) applied the method to blossom time series of *Prunus avium* L., *Galanthus nivalis* L. and *Tilia platyphyllos* SCOP. The functional behaviour of these series is represented by three different models: the constant

model, the linear model and the change point model. Their results provide a quantitative representation of what was previously inferred from the same data by less involved methods. The model comparison option of the Bayesian theory allows the evaluation of which one, out of the chosen group of models, is best suited to describe the trend that is hidden in the data. For the three time series at Geisenheim, it turns out that the most likely model is the change point model. The resulting change point probability has the maximum near 1985 (0.070) for cherry blossom and, with a quite similar distribution, a maximum near 1984 (0.090) for lime tree blossom. The change point probability distribution of snowdrop blossom is much broader, even multi-modal, with a maximum near 1986 (0.055) and a secondary maximum (0.020) near 1964. The rate of change determined by the change point model reaches  $-1.5 \text{ days yr}^{-1}$  in 2002 for snowdrop blossom, and around  $-0.6 \text{ days yr}^{-1}$  both for cherry and lime tree blossom.

Several studies report time of season differences with the highest advances usually in early spring, and notable advances of succeeding phenophases in full spring and early summer (e.g. Bradley et al. 1999, Defila and Clot 2001, Menzel et al. 2001). Sparks and Smithers (2002) suggest higher temperature changes in early in the season as the reason for this differentiation. The relative order of changes revealed for these three species' blossom series at Geisenheim accords with other results: regression coefficients from mean anomaly curves of Germany (1951–2000, Menzel 2003) ranged from  $-0.25 \text{ days yr}^{-1}$  for snowdrop, to  $-0.14 \text{ days yr}^{-1}$  (lime tree) and  $-0.09 \text{ days yr}^{-1}$  (cherry). It is evident that their absolute magnitude for the 1951–2000 period is much smaller than rates of change determined for the year 2002 with the change point model. A recalculation of the regressions in Menzel (2003) for the 1985–2000 period revealed advances of  $-1.42 \text{ days yr}^{-1}$  for snowdrop blossom,  $-0.67 \text{ days yr}^{-1}$  for cherry blossom and  $-0.86 \text{ days yr}^{-1}$  for lime tree blossom. These average rates of change for Germany mirror the results of our new method based on Bayesian theory.

Over most of the century, there is essentially zero change; however, from the mid-1980s onwards, the rate of change is negative for cherry and lime tree blossom. This finding is consistent with the results of other studies (e.g. Scheifinger et al. 2002, Chmielewski and Rötzer 2002) that describe a discontinuous shift towards earlier occurrence dates in the late 1980s and almost no significant trends before that date. However, the negative rate of change in snowdrop blossom is not evident prior to 1992; although the rates of change are relatively high in the 1990s they are associated with a considerable uncertainty range.

The proposed new method of selecting models to describe the trend in phenological time series has major advantages compared to the traditional statistical approach of linear regression. Figure 11.2 displays the slopes of the linear regression and the corresponding significance by the Mann–Kendall trend test for all possible combinations of starting (x-axis) and ending year (y-axis) with 10 or more years of observation of cherry blossom at Geisenheim. This first example clearly demonstrates that the resulting trends start to be representative in the temporal scale when more than 30 years are included. The main obstacle of this traditional approach is evident: the rate of change strongly depends on the time period and no distinct rate of change for single years can be given.



**Fig. 11.2** Trend matrix: Linear regression coefficients and their significance by the Mann–Kendall trend test for *Prunus avium* blossom time series at Geisenheim/Germany. (.1  $Q1 \geq 1. .2, 1 Q1 > 2$ )

However, all time series ending in 1989 and later reveal advancing trends, especially if they start in the second half of the 20th century. The corresponding results for lime tree (trend matrix not displayed) are very similar to Fig. 11.2. The trend matrix for snowdrop (not shown) is even more heterogeneous because snowdrop blossom was observed extremely early in several years between 1910 and 1923, and thus nearly all time series starting before 1920 reveal delayed blossom.

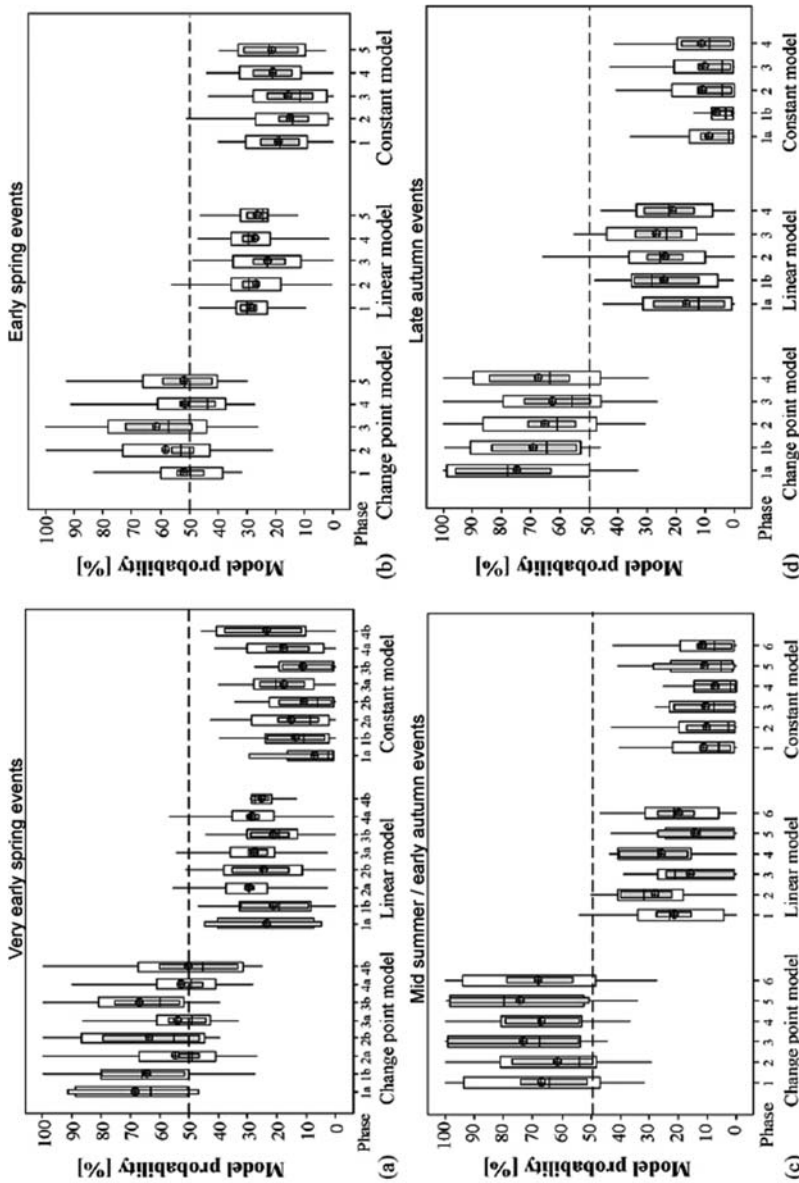
**Example 2 The Use of Bayesian Analysis to Detect Recent Changes in Phenological Events Throughout the Year (Schleip et al. 2006)**

The paper of Schleip et al. (2006) focused on recent changes in phenological events throughout the year. They analysed 2600 observational time series in Europe and 19 phenological phases of different seasons (Table 11.1). Schleip et al. (2006) found that in all seasons (very early spring, early spring, mid summer and early autumn, late autumn) and for all phases the change point model possessed, on average, the highest model probabilities (Fig. 11.3).

**Table 11.1** Indicator species of the four phenological seasons (very early spring, early spring, mid summer/early autumn and late autumn) with their phenological seasons, identification codes and numbers of investigated stations

Season	Species	Common name	Phenological stage	Code	Number of stations
Very early spring	<i>Anemone nemorosa</i> L.	Wood anemone	Beginning of flowering	1a	5
	<i>Corylus avellana</i> L.	Hazel	General flowering	1b	17
	<i>Galanthus nivalis</i> L.	Common snowdrop	Beginning of flowering	2a	102
	<i>Tussilago farfara</i> L.	Colt's foot	General flowering	2b	26
Early spring	<i>Aesculus hippocastanum</i> L.	Horse chestnut	Beginning of flowering	3a	37
	<i>Betula pendula</i> Roth	Silver birch	General flowering	3b	19
	<i>Fagus sylvatica</i> L.	Common beech	Beginning of flowering	4a	106
	<i>Prunus avium</i> L.	Wild cherry	General flowering	4b	20
	<i>Prunus spinosa</i> L.	Blackthorn	Beginning of flowering	1	52
	<i>Aesculus hippocastanum</i> L.	Horse chestnut	General flowering	2	130
	<i>Betula pendula</i> Roth	Silver birch	Leaf unfolding	3	49
	<i>Fagus sylvatica</i> L.	Common beech	Leaf unfolding	4	49
	<i>Prunus avium</i> L.	Wild cherry	Beginning of flowering	5	18
	<i>Prunus spinosa</i> L.	Blackthorn	Beginning of flowering	5	18
Mid summer and early autumn	<i>Aesculus hippocastanum</i> L.	Horse chestnut	Ripe fruit	1	57
	<i>Colchicum autumnale</i> L.	Autumn crocus	General flowering	2	14
	<i>Malus domestica</i> Borkh.	Apple	Ripe fruit	3	16
	<i>Prunus americana</i> Marsh.	American plum	Ripe fruit	4	13
	<i>Tilia cordata</i> Mill.	Small leaved lime	General flowering	5	8
	<i>Sambucus nigra</i> L.	Elderberry	Ripe fruit	6	40
	<i>Aesculus hippocastanum</i> L.	Horse chestnut	Autumn colouring	1a	30
	<i>Betula pendula</i> Roth	Silver birch	Leaf dropping	1b	16
	<i>Fagus sylvatica</i> L.	Common beech	Autumn colouring	2	74
	<i>Malus domestica</i> Borkh.	Apple	Autumn colouring	3	43
Late autumn	<i>Aesculus hippocastanum</i> L.	Horse chestnut	Autumn colouring	4	28
	<i>Betula pendula</i> Roth	Silver birch	Autumn colouring	1a	30
	<i>Fagus sylvatica</i> L.	Common beech	Autumn colouring	1b	16
	<i>Malus domestica</i> Borkh.	Apple	Autumn colouring	2	74



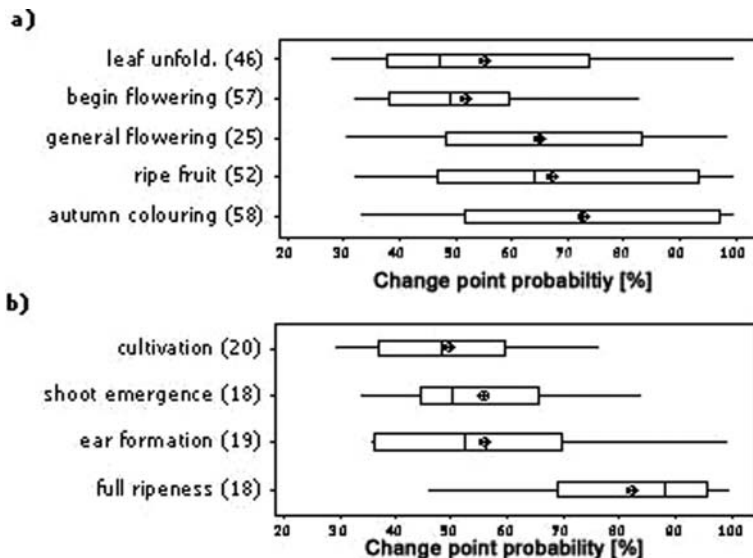


**Fig. 11.3** Boxplots of the one change point, linear and constant model probabilities for the four seasons: (a) very early spring, (b) early spring, (c) mid summer/early autumn and (d) late autumn (code numbers of the indicator species in Table 1.1). Ninety five percent confidence interval for the median is marked as the inner grey box, the 2.5th percentile is found at the lower end and the 7.5th percentile is found at the upper end of the box. The range is marked as black vertical line, the median as black horizontal line in the boxes. The mean is marked as circle with cross. The horizontal dashed line marks the 50% change point probability line

In particular, the phases at the middle and at the end of the year were characterised by higher change point model probabilities (see Fig. 11.3c and d); almost all time series of mid summer, early autumn and late autumn season had median values of over 60%. The highest change point model probability was reached in late autumn by *Aesculus hippocastanum* leaf colouring (Fig. 11.3d). No significant differences concerning model probabilities existed between forest trees, fruit trees and other plants. The probabilities of the linear model mostly ranged between 20 and 30%; but in mid summer to late autumn the constant model had very low probabilities (Fig. 11.3c, 10% on average).

In Fig. 11.4 the results of analysis of phenological phases across the year of the two selected species, horse chestnut (*Aesculus hippocastanum*) and common oat (*Avena sativa*), are displayed. Both species revealed a nearly continuous increase of mean and median probabilities of the change point model from the beginning of the growing period (leaf unfolding, flowering) until its end (full ripeness, autumn colouring).

The results of both Figs. 11.3 and 11.4 indicated that the probabilities of the three different models to describe the observational records clearly changed with season. In general, observed changes at the end of the growing season were more abrupt; thus, the change point model was noticeably superior for description of these time series. The independent results for single species in Fig. 11.4 clearly confirm the results of Fig. 11.3 and prove that they are not an artefact of studying different species' phases in different seasons.



**Fig. 11.4** Horizontal boxplots of change point probabilities for phenological stages across the year (for description see Fig. 11.3, numbers of stations in brackets). The definition of the phenological stage labelled “cultivation” includes all processes which involve a tilling and manipulation of the soil such as ploughing, disk harrowing and seed bed preparation

### 11.3.1.3 Discussion

The two examples compared three models, the constant, linear and change point models, using a new method for the analysis of phenological time series based on Bayesian concepts, recently presented by Dose and Menzel (2004).

The model comparison gives new insight into the type of changes. Two model types were identified as less probable, thus less important; the linear model type which suggests a constant change, perhaps due to a gradual change in climate and the constant model, which can be linked to the idea of no changes in the underlying triggering factors or expressed time lags in their reaction.

The clear preference for the change point model signifies that there are non-linear changes in the phenological. Semenov et al. (2004) have already emphasised that phenological data are non-linear functions of the temperature-regime characteristics of surface air. Particularly the second example proved that long-term phenological time series of key phases (Table 11.1, Fig. 11.3) for four seasons (very early spring, early spring, mid-summer/early autumn, and late autumn) could be described better by the change point model than by traditional methods. In the model comparison, the change point model outperforms the conventional linear and constant models by far. It is important to note that we identified relevant and mostly abrupt changes in all phenological seasons. We even reveal higher change point model probabilities for autumn events than those in the spring. We can conclude that the change point model was superior in all cases. Seasons at the end of the year exhibited the highest probabilities for the change point model.

This tendency was confirmed for two selected species, horse chestnut and common oat (Fig. 11.4) with a nearly continuous increase of change point model probabilities from stages at the beginning until those at the end of the year. These results suggest that subsequent phases later in the growing season integrate more and longer positive temperature anomalies.

## 11.4 Correlation of Phenological Data with Temperature

### 11.4.1 Overview

The recent quantification of changes in time series of phenology data with Bayesian methods has provided compelling evidence for nonlinear changes during the last 20 years. Dose and Menzel (2006) correlated the phenological observations with spring temperature time series. They compare two alternatives models  $M_a$ : temperature and blossom onset time series evolved independently and  $M_b$ : temperature and blossom onset time series exhibit coherence.

Schleip et al. (2008) analysed rates of change and the relationship between temperature changes and bud burst of Norway spruce in the 51 year period, 1953–2003. This study does not only deliver quantitative results on the correlations between temperature and Norway spruce bud burst in Germany, but it also offers new

insights into model improvement and to methods for the understanding of ecological responses to climate change.

### 11.4.2 Methods

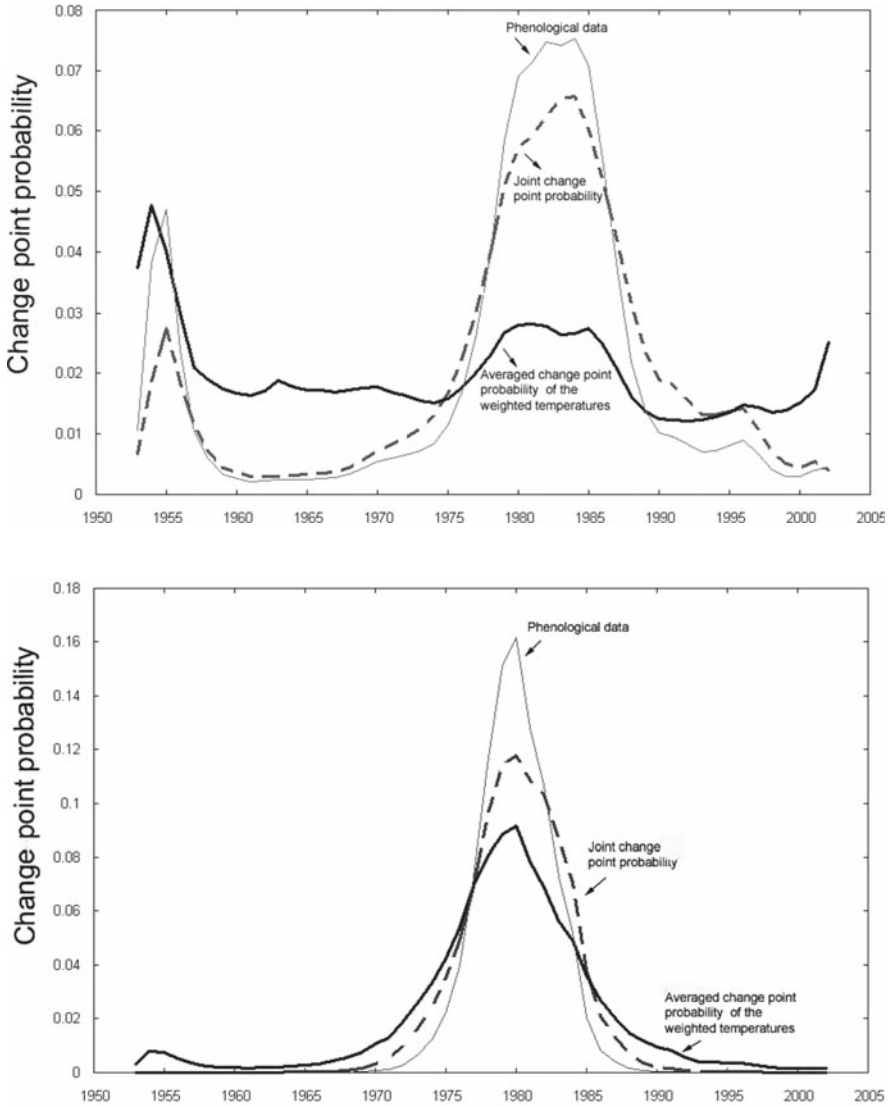
Figure 11.5 exhibit the change point probabilities as a function of time for a temperature (thick dashed line) and a phenological time series (continuous line) as well as their overlap renormalized to unit area (thin dashed line). The upper panel shows a case of small overlap, characteristic of a small coherence factor and the lower panel a case of large overlap characteristic of a high coherence factor.

The calculation of the coherence factor relates to the change point distributions in the following way: the variable “change point position” (E) is eliminated using the Bayesian marginalisation rule. With a flat prior distribution for the change point position this amounts to averaging over all  $N-2$  change point positions per series. Note that  $N$  does not need to be identical to the number of observations, because the algorithm tolerates missing data. The calculation of the probability  $p(x)$  that temperature and phenology observations evolve either independently or coherently (= synchronously) reduces to performing this average independently for the change point positions in the temperature (ET) and in the phenology series (EP) or for  $ET = EP$  only. The ratio of probabilities  $p(\text{coherent})/p(\text{independent})$  is equivalent to a Bayes Factor. In the absence of qualified prior information the Bayes Factor equals the posterior odds (Dose and Menzel 2006). The Bayes Factor will be called the coherence factor henceforth. A coherence factor above one signifies that the two time series are more probably synchronous than independent.

In the recent work of Dose and Menzel (2006) the phenological time series of snowdrop, cherry and lime tree at Geisenheim were related to the three-month mean temperatures January – March, February – April and March–May. Schleip et al. (2008) generalized the temperature averaging and chose as the average effective temperature  $T(y_i)$  in year  $y_i$

$$T(y_i) = \sum_{k=1}^{k_{\max}} w_k \cdot T_k(y_i), \quad \sum w_k = 1, \quad w_k > 0, \quad (11.13)$$

where  $T_k(y_i)$  are the average temperatures in month or week  $k$  of year  $y_i$ ,  $w_k$  are positive weight coefficients that add up to unity and  $k=1$  is either associated with January or with the first week of the year, while  $k_{\max}$  is the last month or week in which the phenological event occurs. The unknown weight coefficients are determined by maximizing the coherence between temperature and the phenological time series. In the first cycle of the calculation ( $n=1$ , where  $n$  is the index of the current cycle of the calculation) we start with an assumption of equal weights  $w_k=1/k_{\max}$  for all  $k$ . These weights are then used to calculate the coherence factor  $C$  using the procedure of Dose and Menzel (2006).



**Fig. 11.5** Distributions of temperature, bud burst and joint (temperature and bud burst) change-point probability of Norway spruce bud burst (*Picea abies* L.) in Schleswig (*upper panel*) and in Hof (*lower panel*). In the upper panel the coherence factor has a value of 1.2 and in the lower panel a value of 3.3. Note that the y-axes have different scales. The thick dashed line symbolises the averaged change point probability distribution of the weighted temperatures for the months January to May. The continuous line represents the probability distribution of the phenological data. The thin dashed line stands for the joint change point probability

For cycle  $n=2$ , a new random set of unnormalized weights is generated according to

$$w_{new} = w_{old} \left( 1 + r * \frac{N^2}{N^2 + 4n^2} \right) \quad (11.14)$$

where  $r$  is a uniform random number  $-0.25 < r < 0.25$ ,  $n$  is the index of the current cycle of the calculation and  $N$  the predetermined number of cycles chosen to find an optimum set of weights.  $w_{new}$ ,  $w_{old}$  are components of vectors with the dimension =  $k_{max}$ . The factor multiplying the random number  $r$  is near unity at the beginning of the calculation, it drops to one half at  $n = N/2$ , and converges to 0.2 for  $n = N$ .  $w_{new}$  must, of course, finally be renormalized to sum to unity.

The relationship between weights and coherence factor is nonlinear and complex. In fact there is no guarantee that the function “coherence factor” exhibits a unique maximum as a function of the  $k_{max}$  weights. This multimodal possibility can be resolved by using a simulated annealing approach, which accounts for the multimodal possibility and finds the global maximum in the presence of one or several lower satellite maxima. The name and inspiration of “simulated annealing” come from annealing in metallurgy, a technique involving heating and controlled cooling of a material to increase the size of its crystals and reduce their defects. The heat causes the atoms to become unstuck from their initial positions (a local minimum of the internal energy) and wander randomly through states of higher energy; the slow cooling gives them more chances of finding configurations with lower internal energy than the initial one. By analogy with this physical process, each step of the simulated annealing algorithm replaces the current solution by a random “nearby” solution, chosen with a probability that depends on the difference between the corresponding function values and on a global parameter  $T$  (called the temperature), that is gradually decreased during the process. The dependency is such that the current solution changes almost randomly when  $T$  is large, but increasingly “downhill” as  $T$  goes to zero. The allowance for “uphill” moves saves the method from becoming stuck at local minima – which are the bane of greedier methods.

For this purpose it is necessary to accept not only uphill steps but, conditional on a certain probability  $p$ , where

$$p = \text{Min}(1, \exp\{(C_{new} - C_{old})/T\}) \quad (11.15)$$

to allow also for downhill moves. The latter can cross a valley and find another possibly higher maximum.  $T$  is the annealing temperature and scales the difference between the new ( $C_{new}$ ) and the old ( $C_{old}$ ) coherence factors. The approach for one step of the calculation is then

1. accept uphill moves with probability one, (i.e. always)
2. if  $C_{new} < C_{old}$  choose a random number  $R$  from a uniform (0,1) distribution and accept the downhill move if

$$\frac{C_{new} - C_{old}}{T(n)} > \ln R \quad (11.16)$$

Currently, there is no general rule for the choice of  $T(n)$ .

The present calculations were done with  $T(n+1) = T(n)/1.01$  (e.g. a one percent decrease of temperature per step). The simulated annealing approach leads to the same approximate optimum as the simple “uphill search” discussed before.

### 11.4.3 Examples

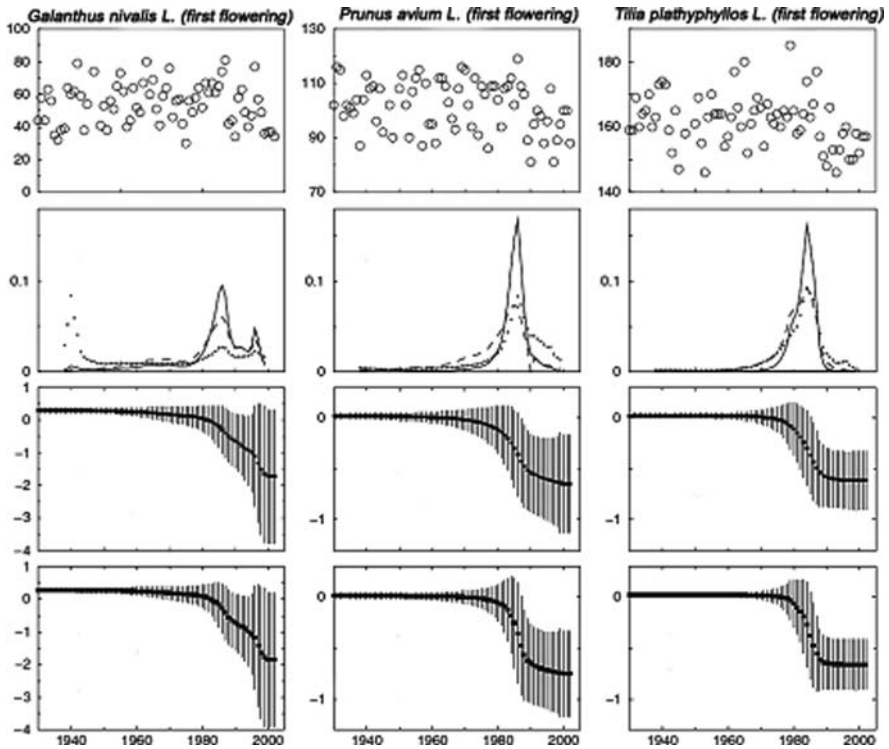
Example 1 Bayesian correlation between temperature and blossom onset data (Dose and Menzel 2006)

Dose and Menzel (2006) compared blossom trends for the coherent and independent hypotheses and found that the transition from trends being slightly positive before 1970 to strongly negative by 200x becomes sharper when the temperature data are included in the analysis (Fig. 11.6).

For the three species considered: snowdrop, cherry and lime tree Dose and Menzel (2006) found factors of 1.05, 2.19 and 3.26, respectively, in favour of coherence. Quantitative differences in the Bayes factors of cherry and lime tree, reflecting different amounts of interdependence, are not evident in traditional correlation analysis. These differences between cherry and lime tree results may be related to different temperature sensitivities. The fact that no preference for a coherent treatment of snowdrop blossom and January–March temperatures was found, although traditional correlation analysis gives a correlation coefficient  $r^2$  of 0.56, raises further questions. Either January–March temperatures are not the most appropriate measure to attribute observed changes in snowdrop blossom to, or other possible triggering parameters, such as soil temperatures or snow cover should be considered, too. Additionally, changes in blossom dates may also be (partly) attributed to other causes, such as changes in variety or microclimatic conditions at top soil and/or ground level which are not mirrored at the 2m height where air temperature is measured.

Thus, the Bayesian answer to the question whether changes in temperature and phenology should be regarded as coherent as was found with cherry and lime trees or independent as in the case of snowdrop also offers deeper biological insight. In conclusion the Bayesian treatment of the problem not only provides us with numbers of well-defined meaning as to which of the two alternative hypotheses  $M_a$ : the evolution of temperature and blossom onset time series is causally independent or  $M_b$ : the two time series exhibit correlation, is supported by the data. In case that  $M_b$  dominates it also allows pooling of temperature and blossom data to arrive at much more precise trend estimates. The return of the Bayesian analysis is therefore much superior to the results of a traditional correlation analysis.

Example 2 Norway spruce (*Picea abies*): Bayesian analysis of the relationship between temperature and bud burst (Schleip et al. 2008)



**Fig. 11.6** The figures in the upper row show the original data on blossom onset. The second row shows change/matching point probabilities for the chosen two segment polygonal as obtained for the temperature data as full dots, for the blossom time series as the dashed trace and the joint probability from the pooled data set as a continuous curve. The third row reproduces blossom trend results obtained earlier on the basis of blossom time-series data only (Dose and Menzel 2004). The lower row shows the corresponding trend predictions based on the joint temperature and blossom data sets

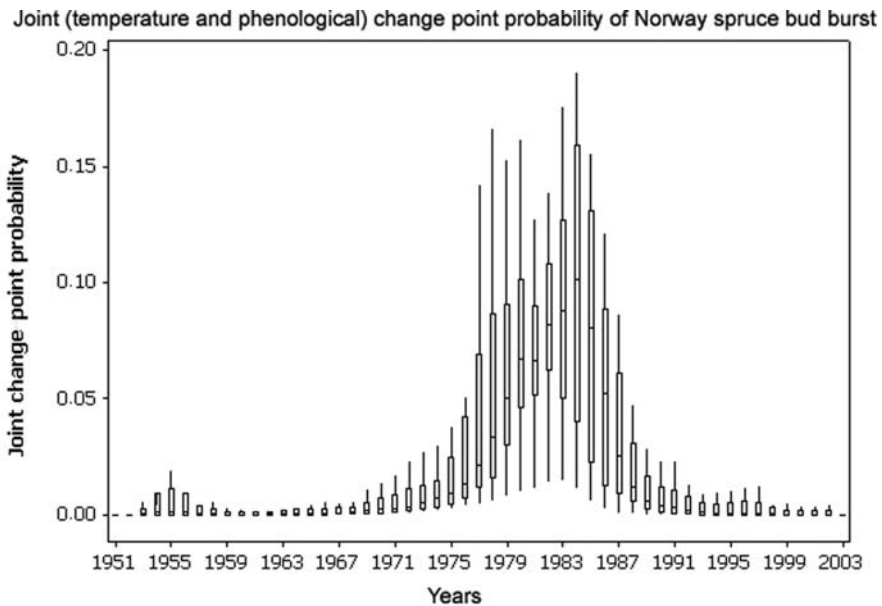
Schleip et al. (2008) applied the Bayesian probability approach when investigating the time series of the phenological phase of bud burst in Norway spruce (*Picea abies* (L.) Karst.) as well as mean monthly and/or weekly temperatures of corresponding climate stations in Germany. They used the Bayesian coherence analysis of Dose and Menzel (2006) to estimate the coherence between phenological onset dates and an effective temperature generated as a weighted average of monthly and weekly means from January to May. Weight coefficients were obtained from an optimization of the coherence factor by simulated annealing.

Most time series of naturally-occurring events in ecosystems do change in a nonlinear way (Dose and Menzel 2004, Schleip et al. 2008). Schleip et al. (2008) showed, using the approach of Dose and Menzel (2004) that linear regression models by themselves are of limited value for the analyses of temperature or phenological time series. Norway spruce bud burst time series (1953–2003) of 17 out



of 18 German stations revealed an abrupt change at the beginning of the 1980s. The change point model proved to be the preferred model with an average model probability of 87% to describe this observed discontinuity. Schleip et al. (2008) showed that temperature time series also exhibited this discontinuity at the beginning of the 1980s. April and May mean temperatures revealed the highest change point probabilities. The advantage of the Bayesian probability method is that it allows an accurate analysis of the relationship between phenology and temperature observations. In all cases investigated in Schleip et al. (2008), the results clearly suggested a coherent development of temperature and phenological time series, with some coherence factors as large as three. Therefore, they expected that change point probabilities derived from the two data sets (joint change point distribution) would be more informative (e.g. better localized in time than that obtained from a single series of data) (see Fig. 11.7).

Norway spruce bud burst represents a phenological phase which shows a prompt response to temperatures of the previous (April) and current month (May) with average temperature weights of 0.48 and 0.28, respectively.



**Fig. 11.7** Box plots of change point probability distributions of joint (temperature and phenological) change point probability at the corresponding 18 climate stations. Change point model probability distributions were calculated for the period 1951–2003. The median is represented by the horizontal line within each box plot. The top of each box is the third quartile (Q3) – 75% of the data values are less than or equal to this value. The bottom of the box is the first quartile (Q1) – 25% of the data values are less than or equal to this value. The lower whisker extends to this adjacent value – the lowest value within the lower limit. The upper whisker extends to this adjacent value – the highest data value within the upper limit

Schleip et al. (2008) calculated model averaged rates of change, using the Bayesian probability approach of Dose and Menzel (2004). Model averaged rates of change are obtained by the superposition of the constant, the linear and the change point model rates of change, weighted by the respective model probabilities. The model averaged rates of change of April and May temperatures have increased from 1951 to 2003, which is equivalent to increased warming. In 2003, May temperature change rates of 18 climate stations ranged from 0.03 to 0.17°C year<sup>-1</sup> whereas in 1951 May temperature change rates ranged from -0.03 to 0.03°C year<sup>-1</sup>. In contrast, change in bud burst of Norway spruce in 2003 was estimated from -0.25 to -0.75 days year<sup>-1</sup> but had showed a delay in 1951. Over most of the investigated period, there was essentially a zero rate of change; but from the 1980s onwards the rate of change was negative for Norway spruce bud burst. This finding is consistent with results of other studies (e.g. Scheifinger et al. 2002, Chmielewski and Rötzer 2002, Dose and Menzel 2004, Schleip et al. 2006) that describe an abrupt change towards earlier occurrence dates in the late 1980s and almost no significant rates of change before that date.

The results of Menzel et al. (2006) and Menzel (2003) underline the findings of Schleip et al. (2008). Menzel (2003) found that the anomaly curve of Norway spruce revealed notable phenological advances of 0.13 days year<sup>-1</sup> during the previous 5 decades (1951–2000). Menzel (2003) detected that, in general, later spring phases (including Norway spruce) responded to March to May temperatures. Menzel (2003) calculated the subset regression between phenological anomalies of bud burst of Norway spruce and the three-monthly running mean temperatures of March, April and May. Her results showed a  $r^2$  of 0.79 and a slope of -4.7 days year<sup>-1</sup>. Menzel (2003) also applied a two-variable model where the month preceding bud burst (April) was chosen as the first variable and the mean temperatures of March to May as the second variable; these explained most of the variability ( $r^2 = 0.85$ ). In the work of Menzel et al. (2006), most phases correlated significantly with mean monthly temperatures of the month of onset and the two preceding months. For 19% of the phenophases the highest correlation was seen with the month of onset, 63% with the preceding month and 18% with that 2 months earlier.

The enhancement of resolution of the approach by weekly or even shorter temperature intervals has pros and cons. On one hand such an enhancement of resolution inherits a loss in the achievable precision and very likely causes unwanted noise. In other words, if we conducted the analysis with a daily resolution, we might get high temperature weights of a certain day which is more likely accidentally and not because of a biological dependence. But, on the other hand, the results of the weekly analysis reveal more specific information about further systematic biological dependences. Beside April and May, the end of February exhibited a systematic accumulation of higher temperature weights.

The state of forcing is often described as a sum of daily rates of forcing (Chuine 2000). Our example suggests that bud burst does not simply react to a rate of forcing with fixed temperature sum or defined threshold value as used by Cannell and Smith (1983), Murray et al. (1989) and Häkkinen (1999) and others. Forcing temperatures rather exhibit a periodic pattern with a smaller first signal at the end of February

and a greater temperature prompt in April and May. However, forcing temperatures have changed in recent decades in a nonlinear way.

As support for more ecophysiological approaches, one could say that they should incorporate specific forcing temperature change patterns rather than temperature threshold sums of previous and current years. Linkosalo (2000) concluded that the formulation of commonly used phenological models seems to be general enough to suit several different plant species and various phenological phenomena. But Linkosalo (2000) also mentioned that it is also possible that the nature of the control mechanism is not straightforward triggering as stated in the same models.

Häkkinen (1999) has already discussed the disadvantages of standard statistical methods because of the dynamic nature of the models of bud development theories. He suggested an alternative approach of a bootstrap and cross validation method for the evaluation of theories based on the numerical comparison of the model mean square errors only.

Chuine et al. (1998) tested four commonly used models to predict the dates of flowering of temperate-zone trees, the spring warming (Hunter and Lechowicz 1992), sequential (Sarvas 1974, Hänninen 1987, 1990, Kramer 1994b), parallel (Landsberg 1974, Hänninen 1987, 1990, Kramer 1994a) and alternating models (Cannell and Smith 1983, Murray et al 1989, Kramer 1994a, 1994b). The main disadvantages of these models are that they are unable to make accurate predictions based on external data (Kramer 1994a). Chuine et al. (1998) stated that the external validity is still not available for the majority of the species. They suggested that a wrong estimation of the starting date of the forcing phase and a wrong estimation of the critical state of forcing may be the reason. The comparison of the accuracy of different models for different species shows that there is no consensus model even if some models seem consistently more accurate than others (Chuine et al. 1998).

## 11.5 Discussion

Our examples indicate that the method of Bayesian analysis combined with the method of simulated annealing may bring a valuable contribution to the estimation of forcing temperatures and model selection.

Phenophases are responding to many meteorological and environmental factors such as light, photoperiod, temperature, precipitation, humidity, wind, soil conditions etc. (Schnelle 1955, Menzel 2002). Despite the many influencing factors, the timing of leaf unfolding and flowering of deciduous vegetation is most likely triggered primarily by temperature. Specifically, chilling temperatures break winter dormancy and subsequent warming temperatures induce budburst (e.g. Chuine et al. 1998, Sparks and Menzel 2002, Rosenzweig et al. 2007).

The comparison of model averaged rates of change of, for example, Norway spruce bud burst time series with those of monthly temperatures that exhibit the highest temperature weights gives us further insights into the relationship. The description of the data in terms of only one model is often unsatisfactory (Dose and

Menzel 2004, Schleip et al. 2006). The Bayesian model comparison analysis allows us to estimate a reliable combined model averaged rate of change. Compared to the commonly used linear regression approach, we are able to provide model averaged rates of change at an annual resolution. This helps us to describe discontinuities and to quantify the direction and speed of the changes. Furthermore the implemented simulated annealing method allows the determination of temperature weight coefficients that show us which temperature changes support phenological change points. It is worth noting that the model averaging process does not alter the shape of the rate of change derived from the change point model. The model averaging procedure adds a counterbalance due to the constant contribution from the linear model and a reduction of the amplitude by the amount of the model probability obtained for the change point model. The results of Schleip et al. (2006, 2008) clearly reveal that the phenological phase has a discontinuity in the 1980s. In the second example we confirmed for several climate stations in Germany that temperatures in April and May had a very similar discontinuity in the 1980s. The reason for this specific timing of change points in the 1980s is most likely linked to altered atmospheric circulation patterns, such as the North Atlantic Oscillation (NAO) (e.g. Menzel 2003).

## 11.6 Conclusion

Regional studies of plant phenology, often using phenological network data, are extremely important for assessing the impacts of global change as they can shed light on regional peculiarities. However, this information is only revealed if the spatial variability can be separated from inherent problems in the temporal significance due to different underlying time periods. This latter point is the crucial limitation of the currently used linear regression approach. By contrast, Bayesian concepts allow the comparison of different models to describe the functional behaviour of phenological time series and even provide annual predictions of rates of changes. Thus, this new approach allows an intensified comparison of regional changes in phenology.

In general, the Bayesian approach provides a unique tool for phenological time series analysis as the reliability of the functional behaviour and of the trend is represented by confidence intervals, which are diagnostically useful as observed odd changes in our study emphasise. Plant phenological research provides fundamental knowledge on the development rhythm of plant species and of influencing factors. Plants have different sensitivities and responses to climate changes which may lead to changes in population dynamics. Differences in their phenological response may affect the competition among species (Kramer et al. 2000) and promote those with a better adaptive response. Changes in species distribution and abundance are expected to result from climate change, which may have positive and negative effects. New crop varieties can become productive in specific regions and unknown diseases or weeds may appear in certain areas. Thus, the phenological responses should be examined at all levels of the plant-environment system

(Beaubien 1996), as a continued trend towards earlier development is very likely to happen.

The frequent observations of a non-linear change underline the importance of Bayesian analyses. Often the strongest changes in the length of the growing season, which is a central clue for the variation of carbon exchange of terrestrial ecosystems, take place at the beginning of the vegetation period. The earlier spring phenophases are the most consistent indicators, however, late spring species benefit more from a prolongation in spring time than early spring species. The reason for this is because late spring species exploit longer days (Schaber 2002). Bayesian nonparametric function estimation is the method of choice for the identification of changes in phenological records and will allow a better large scale attribution of these changes to the temperature evolution in the second half of the twentieth century.

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# Chapter 12

## Smoothing Methods

Adrian M.I. Roberts

**Abstract** Regression methods are often used to explore the dependence of the timing of natural events on the weather. These methods are generally reasonable straightforward to apply, being available in numerous software packages. Weather data are commonly aggregated to monthly means, so, for example, the date on which a particular species flowers each year might be regressed on the monthly mean temperatures during the period preceding flowering. This aggregation has the benefit of reducing problems due to multicollinearity; temperatures between successive days and weeks tend to be highly correlated.

In this chapter, we describe regression methodology that can be applied to correlated predictor variables, such as daily temperature records, avoiding difficulties due to multicollinearity. This method, called penalised signal regression, is based on the observation that the regression coefficients for successive days should be similar in size. Differences in coefficients between neighbouring days are penalised. This results in a smooth curve of regression coefficients that is easily interpretable. We describe several alternative methods that employ this idea and explain how to apply penalised signal regression in practice.

**Keywords** Penalised regression · Phenology · *P*-spline · Smoothing

### 12.1 Introduction

There is considerable interest in the relationships between the timing of natural events and weather data, particularly given the current concerns about climate change and its influence on ecology (Fischlin et al. 2007). Methods for examining such relationships fall into two classes: model based and association

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based. In the case of the former, models are built on an understanding of the physiological processes that determine when the event occurs (e.g. thermal time models (Chuine et al. 2003, Trudgill et al. 2005)). Models tend to be non-linear, though sometimes it is possible to approximate with linear models (Thompson and Clark 2006). Association based methods, on the other hand, are not based on any particular biological model but merely attempt to quantify the relationship with weather data.

Association based methods tend to be straightforward to apply routinely, requiring less tailoring to particular circumstances. Conclusions can be drawn directly or the methods can be used as exploratory tools to suggest specific biological models. In particular, they can highlight secondary effects that otherwise might be missed (e.g. Fitter et al. 1995, Sparks et al. 2000).

Regression analysis (Draper and Smith 1981) is a class of association based methods that is widely used in phenology, in particular stepwise regression (Fitter et al. 1995, Sparks and Carey 1995, Roy and Sparks 2000). Linear regression has the benefit of flexibility; for example, it is possible to accommodate non-normal responses, multiple effects, covariates and correlated errors. In phenological applications, weather data is usually aggregated to averages over a month or more, even though daily observations may be available. This avoids both numerical problems and difficulties with interpretation arising from the high dimensional and correlated nature of daily weather data. However, aggregation is an unsatisfactory solution since information is lost.

In this chapter we describe a recently introduced approach to examining the relationship between phenology and weather (Roberts 2008). This, being based on linear regression, retains the benefit of flexibility. However, it can be used with weekly or daily weather data and gives results that are intuitively attractive.

To illustrate the concepts, we draw on the Last family records (Last et al. 2003, Roberts et al. 2004). The Last family made weekly records of the species in flower in their garden in East Lothian, Scotland, from 1978. From these records, we have determined the first dates of flowering for 208 species and cultivars from 1978 to 2001. We also have daily weather data from the Royal Botanic Garden Edinburgh. Here we will largely focus attention on one species, the European rowan or Mountain ash (*Sorbus aucuparia*), and the influence of temperature. Over the period, Rowan started flowering between 23 April (1993) and 3 June (1979), a range of 41 days. The mean date of first flowering was 16 May. We use here maximum air temperature; this gave the best stepwise regression results over all the species of the five temperature measurements available (Roberts et al. 2004).

We will start by giving an overview of some regression methods used in phenology (Section 12.2), motivating the need for new method. We then illustrate the smoothing approach (Section 12.3), demonstrating some of its advantages. This method is described in more detail (Section 12.4 and 12.5), leading onto a description of alternative approaches (Section 12.6). Extensions to the approach are then detailed (Section 12.7), including ways of analysing many species simultaneously. Finally, software options for implementing the approach are detailed in Section 12.8.

## 12.2 An Overview of Regression Methods for Exploring Relationships with Weather Data

There are several methods available based on linear regression to explore relationships between phenological records and weather data. The most straightforward is simple linear regression, where the phenological response is regressed on a single weather variable. The weather variable could be daily or aggregated. In Table 12.1 we show the results of regressing the first flowering dates of Rowan on temperature data aggregated into months. The regression coefficients (slopes) show the effect of a 1°C rise in temperature in that month, with a negative coefficient indicating an advance in flowering. The largest correlations are found with temperatures in the months February and March, giving an advance in flowering with higher temperatures. January (advance) and October (delay) also have statistically significant correlations at the 10% level.

Next we illustrate the use of multiple linear regression to look at the effects of several weather variables simultaneously. This method does not work well if the variables are highly correlated, otherwise known as multicollinearity, or if there is a large number relative to the number of observations (Draper and Smith 1981). In such cases, regression coefficient estimates can be highly sensitive to small changes in the model or data. This makes it harder to make interpret results. In our data set, correlation coefficients between consecutive daily temperatures average 0.63 and are higher in the period November to March. Monthly temperatures are less serially correlated, with coefficients averaging 0.15. Even so the correlation coefficients between January and February, and February and March are quite high at about 0.5. It clearly makes sense to use aggregated temperatures for multiple regression to avoid issues with multicollinearity. In Table 12.2 we show the results of regressing the first flowering dates of Rowan on monthly temperature data from July of the

**Table 12.1** Regression coefficients (days/°C) and correlation coefficients for simple linear regression by least squares of Rowan first flowering dates on each month mean temperature in turn, from July of the previous year to May of the year of flowering

Month	Jul	Aug	Sep	Oct	Nov	Dec	Jan	Feb	Mar	Apr	May
Coefficient	0.3	-0.2	-4.1	3.2	0.7	0.8	-4.0	-4.9	-6.5	-2.7	-4.2
Correlation	0.02	-0.02	-0.30	0.38	0.07	0.10	-0.55	-0.76	-0.72	-0.26	-0.37

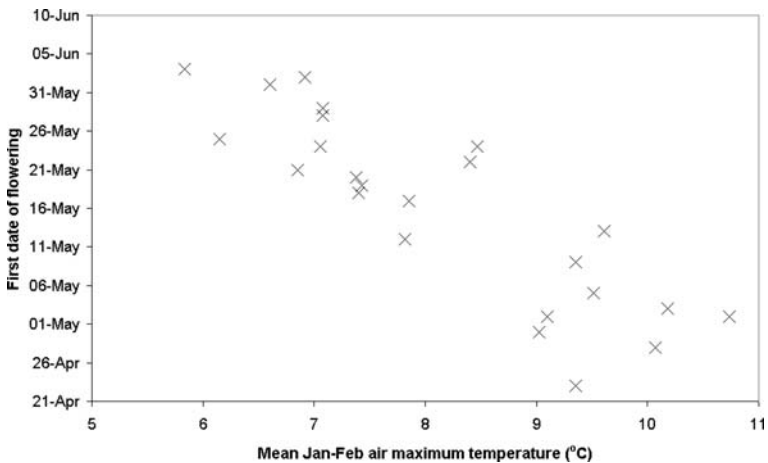
**Table 12.2** Regression coefficients (days/°C) for multiple linear regression by least squares of Rowan first flowering dates all of the monthly mean temperatures from July of the previous year to May of the year of flowering

Month	Jul	Aug	Sep	Oct	Nov	Dec	Jan	Feb	Mar	Apr	May
Coefficient	1.2	1.3	4.5	0.3	0.0	2.3	-0.3	-3.8	-4.7	-0.1	-2.3

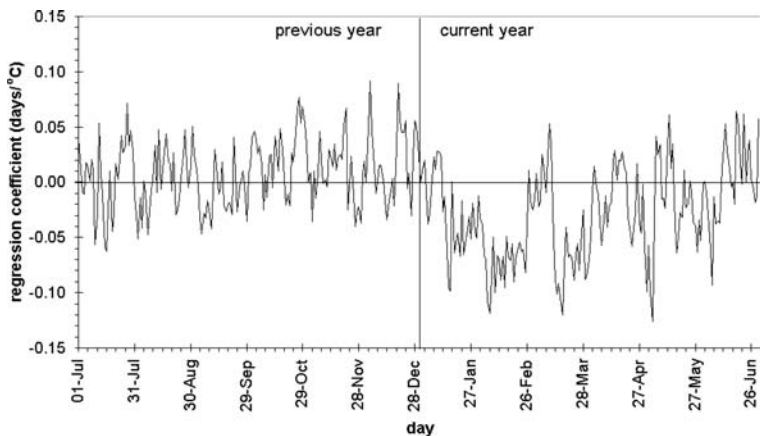
previous year to May of the year of flowering. By summing the regression coefficients, we see that the predicted effect of an overall 1°C rise in temperature over the year is a 1.6 day advance in the start of flowering. Again the largest effects are associated with February and March. Interestingly, September now is linked to a delay in flowering with rising temperature (c.f. Table 12.1); this inconsistency may be due to the relatively low number of observations and the correlations between the months.

Stepwise regression is a variation on multiple regression in which the aim is to select those predictor variables that “best” explain the response. This is done in an incremental process by gradually building the regression from a model with no explanatory variables by adding terms that sufficiently improve the model (forward selection) or by dropping terms that no longer have a sufficient effect (backwards elimination). The procedure is finalised once no variables can be added nor deleted. For a more detailed explanation, see Draper and Smith (1981). Stepwise regression is commonly used in phenology (e.g. Fitter et al. 1995, Sparks and Carey 1995, Roy and Sparks 2000, Keatley et al. 2002), having the benefit of focussing attention on the most influential variables. We apply it here to the Rowan example, using the mean temperatures in the months from July of the year prior to flowering up to May of the year of flowering. We use a 1% cut-off significance criterion for entry and exit of terms. The procedure selects the mean temperatures in February and March and these have regression coefficients  $-3.5$  and  $-4.2$  days/°C respectively. Given an overall rise in temperature of 1°C, the model predicts an advance in flowering of 7.7 days. It is clear that these two months have an important association with the timing of flowering (Fig. 12.1).

Several regression methods have been developed to cope with high dimensional, correlated arrays of predictor variables, primarily for chemistry applications. These



**Fig. 12.1** First flowering dates for Rowan plotted against the mean maximum air temperature over February and March



**Fig. 12.2** Partial least squares regression applied to Rowan first flowering dates with regressors being the daily maximum air temperatures from 1 July of the year prior to flowering and the preceding year to 30 June of the year of flowering. The line interpolates the regression coefficients

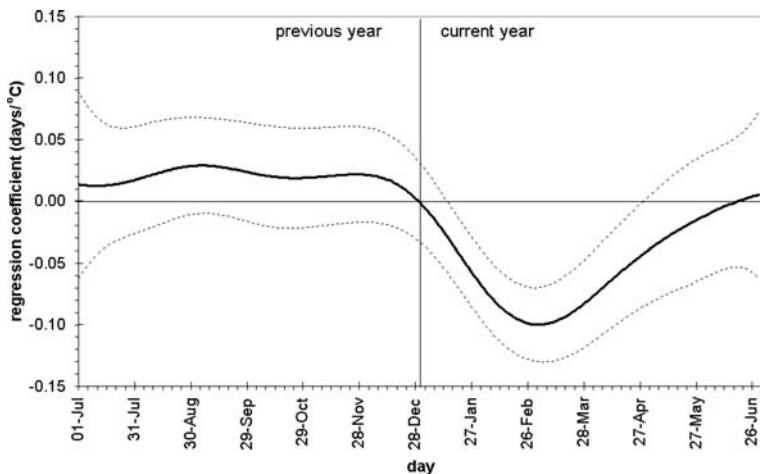
include ridge regression, principal component regression and partial least squares regression (Hastie et al. 2001, Frank and Friedman 1993). We show how one of these, partial least squares, performs with the Rowan data. Partial least squares regression works by finding multivariate projections of the predictor data that are most highly associated with the response variable. By selecting the best of these, the dimensionality of the predictor array can be reduced. The number of projections or components required is chosen by a set criterion – we use the cross-validated prediction error (see Section 12.5). For the Rowan example, we choose to use the daily temperatures from 1 July of the year prior to flowering to 30 June of the year of flowering, giving a total of 365 predictor variables. The resulting regression coefficients for the Rowan example are shown in Figure 12.2, where the number of components was chosen to be two. There is some sign of the relationship with temperatures early in the year of flowering but the graph is difficult to interpret because of the jagged nature of the coefficients.

### 12.3 Improving on regression by smoothing

One of the limitations of the more traditional regression methods (see also Chapter 3) such as multiple regression and stepwise regression for phenology is that it is necessary to aggregate weather data, thus resulting in loss of information. Other regression methods, such as partial least squares, that have been developed to cope with many correlated variables give results that are not always easy to interpret. The method that we describe here, using the concept of smoothing, can cope with weekly or daily weather variables and gives results that are interpretable.

This smoothing concept is based on the idea that regression coefficients for consecutive days should have similar values. We can achieve this through a process of smoothing the regression coefficients. There are a number of potential mechanisms for achieving this; here we principally concentrate on the approach of penalising differences between consecutive regression coefficients. This is known as penalised signal regression. Whereas in standard linear regression, the regression coefficient estimates are found that optimise the fit of the model to the data according to the least squares criterion (Draper and Smith 1981), in penalised signal regression estimates are found that both fit the data well and which have small differences between consecutive coefficients. This approach is explained in greater depth in Section 12.4. There are a number of variations on this general idea and these are detailed in Section 12.6.

We illustrate the penalised signal regression approach using the Rowan example (Fig. 12.3). Again we use the daily temperatures from 1 July of the year prior to flowering to 30 June of the year of flowering as predictors. The particular method that we employ for this analysis is known as *P*-spline signal regression (Marx and Eilers 1999) (see Section 12.6). The advancing effect due to the temperatures in the period prior to flowering is clear, with the peak being around 4 March,  $2\frac{1}{2}$  months before the mean date of flowering. The lines indicating two standard errors above and below each regression coefficients help in the interpretation; there is apparently little effect of temperatures in the calendar year before flowering. A note of caution should be added here – as for all the alternative regression methods, the quality of results will depend on the number of observations (years) available. With more observations, main effects should be more sharply defined and secondary effects may become evident.



**Fig. 12.3** *P*-spline signal regression applied to Rowan first flowering dates with regressors being the daily maximum air temperatures from 1 July of the year prior to flowering and the preceding year to 30 June of the year of flowering. The thick line interpolates the regression coefficients and the dotted lines represent two standard errors above and below these

## 12.4 Some Mathematical Detail

In this section, we describe one of the more straightforward implementations of the penalised signal regression approach. In least squares regression, the estimates of regression coefficients are found by minimising the sum of squared residuals. To constrain the regression coefficients to be similar, a penalty term is added to the sum of squared residuals before minimisation. This method is described by Eilers (1991) and Elston and Proe (1995). Note that the latter adopted a likelihood approach rather than least squares, but these are equivalent for a regression model with independent normal errors.

For a standard multiple linear regression model  $\mathbf{y} = \mathbf{X}\boldsymbol{\beta} + \boldsymbol{\varepsilon}$ , where  $\mathbf{y}$  is a vector of responses for the  $n$  years observed,  $\mathbf{X}$  is a  $n$  by  $p+1$  matrix corresponding to the  $p$  predictor variables plus a column of 1's for the intercept,  $\boldsymbol{\beta}$  is a vector of regression coefficients  $\{\beta_i\}$  including the intercept and  $\boldsymbol{\varepsilon}$  is a vector of independent normally-distributed errors with variance  $\sigma^2$ , the regression coefficients are estimated by minimising the expression

$$(\mathbf{y} - \mathbf{X}\boldsymbol{\beta})^T (\mathbf{y} - \mathbf{X}\boldsymbol{\beta}) + \lambda \boldsymbol{\beta}^T \mathbf{D}^T \mathbf{D} \boldsymbol{\beta} \quad (12.1)$$

The first part of Equation 12.1 is the sum of squared residuals used in least squares and the second part is the difference penalty term. The parameter  $\lambda$  determines the balance between the sum of squares term and the penalty and thus controls the degree of smoothing. The choice of  $\lambda$  and the effect on the coefficient estimates is discussed in 12.5.  $\mathbf{D}$  is a matrix that applies differencing to the coefficients  $\boldsymbol{\beta}$  and has  $p+1$  columns. For given  $\lambda$ , estimates  $\hat{\boldsymbol{\beta}}$  of  $\boldsymbol{\beta}$  are found by minimising (1). There is an analytic solution given by:

$$\hat{\boldsymbol{\beta}} = (\mathbf{X}^T \mathbf{X} + \lambda \mathbf{D}^T \mathbf{D})^{-1} \mathbf{X}^T \mathbf{y} \quad (12.2)$$

and standard errors for  $\hat{\boldsymbol{\beta}}$  can be found using:

$$\text{var}(\hat{\boldsymbol{\beta}}) = \hat{\sigma}^2 (\mathbf{X}^T \mathbf{X} + \lambda \mathbf{D}^T \mathbf{D})^{-1} (\mathbf{X}^T \mathbf{X}) (\mathbf{X}^T \mathbf{X} + \lambda \mathbf{D}^T \mathbf{D})^{-1} \quad (12.3)$$

where  $\hat{\sigma}^2$  is the estimate of the residual variance.

Different orders of differencing can be employed. First order differences correspond to simple differences between consecutive coefficients:  $\beta_i - \beta_{i+1}$ . Higher order differences correspond to polynomial contrasts and can be calculated using the recursive formula (Marx and Eilers 1999):

$$\mathbf{D}_{j+1} = \mathbf{D}_1 \mathbf{D}_j \boldsymbol{\beta} \quad (12.4)$$

where  $\mathbf{D}_j$  is the difference matrix of order  $j$ . For example, second order differences are of the form  $\beta_i - 2\beta_{i+1} + \beta_{i+2}$  and third order of the form  $\beta_i - 3\beta_{i+1} + 3\beta_{i+2} - \beta_{i+3}$ . The order of difference applied will have some effect on the resulting estimates of coefficients; for example, a third order difference matrix will penalise solutions that

are not locally quadratic. Eilers and Marx (2003) suggest comparing different low orders, say from one to three. In our experience, we find that third order differences give satisfactory results with daily temperature measurements.

Eilers and Marx (2003) suggest the inclusion of a further penalty term, known as a ridge penalty, which has the effect of shrinking the regression coefficients towards zero. This is also used in ridge regression (Hastie et al. 2001). The expression (12.1) becomes:

$$(\mathbf{y} - \mathbf{X}\boldsymbol{\beta})^T (\mathbf{y} - \mathbf{X}\boldsymbol{\beta}) + \lambda \boldsymbol{\beta}^T \mathbf{D}^T \mathbf{D} \boldsymbol{\beta} + \gamma \boldsymbol{\beta}^T \boldsymbol{\beta} \quad (12.5)$$

with solution given by:

$$\hat{\boldsymbol{\beta}} = (\mathbf{X}^T \mathbf{X} + \lambda \mathbf{D}^T \mathbf{D} + \gamma \mathbf{I}')^{-1} \mathbf{X}^T \mathbf{y} \quad (12.6)$$

where  $\mathbf{I}'$  is an identity matrix augmented with zeros to allow for the intercept – this is not penalised.

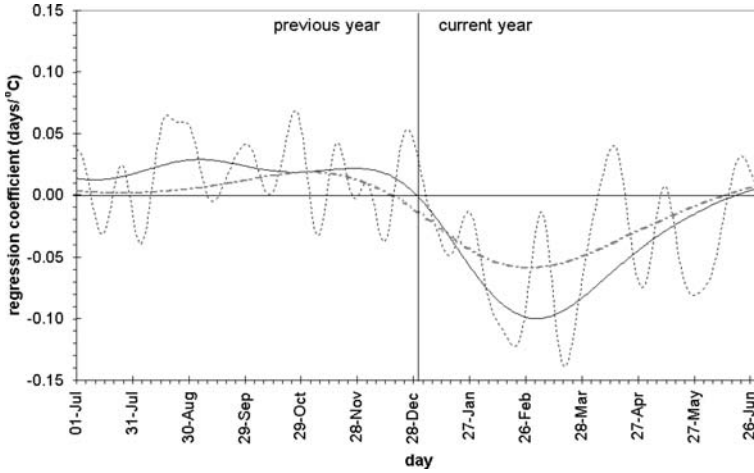
The additional term in Equation 12.5 is proportional to the sum of squares of the regression coefficients. Its importance is controlled by the ridge parameter  $\gamma$ ; see Section 12.5 for information on choosing  $\gamma$ . We have found the inclusion of a ridge penalty beneficial in phenology applications.

## 12.5 Choosing the Degree of Smoothing

As mentioned above, the smoothness of the profile of regression coefficients is controlled by the smoothing parameter  $\lambda$ . Small values of  $\lambda$  produce wiggly solutions and large values tend to produce curves that look more like low-order polynomials (Fig. 12.4). These correspond to greater and less complexity, respectively. The degree of complexity can be represented by the *effective degrees of freedom*,  $d$  (Marx and Eilers 1999). In the Rowan example shown in Figure 12.4, the optimal solution (also shown in Fig. 12.3) has 5.6 degrees of freedom, and the under- and over-smoothed solutions have 15.4 and 2.4 degrees respectively. The effective degrees of freedom are calculated using the formula:

$$d = \text{trace} \left( (\mathbf{X}^T \mathbf{X} + \lambda \mathbf{D}^T \mathbf{D} + \gamma \mathbf{I}')^{-1} \mathbf{X}^T \mathbf{X} \right) - 1 \quad (12.7)$$

The choice of both  $\lambda$  and the ridge parameter,  $\gamma$ , may be made by subjective means, using visual judgement of the results, or, preferably, by more objective means using quantitative criteria. Commonly employed quantitative methods include cross-validation, the Akaike Information Criterion (AIC) and the Bayesian Information Criterion (BIC) (Marx and Eilers 1999, Hastie et al. 2001). These methods will result in different choices of  $\lambda$  and  $\gamma$ , particularly with low numbers of observations. Here we describe the most conceptually simple of these methods, cross-validation.



**Fig. 12.4** Comparison of curves produced by optimal, under and over-smoothing using  $P$ -spline signal regression applied to Rowan first flowering dates with regressors being the daily maximum air temperatures from 1 July of the year prior to flowering and the preceding year to 30 June of the year of flowering. The black line interpolates the regression coefficients the optimum choice of  $\lambda$ , the black dashed line is under-smoothed and the grey dot-dash line is over-smoothed

The objective in cross-validation is to assess how well the model will predict the timing of events in future years. This is done by portioning the data into a training set, to which the model is fitted and regression coefficients estimated, and a test set, which is used to assess the quality of predictions using these estimates. In particular, in leave-one-out cross-validation (Hastie et al. 2001), the training set is made up of all years but one and the test set is the remaining year. The prediction of the phenological response,  $\hat{y}_{-i}$ , for this year,  $i$ , based on the model estimated from the other years is compared to the observed response,  $y_i$ . By cycling through all of the years, using each in turn as the test set, we can build up an estimate of the standard error of prediction,  $\hat{\sigma}_{cv}$ , thus:

$$\hat{\sigma}_{cv} = \sqrt{\frac{1}{n-1} \sum_{i=1}^n (y_i - \hat{y}_{-i})^2} = \sqrt{\frac{1}{n-1} \sum_{i=1}^n \frac{(y_i - \hat{y}_i)^2}{(1 - h_{ii})^2}} \quad (12.8)$$

where  $\hat{y}_i$  is the prediction of the response for year  $i$  based on a model estimated from all years including  $i$ , and  $h_{ii}$  is the  $i$ th diagonal element from the hat matrix given by  $\mathbf{X}(\mathbf{X}^T\mathbf{X} + \lambda\mathbf{D}^T\mathbf{D} + \gamma\mathbf{I})^{-1}\mathbf{X}^T$ . The second equivalence in Equation 12.8 reduces computations considerably.

To find the optimal penalty parameters, it is sufficient to calculate  $\hat{\sigma}_{cv}$  on a logarithmic grid of values for  $\lambda$  and  $\gamma$ . Of course it is important to explore the parameter space fully. It should be noted that multiple local optima may be present, particularly with low numbers of years. In such cases, judgement may be required to select the most appropriate solution and it is worthwhile examining a plot of  $\hat{\sigma}_{cv}$  against  $\lambda$  and  $\gamma$ .



## 12.6 Alternative Methods

In Section 12.3, we detailed one particular variation of penalised signal regression by Elston and Proe (1995). Here we outline other possibilities.

The first of these variations transforms the basic penalised regression approach of Equation 12.4 into an equivalent linear mixed model (Searle et al. 1992) as described in Sims et al. (2007). Here the difference penalty is interpreted as a random effect on the differences between the regression coefficients. So  $D\boldsymbol{\beta} \sim N(\mathbf{0}, \sigma_\lambda^2 \mathbf{I})$ . Fixed effects are required for low order polynomials in the regression coefficients representing the difference between  $X\boldsymbol{\beta}$  and  $D\boldsymbol{\beta}$  – see Sims et al. (2007) for more detail. The polynomials have orders up to the order of the difference less one. The mixed model parameters can then be estimated by residual maximum likelihood (REML) (Patterson and Thompson 1971, Searle et al. 1992). A feature of the mixed model parameterisation is that the degree of smoothing is estimated directly through the variance component  $\sigma_\lambda^2$  since  $\lambda = \sigma^2 / \sigma_\lambda^2$ . Welham et al. (2007) noted that estimates of  $\lambda$  tend to be larger with this mixed model approach than through cross-validation. However, current REML implementations may be unable to cope with the very large numbers of predictors that one may use with daily weather measurements, perhaps due to conditioning problems. For example, we were unable to process the Rowan example using the REML procedure in GenStat<sup>®</sup> with 365 daily temperatures as predictors; in contrast the penalised regression parameterisation of Equation 12.1 can be computed quite quickly.

In a similar manner to which the penalised regression is reparameterised into a mixed model, it can also be placed into a Bayesian framework (see Chapter 11 and Gelman et al. 2004). Here  $D\boldsymbol{\beta}$  is given a normal prior with zero mean and variance-covariance matrix  $\sigma_\lambda^2 \mathbf{I}$ . It is also necessary to place priors on the low order polynomials of the regression coefficients remaining after  $D\boldsymbol{\beta}$  is accounted for, i.e. such that  $D\boldsymbol{\beta} = 0$ . As with the mixed model, the degree of smoothing is related to  $\sigma_\lambda^2$ . A hyper-prior is required for  $\sigma_\lambda^2$ : the form of this may have a marked effect on the results, particularly if the number of years is low, so it is important to consider this carefully. Distributions that might be considered are the inverse gamma for the variance or uniform for its square root, the standard deviation. The parameters of the prior could be informed by experience from analyses of other similar data. Markov chain Monte Carlo (MCMC) (Gilks et al. 1996) is a flexible simulation-based approach for fitting Bayesian models. Note that for both the mixed model and Bayesian formulations, it is not straightforward to incorporate a ridge penalty along with the difference penalty since  $\boldsymbol{\beta} \sim N(\mathbf{0}, \sigma_\gamma^2 \mathbf{I})$  and  $D\boldsymbol{\beta} \sim N(\mathbf{0}, \sigma_\lambda^2 \mathbf{I})$  conflict.

Finally, Marx and Eilers (1999) introduced *P-spline signal regression* (PSR) as a way of reducing computational problems associated with very high numbers of predictors. The approach is similar to that outlined in Section 12.4 except that the regression coefficients are projected onto a lower dimensional and smooth basis. The basis chosen is based on *B-splines*. *B-splines* consist of polynomial pieces, joining at defined points known as knots. The number of knots spanned by each piece is determined by the degree of the spline. For example, the pieces of *B-splines* of

degree two are quadratic and span four knots (including the ends). Eilers and Marx (1996) give more detail on  $B$ -splines. Marx and Eilers (1999) suggest that cubic  $B$ -splines are sufficient in most applications of PSR.

A linear transformation,  $\mathbf{B}$ , based on these  $B$ -splines reduces the dimensionality of the coefficients and places the coefficients on a smooth curve,  $\boldsymbol{\alpha}$ , with lower dimension  $p^*$ , so that  $\boldsymbol{\beta}=\mathbf{B}\boldsymbol{\alpha}$  where  $\mathbf{B}$  has dimension  $p^*$  by  $p$ . A penalised signal regression is then carried out as specified in Section 12.4, with  $\boldsymbol{\alpha}$  replacing  $\boldsymbol{\beta}$  and  $\mathbf{U}=\mathbf{ZB}$  replacing  $\mathbf{X}$ . The difference penalty serves to smooth the coefficients further. Eilers and Marx (2003) recommend choosing a large number of knots. This can be higher than the number of years without causing numerical problems; in the Rowan example, we were able to use 100 knots.

It is also possible to place PSR into a mixed model framework (Currie and Durban 2002, Welham et al. 2007). The use of  $B$ -spline transformation should improve numerical properties with larger numbers of predictors.

PSR offers perhaps the most flexible approach of those detailed here, being able to cope with very high numbers of predictors, and having software available (see Section 12.8). In the Rowan example shown in Figure 12.4, we used cubic  $B$ -splines with 100 knots and both third order difference and ridge penalties.

## 12.7 Extending the Method

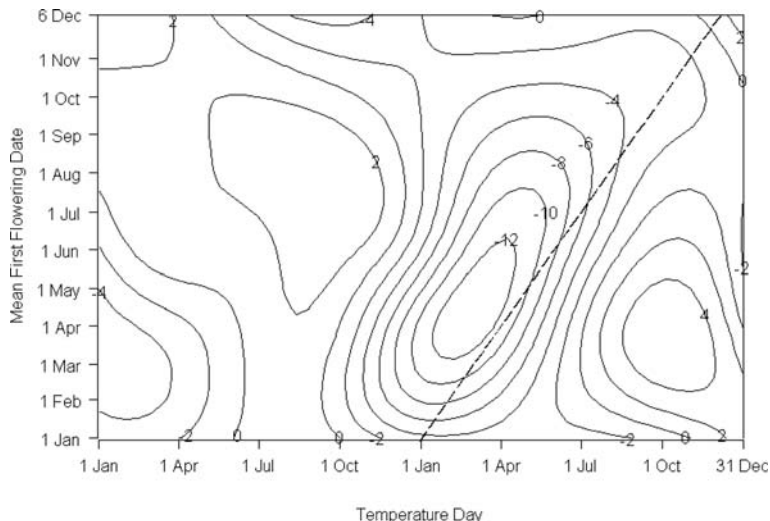
The basis of the approach is in regression. This allows several options for extending and generalising the method:

1. Inclusion of covariates as additive effects. For example, we might be particularly interested in covariates that represent the state of the species in the previous year. The formulae in Section 12.4 can easily be generalised to include additive covariates – these only affect the least squares part of Equation 12.1.
2. Inclusion of covariates as multiplicative effects. This allows examination of the effect of the covariate on the form of the regression coefficient curve rather than just its height. For example, we might be interested in the effect of latitude. The method is more complex and is outlined below.
3. Inclusion of more than one set of predictors. For example, the effects of daily temperature and rainfall may be of interest; therein we have a two-dimensional surface of regression coefficients. The method is outlined below.
4. Correlated error terms. This could be used to represent the effect that the previous year's response might have on the current year's outcome.
5. Non-normal distributed responses. Marx and Eilers (1999) demonstrate that the approach can be extended using a generalised linear regression method (McCullagh and Nelder 1989). The range of possibilities then includes distributions such as the binomial and Poisson.

The *P*-spline approach outlined above can be expanded to investigate the effect of one or more covariates, for example latitude, on the regression coefficients (Eilers and Marx 2003) or to study how two or more banks of predictors, such as daily temperature and rainfall measurements, affect the phenological response (Marx and Eilers 2005). In both cases a smooth surface of regression coefficients is produced. In parallel to ordinary PSR, the regression coefficients are transformed onto a smooth surface using tensor-products of *B*-splines. Tensor-products (a matrix operation) of one-dimensional *B*-splines give a mathematically simple way to extend the idea of *B*-splines to two or more dimensions – see Eilers and Marx (2003) for a fuller description. These provide a flexible basis yet economical basis for representing a surface. The degree of smoothing is again smoothed by difference penalties: one for each dimension of the surface. Note that the computational cost of the method is related to the product of number of knots in each dimension; Marx and Eilers (2005) recommend that this product is limited to 1000.

We illustrate multidimensional PSR to investigate the effect that the date that a species tends to start flowering has on the relationship of its phenology with temperature. In this case we are examining the effect of a covariate, the mean date of flowering, on the form of the 1-d PSR curve. Over the range of mean flowering dates, this forms a 2-d surface of regression coefficients. Since the mean flowering date is a covariate, we centre the flowering dates for each species by subtracting their mean. To avoid those species with greater responses to temperature dominating the analysis, we scale the centred flowering dates by dividing by the standard deviation of flowering dates for the species. The 2-d surface of regression coefficients that we wish to produce has one axis representing the daily temperatures and the other representing the effect of the mean date of flowering; the 2-d PSR method forms a 2-d regression coefficient surface using tensor-products of *B*-splines, one for each axis direction, which is constrained using separate penalties, again one for each axis.

Figure 12.5 shows the regression coefficient surface produced by applying this approach to 208 species from the Last family data set. These have mean first flowering dates ranging from 1 January to 27 November. The regression is on daily maximum air temperature from 1 January of the year preceding flowering to 31 December of the year of flowering. Thirty cubic *B*-splines are used in each direction (to keep the product below 1000) along with third order difference penalties (as for the one-dimensional PSR). A ridge penalty is also included. We found that the penalty parameters chosen by cross-validation produced a rather wiggly surface. To aid interpretation, the surface illustrated is based on a greater degree of smoothing, though the increase in cross-validated prediction error is small. The surface is dominated by a diagonal trough, representing negative regression coefficients. This shows that the period when increasing temperatures has the effect of advancing flowering tends to be later for later species. For January flowering species, the key period when temperature most affects timing of flowering tends to be about a week prior to the mean date of flowering; for August species, the key period is about three months before the mean date.



**Fig. 12.5** Contour plot of the regression coefficient surface produced by two-dimensional  $P$ -spline signal regression applied to the standardised flowering dates of 208 species with daily temperatures for the year of flowering and the preceding year as regressors and mean date of flowering as a covariate. The surface has been scaled by the mean of the standard error to simplify interpretation. The dashed line indicates where the temperature day is equal to the mean flowering date. This figure is reproduced from Roberts (2008) with the kind permission of Springer

## 12.8 Software

Although off-the-shelf software is not available for the basic penalised signal regression method (Section 12.4), it is relatively straightforward to implement this with software that permits matrix manipulations. Statistical packages with such facilities include SAS<sup>®</sup>, S-PLUS<sup>®</sup>, R and GenStat<sup>®</sup> (Payne et al. 2008). To implement the mixed model approach, software with both a REML procedure and matrix manipulations will be required. Again SAS<sup>®</sup>, S-PLUS<sup>®</sup>, R and GenStat<sup>®</sup> have such facilities. For a Bayesian framework, there are software packages that carry out MCMC for certain classes of models, including WinBugs (Lunn et al. 2000). Marx and Eilers have produced S-PLUS<sup>®</sup> code for their 1-d and multidimensional  $P$ -spline signal regression methods (see <http://www.stat.lsu.edu/faculty/marx/>).

## 12.9 Conclusions

We have described here a flexible approach to exploring relationships between the timing of natural events and weather data. It allows use of daily weather measurements without the need to aggregate. It can be extended in various ways, permitting, for example, the examination of weather relationships across many species.

As mentioned in the Introduction, biologically-based models such as thermal time models provide an alternative route to investigating the relationship between the phenological response and weather. The relationship between such models and the penalised regression approach is of interest. In particular, can the results from penalised regression models be used to guide the selection of particular thermal time models? This is the subject of ongoing research. The research will also include an evaluation of the number of years on the quality of the penalised regression model and comparison of alternative methods (Section 12.6) and criteria for selecting the degree of smoothing (Section 12.5).

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## Chapter 13

# Accounting for Correlated Error Structure Within Phenological Data: a Case Study of Trend Analysis of Snowdrop Flowering

Natalie Kelly

**Abstract** Given that phenological studies can provide insight into some of the climate change driven alterations in global ecosystems, easily understood but valid statistical analyses are paramount. Results from studies of trends in phenophases at a regional level provide more powerful evidence of climate change; and such studies require observations from multiple locations. However, data containing phenophase time series from multiple locations has an inherent correlated error structure which may render standard statistical methods invalid. This chapter explores the problems in statistical inference that can arise from applying naïve techniques to data containing correlated error and provides two alternative modelling approaches for more valid analyses. These alternative modelling approaches – data resolution and random effects modelling – are extensions of simple linear regression. These modelling approaches are described in detail, compared and discussed in the context of potential questions, data and analysis issues in phenological research. A case study of trends in flowering of the spring bulb snowdrop (*Galanthus nivalis* L.) across England is used to demonstrate these alternative modelling approaches. For the period 1952–2000, snowdrop flowering advanced approximately 6.5 days (SE = 0.10) per decade across England. Snowdrop flowering was also estimated to advance approximate 3.9 days (SE = 0.52) for every 1°C increase in mean January air temperatures during the same period.

**Keywords** Climate change · Correlated data · England · *Galanthus nivalis* L. · Phenology

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## 13.1 Introduction

Phenology is the study of the periodicity of biological events such as flowering and leaf set in plants or trees, or migration and breeding in animals (Lieth 1974). A fundamental aim of phenological research is to link the variation in periodicity of such events – known as phenophases – to climate variables, such as air temperature and rainfall, and other environmental or geographical covariates like pollution or latitude. As it is often the case that phenophases are sensitive to changes in climate, especially temperature (Dose and Menzel 2006), phenological data can provide insight into effects of climate change upon natural systems (Sparks et al. 2000, Rosenzweig et al. 2007). With a high likelihood of profound changes in the functioning of global ecosystems with climate change (Parmesan and Yohe 2003, Thompson and Clark 2006, Cleland et al. 2007), valid statistical analyses of phenological data are paramount.

Observations of a given phenophase are made annually, usually at the same geographical location and by the same observer. Records of a phenophase of a particular species, or collection of phenophases, at a single location may span many decades or, as in the famous (and rare) example of the Marsham series, one family in Norfolk, England, recorded the dates in spring of the appearance of a small number of common plants and animals for nearly two centuries from 1736 (Margary 1926, Sparks and Carey 1995). Phenological data are therefore longitudinal; a name which is traditionally applied to repeated observations of individual sample units through time. However, repeated observations will not be independent and so are likely to be correlated. As one of the primary assumptions of many common statistical tests is that data are comprised of independent samples, correlation must be accounted for in order to draw valid and efficient inferences about the parameters of interest. This is a particularly important consideration if phenophase series from multiple locations are to be analysed together in order to draw inferences about regional level processes.

This chapter describes both the consequences of correlated data and how to apply valid statistical analysis to phenological data. To assist in this, a case study of trend detection in snowdrop flowering at a number of locations across England is presented. To appeal to varying levels of statistical knowledge, two methods for modelling correlated data are demonstrated and compared against a model which ignores correlation – one simple and the other more sophisticated, and both based on simple linear regression. This chapter assumes knowledge of regression analysis and linear models and the basic properties of expectations and variances. For a primer on these topics, readers are directed to references such as McCullagh and Nelder (1989). As the intention of this chapter is to introduce statistical methods that account for correlated data in a phenological context, statistical notation has been kept as simple as possible. If readers wish to explore further the underlying statistical theory, references such as Pinheiro and Bates (2000), Verbeke and Molenberghs (2000) and Diggle et al. (2002) are recommended.



## 13.2 Trend Detection and Regional-Level Analyses with Phenological Data

### 13.2.1 Trend Analysis

A common analysis of phenological data involves testing for the presence of a trend in a phenophase of a given species over time or with an associated climate covariate, such as air temperature (i.e.  $H_0$ : trend = 0 days per unit of time or climate covariate). Detection of the presence and magnitude of a trend in a phenophase can indicate the present cumulative impact of climate change on a species or aid in the prediction of future changes, either with time or a given climate covariate (Sparks and Menzel 2002). If assessed against time, a trend in a phenophase may then be reported as a change in days over the study period, per year or per decade (Dose and Menzel 2004). This type of analysis is empirical, using purely statistical concepts to direct model building (Cleland et al. 2007). However, the results of such empirical analyses can be used further to inform process-based or physiological modelling (e.g. Chuine and Beaubien 2001).

Modelling of trends in phenological data series, whether using the slope estimate or measure of correlation, has the general structure of simple linear regression,

$$y_k = \beta_0 + \beta_1 x_k + e_k \quad (13.1)$$

where  $x$  is the explanatory variable (time or environmental covariate),  $y$  is the realisation of a phenophase usually expressed as a yearday (i.e. number of days since December 31), and  $k$  represents the  $k$ th sample. The error term  $e_k$  accounts for unexplained variability, and is assumed to be Gaussian and independently distributed in a population, with a mean of zero and a common variance of  $\sigma^2$ . The parameters,  $\beta_0$  and  $\beta_1$ , are the intercept and slope, respectively. A model of this type treats phenophase data – both yearday and year values – as variables that are continuous with a Gaussian distribution. The significance of the slope or trend estimate is usually tested using either a  $t$ - or  $F$ -test (e.g. as used in a phenology context by Abu-Asab et al. 2001). When year is treated as an explanatory variable, a positive trend estimate corresponds to a delay in a phenophase and a negative trend estimate to an advance of a phenophase over the study period. While the parameter estimate from a trend model is referred to as a slope, it becomes a trend when considered in the context of the study.

This method assumes linearity in the response of the phenophase with time or climate covariates; although there may be little basis for this assumption (Sparks and Carey 1995, Dose and Menzel 2004, 2006). It is important to note, however, that a linear function allows for a simple approximation of the direction and magnitude of a trend and that estimated linear rates are easily understood and palatable to both scientists and policy makers (Weatherhead et al. 1998). For simplicity, only linear relationships are considered in this chapter, but some discussion of modelling

non-linearity in phenological data is offered in Dose and Menzel (2004, 2006) and Roberts (2008).

### ***13.2.2 Detecting Trends in Phenophases at the Regional Level***

The Intergovernmental Panel of Climate Change (IPCC) has made repeated reference to the importance of testing for changes in biological processes at the regional level or across a geographical scale of a hundred or so kilometres (Gitay et al. 2001, Rosenzweig et al. 2007). Ecological theories gain weight when able to be generalised across geographical regions, suites of species, life forms, age classes, etc (Beck 1997). Likewise, the validity of applying the results of phenophase trend analysis at a regional level can be strengthened with the inclusion of series of observations from multiple locations within the region of interest. In addition, including data from multiple locations in an analysis will also lessen the effects of outliers arising from unusual seasonal weather or observation error (Häkkinen et al. 1995). Although the existence of multiple-location phenological data is reasonably rare, the rise in popularity of phenological networks will ensure more of such data is available in the future (Cleland et al. 2007).

There has been some discussion in the phenology literature about the representativeness of locations of phenophase observations (e.g. Roetzer et al. 2000, Thompson and Clark 2006 and Siljamo et al. 2008). It is thought that data from individual locations may unduly influence or bias models of phenological change, particularly through factors that cannot be controlled for or quantified. Each location will have a unique suite of confounded characteristics that will influence the variance in a phenophase. Firstly, it is likely that each location will have an individual observer that may have their own interpretation of the phenophase and bias is, therefore, introduced through scientific methodology (Siljamo et al. 2008). The localised climate at each location will also influence the phenophases, but unless a weather station is placed nearby, these subtle variations in climate will not be recorded (Thompson and Clark 2006, Siljamo et al. 2008). Further, it is realistic to assume that genotypes of species spread across a study region may vary enough to express a different phenophase, even with comparable climatic conditions. The combination of all these factors will lead to a phenophase systematically occurring a few days earlier at one location or a few days later at another compared to the mean of a population of locations. These sources of variation may be accounted for with a covariate analysis, but this would require a great deal more information to be collected; which may be a particularly onerous task if attempted retrospectively (Linkosalo et al. 1996). It is perhaps best, therefore, to concede that each location will have a certain amount of random variation that differs between locations and that cannot be realistically quantified.

Fortunately, if the geographical positions of locations of phenophase series arise randomly – which is probably a fair assumption given a large proportion of phenological data is sourced from amateur observers – means and trend estimates

derived by combining these data are going to be unbiased for the greater underlying population, regardless of the consequences for the associated variance. To this end, some consideration has been given to the problem of combining phenophase series from locations which vary from one another as described above. The basic idea of methods introduced by Häkkinen et al. (1995) and further developed by Schaber and Badeck (2002) involves comparing the series from each location and estimating the location-wise bias. This location-wise bias is considered systematic for each location. Put in simplest terms, by estimating and accounting for location-wise bias, the residual errors in trend estimate models were decreased, providing more power to detect the presence of trends. This type of model is known as a random effects model, where location-wise effects can be considered either fixed or random (definition expanded upon below). Although not directly discussed by either Häkkinen et al. (1995) or Schaber and Badeck (2002), these very same models can be used to account for correlations in longitudinal data.

### **13.3 Statistical Analysis of Snowdrop Flowering Data**

The analysis presented here aims to explore three models that differ in how they account for correlations between observations of a phenophase within a given location. A comparison between the models is presented, based on two common parameters of interest in analyses of trends in phenological data: the estimate of the trend and its standard error. To illustrate this, a case study of spring flowering of snowdrop is presented, where the aim is to identify trends in flowering over time and with a changing climate covariate across the latter half of the twentieth century over a region of England. After the case study is introduced, each model to be explored will be described in turn.

#### ***13.3.1 Case study***

Phenological studies will almost certainly be observational and therefore rely on correlation analysis for inference (Parmesan and Yohe 2003, Sparks and Tryjanowski 2005). Unfortunately, causal relationships are notoriously difficult, if not impossible to prove with observational studies. In recognition of this problem, the IPCC produced guidelines to strengthen inferences from correlation analyses on observational studies (outlined in Gitay et al. 2001 and implied in Rosenzweig et al. 2007). In particular – and with specific reference to the influence of air temperature on biological events (Root et al. 2003) – studies must positively identify three relationships, viz., that there is a significant correlation between a species trait and air temperature; the species trait has changed significantly over the study period; and that there has been significant change in air temperature over the study period. Owing to the number of studies finding significant increases in air temperatures across England over the twentieth century (e.g. Harvey and Mills 2003 and Karoly

and Stott 2006), the current study of snowdrop flowering will only focus on two of the criteria for detecting causal relationships, namely the relationship between a phenophase and air temperature (henceforth referred to as temperature), and the relationship between a phenophase and time.

Snowdrop or fair-maid-of-February (*Galanthus nivalis* L.) is a spring ephemeral and one of the earliest flowering bulbs across Europe. Snowdrop grows up to a height of 15–20 cm, with a single white, bell-shaped flower, which appears between January and March (Aschan and Pfanz 2006). Like other spring ephemerals of deciduous forests, snowdrop appears shortly after snow melt to take advantage of the increased light available in early spring before the upper canopy develops (Lapointe 2001). Therefore, it is likely that snowdrop phenology is highly influenced by snowmelt (Galen and Stanton 1995) and, as a corollary, will be sensitive to changes in growing season (Schwartz et al. 2006). Snowdrop is a popular plant in phenological datasets as it is widely associated with the coming of spring and is, therefore, a sentimental favourite (Sparks and Collinson 2003).

The case study data are comprised of four series of first annual snowdrop flowering. The locations, viz. Walsall in the West Midlands, Ponteland in Northumberland, Norwich in Norfolk and Sheffield in Yorkshire are reasonably spread out across England (see Table 13.1 for details). Each series was recorded by an amateur observer, in a consistent manner, over the period of each series and was completely independent of the others. Although all four snowdrop flowering series have different starting years, they all cover the last two decades of the twentieth century; a period widely noted for substantially increased temperatures across England (Sparks and Menzel 2002). Mean minimum and maximum monthly temperatures (near-surface) for each series, as estimated by the closest weather station to each of the four locations, were obtained from The Met Office website.<sup>1</sup> Mean monthly temperature was calculated as the average of the mean minimum and maximum temperatures. The flowering date is presented as yearday. A basic analysis of the Norfolk series appeared in Sparks and Manning (2000) and the West Midlands, Yorkshire and Norfolk series appeared in Sparks and Collinson (2003). Given the consistency of the Central England temperature series over the general region containing the four study locations (Harvey and Mills 2003), a reasonable level of regional homogeneity in climate is assumed.

Exploring which temperature variables – temperatures from different months, or combinations and interactions of these variables – is a complete modelling exercise in itself (e.g. Sparks and Carey 1995 and Keatley et al. 2002). In earlier studies of the phenology of spring flowering plants in England, monthly temperatures from the previous year were of less importance than those of winter and early spring (Fitter et al. 1995, Sparks and Carey 1995, Fitter and Fitter 2002). Therefore, for the purposes of this study, only mean January temperature has been selected as a climate covariate to explain variation in snowdrop flowering. Finally, it has been

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<sup>1</sup>The United Kingdom's Government weather service, The Met Office; <http://www.metoffice.gov.uk/>

**Table 13.1** Geographical information for each location studied along with details of the nearest weather station. A general distance between each location and the respective weather station is included for interest

Location of observations	Latitude	Longitude	Altitude	Period of obs.	Location of weather station	Latitude	Longitude	Altitude	Distance from obs location
West Midlands (Walsall)	52° 35' N	1° 58' W	120 m	1976–2000	West Midlands (Shawbury)	52° 46' 60" N	2° 38' 60" W	72 m	50 km
Northumberland (Ponteland)	55° 03' N	1° 44' W	60 m	1952–2000	Northumberland (Durham)	54° 46' 0" N	1° 34' 0" W	102 m	30 km
Norfolk (Norwich)	52° 37' N	1° 17' E	20 m	1965–1999	Norfolk (Cambridge)	52° 12' 18" N	0° 10' 30" E	26 m	90 km
Yorkshire (Sheffield)	53° 22' N	1° 27' W	65 m	1980–2000	Yorkshire (Sheffield)	53° 22' 0" N	1° 27' 0" W	65 m	0 km

suggested that by ignoring the date of the vernal equinox, bias can be introduced into analyses of the start of spring (Sagarin 2001). As such bias has been generally thought of as negligible (Menzel 2003), no consideration was given to the yearly timing of the vernal equinox in the analyses of snowdrop flowering presented here.

### 13.3.2 *Modelling Correlated Data*

Data that are classed as *correlated* contain groups or clusters of observations that are stochastically related in some way. Within each cluster, all observations are influenced similarly by inherent qualities of the cluster itself and will typically display positive correlation. That is, within-cluster observations will be more similar, on average, than observations from other clusters. A single sample unit might be considered a cluster by itself, but there may also be multiple sample units within a cluster. There are three common sources of clustering in data, namely, nesting of sampling units, splitting of sample units and repeated observations taken on sample units (Schabenberger and Pierce 2001). The third clustering type is the most relevant to analyses of trends within phenological data. A phenological series is comprised of observations made each year at a single location and, therefore, can be considered *longitudinal*. Other hypothetical examples of clustering in phenological data might include phenophases recorded by a single observer at multiple locations or multiple observers at a single location. At the very least, phenological data is clustered at the location level and this should be considered during analysis and subsequent inference.

In measuring changes in response variables within individual clusters over time, the central aim of longitudinal studies is to quantify the relationships between these changes and both time and any associated global or cluster-specific covariates. However, the potential presence of within-cluster correlation invalidates the assumption of independence of observations, as required for many common statistical analyses; this may then return produce misleading results in subsequent analyses. For example, if a model is specified to make a comparison between clusters and no consideration is given to the within-cluster correlation, the standard error associated with the cluster-wise parameter estimate may be too small. This may, in turn, lead to confidence errors that are too narrow or a  $p$ -value that is too small and, therefore, an inflation of the significance of a parameter estimate. Alternatively, if a model is specified to estimate change across a number of clusters, between-cluster variance may produce a standard error that is too large, decreasing the power of any statistical tests applied to the data. In this instance, pertinent information is wasted.

Fortunately, statistical methods are available that account for within-cluster correlation and provide valid models for subsequent interpretation. Such models provide an alternative to *naïve pooling*; or ignoring within-cluster correlation during analysis (Burton et al. 1998). In particular, if the response variable has a Gaussian distribution – or, alternatively, normality can be approached through transformation – analyses that account for within-cluster correlations are usually a

generalisation of simple linear regression. As an aside, this generalisation results from a more flexible way in which the covariance matrix of the random errors is specified (Fitzmaurice et al. 2004). For simplicity, the following discussion of models for clustered data is confined to responses that are continuous with a Gaussian distribution; a common feature of phenophase data. Discussion of clustering will also largely be confined to longitudinal data, but some consideration will also be given to cross-sectional analyses, where data are collapsed over time.

To correctly model clustered data, both the mean response and the within-cluster correlation structure must be modelled (Liang and Zeger 1993). Three modelling methods are presented here – a naïve pooled model, a data resolution model and a random effects model – all based upon simple linear regression. Notation which applies to each of the models is specified below:  $y_{ij}$  is snowdrop flowering phenophase in year days,  $i$  represents each of the four locations (i.e.  $N = 4$ ) and  $j$  each year a phenophase was recorded for each location ( $j = 1, 2, \dots, n_i$ ). Note that values of  $n$  can vary with location,  $i$ . Covariates to be tested are year as a raw value,  $t_{ij}$ , and mean January temperature ( $^{\circ}\text{C}$ ),  $m$ . As  $y$  and  $t$  both carry the subscripts  $i$  and  $j$ , both are able to vary by location and with time point.

### 13.3.3 Naïve Pooled Analysis

The simplest model presented in this chapter is a *naïve pooled model* where no consideration is given for the location grouping within the snowdrop flowering data. A simple linear regression provides least squares estimates of slope and intercept and all data is weighted equally. The naïve pooled model is specified as:

$$y_{ij} = \beta_0 + \beta_1 t_{ij} + e_{ij} \quad (13.2)$$

where  $\beta_0$  is the intercept,  $\beta_1$ , the slope or estimate of change in snowdrop flowering associated with a one year increment across the region represented by the four locations,  $e_{ij}$  is a Gaussian distributed error term, which is uncorrelated with  $t$ . If  $t$  is substituted with  $m$ , the slope is an estimate of change in snowdrop flowering associated with a  $1^{\circ}\text{C}$  increase in mean January temperature. The statistic for the testing the significance of a slope,  $\beta_1$ , is given by:

$$\text{test statistic} = \frac{\hat{\beta}_1}{\text{SE}(\hat{\beta}_1)} \quad (13.3)$$

with  $\left( \sum_{i=1}^N n_i \right) - 2$  degrees of freedom.

Tests of this type are known generally as *Wald* tests and are constructed in order to test significance of model parameter estimates (Wald 1943). The test statistic is compared against a standard Gaussian distribution with a null hypothesis that the population slope is zero. However, since the properties of the Gaussian distribution

tend to break down with smaller sample sizes, the  $t$ -distribution can be used instead to provide a more robust test.

### 13.3.4 Data Resolution Model – Averaging over Location-Wise Trend Regressions

The next simplest approach to the analysis of snowdrop flowering from multiple locations would be to resolve the repeated measures at each location by producing a summary statistic and then use that statistic as if it was the primary data (Feldman 1988, Burton et al. 1998). An appropriate summary statistic would be the slope estimate from simple linear regression of the date of snowdrop flowering over time, or with a climate covariate, estimated for each location, with its associated standard error. After a slight modification to (13.2), the within-location simple linear regression is given by:

$$y_{ij} = \beta_{0i} + \beta_{1i}t_{ij} + e_{ij} \quad (13.4)$$

where  $\beta_{1i}$  the slope for location  $i$ . This method is based on the assumption that there is an underlying population slope describing the change in the date of snowdrop flowering across the region of interest. Furthermore, the least-squares estimates of the slope parameters,  $\beta_{1i}$ , are unbiased for the snowdrop population across the region of interest, regardless of the within-location correlation structure (Diggle et al. 2002, Murtaugh 2007). Finally, it is assumed that each estimate of  $\beta_{1i}$  has a Gaussian distribution. As described by Murtaugh (2007), an appropriate summary statistic of  $\beta_{1i}$  is a weighted mean of the location-wise slope estimates – where such weights are proportional to the squared standard errors of the location-wise slope estimates – given by:

$$\hat{\beta}_1 = \frac{\sum_{i=1}^N w_i \hat{\beta}_{1i}}{\sum_{i=1}^N w_i} \quad (13.5)$$

using

$$w_i = \frac{1/[\text{SE}(\hat{\beta}_{1i})]^2}{\sum_{i=1}^N (1/[\text{SE}(\hat{\beta}_{1i})]^2)} \quad (13.6)$$

where

$$\sum_{i=1}^N w_i = 1. \quad (13.7)$$



Using the assumption that the slope estimates for each location are independent, (i.e. it is unlikely that the snowdrop flowering at one location will influence flowering at another), the standard error of the weighted average, (13.5), is calculated as,

$$SE(\hat{\beta}_1) = \sqrt{\frac{\sum_{i=1}^N w_i(\hat{\beta}_{1i} - \hat{\beta}_1)^2}{N-1}}. \quad (13.8)$$

With  $\hat{\beta}_{1i}$  and the associated standard error, the test statistic for the test of significant slope is as specified by (13.3), but with degrees of freedom,  $N-1$ .

### 13.3.5 Random Effects Model

The final and most complex model considered in this chapter explicitly accounts for location-wise correlation.

Consider the simple linear regression model represented in (13.1) or (13.2). With such linear regression models, the errors,  $e_k$  or  $e_{ij}$ , are assumed to be Gaussian and independently distributed across the population, with a mean of zero and a common variance of  $\sigma^2$ . However, as previously described, the model errors cannot be assumed independent with longitudinal data; but will instead be correlated to some degree. Furthermore, the model given by (13.2) specifies that the intercept and slope will be the same for all clusters, that is there is only one value each of  $\beta_0$  and  $\beta_1$ . As described in Häkkinen et al. (1995) and Schaber and Badeck (2002), it is beneficial to add individual location-specific effects into the model to account for different rates of change in the phenophase, in addition to the problem of non-independence between observations (Fitzmaurice et al. 2004). The model represented by (13.2) then becomes:

$$y_{ij} = \beta_0 + \beta_1 t_{ij} + v_{0i} + e_{ij} \quad (13.9)$$

where  $v_{0i}$  represents the influence associated with location  $i$ , or its influence on the repeated observations within  $i$ . Other components are as specified in previous models. The model containing location-wise effects can be re-written as a two-level model, where the first level reflects the within-cluster component,

$$y_{ij} = b_{0i} + b_{1i} t_{ij} + e_{ij} \quad (13.10)$$

and the second level reflects the between-cluster component,

$$b_{0i} = \beta_0 + v_{0i} \quad (13.11)$$

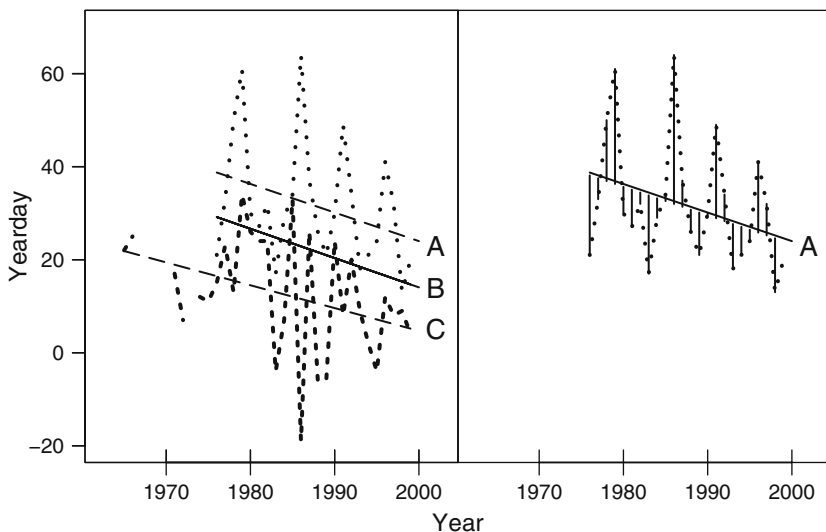
$$b_{1i} = \beta_1. \quad (13.12)$$

Model (13.9) specifies that the intercept for the  $i$ th location is a function of a population level intercept,  $\beta_0$ , which is altered by the addition of a unique contribution,  $\nu_{0i}$ , for that location. It is assumed that the slopes are equal across the population, estimated to be  $\beta_1$ ; that is the slope for each location is parallel to a population level slope. Readers may recognise this model format to be similar to that of an analysis of covariance (ANCOVA), where the intercepts and slopes of different treatments or factors may vary. Accordingly, it is possible to add a further parameter,  $\nu_{1i}$ , to account for the unique contribution of a given cluster to the slope estimate. However, during exploratory data analysis of the snowdrop flowering data, an ANCOVA model – where individual slopes and intercepts were assigned to each location – provided no evidence that the slopes for each location were anything but parallel (data not shown). Therefore, in the interests of brevity, the slope and intercept random effects model will not be pursued here.

The process that the cluster-wise effect,  $\nu_{0i}$ , represents is at the centre of modelling with correlated data. As it is typical that clusters are considered to be representative of an underlying population, and that the clusters have been randomly selected, the cluster-specific effects  $\nu_{0i}$  may be considered a *random effect*. Specifically, a random effect represents parameters that vary from cluster to cluster and, therefore, account for the natural heterogeneity that arises from unmeasured factors (Liang and Zeger 1993). Realisations of  $\nu_{0i}$  are considered to be representative of that underlying population, where it is commonly assumed that  $\nu_{0i} \sim N(0, \sigma_{\nu_0}^2)$ . With the addition of  $\nu_{0i}$  to (13.2), the distribution of the errors  $e_{ij}$  are then considered to have a Gaussian distribution and be *conditionally independent* across the population with a mean of zero and a common variance  $\sigma^2$ . The conditional independence can be assumed due to the presence of random cluster specific effects,  $\nu_{0i}$ ; with the influence due to individual clusters removed from errors (Hedeker 2004).

As the response  $y$  across  $t$  is shifted by a random amount,  $\nu_{0i}$ , for each cluster, but that  $y \sim t$  is still parallel for all sample units, this model is often referred to as a *random intercepts model*. The random intercepts model is demonstrated in the *left panel* of Fig. 13.1, where annual observations of phenophases for two locations – A and C – are plotted with a theoretical population-level response, B. The population slope specified by is  $\beta_1$ , and the population intercept by  $\beta_0$ . The vertical shift to take trend-line B to either A or C would represent  $\nu_{0A}$  and  $\nu_{0C}$ , respectively. Cluster-wise variation around the population level response is represented by  $\sigma_{\nu_0}^2$ ; that is if the value of  $\sigma_{\nu_0}^2$  is close to zero, there would be little variation among the clusters. Finally, the within-location variation is demonstrated in the *right panel* of Fig. 13.1. During standard model fitting for random effects model, the actual random effects are not estimated per se, but instead the parameters of their distributions (i.e.  $\sigma_{\nu_0}^2$  and  $\sigma^2$ ) are estimated.

In contrast to random effects, *fixed effects* are those explanatory variables associated with an entire population or repeatable experimental treatment. Although referred to here as a random effect model, a model with both fixed and random effects are also known as mixed effects models, multilevel models and random coefficient models (list not exhaustive) (Hedeker 2004). Deciding whether a given



**Fig. 13.1** Sources of variability in longitudinal data, demonstrated using snowdrop flowering data from two locations. *Left:* Between-location (A and C) heterogeneity (---), compared to a population trend (B) (—). *Right:* Within-location (A) variation around a location-wise trend (—)

cluster variable is fixed or random will depend on how the levels of the variable that appears in the study were selected. For example, if a phenological study contained data from multiple randomly selected locations, and the aim of a study is to apply the results to a wider region, then location would be considered a random effect. If instead the aim is to model phenophases at deliberately selected locations, then location would be treated as fixed effect. The consequence of treating location as a fixed effect, however, is that model results cannot be extrapolated to a wider regional level. Either way, if year is added to the phenophase trend model as a covariate, then it would probably be considered a fixed effect. In summary, a random effects model allows the flexibility to estimate both the population level mean response and the cluster response, depending on research aims.

With the inclusion of a random effect in a model to account for within-cluster correlation, there is an assumption that all observations within a cluster are equally correlated. For example, the inclusion of a cluster-wise random effect leads to the decomposition of variance of as response as:

$$\text{Var}(y_{ij}) = \sigma_{v0}^2 + \sigma^2 = \sigma_{\text{null}}^2 \tag{13.13}$$

where  $\sigma_{\text{null}}^2$  is the total variance of the pooled response values; that is a null model. The within-cluster correlation,  $\rho$ , can be estimated by:

$$\rho = \frac{\sigma_{v0}^2}{\sigma_{v0}^2 + \sigma^2} \tag{13.14}$$

That is if  $\sigma_{v0}^2 = 0$ , within-cluster correlation reduces to 0. The value  $\rho$  is also an estimate of the proportion of unexplained variance in the response variable that is at the cluster level (Moerbeek et al. 2003). However, the assumption of constant correlation within a cluster is usually unrealistic, particularly if clustering occurs through repeated observations. Very often with time series or longitudinal data, observations that are close in time will be more similar than those further apart. This is known as *serial correlation*; a specific example of which would be autoregressive correlation. Another type of correlation structure is known as *unstructured*, where the correlation between each pair of observations is estimated individually – which is computationally intensive and requires a completely balanced design. The correlation structure used to model a random effect (as a random intercept) is known as *exchangeable* or *compound symmetry*, where, as described before, each observation is assumed to be correlated equally (Horton and Lipsitz 1999). It is, however, common that the signal of serial correlation is swamped by random effects (Diggle et al. 2002). During exploratory data analysis of the snowdrop flowering data, a number of serial correlation models were tested, but none were found to explain location-wise correlation structure better than the pure random effect (as a random intercept; data not shown). Therefore, only the exchangeable correlation structure is considered here.

Specifying the test statistic for the test of a significant slope for a fixed effect is not as straight forward as that described for the naïve pooled and data resolution models; particularly for small sample sizes (i.e.  $N < 10$  (Feldman 1988)) and unbalanced data (Manor and Zucker 2004). It is standard that estimates of precision and subsequent analysis upon fixed effects are based on their asymptotic distribution – a property known to break down with small sample sizes (Kenward and Roger 1997). However, a number of methods are available to correct for small sample biases in inferences for fixed effects with random effects models. Readers are directed to Kenward and Roger (1997), Fouladi and Shieh (2004) and Manor and Zucker (2004) for more details on this problem. Generally speaking, popular statistical packages allow for approximations for dealing with small sample sizes and unbalanced data in estimating the significance of fixed effects within random effects models.

There are two main methods for modelling correlated error structure – which must be calculated before the fixed effects parameters can be estimated – namely, maximum likelihood (ML) and restricted maximum likelihood (REML). Both methods are readily available in popular statistical analysis packages; and choosing between the two can be a source of consternation to those new to modelling with random effects (Murtaugh 2007). In general, both methods are based on likelihoods and so benefit from the principles of consistency, efficiency and asymptotic normality. Furthermore, the two methods are asymptotically equivalent. In basic terms REML is better at estimating and then finding the most appropriate correlation structure (Fitzmaurice et al. 2004). In contrast, ML is more appropriate for comparing nested fixed effects. In most cases the estimates of the fixed effects parameters will be similar, although probably not exactly the same (Pinheiro and Bates 2000). It is often worthwhile fitting a random effects model with both ML and REML methods to check if the parameter estimates of the fixed effects vary greatly. If there is substantial variation in the parameter estimates, then Diggle et al.

(2002) recommend using the REML method. The REML method was selected for the analyses presented in this chapter.

Although the design and structure of longitudinal data may suggest that there could be significant amounts of within-cluster correlation, it may be that the addition of random effects are not necessary. A common method for testing the significance of random effects is to compare the fit of models both with and without random effects, with fixed effects remaining unchanged. However, non-nested models or models estimated using REML cannot be compared using likelihood ratio-tests. Instead Akaike's information criterion (AIC) can be used to indicate the best model (Akaike 1974):

$$\text{AIC} = -2 \times (\ln L_{\max}) + 2 \times p \quad (13.15)$$

where  $p$  is the number of unknown parameters estimated in the model; and  $\ln L_{\max}$  the log-likelihood maximum function evaluated at the REML estimates. The AIC provides a measure of fit for a particular model, which is penalised by the number of parameters estimated. When all models are fitted to the same data, the model with the lowest AIC value provides the most parsimonious representation of the data.

### 13.3.6 Collapsing Across Time

A variable representing de-trended snowdrop flowering responses – where the year trend was removed – was created and used to model the effect of changing the mean January temperature on snowdrop flowering. As the trend with time was removed from this snowdrop flowering data, it is valid to assume there is no natural ordering for these observations. It may be appropriate, therefore, to collapse over the time dimension and to model de-trended flowering responses as a function of temperature only; an analysis known as *cross-sectional*. Such a model would allow interpretation of the physiology or autecology of the species in addition to aiding prediction of changes in phenology with changes in climate.

The effect mean January temperature on de-trended snowdrop flowering data was also modelled using the three models described, but with no consideration given to time. With addition of a location-wise random effect, the de-trended snowdrop flowering data is assumed to be conditionally independent; and the mean January temperature is treated as a fixed effect.

### 13.3.7 Software

The fixed effects models (naïve pooled and data resolution models) were fitted in R v2.7.1 (R Development Team 2008). The random effects models were also fitted in R, but using the *nlme* library v3.1-89 (Pinheiro et al. 2008); specifically the “lme” function. The “lme” function produces sensible restricted likelihood estimates from unbalanced data (Pinheiro and Bates 2000), which is of benefit in this study. It is also

possible to analyse random effects models in R using a library called *lme4* (Bates et al. 2008); both libraries are available from the Comprehensive R Archive Network (CRAN).<sup>2</sup> The *nlme* library provides an approximation for testing the significance of fixed effects with small sample sizes and unbalanced data (Pinheiro and Bates 2000).

### 13.3.8 Model Diagnostics

If the variance of the date of snowdrop flowering around a mean response profile appeared to increase over time, it may be worthwhile to apply a log transform to the date variable before formally fitting any models. No transformation was applied to the snowdrop data, however, as variance does not seem to increase with time.

As with most statistical modelling techniques, it is important to test the underlying assumptions using model diagnostics. To check the distributional assumption of the errors, plots of residuals versus predicted values were produced. If the model is correctly specified, residuals should have mean zero and a distribution that is Gaussian. However, checking the distribution of the between-cluster variance is arguably difficult with such a small sample size (i.e.  $N = 4$ ). The effects of influential points were also checked. However, although the values before 1960 (i.e. those from Northumberland) are deemed to be influential points, with high leverage, they were not deemed to have a significant role in influencing parameter estimates, as judged by leave-one-out statistics.

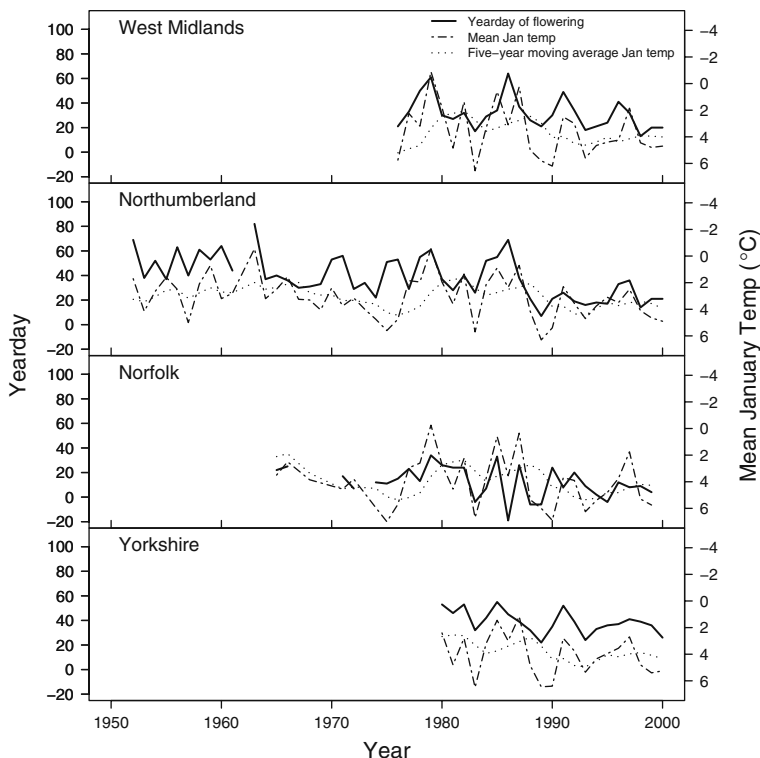
## 13.4 Results

### 13.4.1 General Observations

The yearday of snowdrop flowering for year and for each location is given in Fig. 13.2. Summary statistics of the timing of snowdrop flowering by location is given in Table 13.2. The de-trended standard deviation was calculated after first removing the location-wise trend line from the raw dates of snowdrop flowering. On average, snowdrop flowers earliest in Norfolk and latest in both Northumberland and Yorkshire. Inter-annual variation in the date of snowdrop flowering was greatest in Northumberland and least in Yorkshire. Upon inspection of Fig. 13.2, the location-wise interannual variation appears to be almost as large as the between-location differences.

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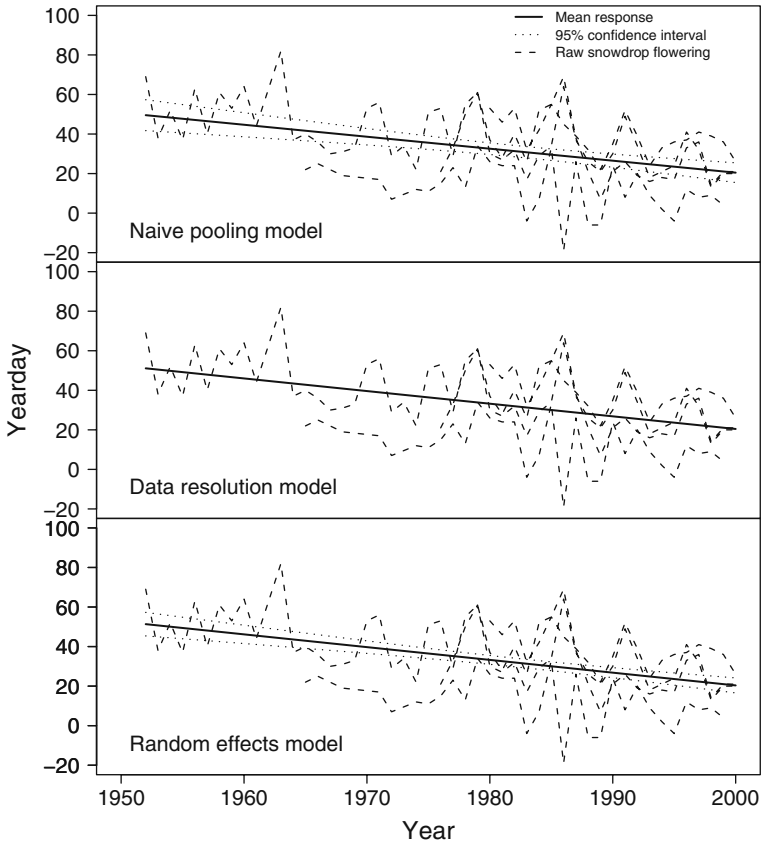
<sup>2</sup>[www.cran.r-project.org/](http://www.cran.r-project.org/)



**Fig. 13.2** Inter-annual variation in date of first flowering of snowdrop across four locations. Note the temperature scale on the right vertical axis has been inverted for clarity. Gaps in the data series for Northumberland and Norfolk represent observations that were lost or never recorded. The minus values refer to snowdrop flowering that occurred in the previous December. A five-year moving average January temperature has been added for comparison

**Table 13.2** Summary statistics of the timing of snowdrop flowering by location

Location of observations	Mean flowering date	Standard deviation (raw)	Standard deviation (de-trended)	Earliest	Latest
West Midlands	Feb 1	13.2	12.4	Jan 14 (1998)	Mar 5 (1986)
Northumberland	Feb 9	17.1	13.9	Jan 8 (1989)	Mar 23 (1963)
Norfolk	Jan 14	12.5	11.5	Dec 13 (1986)	Feb 4 (1979)
Yorkshire	Feb 9	9.4	8.2	Jan 23 (1989)	Feb 25 (1985)



**Fig. 13.3** Results of naïve pooled, data resolution and random effects models of the date of snowdrop flowering over time, with a 95% confidence interval for  $E(y_{ij})$  (mean response) at a given value of  $t_{ij}$  (time in years), as superimposed upon the raw data

### 13.4.2 Trend Results

Each of the three models yielded highly significant year effects for snowdrop flowering, despite large inter-annual variation, Fig. 13.3. Using the parameter estimates from the random effects model, the interpretation is that snowdrop flowering has advanced by 6.5 days per decade ( $SE = 0.10$ ) from 1952 to 2000 across the region represented by the four locations, Table 13.3. Likewise, each of the three models also produced highly significant mean January temperature effects for de-trended snowdrop flowering, Fig. 13.4. Again, using the random effects model for interpretation, the date of snowdrop flowering advanced around 3.9 days ( $SE = 0.52$ ) for each  $1^\circ\text{C}$  increase in mean January temperature across the region represented by the four locations, Table 13.4.



**Table 13.3** Parameter estimates, associated standard errors and test results for each model for the analysis of date of snowdrop flowering over time. Results for null model included for comparison

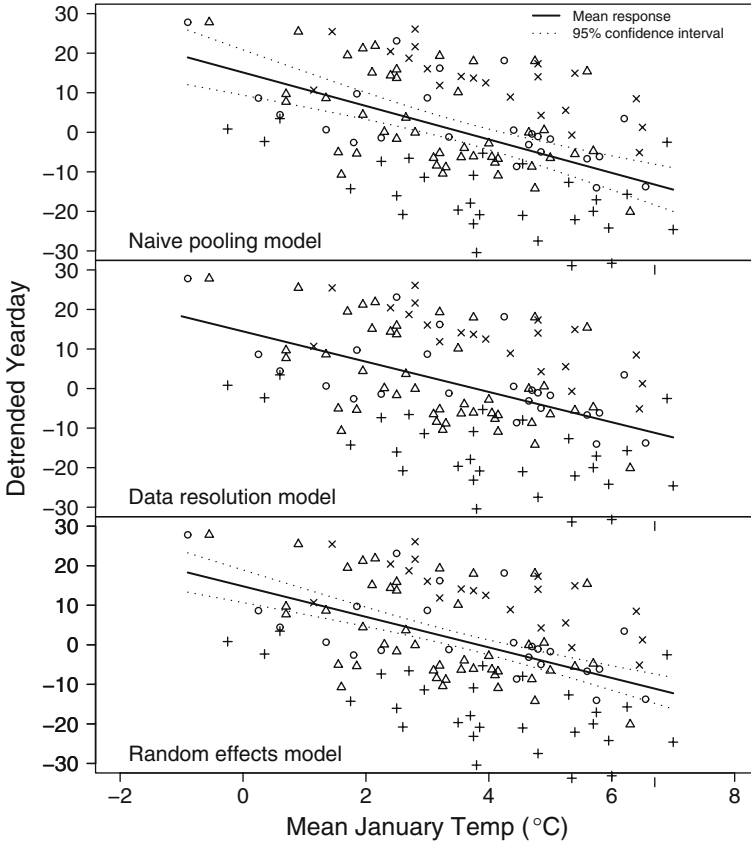
Model	Parameter	Estimate	Standard error	t	p <	AIC
Null	$\bar{x}$	30.91	1.59	19.49	0.0001	1076.5
	$\sigma^2$	314.33	—	—	—	—
Naïve pooling	$\beta_0$	1231.99	236.91	5.20	0.0001	1054.7
	$\beta_1$	-0.61	0.12	-5.07	0.0001	—
	$\sigma^2$	262.11	—	—	—	—
Data resolution	$\beta_0$	1298.44	111.97	11.59	0.0002	—
	$\beta_1$	-0.65	0.05	-11.83	0.0002	—
Random effects	$\beta_0$	1311.35	201.96	6.49	0.0001	999.4
	$\beta_1$	-0.65	0.10	-6.35	0.0001	—
	$\sigma_{v0}^2$	161.01	#	—	—	—
	$\sigma^2$	151.52	#	—	—	—

#Standard errors for the estimated covariance parameters are not reported in model output provided by *nlme* (Pinheiro et al. 2008) in R

### 13.4.3 Comparison of the Three Methods

For both analyses of snowdrop flowering over time and with mean January temperatures, the data resolution and random effects models gave similar slope estimates, Tables 13.3 and 13.4. For snowdrop flowering over time, the slope estimated by the naïve pooled model was less negative than those of the other models. In weighting each data point equally and not considering their origin, the vertical spread of the snowdrop flowering dates, particularly in the influential end year values (i.e. around 2000) forced the slope estimate from naïve pooled model to be shallower. This dampening effect is negated in the data resolution and random effects models where slope estimates for each location are calculated before being weighted and summarised together for population-level inferences. The slope dampening effect is reversed for the de-trended snowdrop flowering against mean January temperatures model, where the naïve pooled regression slope is more negative than those from the other models. Here warmer mean January temperatures and earlier flowering in Norfolk is combined and weighted equally with the colder temperatures and later flowering in Yorkshire to produce a steeper slope estimate, Figs. 13.2 and 13.4.

For the analysis of snowdrop flowering over time, the standard error of the slope estimate for the data resolution model was around 50% that returned for the random effects model, Table 13.3. With balanced data, these two values would be expected to be similar (Feldman 1988, Moerbeek et al. 2003). In this example, the discrepancy can be explained by the lower weights assigned to a location-wise slope estimate which was further away from the mean (i.e. that for Yorkshire), Table 13.5. If the numbers of years at each location were more equal, it is likely that the standard errors of the location-wise slope estimates would also be more similar; this would lead to more equal weighting in (13.8), and a larger standard error of the population level slope estimate, putting it closer in size to that returned by the random effects model.



**Fig. 13.4** Results of naïve pooled, data resolution and random effects models of de-trended date of snowdrop flowering by mean January temperature (°C), with a 95% confidence interval for  $E(y_{ij})$  (mean response) at a given value of  $m_{ij}$  (mean January temperature), as superimposed upon the raw data. Symbols correspond to each location: West Midlands, ○; Northumberland, △; Norfolk, +, and Yorkshire, ×

It is likewise usually expected that the standard error of the slope estimate will be smaller for naïve pooled models than in either the data resolution or random effects models, due to positive correlations between observations within a single cluster (e.g. Feldman 1988, Moerbeek et al. 2003 and Murtaugh 2007). However, in this example, the standard error of the slope estimate – for both snowdrop flowering against time and with mean January temperature – for the naïve pooled model is larger than those from the other models, Tables 13.3 and 13.4. This can be attributed to the relative size of the within-location variation resulting from high interannual variation as compared to between-location differences.

With so much interannual variation, it is almost surprising that the addition of the location-wise random effects was deemed to improve the model. However, a great deal of the error variance ( $\sigma^2$ ) in the naïve pooled model is explained by

**Table 13.4** Parameter estimates, associated standard errors and test results for each model for the analysis of de-trended date of snowdrop flowering with mean January temperatures. Results for null model included for comparison

Model	Parameter	Estimate	Standard error	t	p <	AIC
Null	$\bar{x}$	0.00	1.44	0.00	1	1052.8
	$\sigma^2$	259.85	–	–	–	–
Naïve pooling	$\beta_0$	15.11	2.89	5.23	0.0001	1024.0
	$\beta_1$	–4.23	0.72	–5.80	0.0001	–
	$\sigma^2$	205.35	–	–	–	–
Data resolution	$\beta_0$	14.45	6.96	2.07	0.0700	–
	$\beta_1$	–3.83	0.39	–9.72	0.0004	–
Random effects model	$\beta_0$	14.80	6.52	2.27	0.0300	953.0
	$\beta_1$	–3.86	0.52	–7.17	0.0001	–
	$\sigma_{\psi_0}^2$	150.80	#	–	–	–
	$\sigma^2$	106.30	#	–	–	–

#Standard errors for the estimated covariance parameters are not reported in model output provided by *nlme* (Pinheiro et al. 2008) in R

**Table 13.5** Location-wise estimates of slope, associated standard error and calculated weights for the data resolution model. Estimates of the intercept parameters included for completion

Snowdrop flowering date ~ year		Detrended snowdrop flowering ~ mean January temperature				
Location	$\hat{\beta}_0$ (SE)	$\hat{\beta}_1$ (SE)	$w_i$	$\hat{\beta}_0$ (SE)	$\hat{\beta}_1$ (SE)	$w_i$
West Midlands	1253.22 (696.18)	–0.61 (0.35)	0.09	16.18 (4.39)	–3.51 (1.08)	0.20
Northumberland	1409.33 (284.04)	–0.69 (0.14)	0.55	19.41 (3.77)	–5.00 (1.10)	0.20
Norfolk	985.61 (432.67)	–0.49 (0.22)	0.24	–5.56 (4.37)	–2.99 (0.98)	0.25
Yorkshire	1545.62 (599.64)	–0.76 (0.30)	0.12	–3.81 (3.56)	–3.81 (0.82)	0.35

adding the random location effect for analysis of both flowering over time and with mean January temperature, Tables 13.3 and 13.4. Using (13.14) and values from Tables 13.3 and 13.4, the within-location correlation for the raw date of snowdrop flowering over time is 0.52; the correlation for de-trended snowdrop flowering by mean January temperature is 0.59. These values are reasonably high and certainly far from the value of zero required for simple linear regression to be appropriate. The relative worth of the adding random effects to the model is tested by directly comparing the random effects model with the naïve pooled model. Given the AIC value for random effects model of 999.4 is lower than that of the linear regression model with no random effects (or naïve pooled model), 1054.7, Table 13.3, it can be concluded that it is important to account for location-wise correlation in fitting models to detect a trend in snowdrop flowering over time. This is mirrored in the models to detect a relationship between mean January temperatures and a de-trended date of snowdrop flowering, where the AIC for the naïve pooled and random effects models were 1024.0 and 953.0, respectively, Table 13.4.

## 13.5 Discussion

### *13.5.1 Application of Analysis of Correlated Data Methods to Phenological Data*

In this chapter, two alternative methods to the naïve pooled model have been presented; both accounting for correlation, but varying in sophistication. Both alternative models are widely described and used within ecological literature, but have been approached to a substantially lesser degree in phenological research. Notable exceptions would be studies by Inouye et al. (2003) and Tøttrup et al. (2006), where the repeated or longitudinal nature of phenological data was accounted for. Furthermore, Sparks and Carey (1995) did incorporate a term to account for serial correlation in a multivariate analysis of changing phenophases, but the method was not fully described. In analysing here a dataset of snowdrop flowering from a number of different locations around England, the salient features of accounting for correlated error structure in phenological data have been demonstrated.

The naïve pooled model ignores location-wise clustering and fits a simple linear regression to equally weighted points. In the naïve pooled model, between-cluster variance is lumped together with the within-cluster, which falsely reduces the estimate of error variance. With a deflated error variance, the likelihood of finding a parameter estimate significant, when it is not, is increased – that is, a false positive or type I error. The reverse was the case in the snowdrop flowering case study, however, where the unbalanced data structure and high interannual variation of the snowdrop flowering produced a larger than expected standard error of the slope estimate for the naïve pooled model. With a higher than expected standard error of the slope estimate, the chance of a false negative or type II error is increased. Either way, in not accounting for any underlying correlations in clustered data, there will be an increase in the likelihood of a spurious result. The results of the naïve pooled models also demonstrate that it is possible that the contribution of location-wise trends to an analysis may be diminished (e.g. population slope estimate was underestimated in the flowering over time model) or may be exaggerated (e.g. population slope was overestimated in the de-trended flowering with temperature model).

The data resolution model uses summary statistics for each location – in this instance, slope and standard error of the slope – which are then treated as raw data in the next step of data analysis. The relatively simple data resolution method is well suited to analyses of trends in phenophases, where inferences are largely based on simple linear regressions which yield summary statistics like slope and its standard error estimate. This method prevents also over-inflation of the apparent sample size (Burton et al. 1998) and returns an unbiased estimate of the population slope. Furthermore, the data resolution model treats the within- and between-location variation separately. In the first step, variances are estimated from the raw flowering data. In the second step, these raw variances are used in estimating a weighting scheme with which location-wise slopes are combined to produce a population-wise slope estimate. While this mean slope estimate is unbiased, the associated standard error estimate may be incorrect if the weighting system is inaccurate. In

the example of snowdrop flowering over time, the unbalanced nature of the data produced high estimates of standard error for some of the locations (i.e. Yorkshire). Subsequently, this decreased the weighting that the Yorkshire location-wise slope estimate received which, in turn, produced a very small standard error of the population slope estimate. This highlights an issue with the data resolution model when using small sample sizes which are coupled with greatly unbalanced data.

The random effects model treated location as a random effect and both year and mean January temperature as fixed effects. There was no interest in estimating the differences in snowdrop flowering between the locations, but the location-wise structure was accounted for regardless. As a result, an unbiased population-wise slope was estimated for trends in snowdrop flowering; the estimation of which accounted for both random location factors that were not directly measured in addition to correlations between observations. Despite large amounts of within-location variation, the addition of the random effects improved the model, according to the AIC. The significance test of the slope parameter is based on an approximation and it is unknown whether it was robust against such a small sample size. This point is recommended for future research. Furthermore, although the addition of early observations from Northumberland were potentially influential to the random effects model, examination of leave-one-out diagnostics revealed they were not so. However, given the potential for even more unbalance in data in phenological studies, this point too warrants future research in order to prove the utility of random effects modelling.

Finally, the sign of a good statistical analysis is the ability to account for sources of correlation and variation in the underlying statistical process (Verbeke and Molenberghs 2000). Although the nature of phenological data may prove challenging to any random effects model, any attempt to account for correlated error structure will yield an improvement to the analysis.

In this study of trends in snowdrop flowering, only mean January temperature was considered as a potentially influential climate covariate. It is, however, reasonable to assume the temperatures across other months of the year or combinations or sums of such temperatures may also influence a phenophase. In the event that the explanatory or predictive value of a number of such climate covariates is to be tested, methods such as forward, backward or stepwise regression may be used (e.g. Sparks and Carey 1995 and Keatley et al. 2002). Model selection of this nature is also possible with random effects models, where selection for fixed effect variables is largely similar to that used in linear models. Naturally, any process of selection of the most informative climate covariates would need to simultaneously account for correlated error structures.

The issue of balanced data sets is very pertinent in phenological studies involving observations from multiple locations. It is unlikely that phenological series collected by different observers will start and end on the same years. Furthermore, due to personal circumstances, yearly observations may be missed altogether within the time series, as occurred with the Northumberland and Norfolk series in the snowdrop flowering case study. In fact, missing data are probably the rule, not the exception in phenological data. Many statistical analyses for longitudinal data are based on the

assumption that data is balanced (Fitzmaurice et al. 2004), where sample units are all measured at a set of common time points. Given likely improvements in analysis of balanced phenological data, there may be the temptation to truncate longer time series to cover the same period. There are studies that have excluded phenophase time series on account of being too short (e.g. Roetzer et al. 2000), but this reflects a need to include time series over a certain length to increase analysis power as opposed to the need to have more balanced data. Fortunately, methods around random effects modelling are usually robust enough to deal with missing data, albeit only if missing on a random basis (Liang and Zeger 1986). For a more in depth discussion of different models of missing data, see Diggle et al. (2002). A simultaneous analysis of phenophases from different locations – regardless of the modelling method selected – will be valid if the bulk of the years comprising the data have observations from each location. In the event that the lengths of phenophase time series vary greatly, as they did in the snowdrop flowering case study, model results must be checked for impact of leverage from the longer time series. Phenological data is hard won and deleting for the sake of balance should never be seriously considered.

It is hoped that the reader now has an appreciation of how misleading statistical analyses can potentially be if pertinent correlated error structures are ignored. It may, however, seem that for studies of phenological trends at the regional level, treating phenological data as longitudinal and properly accounting for within-cluster correlation is a negative, requiring much more knowledge about statistical methods. To begin with, solutions for dealing with within-cluster correlations in longitudinal studies do not necessarily need to be complex. Being mindful of potential issues arising from small sample sizes and unbalanced data – factors which are going to be almost universal in phenological research – the data resolution method can provide a quick and easy method to account for correlation structures. For those wishing to employ more sophisticated analyses that are a little more robust against small sample and unbalanced data issues, the random effects model is available. However, anybody considering using a random effects model in phenological research should not do so uncritically (Feldman 1988). Assumptions concerning the distribution of data and errors have been outlined above and these should be thoroughly tested. Finally, correlated error structures are an essential feature of phenological data. With relatively little effort combined with readily available software, in addition to resources like this chapter, it is hoped that the use of random effects modelling in phenological research will expand.

### ***13.5.2 Changes in Snowdrop Flowering Phenology***

The results of modelling the phenophase of snowdrop flowering over time and as a function of temperature presented here suggest there has been a shift across England over the second half of the twentieth century. From the early 1950s to 2000, this study detected an advance in snowdrop flowering of 30.7 days – or approximately

6.5 days earlier per decade. This estimate is somewhat larger than those reported for Germany where snowdrop flowering advanced by 2.5 days per decade between 1951 and 2000 in one study (Menzel 2003) and between 2.9 and 3.7 per decade between 1951 and 1995 in another (Roetzer et al. 2000). The slower rate of advance of snowdrop flowering in Germany as compared to England may be attributed to less warming and less fluctuating continental temperatures (Menzel et al. 2006). This study also detected a significant relationship between the timing of snowdrop flowering and mean January temperatures; with a shift of approximately 3.9 days earlier with every 1°C increase. This concurs with an estimate of the advance in snowdrop flowering across the United Kingdom of 3.4 days with each 1°C increase in Central England temperature by Sparks et al. (2000).

On balance, this shift in snowdrop flowering phenology is likely to be a result of climate change, particularly through increases in air temperatures (Root et al. 2003). There is evidence to suggest that temperatures across England have been increasing over the past decades. According to analyses on the Central England temperature (CET), there has been a 1°C increase in annual-mean temperature since 1960 (Karoly and Stott 2006). Of particular relevance to spring ephemerals is the increase of 1.5°C in spring Central England temperatures from the 1970s (Harvey and Mills 2003). When combined with these published findings of increases in temperatures across England, the results presented here provide compelling evidence of a causal link between changing snowdrop flowering in England and extant climate change. This evidence is strengthened by the relative long length of the phenological series analysed, particularly from Northumberland, with 48 years of snowdrop flowering observations; and by the large area of England represented by the series (approximately 25,000 km<sup>2</sup>). However, since this study only covers a period of 48 years at most, it is not appropriate to suggest the results reflect long-term patterns in phenology of snowdrop flowering. Regardless, this study does present evidence of a strong fingerprint for change in the phenology of early flowering bulbs in England between 1952 and 2000.

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# Chapter 14

## Modelling the Flowering of Four Eucalypt Species Using New Mixture Transition Distribution Models

Irene L. Hudson, Susan W. Kim, and Marie R. Keatley

**Abstract** The multivariate relationship between the probability of flowering, in relation to two discrete states of rainfall and of temperature (high/low), is investigated via a mixture transition distribution (MTD) analysis, which allows for a different transition matrix for each lag (up to 12 months backwards in time) to present flowering via a so-called MTDg analysis. The conventional mixture transition distribution (MTD) model considers the effect of each lag to the present independently, and uses equal transition matrices among different lags. Flowering data consisted of monthly flowering records of *E. leucoxyton*, *E. microcarpa*, *E. polyanthemos* and *E. tricarpa* (1940 and 1970). We extend the MTDg model to allow for interactions (between rain and temperature) to account for changes in the transition matrices amongst the differing lags. The MTDg model with interactions shows that the flowering of *E. leucoxyton* and *E. tricarpa* behave similarly with temperature (both flower at low temperature) and have a positive relationship with flowering intensity 11 months ago. *Eucalyptus microcarpa* behaves differently, in that it flowers at high temperature. MTDg analysis also found a highly significant interaction between mean temperature and rainfall for *E. polyanthemos*, in that *E. polyanthemos* does not tend to flower during the winter time (when it is cold and wet). Rainfall has a direct positive impact only on *E. tricarpa*. These four species are influenced by temperature (and to a lesser extent rainfall) and as a consequence their flowering phenology will possibly change in response to climate change.

**Keywords** Climate · Interactions · Discrete transition states · Flowering · Mixed transition distribution (MTD and MTDg)

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## 14.1 Introduction

Eucalypts as a genus dominate much of the Australian landscape. Studies examining the phenology of this genus have had two main periods from the late 1950s to the 1960s (Ashton 1956, Fielding 1956, Harris 1956, Gill 1966) and then the 1990s (Harrison et al. 1990, Bassett and White 1993, Bassett 1995, Keatley 1999). Keatley et al. (2002) represents one of the first attempts to utilise Australian phenological data, using more than 30 years of monthly flowering readings to detect responses to climate change. Phenological indicators (e.g. date of first and last flowering, first arrival of migrating birds) are used as proxies of global climate change (Root et al. 2003, Hudson et al. 2005, Rosenzweig et al. 2008). Long-term (1940–1971) synchrony of four *Eucalyptus* species was recently quantified mathematically at the population-level (Keatley et al. 2004, Kim et al. 2008). Keatley et al. (2002) reported that changes in temperature are likely to translate to changes in flowering commencement time. The magnitude of these shifts (Keatley et al. 2002) is greater than the average reported in meta analysis studies (Root et al. 2003, Parmesan and Yohe 2003, Parmesan 2007, Parry et al. 2007) but in agreement with the results for some individual species in other studies (Abu-Asab et al. 2001, Fitter and Fitter 2002, Peñuelas et al. 2002).

Earlier Hudson et al. (2003) identified upper temperature thresholds for *E. leucoxylon* flowering and showed that *E. leucoxylon* flowering is influenced by temperature whose effect is non-linear. GAMLSS modelling (Chapter 10 and Hudson et al. 2009) of the four species (*E. leucoxylon*, *E. microcarpa*, *E. polyanthemos*, and *E. tricarpa*) showed non-linear impacts of temperature on flowering, where, the main temperature drivers: for *E. leucoxylon* is minimum temperature, maximum temperature for *E. polyanthemos*, both minimum and maximum temperatures for *E. tricarpa*, and mean temperature for *E. microcarpa* ( $P < 0.0001$ ). Reproductive success may also be influenced by shifts in flowering onset (Hudson et al. 2003). Indeed Keatley and Hudson (1998) showed there is an optimal time for species to flower, depending on bud and fruit volume. Recently Keatley and Hudson (2007) found monthly flowering probabilities, and mathematically derived peak month, flowering commencement month and cessation month for the same aforementioned species.

The aim of this chapter is to demonstrate, using two case studies (see Kim et al. 2008, 2009), how to model the multivariate relationship between the probability of flowering (on/off) in relation to two discrete states of rainfall and of temperature (high/low) via a generalized mixture transition distribution (MTD) analysis, which allows for a different transition matrix for each lag (up to 12 months backwards in time) to present flowering, the so-called MTDg analysis (Raftery 1985, Berchtold 2006) extended to incorporate complex interactions between the covariates (here climatic predictors). The idea of the mixture transition distribution (MTD) model is to consider independently the effect of each lag to the present, instead of considering the effect of the combination of lags as in the case of the more traditional pure Markov chain process (Brémaud 1999). The assumption underpinning the MTD

model, namely the equality of the transition matrices among different lags, is a strong assumption in that we can expect differing transition matrices across differing lags in practice.

For this current chapter, an extended model for a MTDg (Berchtold 2006) analysis, which accommodates interactions was developed. This work extends both MARCH and the work of Kim et al. (2005, 2008) to allow for differing transition matrices amongst the lags for MTD modelling the flowering of the same four eucalypt species and climate time series studied here, respectively.

## 14.2 History and Approach

Earlier studies by Kim et al. (2005, 2008) extended the MARCH software (Berchtold 2006) for MTD modelling of the flowering records of the same four eucalypt species and climate time series studied here. For this current study, an extended model for a MTDg (Berchtold 2006) analysis, which accommodates interactions is developed (see Kim et al. 2009). As in Kim et al. (2008), we develop here, an extended model which accommodates interactions using the AD Model Builder™ (Fournier 2000). As already mentioned this extends both MARCH and the work of Kim et al. (2005, 2008). Our model is different to MARCH's MTD models, in terms of incorporating interactions between the covariates and also in its minimization process, namely AD Model Builder™ (Fournier 2000), which uses auto-differentiation as a minimization tool. This was shown to be computationally less intensive than MARCH (Kim et al. 2008, 2009).

Here we develop the MTDg model with interactions model to account for changes in the transition matrices of flowering amongst the differing lags (up to 12 months prior). Four climatic predictors are incorporated into the MTDg modelling of eucalypt flowering. As in Kim et al. (2005, 2008) we accommodate interactions for the MTDg model. The MTD model with interactions was first defined by Kim et al. (2008) and the MTDg model was given by Berchtold (2004).

### 14.2.1 *The Models*

In the next sections we follow the development of Berchtold and Raftery (2002), defining first the well known Markov chain formulation, then describing the mixture transition distribution (MTD) model, as first introduced by Raftery (1985) for the modeling of time-homogeneous high-order Markov chains; then we develop the MTDg model. Lastly both the MTD and MTDg models are extended to incorporate covariates.

### 14.2.1.1 Markov Chains

The Markov chain is a probabilistic model used to represent dependences between successive observations of a random variable. The Markov chain model was introduced by Andrej Andreevic Markov at the beginning of the twentieth century and is used in many disciplines, including mathematical biology, internet applications, economics, meteorology, geography, biology, chemistry, physics, behaviour, social sciences and music. For a comprehensive treatment of Markov chains and early applications, see Brémaud (1999). Seneta (1996) provides an account of Markov’s motivations and the theory’s early development.

Here we consider a discrete-time random variable  $X_t$  taking values in the finite set  $\{1, \dots, m\}$ . The aim of Markov chains is to predict the value of  $X_t$  as a function of the values taken by previous observations of this same variable.

#### First-Order Markov Chain

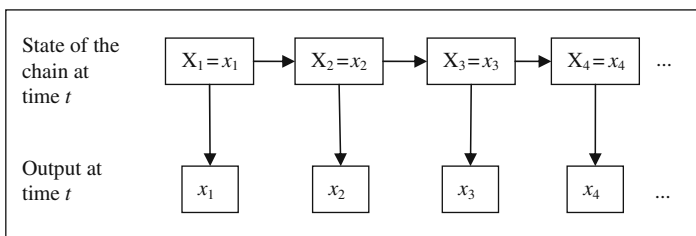
In a first-order homogeneous Markov chain, we make the assumption that the whole past of a random process is summarized by the knowledge of the last observation only. Figure 14.1 represents the dependence relation between successive observation of a Markov chain.

Mathematically, we write

$$P(X_t = i_0 | X_0 = i_t, \dots, X_{t-1} = i_1) = P(X_t = i_0 | X_{t-1} = i_1) = q_{i_0 i_1}(t) \quad (14.1)$$

where  $i_t, \dots, i_0 \in \{1, \dots, m\}$ . If we suppose that the probability  $q_{i_0 i_1}(t)$  is time-invariant, it is replaced by  $q_{i_0 i_1}$  and we have a homogeneous Markov chain. Considering all combinations of  $i_1$  and  $i_0$ , we construct a transition matrix  $Q$ , each of whose rows sums to 1:

$$Q = \begin{matrix} & \begin{matrix} X_t \\ X_{t-1} \end{matrix} & \begin{matrix} 1 & \cdots & m \end{matrix} \\ \begin{matrix} 1 \\ \vdots \\ m \end{matrix} & \begin{bmatrix} q_{11} & \cdots & q_{1m} \\ \vdots & \ddots & \vdots \\ q_{m1} & \cdots & q_{mm} \end{bmatrix} \end{matrix}$$



**Fig. 14.1** A first-order Markov chain. The probability of observing a particular output at time  $t$  depends on the output observed at time  $t-1$



$X_t = 1$  because of the different value taken by  $X_{t-1}$ . The probability of this transition is then 0 and this element is considered to be a structural zero. Each possible combination of  $l$  successive observations of the random variable  $X$  is called a *state* of the model. The number of states is equal to  $m^l$  ( $3^2=9$  in this example). In the case of a first-order Markov chain, each value taken by the random variable  $X$  is also a state of the model. The relationships (14.3) and (14.4) defined in the case of a first-order Markov chain still hold. Irrespective of what the order is, there are  $(m-1)$  independent probabilities in each row of the matrix  $Q$ , the last one of which is completely determined by the others since each row is a probability distribution summing to 1. The total number of independent parameters to be estimated is thus equal to  $m^l(m-1)$ . Given a set of observations, these parameters can be computed as follows. Let  $n_{i_l \dots i_0}$  denote the number of transitions of the type  $X_{t-l} = i_l, \dots, X_{t-1} = i_1, X_t = i_0$  in the data. The maximum likelihood estimate of the corresponding transition probability  $\hat{q}_{i_l \dots i_0}$  is then

$$\hat{q}_{i_l \dots i_0} = \frac{n_{i_l \dots i_0}}{n_{i_l \dots i_{1+}}}, \tag{14.7}$$

Where

$$n_{i_l \dots i_{1+}} = \sum_{i_0=1}^m n_{i_l \dots i_0} \tag{14.8}$$

and the log-likelihood of the entire sequence of observations is written

$$LL = \sum_{i_l \dots i_0=1}^m n_{i_l \dots i_0} \log(\hat{q}_{i_l \dots i_0}) \tag{14.9}$$

### 14.2.1.2 The MTD Model

Let  $\{X_t\}$  be a sequence of random variables taking values in the finite set  $N = \{1, \dots, m\}$ . In an  $l$ th-order Markov chain, the probability that  $X_t = i_0, i_0 \in N$ , depends on the combination of values taken by  $X_{t-l}, \dots, X_{t-1}$ . In the MTD model, the contributions of the different lags are combined additively. Then

$$P(X_t = i_0 | X_0 = i_t, \dots, X_{t-1} = i_1) = \sum_{g=1}^l \lambda_g P(X_t = i_0 | X_{t-g} = i_g) = \sum_{g=1}^l \lambda_g q_{i_g i_0} \tag{14.10}$$

where  $i_t, \dots, i_0 \in N$ , the probabilities  $q_{i_g i_0}$  are elements of an  $m \times m$  transition matrix  $Q = [q_{i_g i_0}]$ , each row of which is a probability distribution (i.e. each row sums to 1 and the elements are nonnegative) and  $\lambda = (\lambda_l, \dots, \lambda_1)'$  is a vector of lag parameters. Note that here we adopt the convention that each *row* of the transition matrix  $Q$  is a probability distribution. Sometimes each *column* of  $Q$  is taken to be a probability distribution. To ensure that the results of the model are probabilities, that is,



$$0 \leq \sum_{g=1}^l \lambda_g q_{i_g i_0} \leq 1 \tag{14.11}$$

the vector  $\lambda$  is subject to the constraints

$$\sum_{g=1}^l \lambda_g = 1 \tag{14.12}$$

where

$$\lambda_g \geq 0 \tag{14.13}$$

Equation (14.10) gives the probability corresponding to each combination of  $i_l, \dots, i_0$  individually. The model can also be written in matrix form, giving the whole distribution of  $X_t$ . Let  $\chi_t$  and  $\hat{\chi}_t$  be the vectors defined by (14.2) and (14.3).

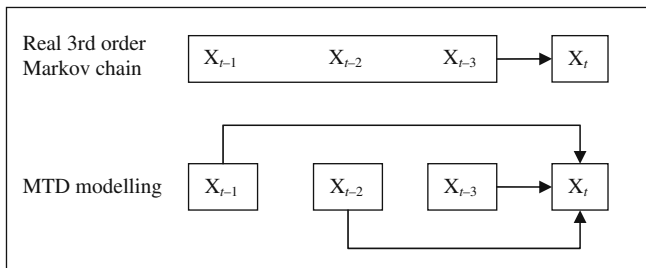
The MTD model can then be rewritten as

$$\hat{\chi}_t = \sum \lambda_g \chi'_{t-g} Q \tag{14.14}$$

Since each row of the transition matrix  $Q$  is a probability distribution and as such sums to 1, this matrix has  $m(m-1)$  independent parameters. In addition, an  $l$ th-order model has  $l$  lag parameters  $\lambda_l, \dots, \lambda_1$ , but by (14.8) only  $(l-1)$  of them are independent. An  $l$ th order MTD model thus has  $m(m-1) + (l-1)$  independent parameters, which is far more parsimonious than the corresponding fully parameterized Markov chain (see Table 14.1). Moreover, each additional lag adds only one parameter to the model.

**Table 14.1** Maximal number of independent parameters for different Markov chains and MTD models

Number of values $m$	Order $l$	Markov chain	MTD model	MTDg model
2	1	2	2	2
	2	4	3	5
	3	8	4	8
	4	16	5	11
3	1	6	6	6
	2	18	7	13
	3	54	8	20
	4	162	9	27
5	1	20	20	20
	2	100	21	41
	3	500	22	62
	4	2,500	23	83
10	1	90	90	90
	2	900	91	181
	3	9,000	92	272
	4	9,000	93	363



**Fig. 14.2** Comparison between a 3rd order Markov chain and its MTD model analogue. In a real high-order Markov chain, the combination of all lags influences the probability of the present. In a MTD model, the contribution of each lag upon the present is considered independently

In the basic MTD model, the same transition matrix  $Q$  is used to model the relation between any of the lags and the present (Fig. 14.2). In MTD modelling, the contribution of each lag upon the present is considered independently. The MTD model approximates high-order Markov chains with far fewer parameters than the fully parameterized model (see Table 14.1). Even though Markov chains are well suited for the representation of high-order dependencies between successive observations of a random variable, as the order  $l$  of the chain and the number  $m$  of possible values increase, the number of independent parameters increases exponentially and quickly becomes too large to be estimated efficiently, or even identifiably, with data sets of the sizes typically encountered in practice (Berchtold and Raftery 2002). Table 14.1 gives the number of independent parameters for different combinations of  $l$  and  $m$  showing the significant reduction in parameters achieved by MTD (and MTDg) modelling compared to conventional Markov chains.

### 14.2.1.3 The MTDg Model

Let  $\{X_t\}$  be a sequence of random variables taking values in the finite set  $N = \{1, \dots, m\}$ . In an  $l$ th-order Markov chain, the probability that  $X_t = i_0, i_0 \in N$ , depends on the combination of values taken by  $X_{t-l}, \dots, X_{t-1}$ . In the basic MTD model, the same transition matrix  $Q$  is used to model the relationship between any of the lags and the present. The idea of the mixture transition distribution (MTD) model is to consider independently the effect of each lag to the present instead of considering the effect of the combination of lags (Fig. 14.2); as in the case of the more traditional pure Markov chain process (Brémaud 1999).

The constraints imposed by the use of only one transition matrix to represent the relation between each lag and the present is sometimes too strong to allow good modeling of the real high-order transition matrix. In this case, it is possible to replace the basic MTD model by a MTDg model. The principle of the MTDg model is to use a different transition matrix of size  $(k \times k)$  to represent the relationship between each lag and the present. The high-order transition probabilities are then written as follows,

$$P(X_t = i_0 | X_{t-1} = i_1, \dots, X_{t-f} = i_f) = \sum_{g=1}^f \lambda_g q_{g i_g i_0} \tag{14.15}$$

where  $q_{g i_g i_0}$  is the transition probability from modality  $i_0$  observed at time  $t-g$  and modality  $i_0$  observed at time  $t$  in the transition matrix  $Q_g$  associated with the  $g$ th lag. In addition to the lag weight parameters  $\lambda_1, \dots, \lambda_f$ , the MTDg model implies the estimation of  $f$  transition matrices  $Q_1, \dots, Q_f$ , for a total of  $f_k(k-1) + (f-1)$  independent parameters. This is much more than involved in the basic MTD model described in the previous section, but this number of parameters remains small compared to the number of independent parameters of a real fully parameterized  $f$ th order Markov chain (see Table 14.1). As a result the MTDg proves valuable in many real world applications, as shown by Kim et al. (2008).

### 14.2.1.4 The MTD Model with Covariates

Though Markovian processes are usually used to describe the behaviour of say a single observed random variable, we oft times believe the behavior to be under the influence of an unobserved hidden process. This is where the modelling of the observed variable may be enhanced if the effect of some covariates could be taken into account in the modelling process. MARCH (Berchtold 2006) is able to incorporate covariates, even if the resulting process is not a real Markovian process. Here we make an abstraction of the possible influence of an additional hidden process, following Berchtold and Raftery (2002). The information set used to predict the probability distribution of  $X_t$  can be decomposed into two parts: the lags of an order  $f$  Markov chain,  $X_{t-1}, \dots, X_{t-f}$ , and a set of  $e$  categorical covariates  $C_1, \dots, C_e$ . Each covariate  $j$  takes a finite number of modalities  $k_j$ . Covariates can either take a fixed value during the whole observed process (gender for instance), or be time dependent (age category, income category, or behaviour for example). The relation between the  $j$ th covariate and  $Y_t$  is summarized in a transition matrix  $D_j$  of size  $(k_j \times k)$ . Each row of  $D_j$  is the probability distribution of observing the  $k$  possible values taken by  $Y_t$  in function of one of the  $k_j$  possible values taken by the covariate.

The MARCH platform (Berchtold 2006) proposes three solutions to combine the lags and covariates information:

1. All available information is directly combined into a single very large transition matrix giving the probability distribution of  $X_t$  given any combination of the values taken by both the lags and the covariates. This matrix is of size  $(k^f \prod_{h=1}^e k_h \times k)$ .
2. The lags of  $X_t$  are considered as an order  $f$  Markov chain with transition matrix  $Q$ , and the covariates are represented through there transition matrices  $D_1, \dots, D_e$ . The information of these  $e+1$  transition matrices is then combined by using a mixture model. Formally, we write

$$\begin{aligned}
P(X_t = i_0 | X_{t-1} = i_1, \dots, X_{t-f} = i_f, C_1 = c_1, \dots, C_e = c_e) \\
= \lambda_1 q_{i_f \dots i_1 i_0} + \sum_{h=1}^e \lambda_{1+h} d_{hj_h i_0}
\end{aligned} \tag{14.16}$$

where  $q_{i_f \dots i_1 i_0}$  is the transition probability corresponding to the Markov chain,  $d_{hj_h i_0}$  is the transition probability between covariate  $h$  and  $X_t$ , and where the weight parameters  $\lambda_1, \dots, \lambda_{1+e}$  sum up to one. By computing all of these probabilities, we can then estimate the full transition matrix computed in the previous solution.

3. Consider the same situation as in solution 2 above, but that the Markov chain associated with the lags of  $X_t$  is replaced by a MTD model. Then,

$$\begin{aligned}
P(X_t = i_0 | X_{t-1} = i_1, \dots, X_{t-f} = i_f, C_1 = c_1, \dots, C_e = c_e) \\
= \sum_{g=1}^f \lambda_g q_{i_g i_0} + \sum_{h=1}^e \lambda_{f+h} d_{hj_h i_0}
\end{aligned} \tag{14.17}$$

where the  $q_{i_g i_0}$  are the transition probability of the MTD model,  $d_{hj_h i_0}$  is the transition probability between covariate  $h$  and  $X_t$ , and where the weight parameters  $\lambda_1, \dots, \lambda_{f+e}$  sum up to one. By computing all of these probabilities, we can then estimate the full transition matrix computed in solution 1 above.

In this chapter we implemented solution 3.

#### 14.2.1.5 The MTD Model with Interactions Between the Covariates

The MTD model above with covariates can also have interaction among covariates. The high-order transition probabilities are then computed as follows:

$$\begin{aligned}
P(X_t = i_0 | X_{t-1} = i_1, \dots, X_{t-f} = i_f, C_1 = c_1, \dots, C_e = c_e, M_1 = m_1, \dots, M_l = m_l) \\
= \sum_{g=1}^f \lambda_g q_{i_g i_0} + \sum_{h=1}^e \lambda_{f+h} d_{hj_h i_0} + \sum_{u=1}^l \lambda_{f+e+u} s_{uv_u i_0}
\end{aligned} \tag{14.18}$$

where  $\lambda_{f+e+u}$  is the weight for the interaction term,  $q_{i_g i_0}$  is the transition probability from modality  $i_g$  observed at time  $t-g$  and modality  $i_0$  observed at time  $t$  in the transition matrix  $Q$ ,  $s_{uv_u i_0}$  is transition probability between covariate  $h_1$  and covariate  $h_2$  interaction term ( $v_u = d_{h_1 j_{h_1}} \times d_{h_2 j_{h_2}}$ ) and  $X_t$ , and where

$$\sum_{g=1}^{f+e+l} \lambda_g = 1 \tag{14.19}$$

and where

$$\lambda_g \geq 0 \tag{14.20}$$

### 14.2.1.6 The Generalized MTDg Model with Interactions between Covariates

The MTD model with interactions above can also have a different transition matrix of size  $(k \times k)$  to represent the relation between each lag and the present. The high-order transition probabilities are then computed as follows:

$$\begin{aligned}
 P(X_t = i_0 | X_{t-1} = i_1, \dots, X_{t-f} = i_f, C_1 = c_1, \dots, C_e = c_e, M_1 = m_1, \dots, M_l = m_l) \\
 = \sum_{g=1}^f \lambda_g q_{g i_g i_0} + \sum_{h=1}^e \lambda_{f+h} d_{h j_h i_0} + \sum_{u=1}^l \lambda_{f+e+u} s_{u v_u i_0}
 \end{aligned}
 \tag{14.21}$$

where  $q_{g i_g i_0}$  is the transition probability from modality  $i_g$  observed at time  $t-g$  and modality  $i_0$  observed at time  $t$  in the transition matrix  $Q_g$  associated with the  $g$ th lag.

In Eq. (14.21),  $s_{u v_u i_0}$  is transition probability between covariate  $h_1$  and covariate  $h_2$  interaction term ( $v_u = d_{h_1 j_{h_1}} \times d_{h_2 j_{h_2}}$ ) and  $X_t$ , and

$$\sum_{g=1}^{f+e+l} \lambda_g = 1
 \tag{14.22}$$

and where

$$\lambda_g \geq 0
 \tag{14.23}$$

### 14.2.1.7 Estimation

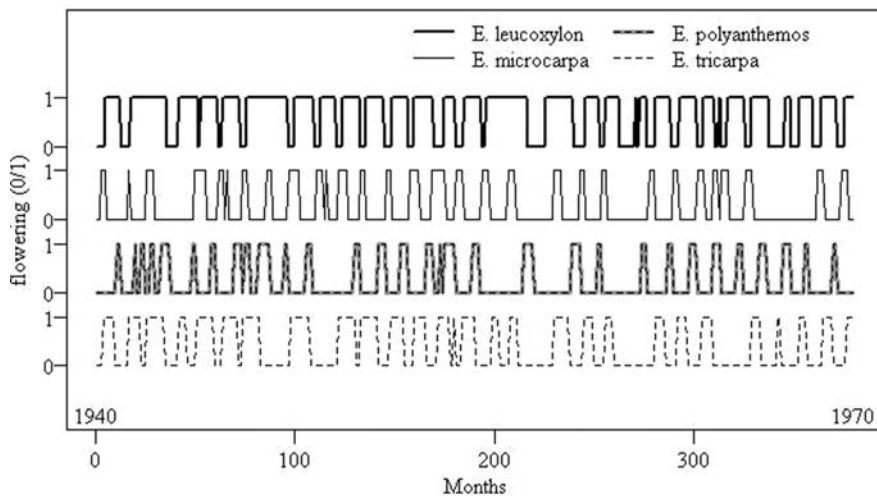
The parameters  $\lambda$  and  $q$  of the MTD model (14.21) can be estimated by minimizing the negative the log-likelihood (NLL) of the model:

$$\text{NLL} = - \sum_{i_1, \dots, i_0=1}^m n_{i_1, \dots, i_0} \log \left( \sum_{g=1}^f \lambda_g q_{g i_g i_0} + \sum_{h=1}^e \lambda_{f+h} d_{h j_h i_0} + \sum_{u=1}^l \lambda_{f+e+u} s_{u v_u i_0} \right)
 \tag{14.24}$$

where  $n_{i_1, \dots, i_0}$  is the number of sequences of the form  $X_{t-1} = i_1, \dots, X_{t-f} = i_f, C_1 = c_1, \dots, C_e = c_e, M_1 = m_1, \dots, M_l = m_l$  in the data. To ensure that the model defines a high order Markov chain, the negative log-likelihood must be minimized with respect to the constraints (14.22) and (14.23). ADMB<sup>TM</sup> was used to minimize the negative the log-likelihood (NLL). This uses auto-differentiation (AUTODIFF) (Fournier 1996) as a minimisation tool, and was shown to be computationally less intensive than MARCH (Kim et al. 2005, 2008). The major advantage of our new model is that its run-time is more than 10 times shorter ( $< 1$  min vs. 2 days) and can be run from a batch file in DOS. Hence multiple models can be tested one after the other in remote mode. The outputs can also be appended into one file to be easily accessed by any graphical software.

### 14.3 Data Sets

Flowering data were sourced from the Box-Ironbark Forest near Maryborough, Victoria, in particular the flowering records of *E. leucoxylo*, *E. microcarpa*, *E. polyanthemos* and *E. tricarpa* (1940–1971). Flowering intensity was calculated by using a rank score (from 0 to 5) based on the quantity and distribution of flowering (Keatley and Hudson 2007). Flowering intensity scores were dichotomised into two discrete states, namely on and off (1/0) flowering (Fig. 14.3) as in Kim et al. (2005). One temperature variant, of the minimum monthly temperature (MinT), maximum monthly temperature (MaxT) and mean monthly diurnal temperature (MeanT), in addition to the monthly rainfall (Rain) were included as covariates in the MTD and MTDg models; along with the temperature by rain interaction effect, for both the MTD and the MTDg models. We used two discrete states, namely low/high (lower than median temperature vs. higher than median temperature) for the temperature variables and less/more (less than the median rainfall vs. more than the median rainfall) for the rainfall variable. The cut-points for the states or low/high (less/more) categories of each climatic covariate are shown in Table 14.2.



**Fig. 14.3** Flowering (0=off/1=on) of the four eucalypts species

**Table 14.2** Cut-points for the climate variables based on medians

Climate variables	Low (less)	High (more)
Minimum temperature (°C)	≤7.65	>7.65
Maximum temperature (°C)	≤20.33	>20.33
Mean diurnal temperature (°C)	≤13.84	>13.84
Rain (mm)	≤40.45	>40.45

## 14.4 Results

The MTD mixing probabilities  $\lambda_g$  and transition probabilities for the four species are given in Tables 14.3 and 14.4, respectively. Flowering intensity of all species was positively and significantly correlated with last month's flowering and with flowering 11 months earlier ( $P < 0.0001$ ); with flowering 12 months earlier for *E. polyanthemos* and *E. microcarpa*. MTD showed a significant 9 month lag for both *E. polyanthemos* and *E. tricarpa*. Rainfall was not a significant main predictor of flowering in all species except *E. tricarpa*. Rain interacts with (mean) temperature for *E. polyanthemos* only. Figure 14.4 shows the relevant transition probabilities for the MTD model of *E. polyanthemos* flowering. MTD models confirm that the main temperature driver is maximum temperature for *E. tricarpa*, and mean temperature for both *E. leucoxyton* and *E. polyanthemos* (Fig. 14.4); and minimum temperature the main temperature driver for *E. microcarpa*'s flowering.

The MTDg mixing probabilities  $\lambda_g$  and transition probabilities for the four species are given in Tables 14.5 and 14.6, respectively. MTDg modelling showed that flowering intensity of all species was positively and significantly correlated with last month's flowering; with flowering 12 months earlier for *E. polyanthemos* and *E. microcarpa*; and with flowering 11 months earlier for all species except *E. microcarpa*. MTDg as did MTD showed a significant 9 month lag *E. tricarpa* only. Rainfall was not a significant main predictor of flowering in all species except *E. tricarpa*. Rain interacts with mean temperature for *E. polyanthemos* only. Figure 14.5 shows the relevant transition probabilities for the MTDg models of all 4 species' flowering.

MTDg models (Tables 14.5 and 14.6), in agreement with the MTD analysis (Tables 14.3 and 14.4), show that the main temperature driver for *E. tricarpa* is maximum temperature, mean temperature for both *E. leucoxyton* and *E. polyanthemos*; and minimum temperature for *E. microcarpa*'s flowering. From the MTDg analysis we summarise as follows: Flowering increases as temperature (minimum) increases for *E. microcarpa*, flowering decreases as temperature increases for *E. leucoxyton* and *E. tricarpa* (driven by mean and maximum temperature, respectively). Rainfall positively impacts on the flowering of *E. tricarpa* (i.e. flowering increases with more rainfall). There is a significant interaction between mean temperature and rainfall on the flowering of *E. polyanthemos* (Table 14.4).

A comparison of the MTDg and MTD analyses show overall similar results. Previous months flowering has a significant positive impact on flowering of the current month for all four eucalypts species, as gleaned by both MTDg and MTD analysis. Flowering at lag 12, the previous year, has a significant positive effect on the flowering of *E. microcarpa* and *E. polyanthemos*, as shown by both MTDg and MTD models. Flowering of 11 months ago has positive effects on flowering of *E. polyanthemos*, *E. leucoxyton*, and *E. tricarpa* from the MTDg models, and on all four species from the MTD analysis. Flowering nine months ago has a significant positive effect on flowering of *E. tricarpa* for both MTDg and MTD; MTD models also found a significant 9 month lag for *E. polyanthemos*.

Table 14.3 MTD mixing probabilities and optimal models

Species	MTD model	Likelihood	lag 1	lag 9	lag 10	lag 11	lag 12	Temp variable	Rain	Temp by rain interaction
<i>E. microcarpa</i>	MinT, rain <sup>+</sup>	115.94	0.544	-	-	0.039	0.274	0.118	0.026	-
	MeanT, rain	116.14	0.534	-	-	0.032	0.275	0.136	-	-
	MaxT, rain	115.98	0.534	-	-	0.031	0.274	0.137	-	-
<i>E. polyanthemus</i>	MinT, rain	139.84	0.554	0.059	-	0.166	0.111	0.064	0.019	0.028
	MeanT, rain <sup>+</sup>	139.36	0.530	0.060	-	0.160	0.105	0.091	0.009	0.045
	MaxT, rain	139.68	0.526	0.059	-	0.160	0.104	0.084	-	0.067
<i>E. leucoxydon</i>	MinT, rain	124.36	0.636	-	-	0.138	0.026	0.179	-	-
	MeanT, rain <sup>+</sup>	120.96	0.611	-	-	0.124	0.042	0.202	-	-
	MaxT, rain	123.81	0.629	-	-	0.148	0.023	0.179	-	-
<i>E. tricarpa</i>	MinT, rain	130.81	0.614	0.045	0.025	0.087	-	0.149	0.079	-
	MeanT, rain	130.64	0.617	0.059	0.009	0.096	-	0.157	0.062	-
	MaxT, rain <sup>+</sup>	129.47	0.609	0.047	0.021	0.093	-	0.166	0.064	-

<sup>+</sup> denotes optimal MTD model, based on the lowest likelihood value.

Covariate effects above 0.03 are considered significant.

- Cells have zero probabilities.



**Table 14.4** Transition probabilities of flowering for the optimal MTD models

Species	Climate effects (temp/rain) (+/-) interaction (-/+) (-/+)	Previous flowering			Temperature			Rain			Temperature by rain interaction					
		off	on	low <sup>1</sup>	high <sup>2</sup>	less <sup>3</sup>	more <sup>4</sup>	low/less	low/more	high/less	high/more	low/less	low/more	high/less	high/more	
<i>E. microcarpa</i>		0.00	1.00	0.00	1.00	1.00	0.00	-	-	-	-	-	-	-	-	
<i>E. polyanthemus</i>		0.01	1.00	0.00	0.34	0.94	0.03	0.88	0.12	0.20	0.96	-	-	-	-	
<i>E. leucoxylon</i>		0.05	1.00	1.00	0.00	0.88	0.94	-	-	-	-	-	-	-	-	
<i>E. tricarpa</i>		0.00	1.00	1.00	0.00	0.00	1.00	-	-	-	-	-	-	-	-	

<sup>1</sup>Cut point for low temperature states: MinT ≤7.64°C, MaxT ≤20.32°C, MeanT ≤13.83°C.

<sup>2</sup>Cut point for high temperature states: MinT >7.65°C, MaxT >20.33°C, MeanT >13.84°C.

<sup>3</sup>Cut point for less rain: rain ≤40.44 mm.

<sup>4</sup>Cut point for more rain: rain >40.45 mm.

- Cells have zero probabilities.

**Table 14.5** MTDg mixing probabilities and optimal models

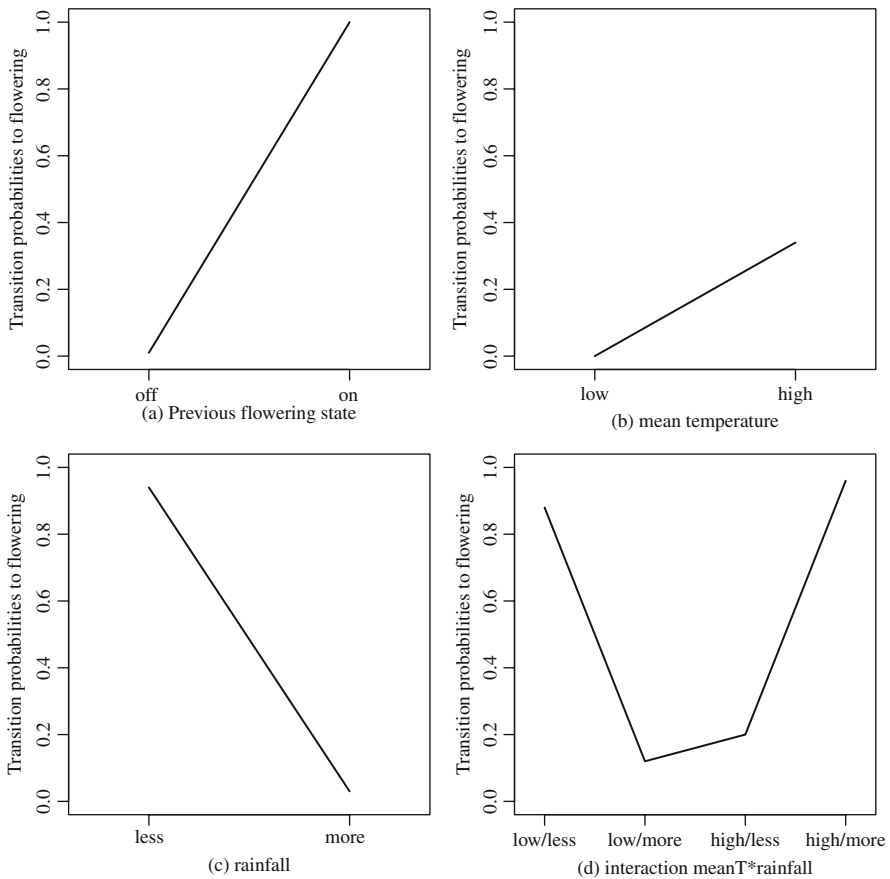
Species	Optimal MTDg model	Likelihood	lag 1	lag 9	lag 11	lag 12	Temp variable	Rain	Temp by rain interaction
<i>E. microcarpa</i>	MinT, rain	-117.61	0.555	-	-	0.300	0.144 <sup>φ</sup>	-	-
<i>E. polyanthemus</i>	MeanT, rain	-140.69	0.663	-	0.186	0.097	0.007	-	0.046
<i>E. leucoxyton</i>	MeanT, rain	-122.36	0.616	-	0.141	-	0.240 <sup>φ</sup>	-	-
<i>E. tricarpa</i>	MaxT, rain	-129.54	0.608	0.053	0.108	-	0.165 <sup>φ</sup>	0.065	-

<sup>φ</sup> Covariate effects above 0.03 are considered significant.

- Cells have zero probabilities.

**Table 14.6** Transition probabilities of flowering for the optimal MTDg models

Species	Climate effects		Previous flowering												Temperature by rain interaction			
	temp/rain	lag 1	lag 9		lag 11		lag 12		temperature		rain	low/less		high/more				
			on	off	on	off	on	off	low	high		low/mo	high/less	high/more				
<i>E. microcarpa</i>	+/-	0.01	1.00	-	-	0.89	0.94	-	1.00	-	-	-	-	-	-	-	-	
<i>E. polyanthemus</i>	-/-	0.05	0.82	0.16	0.03	0.02	0.97	-	0.96	0.10	0.99	0.98	0.55	0.81	-	0.56	1.00	
<i>E. leucoxylon</i>	-/-	0.02	0.99	-	0.06	0.06	1.00	0.93	0.90	0.99	0.15	-	-	-	-	-	-	
<i>E. tricarpa</i>	-/+	-	1.00	-	-	-	1.00	-	-	1.00	-	-	1.00	-	-	-	-	

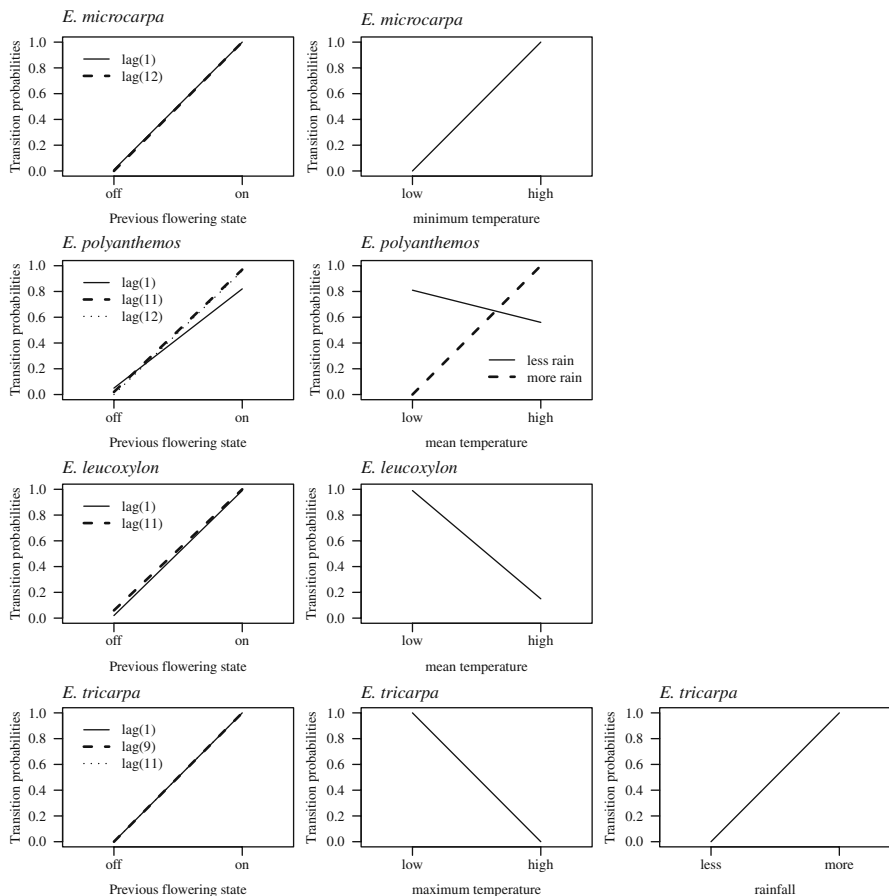


**Fig. 14.4** Transition probabilities to flowering from (a) previous flowering state (on/off), (b) mean diurnal temperature state (low/high), (c) rainfall state (less/more) and (d) temperature by rainfall interaction state for *E. polyanthemus*

## 14.5 Discussion

The MTD and MTDg models with interactions show that the flowering of *E. leucoxylo*n and *E. tricarpa* are influenced similarly by temperature (both flower at low temperature) and exhibit a positive relationship with flowering 11 months ago. For *E. leucoxylo*n this is because it has two months in which flowering commencement is almost equally likely: April and June, 0.36 and 0.39, respectively (Keatley and Hudson 2007). The reason is less clear for *E. tricarpa* as the probability of flowering commencement 11 months prior is low, 0.04.

The flowering of *E. microcarpa* behaves differently from *E. leucoxylo*n and *E. tricarpa*. *Eucalyptus microcarpa* flowers at high temperature and its flowering has a significant and positive relationship with flowering a year ago. This illustrates



**Fig. 14.5** MTDg transition probabilities to flowering from previous flowering state (on/off), temperature state (low/high), and rainfall state (less/more) for the four eucalypts species

this species is more consistent as to when it starts flowering (i.e. *E. microcarpa* has a probability of commencing flowering 12 months before of 0.67 compared to *E. leucoxylon* and *E. tricarpa*, respectively 0.41 and 0.39) (Keatley and Hudson 2007).

The MTD and the MTDg model found a significant interaction between two climate variables, mean temperature and rainfall on the flowering of *E. polyanthemos*. As flowering is viewed as either “off” or “on” this interaction appears to be delineating *E. polyanthemos*’ flowering period. It usually commences flowering in late spring – as mean temperature is increasing and rainfall is decreasing and ceases in early summer; just prior to the warmest mean temperature and lowest rainfall. An alternative interpretation of this interaction could also be that as flowering is viewed as either “off” or “on” it is delineating the climate profile during *E. polyanthemos*’ flowering period.

These four species examined here are influenced by temperature (see also Keatley et al. 2002) and in some instances are influenced by rainfall; and as a consequence their flowering phenology will change in response to climate change. These changes can be regarded as the short-term impacts of climate change (Rehfeldt et al. 2004). The longer-term consequences are changes in their individual reproductive success and distribution. These changes in phenology will in turn have an impact on other species (e.g. 20% of vertebrate species where these species occur, box-iron bark forests, are nectar dependent (Traill 1991)). Mac Nally et al. (2009) have related a crash in the number of birds in these systems to a reduction in nectar; reflective of reduced flowering intensity and thus food, between 2002 and 2007. The apicultural industry is also likely to be affected as these species are some of the main producers of honey in Australia (Victorian Environment Assessment Council 2001) and therefore changes in flowering would have significant economic consequences.

Future work will entail the modification of the MTD and MTDg models discussed here to incorporate all the three temperature variants, rainfall main effects and their interactions. Multivariate MTD (M-MTD) models are also the topic of future work. It is anticipated that our M-MTD models (with a multiplicity of covariates) may be more sensitive than MTD and MTDg models in establishing temperature by rainfall interactive effects on flowering. Indeed the influence of rain on these species needs further examination as its effect has been shown to range from none (Porter 1978, Keatley and Hudson 2000) to a significant but minor effect (i.e. temperature has a much greater influence) (Wells 2000, Keatley and Hudson 2000, Keatley et al. 2002); to significant with a major influence (Wilson and Bennett 1999, Kim et al. 2005, Mac Nally et al. 2009). Given these mixed results indications are that, as in semi-arid woodlands, there is a rainfall threshold required before flowering can occur (Porter 1978, Hodgkinson and Freudenberger 1997).

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# Chapter 15

## Life History Mediated Responses to Weather, Phenology and Large-Scale Population Patterns

Esa Ranta, Jan Lindström, Veijo Kaitala, Elizabeth Crone, Per Lundberg, Tatu Hokkanen, and Eero Kubin

**Abstract** Using a threshold-triggering framework, we extend the Moran effect to also cover timing of life history events. With two varieties of the model we demonstrate emergence of synchrony in seasonal and annual timing that levels off against distance between sampling sites compared. In the first model we address within-season timing over years. The Finnish data on leafing of European aspen support the model predictions in all detail explored. In the second example the focus is on annual match of seed production in the Finnish Scotch pine and Norway spruce. The model predictions find their match with the data. We show that it is possible to extend Moran's (1953) idea to encompass events not directly regulated by density-dependent feedback. It is perhaps not too surprising that phenological events can be synchronized in much the same way as population fluctuations.

**Keywords** Life history · Phenology · Spatial synchrony · The Moran effect · Threshold-triggering

### 15.1 Introduction

An eminent Australian statistician, P.A.P. Moran (1953) was the first one to draw ecologists' attention to the fascinating fact that densities of many populations of a given species fluctuate in step over time. He also provided a model to show how synchrony may arise. Pat Moran's argument was very elegant in its simplicity: if spatially separate populations were subjected to similar density-dependent feedback in their renewal process, spatially correlated external disturbance would synchronize

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To honor of Patrick Alfred Pierce Moran 1917–1988: the father of the Moran effect

population fluctuations. In addition, correlation between these population fluctuations would eventually match the correlation between the forcing terms (see also Ripa and Ranta 2007). Perhaps demonstrating how much Moran was ahead of his time, ecologists ignored Moran's model for several decades, until Royama (1992) reintroduced it in an influential monograph. To use a well-worn cliché, the rest is history; the so-called "Moran effect" has been very much in the limelight of ecological literature since Royama's 1992 book (for reviews, see Ranta et al. 1997, 2006, 2007, Liebhold et al. 2004).

For historical reasons, the Moran effect has been considered as the synchronizing agent of population fluctuations (Ranta et al. 1997, 2006, 2007). Here, we discuss the role of Moran effect in synchronizing phenological events. In particular, we are interested in landscape and population level causes of timing of life history events to external triggers. Hence, phenology for us is: "the relationship between a regularly recurring biological phenomenon and climatic or environmental factors that may influence it" (Encarta® World English Dictionary© 1999, Microsoft Corporation). Such events include calendar timing of episodes such as spring arrival, onset of egg laying, hatching of chicks, moult and autumn departure in birds; timing of reproduction in mammals and fish; emergence of adult insects and timing of diapause and hibernation; leafing, flowering, and fruit production in plants. Note that many of those phenomena are inherently closely associated with factors directly tied to population growth. The Moran effect on population fluctuations and on phenological life history processes are thus very closely related.

To lessen our burden, we limit the analyses presented here to two kinds of life history events, those that make immediate use of resource availability, and those that need accumulation of resources before being realized. Drawing on life-history theory (e.g. Stearns 1992), we call these income and capital strategies, respectively. These are the ends of a continuum of strategies; so demonstrating the possible population and landscape level consequences of life history decisions made at these end points of this continuum captures the range of possible outcomes. Leafing in trees is an example of an income strategy. Leafing phenology is cued by temperature at a particular site in a particular year, so we expect leaf production to reflect (for most part) conditions in the current year (Arft et al. 1999). Seed production in trees is an example of a capital strategy. In northern latitudes, many tree species produce seeds (cones, or berries) synchronously in some years, followed by a few low seed production years to the next mass production of seeds (Kelly and Sork 2002), suggesting that seed production in one year reflects resource allocation from stored resources as well as resource gain in that year (see, e.g. Hoch et al. 2003). Indeed, reproductive activity of trees in forests often fluctuates between years with a large variance, and their flowering and fruit production are synchronized over a long distance, even across species and higher taxa (Koenig and Knops 1998, 2000, Koenig et al. 1994, 1999). Therefore, in order to ask whether weather events synchronize seed production, we need to understand how individual trees store and allocate resources over time.

To facilitate our argument, we first show how a simple statistical tool – measuring synchrony (the temporal match of events in space and time) – helps us uncover significant features that lie in the space-time domain of ecologically significant income

processes such as leaf phenology. We then introduce a resource-based model of mast seeding in plants (c.f., Büsgen and Münch 1929, Yamauchi 1996, Isagi et al. 1997, Satake and Iwasa 2002, Rees et al. 2002). Masting, or mast seeding, is the synchronous and highly variable seed production between years by a population of plants (e.g. Kelly 1994). A number of hypotheses have been proposed to explain evolutionary advantages of masting (Janzen 1971, Silvertown 1980, Nilsson and Wästljung 1987, Norton and Kelly 1988, Smith et al. 1990, Kelly et al. 2001, just to name a few). However, we are interested in evaluating a mechanistic explanation of masting as a function of fluctuations in available resources due to variable environmental conditions such as temperature and precipitation.

Synchrony is simply defined here as “occurrence at the same time” (Encarta® World English Dictionary© 1999, Microsoft Corporation). Quite obviously, events such as the arrival of spring (according to some appropriate definition), should potentially serve as a strong synchronizing agent. It is well known that many natural processes are indeed synchronized (Ranta et al. 2006). When referring to population dynamics the degree of synchrony is often measured as the cross-correlation of population sizes in two spatially separate locations (references in reviews by Ranta et al. 1997, 2006, 2007). When the correlation approaches one, the two populations fluctuate roughly hand in hand, when the correlation is close to negative one, they are completely out of phase, and when it is close to zero, there is no correlation between the population sizes at the two locations. Obviously, depending on the kind of data it might be advisable to use some other measure of the population synchrony than temporal correlation. For example, in phenological research, synchrony could be measured as the difference in time when a life history event takes place but in different study populations.

Typically, synchrony tends to decrease with distance – the closer the populations are in space, the higher the temporal match is. This distance-dependence of synchrony can have two causes (Ranta et al. 1997, 1999). First, the populations may share the same environmental driver and respond in a similar fashion to it (flowering and leafing in plants, onset of nesting in birds), and populations separated by smaller distances may experience more similar timing of environmental events. Second, there may be a high degree of exchange of individuals between the two populations (valid for dispersing organisms only). Both effects tend to be more matching the closer the populations are in space. Hence, when the synchrony measure between any two populations in a set of spatially separate habitats or patches, is plotted against distance between them, there is usually a negative slope of that relationship. The more global the Moran effect is (i.e. high spatial autocorrelation in environmental factors), the less synchrony levels off with distance and the slope becomes shallower. The more localized the Moran effect is, the steeper the slope. Ranta et al. (2006: Chapter 4) provide a fuller account on the definitions and the statistics involved here.

Population synchrony is not just a statistical phenomenon. If, for example, *per capita* dispersal is constant, then many individuals are dispersing at high population densities over large areas, but far less so when the population densities are simultaneously low in nearby habitats or patches. This means that gene flow will be pulsed over time and that “crunch” years with small population densities, and

therefore increased likelihood of local genetic drift, will occur. In other words, greater synchrony means less potential for genetic or demographic rescue effects (Brown and Kodric-Brown 1977, Tallmon et al. 2004).

## 15.2 Space-Time Synchrony of Phenology Events

We aim to show that the Moran effect (i.e. a common external perturbation) is capable of synchronizing two differing life history events, exemplified with leafing in European aspen (*Populus tremula*) and mast seeding in both Scotch pine (*Pinus sylvestris*) and Norway spruce (*Picea abies*) in Finland. In proving the latter we do not need to call for the concept of “pollen coupling” (Satake and Iwasa 2002). Indeed, in each case a simple threshold-triggering mechanism works. In the first example we address within-season timing over years, in the second example the focus is on the annual match of seed production in the two most common forest trees in Finland. However, we emphasize that synchrony here refers to timing of leafing within years, and seed production among years, not to population dynamics.

### 15.2.1 Threshold-Triggered Phenology

Consider the onset of leafing (more precisely, when leaves have reached their final size) along a temperature gradient, as a metaphorical starting point. The annual steepness of the gradient (i.e. the slope of temperature over space) represents the possible strength of the Moran effect. In years when the slope is shallow, the threshold is reached almost simultaneously everywhere. This would correspond to a situation where a large-scale weather pattern prevails on large range. In contrast, when the slope is steep, one end of the gradient has higher temperatures earlier, resulting in earlier leafing in that end of the gradient. However, local conditions are also going to affect the phenological event in question, as different places will have different wind conditions and geographical features, for instance. To accommodate such variation, we add local noise to the overall pattern, affecting the temperature accumulation towards the threshold needed for leafing. Thus, one can imagine sampling stations located along a temperature gradient, where local conditions are also recorded. We let the Moran effect influence the annual slope of the gradient, and the resulting data are observations of seasonal timing of the phenology event in the sampling stations. Such data render it easy to define spatio-temporal patterns of synchrony.

#### 15.2.1.1 Phenology of Leafing in the European Aspen in Finland

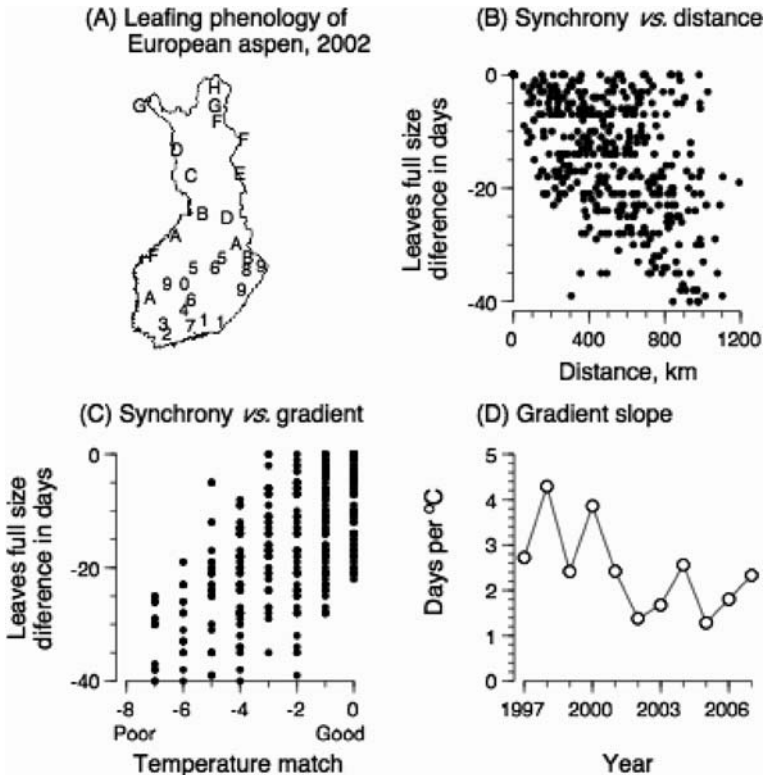
To make this conceptual model concrete, we turn to real data. In this particular case, we have the 1997–2007 leafing records (i.e. when leaves reach their full size) of European aspen from 30 sampling stations in Finland. The method of selecting

the target trees of local origin and undertaking the phenological observations are described in Kubin et al. (2007). The observations are made individually by observing five medium-sized and healthy trees. The trees are selected either from an observation stand or from a separate location according to the situation, and they are marked and numbered. The leaf has reached its full size when it does not grow any bigger. To verify this, cross measurements (width and length of individual leaves) were used (for more details see Kubin et al. 2007).

We take 2002 as an example year and plot the dates on the map of Finland (Fig. 15.1a). In this year the gradient to reach full-sized leaves is 40 days across the country. The threshold temperatures are encountered earlier in South and West than in North and East of Finland. The model suggests (in statistical terms), provided there is a geographical gradient, that the temporal match in timing is highest at close ranges and that it decreases with increasing distance. Not surprisingly, this pattern is found despite that there is huge scatter in the aspen synchrony data ( $r_{464} = -0.60$ ; Fig. 15.1b). To illustrate the basic elements of the threshold-triggering model, we have taken May temperature isoclines (1971–2000 data at 1°C isoclines available at [http://www.fmi.fi/saa/tilastot\\_134.html](http://www.fmi.fi/saa/tilastot_134.html)) as a preliminary surrogate of the environmental gradient.

With such data we can replace the geographical distance data with temperature distance data. Graphing leafing synchrony against temperature synchrony suggests a positive co-variation between the two variables (Fig. 15.1c;  $r_{464} = 0.74$ ), somewhat stronger than the relationship between synchrony and distance. This can be repeated for all the 11 years we have data on leafing in the European aspen. As the temperature data are long-term averages, while the aspen data are annual, one would expect to see annual variation in the slope of the relationship between synchrony of leaf in full size vs. temperature match along the nation-wide geographical range. This is the case (Fig. 15.1d); the slope varies between 1 and 4 days per one °C difference between the sampling sites.

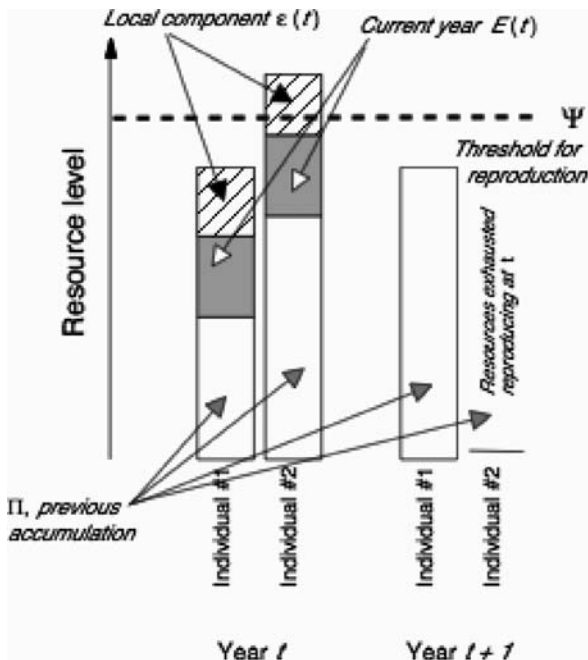
We consider some, yet unknown, accumulated temperature sum needed for reaching full-sized leaves in aspen. Using the 1971–2000 temperature isoclines (or their synchrony across Finland) approximates this threshold. Annual temperature variation in the leaf-growing season is reflecting variation the triggering threshold. Thus, the Moran effect can be partitioned into its components: long-term average, and annual deviations from it. We used these 11 years of data on the relationship between synchrony in flowering dates and temperature match across Finland, to estimate the relative contributions of match in temperature and years to the slopes in Fig. 15.1d. Normalized regression coefficients for temperature synchrony and year are 0.57 (standard error = 0.01) and 0.09 (standard error 0.01), respectively. Therefore, the annual component of the Moran effect plays a minor role in synchrony relative to the long-term average. Nonetheless, Fig. 15.1d suggests intriguingly that the long-term average climate conditions could be becoming a worse predictor of annual synchrony over time (a generalized linear model with year x slope interaction gives a normalized coefficient  $-0.13$  (standard error 0.01) supporting the conclusion of negative trend).



**Fig. 15.1** (a) Leafing phenology of European aspen in Finland 2002. The numbers and letters on the map refer to the date on which leaves reached full expansion (1 = 24/5; 2 = 25/5; 3 = 28/5; 4 = 1/6; 5 = 8/6; 6 = 11/6; 7 = 12/6; 8 = 13/6; 9 = 15/6; 0 = 16/6; A = 18/6; B = 22/6; C = 24/6; D = 29/6; E = 5/7; F = 6/7; G = 11/7; H = 13/7) and their locations indicate the position of sampling stations on the map. (b) Based on the data in (a) one can simply calculate synchrony in the temporal match of leafing in the aspen and graph the data against the geographic distance of the sampling stations. The finding is a leveling off of the synchrony against distance ( $r = -0.603$ ; slope  $-0.026$ ). (c) Instead of distance one can use long-term (1970–2001) temperature isoclines as a measure of phenological proxy between the sampling locations. The leafing synchrony is graphed against the measure of temperature synchrony ( $r = 0.736$ , slope 4.29). (d) The slope (days per a degree of °C difference) of regression lines (synchrony in leafing versus synchrony in temperature; see panel (c)) graphed over the study years 2001–2007

### 15.2.2 Phenology of Mast Seeding

Here we formulate the resource allocation by plants into an individual based model of seed production. Our model was inspired by resource matching as described by Büsgen and Münch (1929), and is very close to that presented by Tuomi et al. (1983, their Fig. 2). It is also conceptually close to models analyzed recently by Yamauchi (1996), Isagi et al. (1997), and Rees et al. (2002) in that individual plants gain resources over time, and then spend them on reproduction when above a threshold level needed for reproduction. To emphasize the similarity to other models and avoid

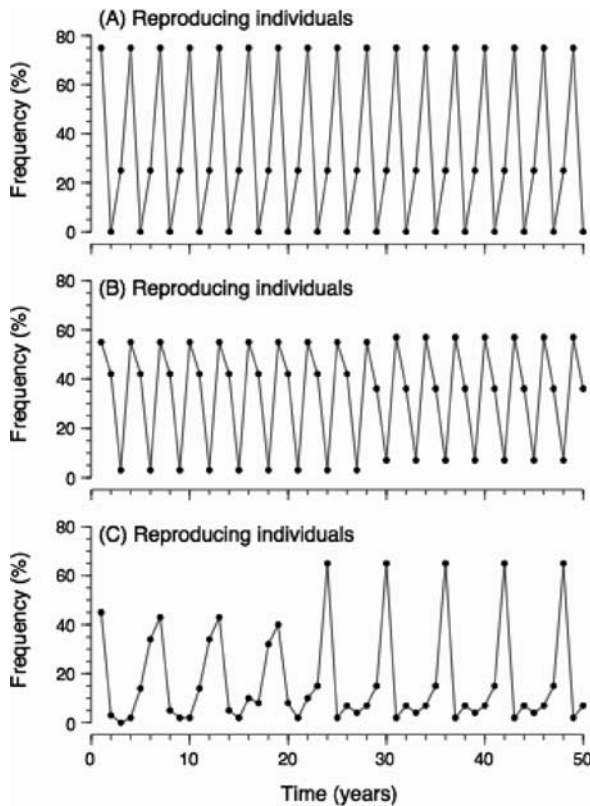


**Fig. 15.2** Schematic structure of the resource-threshold model (more details in Box 13.1). The two individuals depicted differ their energy levels accumulated for reproduction ( $\Pi_i$ , white sections of the columns). On the ongoing season both gain energy,  $E(t)$  (grey sections), for reproduction modulated by local modifiers,  $\varepsilon(t)$  (hatched sections), not necessarily the same for all individuals. Once the energy accumulated exceeds the threshold  $\Psi$  needed for reproduction, breeding takes place all reserves are depleted. The next season those individuals start energy accumulation from scratch, while those that did not hit  $\Psi$  stay with their reserves to the next breeding season

confusion in the definition of resource matching (c.f., Rees et al. 2002, Monks and Kelly 2006), we refer to our model as a resource-threshold model of seed production. With this model, we evaluate periodicity and patterns of spatial synchrony in reproductive events in perennials across geographical ranges. For this purpose, we consider again a set of localities along an environmental gradient as in Section 15.2.1, where – for instance – temperature in one end is higher than in the other end (e.g. due to latitude or altitude).

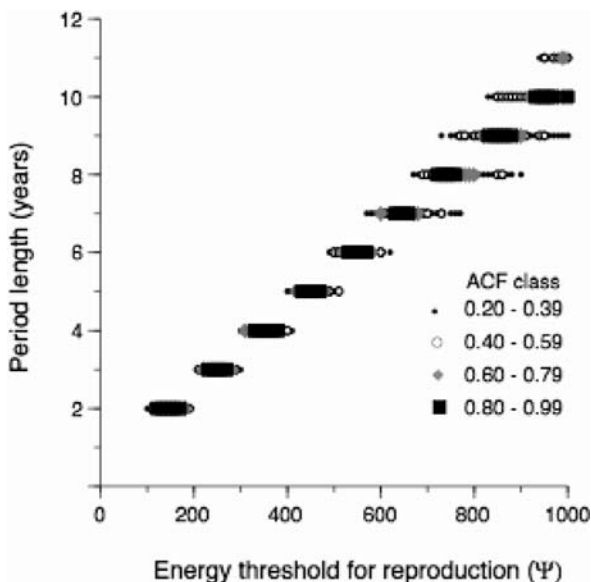
The model (Fig. 15.2; Box 15.1) is built on individual-level accumulation of energy reserves  $\Pi_i(t)$  for reproduction. The reserves are either increased by energy gained during the growing season,  $E(t)$ , or used up if reproduction takes place (Box 15.1). Individuals may experience variation due to local conditions:  $E'_i(t) = \mu'_i(t) E(t)$ , (here  $\mu$  is taken from uniformly distributed random distribution between  $1-w_L$  and  $1+w_L$ ). Reproduction takes place once the accumulated reserves exceed the threshold  $\Psi$  for reproduction. The reserves are completely depleted during reproductive events. The model poses an immediate observation, also seen in the data (Figs. 15.6 and 15.7): all individuals do not reproduce simultaneously!

With annual variation in  $E(t)$ , and with individual differences in energy accumulation due to local differences, we find the following. When  $E(t) > \Psi$  all individuals in all sites will reproduce every year (consistent with the results of Isagi et al. 1997, Satake and Iwasa 2000). This is one of the extreme ends of the income-capital reproduction continuum: the income is put directly to reproduction. In contrast, if the energy demand for reproduction is higher than annual availability (i.e.  $\Psi < E(t)$ ) reproduction becomes periodic, and the period length between the peak years of reproduction increases with increasing difference between  $E(t)$  and  $\Psi$  (Figs. 15.3 and 15.4). This is another testable prediction generated by



**Fig. 15.3** Examples of the temporal dynamics the resource-threshold model can generate. The threshold is  $\Psi = 250$ , annual availability,  $E(t)$ , is uniformly distributed random numbers between 80 and 120 plus  $\varepsilon_t(t)$  with  $w = 0.01$  in (a) and  $w = 0.05$  in (b). The population is  $n = 100$  individuals with initial  $\Pi_i$  taken from uniform random numbers between 50 and 150. In both cases there is a three-year periodicity but the overall pattern differs. In (a) peak (year  $t$ ) is followed by a crash at  $t + 1$ , modest recovery at  $t + 2$ , and a peak of reproduction at  $t + 3$ . In (b) there are still a fair proportion of individuals reproducing after the peak year. The reproduction statistics are taken after a transient period of 100 time steps has elapsed. (c) An example with a six-year periodicity,  $\Psi = 550$ ,  $w = 0.025$ , otherwise as in (a) and (b)

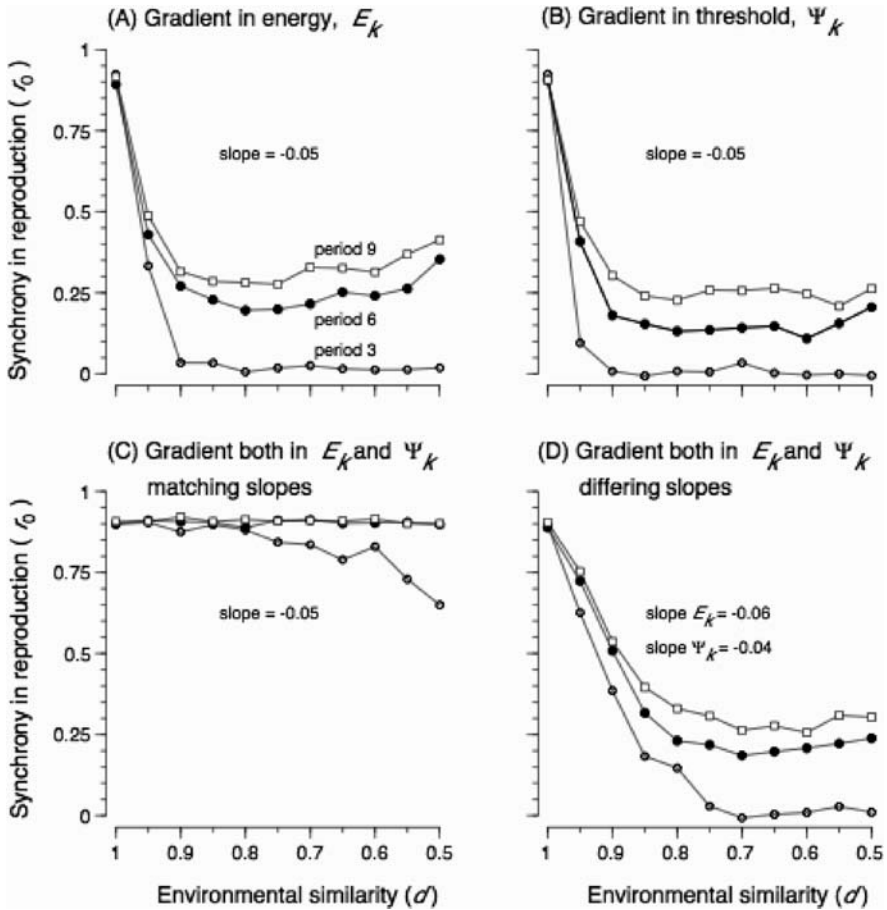




**Fig. 15.4** Period length as a function of the energy threshold for reproduction  $\Psi$ , when  $E(t)$  is uniformly distributed random numbers between 80 and 120 with  $\varepsilon_i(t)$ , when  $w = 0.01$ . The population is  $n = 100$  individuals with initial  $\Pi_i$  taken from uniform random numbers between 50 and 150. The autocorrelation statistics (only positive coefficients are indicates starting from 0.2; inset) are taken from time series of 100 steps long after a transient period of 100 time steps has elapsed. A matching graph (not shown here) can be achieved by keeping the threshold  $\Psi$  fixed and by reducing the  $E(t)$ : when  $E(t)$  gets smaller and smaller the period length of reproduction increases

the model. Note that one has the same effect by keeping  $\Psi$  constant and by reducing  $E(t)$ .

This resource-threshold model is easy to extend into a spatial context. Assume that there are  $N$  sites, perhaps along an environmental gradient. The regions may differ in many ways in terms of the resource-threshold model, as outlined above. Introducing differences (i) in  $E_k(t)$ , would imply more energy in the south (lowlands) than the north (at high altitudes), for instance. Alternatively, there could be (ii) gradient differences in  $\Psi_k$ , or (iii)  $E_k(t)$  and  $\Psi_k$  could co-vary along the gradient either with matching or different slopes. We demonstrate this by taking two localities, A and B, that are either matching ( $E_B = E_A$ ), or more apart (e.g.  $E_B = dE_A$ , where  $d < 1$ ; Box 15.1). We measure the temporal match between these two localities by calculating cross correlation with time lag zero,  $r_0$  (e.g. Ranta et al. 1995, 2006). Presenting the gradient similarity this way makes the ambient environments in A and B spatially autocorrelated (Ranta et al. 1999). The full model is presented in Box 15.1. Note that the Moran effect in the present model is in the  $E$ , provided it is not constant over years. This is similar to the threshold-triggered phenology model in Section 15.2.1. When  $E(t)$  comes from a frequency distribution, nothing prevents it from having a long-term trend, or temporal structure (autocorrelation).



**Fig. 15.5** Synchrony (measured with cross correlation with lag zero,  $r_0$ ) in reproduction between populations increasingly with environmental similarity ranging from perfect match  $d = 1$  to  $d = 0.5$ . In each panel synchrony level is evaluated for reproductive periodicities of three, six and nine years. The population size in each unit is  $n = 100$  individuals with initial  $\Pi_i$  taken from uniform random numbers between 50 and 150. The synchrony statistics are taken from time series of 100 steps long after a transient period of 100 time steps has elapsed. The gradient can be either in  $E_k$  (a) or  $\Psi_k$  (b). If the gradient is both in  $E_k$  and  $\Psi_k$ , it can be with matching slopes for  $E_k$  and  $\Psi_k$  (c), or slopes for  $E_k$  and  $\Psi_k$  can differ (d)

We leave exploration of these aspects outside the present treatment, as they would take so much space.

We observe that spatial synchrony, the degree of temporal match in space, reduces rapidly with increasing environmental dissimilarity with the gradient being either in  $E_k$  or  $\Psi_k$  (Fig. 15.5a, b). The main reason for this fast decline in synchrony is that the two populations start to fluctuate with different periodicity (Fig. 15.5).

Period length of the reproductive dynamics between the sites also affects the level of synchrony. The larger the difference, the lower is the temporal match of reproduction. Interestingly, when the gradient influences simultaneously, and with matching slopes, both  $E_k$  and  $\Psi_k$ , we observe only a minimal decay in synchrony along the environmental gradient (Fig. 15.5c). Finally, when both  $E_k$  and  $\Psi_k$  change along the environmental gradient but with different slopes (regardless of which one is steeper) the synchrony decay against decreasing values of  $d$  becomes shallower (Fig. 15.5d).

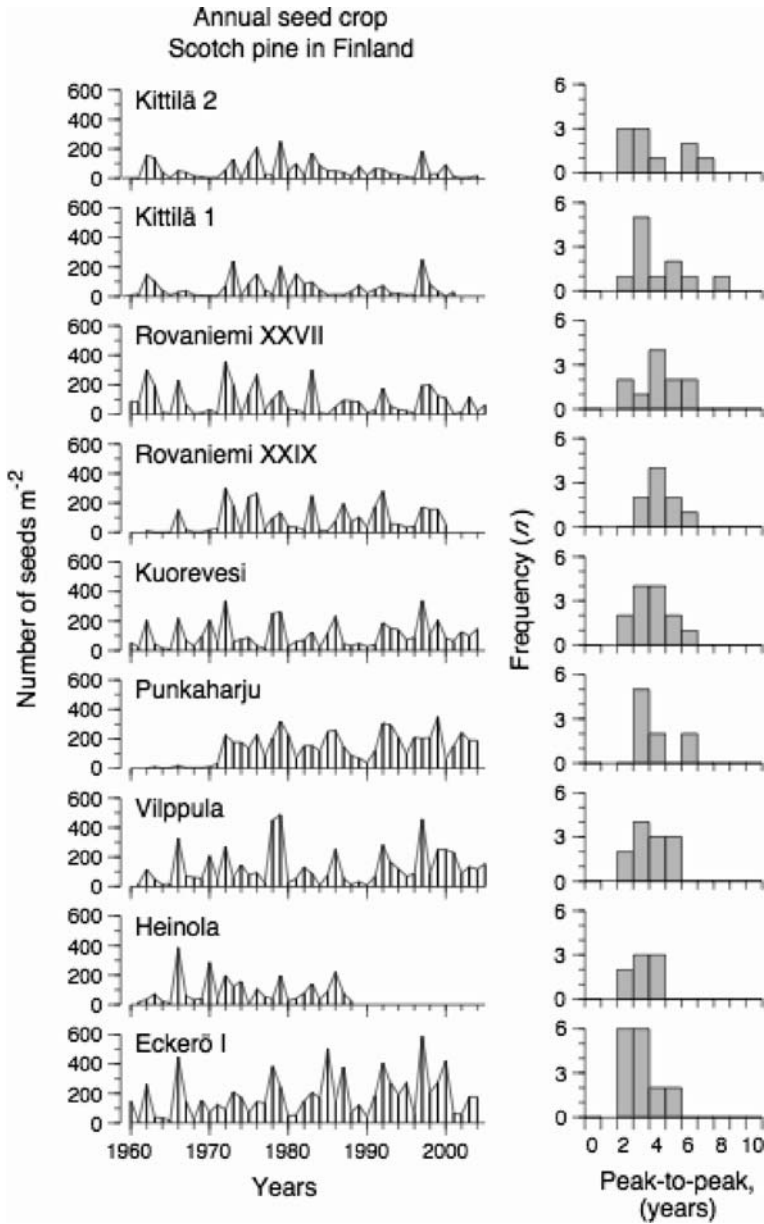
### 15.2.2.1 Seed Crop in Pine and Spruce in Finland

The most important factors influencing the seed crop include variations in climatic and weather conditions, and the internal anatomical, physiological and genetic characteristics of the trees (e.g. Sarvas 1962). There are also other factors regulating the abundance and quality of the seed crop, such as site fertility, stand structure, topography and damages. These factors can be depicted by means of a seed crop concept model (Hokkanen 2000), which illustrates the complexity and multi-phased nature of the ecological process resulting in a seed crop.

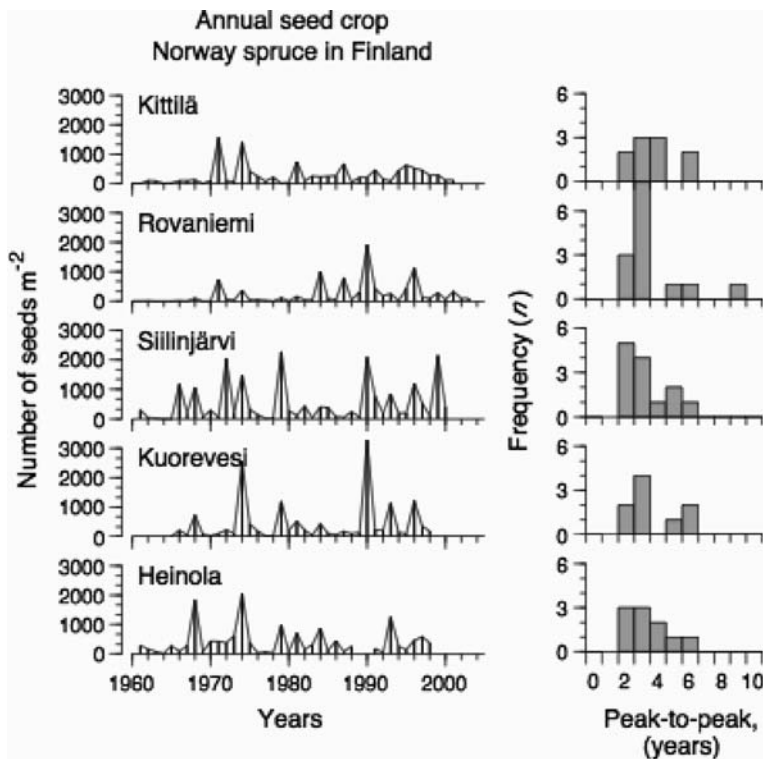
At the end of the 1950's Risto Sarvas, an ingenious forest ecologist, established a nation-wide network monitoring the litter fall, flowering and seed crops of trees in Finland. At its peak, the network included 47 pine and 21 spruce sample plots in different parts of Finland. At present, almost fifty years later, the litter collection is still ongoing at 12 original sample plots. The litter fall collection and seed crop sampling system is described in detail by Sarvas (1962), Koski and Tallqvist (1978), and Kouki and Hokkanen (1992).

Long-term data of Scotch pine and Norway spruce seed crops in Finland immediately corroborate one prediction of this individual based resource-threshold model: reproduction in these trees is not evenly distributed in time. Rather, the data suggest some periodicity in time (Figs. 15.6 and 15.7; compare with Fig. 15.3). Some years are markedly better in terms of seed production than others. In good seed production years pine is capable of producing *ca.* 200 seeds per  $m^2$ , the corresponding capacity for spruce being *ca.* 1000 seeds. In lean years, these numbers are much reduced. However, in those years, the seed production is not reduced evenly, but only some trees produce seeds, whereas in good seed years practically all trees are known to reproduce (Koski and Tallqvist 1978). These observations are in accordance with the model (e.g. Fig. 15.3).

Periodicity of the incidence of life history events is one of the most profound predictions of the resource-threshold model (Fig. 15.3). We addressed the periodicity of the annual seed crop in pine and spruce by using the peak-to-peak analysis (Packard et al. 1980, Rinaldi et al. 2001). In principle, this method calculates intervals between years of high seed production. Frequency distributions of intervals (in years) from one peak to another are shown in Figs. 15.6 and 15.7. As the seed production in both pine and spruce are periodic in Finland, this matches another major prediction of the model in two species.



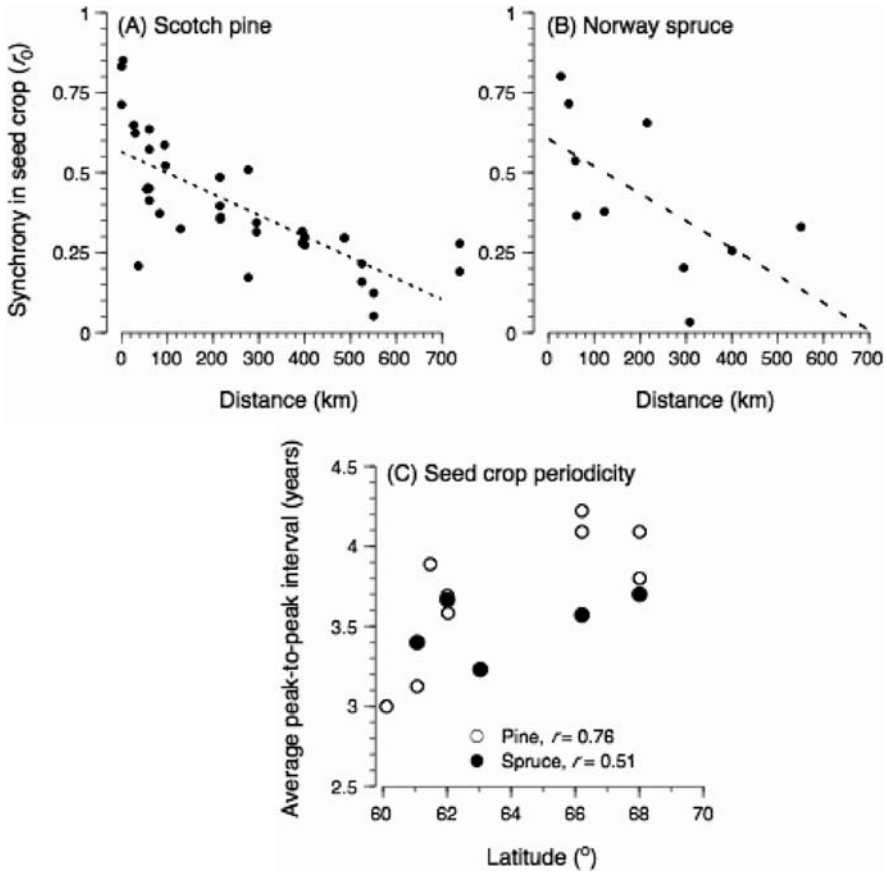
**Fig. 15.6** Annual seed crop in pine in nine localities in Finland (arranged from bottom to top in south to north order). The right-hand histograms give the frequency distribution of peak-to-peak seed years



**Fig. 15.7** Annual seed crop in spruce in five localities in Finland (arranged from bottom to top in south to north order). The right-hand histograms give the frequency distribution of peak-to-peak seed years

Given a resource gradient, or a gradient in the threshold, or both (but with differing slopes), the resource-threshold model suggests that if populations compared are from different parts of the gradient, the degree of synchrony in reproduction decreases with distance. The temporal mismatch in seed production is expected to increase with difference in the ambient environments (Fig. 15.5), and this is another feature readily seen in the pine and spruce data: the synchrony in seed production clearly decreases with increasing distance, perhaps with a steeper slope against distance for spruce than pine (Fig. 15.8a, b).

An interesting fact that we would like to point out is the almost total absence of synchrony between the seed crops in pine and spruce in the same (or very closely situated) stands (Heinola:  $r_0 = 0.09$ ; Kuorevesi;  $r_0 = 0.09$ ; Rovaniemi:  $r_0 = -0.11$  or  $-0.30$ ; Kittilä:  $r_0 = -0.11$  or  $-0.13$ ). These observations show – if nothing else – that the two tree species are either different in their match to resources, or to the threshold needed for reproduction. In fact, this is yet another indication that the resource-threshold model captures some relevant features of the expected life history responses to environmental cues: different species respond to the ambient environment differently (depending on their life histories and thresholds).



**Fig. 15.8** Seed crop synchrony in (a) pine and (b) spruce graphed against geographical distance between the sampling sites. The time series data, based on which the synchrony values are calculated are shown in Figs. 15.6 and 15.7. (c) Seed crop periodicity in pine and spruce against latitude (correlation coefficients are inserted)

The model also suggests – provided that there is a gradient in the resource availability for reproduction – less energy towards north, or in higher altitudes – that the periodicity of the reproduction increases. Calculating averages of the peak-to-peak intervals (right-hand histograms in Figs. 15.6 and 15.7) and plotting the values against latitude of the time series shows that there is indeed an increasing trend in period length towards north (Fig. 15.8c).

### 15.3 Discussion

We have shown with the threshold-triggered phenology model (Section 15.2.1) that the conceptual framework of Moran effect can be extended beyond its original domain in explaining large-scale synchrony in fluctuations of population size.

Here, instead of focusing on synchrony in the overall size of the populations in time and space, we looked at the timing of different phenological events, such as seed production in trees. The model incorporates the idea of a Moran effect by letting an environmental gradient represent the original spatially autocorrelated, density-independent perturbation. The other essential component of the original idea by Moran (1953) concerned the shared structure of density-dependence by the spatially separated populations. When transferring the Moran effect to govern life history events one has to be particularly careful when referring to density dependence and when not. With our two examples, accompanied with explicit Moran noise, we have shown that it is possible to extend Moran's (1953) idea to encompass events not directly regulated by density-dependent feedback. Against this background, it is perhaps not too surprising that phenological events can be synchronized in much the same way as population fluctuations (e.g. Antonovics and Levin 1980).

Similar to our first example, Tryjanowski et al. (2006) monitored first flowering of Early dog violet (*Viola reichenbachiana*) and Horse chestnut (*Aesculus hippocastanum*) over 26 years in Poland and the United Kingdom. They presented annual observations of first flowering dates (*y*-axis) graphed against mean temperature (*x*-axis) in February–March in both countries. For comparison, we generated measures of flowering and temperature synchrony from their data. Calculating the slope (as in Fig. 15.1c) we observe that the synchrony in first flowering dates is shallower in Poland (violet: 2.9 days difference per °C, standard error = 0.25; chestnut 1.6±0.20) than in the United Kingdom (violet: 8.4±0.54; chestnut: 4.2±0.64). This analysis substantiates Tryjanowski et al.'s conclusion that flowering records show much stronger temperature sensitivity in the United Kingdom (where temperatures are much warmer than in the same period in Poland) compared to Poland. With statistical modeling, one can quantify the contribution of the country effect: in the violet data it is almost as strong (based on normalized regression coefficients) as the temperature synchrony effect (violet: 0.47±0.03 vs. 0.58±0.03, country and temperature, respectively; chestnut: 0.47±0.04, vs. 0.32±0.04). This finding suggests that exploring effects of phenotypic plasticity or adaptation to local conditions would be a potentially profitable direction for extending the threshold-triggered phenology model. Incidentally, with the aspen data (Fig. 15.1c, d) if we split Finland into two halves (at 63°N), for the 11 -year period we get the average slope for the southern part to be 2.5 while it is 2.2 for the northern part. A paired t-test found this difference to be statistically significant ( $t_{10} = 2.24$ ,  $p < 0.05$ ). Hence, the data on aspen and violet and chestnut are matching, steeper slope in warmer temperatures. This finding is perhaps an indication that the threshold temperature for the phenology event is somehow related to long-term ambient temperature during the critical period for the life history event in question.

Synchrony in seed production is even more directly analogous to population-dynamic Moran effects. In population dynamics, the Moran effect influences population renewal process that is not very far from seed production. In addition, fluctuations in resource gain can be considered as representing the spatially autocorrelated perturbation, and as resource depletion within individual plants encompasses these fluctuations, this process becomes directly analogous to density dependence within populations. To fully develop the analogy, recall that population dynamic

Moran effects occur because population dynamics are regulated through density-dependent feedback loops (e.g. Royama 1992): once populations are depressed (or elevated) by climate in a particular year, endogenous processes tend to return population sizes towards carrying capacity; this (with or without resonance) tends to keep populations synchronized in future years.

Similarly, resource depletion in individual plants leads to periodic seed production, at least at the capital end of the resource allocation continuum. After a high-resource year, all plants reproduce, all plants deplete their resources below the threshold, and all plants are all part of the same cycle. A key component of this result is that seed production by individuals is inherently periodic over time in our resource-threshold model. For example, Satake and Iwasa (2002) analyzed Moran effects as a possible synchronizing force in seed production using a heuristically similar model of resource depletion. Their model predicted chaotic patterns of seed production by individuals over most regions of parameter space, and therefore autocorrelated fluctuations in resource availability did not synchronize seed production. However, even in their model, Moran effects occurred in the small region of parameter space where seed production by individuals was approximately cyclical. Therefore, we might expect Moran effects to be stronger for phenology of traits that draw on capital resources, such as seed production.

It is interesting to revisit evolutionary theories about mast-seeding in light of the potential for Moran effects to cause synchronous mast seeding. Resource matching has been viewed as a kind of a null hypothesis as it assumes no evolutionary benefits (Rees et al. 2002). It is possible that masting is just a consequence of physiological constraints or selection for reproduction based on stored resources in a variable environment, not necessarily a consequence of selection due to benefits of mast seeding per se, such as predator satiation. Alternatively, it is possible that selection for mast seeding acts to favor life histories at the capital end of the continuum, so that Moran effects are more effective in synchronizing plant reproduction.

The two explanations are not necessarily mutually exclusive. It is quite possible that the primary reason for the observed patterns is based on the physiological constraint mechanism and that that in turn might give predator satiation an advantage that could fine-tune the response to a variable environment. But since plant population dynamics rarely seem to be seed limited (Clark et al. 2007), it is perhaps more likely that what we see is life history and physiologically driven response to the mixed effect of resource acquisition, resource storage and environmental variability with no deeper direct adaptive significance. In either case, it is clear that evaluating mechanisms of synchrony in seed production needs to be done in the context of mechanisms of resource allocation and storage over time, in response to fluctuations in resource availability.

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## Chapter 16

# Applications of Circular Statistics in Plant Phenology: a Case Studies Approach

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**Abstract** Phenology is the study of recurring biological events and its relationship to climate. Circular statistics is an area of statistics not very much used by ecologists nor by other researchers from the biological sciences, and indeed not much visited, till recently in statistical science. Nevertheless, the connection between the evaluation of temporal, recurring events and the analysis of directional data have converged in several papers, and show circular statistics to be an outstanding tool by which to better understand plant phenology. The aim of this chapter is to assess applications for circular statistics in plant phenology and its potential for phenological data analysis in general. We do not discuss the mathematics of circular statistics, but discuss its actual and potential applications to plant phenology. We provide several examples at various levels of application: from generating circular phenological variables to the actual testing of hypotheses, say, for the existence of certain a priori seasonal patterns. Circular statistics has particular value and application when flowering onset (or fruiting) occurs almost continuously in an annual cycle and importantly in southern climates, where flowering time may not have a logical starting point, such as mid-winter dormancy. We conclude circular statistics applies well to phenological research where we want to test for relationships between flowering time and other phenological traits (e.g. shoot growth), or with functional traits such as plant height. It also allows us to group species into annual, supra-annual, irregular and continuous reproducers; to study seasonality in reproduction and growth; and to assess synchronization of species.

**Keywords** Circular statistics · Phenology · Phenological methods · Seasonality · Vector analysis

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## 16.1 Introduction

The relevance of phenology, the study of recurring biological events and their relationships to climatic factors, has increased exponentially over the last decade, as phenology can be used to understand the effects of climatic changes on plant and animal life cycles (Menzel 2002, Schwartz 2003). However, the issue of comparability among phenological studies remains a challenge due to the wide range of methods applied in the collection and evaluation of plant phenology data (Chapters 5, 6 and 20). When we consider the lack of world wide standards for data collection, [as an exception we can cite the Europeans through COST Action 725 (COST 2008), that have developed a standard; see Chapter 5 for further discussion], and the need for core methods of analysis for phenological data, we start to appreciate the difficulties faced by plant phenologists worldwide.

Circular statistics is an area of statistics not much used by ecologists and other researchers from the biological sciences (Fisher 1993). Circular (or directional) statistics is the specific sub-discipline of statistics that deals with directions (unit vectors), axes (lines through the origin) or rotations. The fact that 0 and 360° are identical angles, so that 180° is not a sensible mean of 2 and 358°, provides an illustration that special statistical techniques are required for the analysis of angular (vector) data.

Environmental applications of circular statistics include long-axis orientations of feldspar laths, cross-bed azimuths of paleocurrents, and orientations of pebbles or rock cores (Fisher 1993). Also, the repeating nature of time increments, such as days, months or years, is captured by the wrapping-around of the circle. Further examples include time of the daily maximum temperature, or occurrence of hurricanes during the year, compass directions, dihedral angles in molecules (Anderson-Cook and Otieno 2002), etc.

Applications of circular statistics are to be found in geology, astronomy (Fisher 1993, Evans 2006) and the medical sciences (Mann et al. 2003). Other applications are spread out across several fields such as meteorology (Svensson et al. 2002, Gritit et al. 2006, Kasprzyk 2006), oceanography (Calsbeek and Smith 2003), geography (Liebhold et al. 2004) and biology (Hemmi and Menzel 1995, Alonso 1997, Novotny and Basset 1998, Morellato et al. 2000, Hamer et al. 2005, Prado et al. 2005, Castro et al. 2007). The growing applications for biological sciences justified a book on directional data methods by Batschelet (1981) and the inclusion of circular statistics in a general textbook (Zar 1999), and more recently in software and computational platforms. See for example, Stata, Matlab (2009) (CircStat in the Statistics Toolbox), the free R-project package for circular statistics, namely CircStats (R Project for Statistical Computing 2009) (see <http://riss.acs.unt.edu/Rdoc/library/circular/html/00Index.html>). Lastly Oriana 2.0 (Kovach Computing Services 2009) (see <http://www.kovcomp.co.uk>), which is the only platform dedicated specifically to circular statistics. Also important is Jammalamadaka and SenGupta's (2001) research monograph on circular data analysis which contains S-plus subroutines for analyzing actual data sets.

It is noteworthy that recently circular statistics is gaining prominence in the highly complex area of computational biology and proteomics (Mardia et al. 2007, Boomsma et al. 2008); also in bird ecology (Sutherland et al. 2004) and in other ecological studies (Herrera 1988, Morellato et al. 2000, Anderson et al. 2005, Ting et al. 2008). For instance, Ting et al. (2008) applied circular vector algebra to characterize seasonal peaks in fruit production (mean date, as an angle) and the length of fruiting seasons (as a circular standard deviation), and circular correlations to connect geography and climate to timing of fruit production in fleshy fruited plant communities.

Most of the earlier animal and plant applications of circular statistics analysis in biological sciences concern the analysis of directional data, for instance, the orientation and direction of movements of animals, such as flight direction of birds and butterflies and the orientation on salamanders and dragonflies (Batschelet 1981, Fisher 1993). Nevertheless, the connection between the evaluation of temporal, recurring events and the analysis of directional data have converged in several papers, and shown circular statistics to be an excellent tool by which to describe and to compare both plant and animal phenology (Herrera 1988, Wolda 1988, 1989, Morellato et al. 1989, 2000, Milton 1991, Alonso 1997, Davies and Ashton 1999, Hamer et al. 2005, Zimmerman et al. 2007). Milton et al. (1982) was one of the first studies to apply circular statistics to analyse phenology.

The aim of this chapter is to assess the applications of circular statistics on plant phenology and its potential for phenological data analysis in general. We do not discuss the mathematics of circular statistics, a rather complex issue, but focus on its actual and potential applications in the science of plant phenology. We provide examples for the application of circular statistics in plant phenology, from the generation of so-called phenological variables to testing hypotheses of random (uniform) versus non-random seasonal patterns. In summary circular statistics includes tests of uniform direction around the circle (which may represent a year), intervals, and tests for comparing two groups of directions, circular graphs, correlations, and regression, among others. Finally, we discuss the still unexplored potential of circular statistics to plant phenological studies. We conclude that circular statistics is a developing field of application for the analysis of plant phenological data; and its application is highly recommended for researchers who aim to unravel phenological patterns and to formally compare and test hypotheses on plant phenology.

## 16.2 Circular Statistics

### *16.2.1 Definition of Circular Scale and Circular Distribution*

The first aspect of application of circular statistics is to understand how the basic parameters of circular statistics correspond to traditional linear statistics. There are classic books (Mardia 1972, Batschelet 1981) and other good sources of information on directional data (Upton and Fingleton 1989, Fisher 1993, Mardia and Jupp 2000,

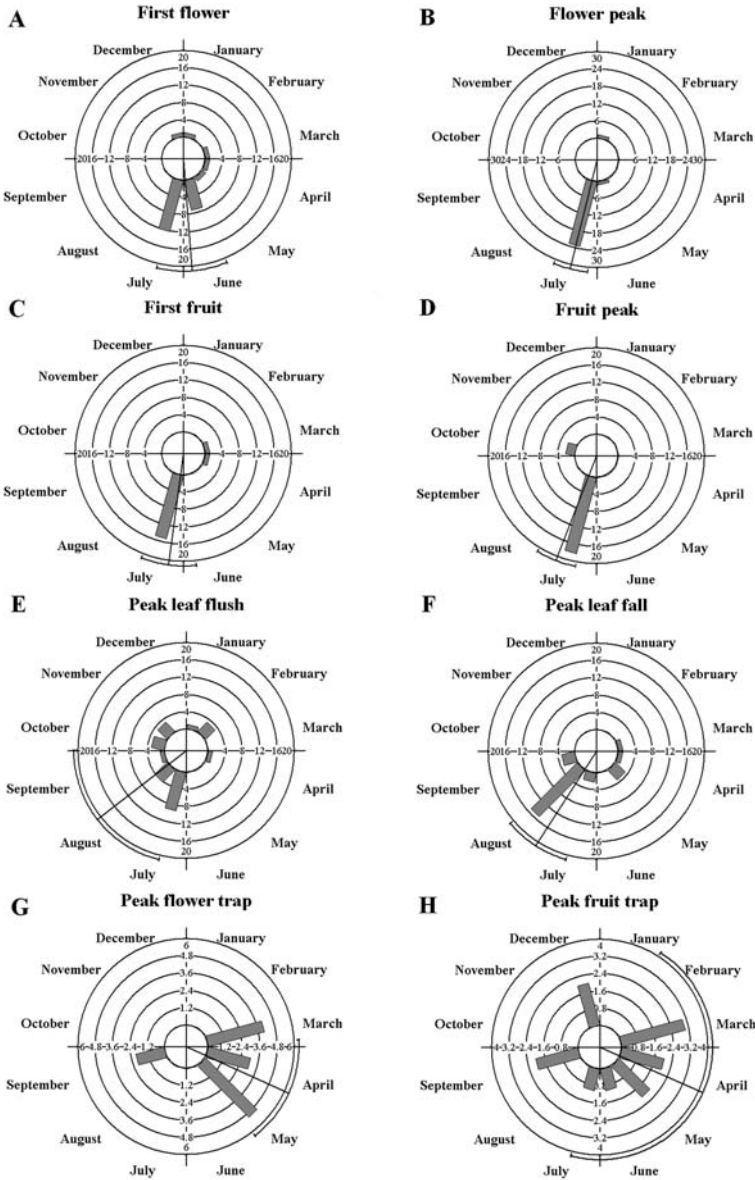
Jammalamadaka and SenGupta 2001), and the literature cited therein. The basics to circular distributions and test statistics of hypotheses for directional data are clearly explained by Zar (1999, or any other edition) for a beginner. To further discuss the applications of circular statistics in plant phenology it is necessary to briefly introduce the terms we use in this chapter and, where appropriate, their correspondence with linear data. The terminology follows Zar (1999), and the definitions are mostly according to Batschelet (1981) and Fisher (1993).

A circular scale is a special type of interval scale, where not only is there no true zero, but indeed any designation of high or low values is arbitrary. The best example of the circular scale are compass directions (North, South, East, West and its intervals), where the circle is divided into 360 equal intervals or degrees. Other illustrations of a circular scale are times of day and months of year, a familiar scale for any phenologist, dealing with daily, monthly or annual cycles. For example, at an annual level, one month of the year corresponds approximately to  $30^\circ$  ( $360^\circ/12$ ) of a circle, and  $\sim 1^\circ$  to one day. Time is also circular when it measures part of a cycle, such as the timing of a daily event; however, time is linear when it measures length of time, such as the number of days since an event.

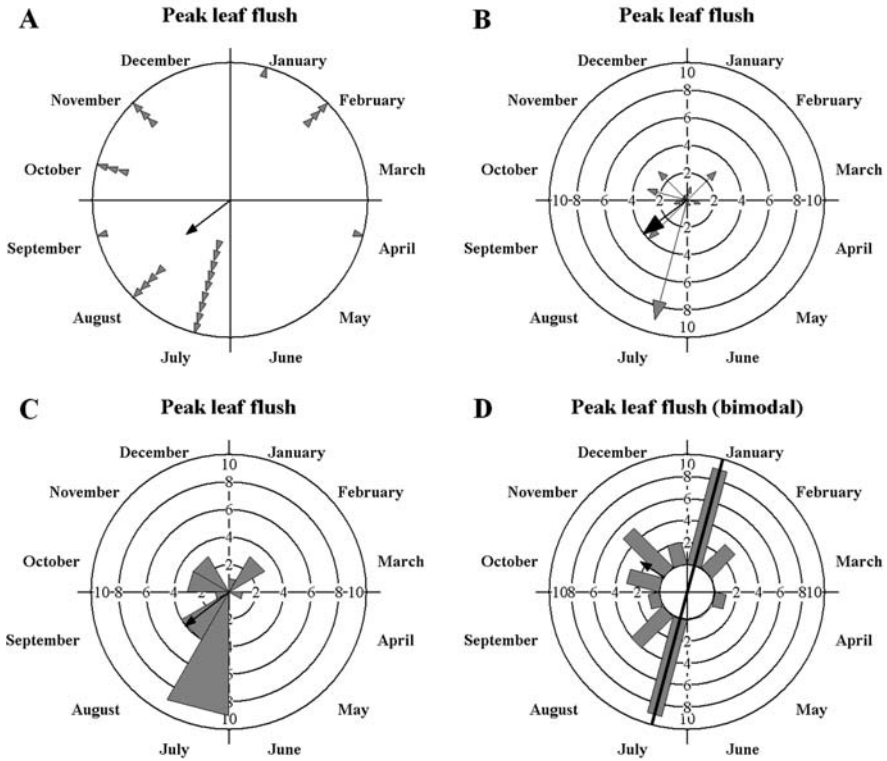
Apart from long standing theoretical reasons, data from circular distributions may not be analysed by traditional linear statistics for empirical reasons even purely based on such arbitrariness of the zero point on the circular scale (Mardia 1975, Batschelet 1981, Zar 1999). Henceforth, any time unit ( $X$ ) can be converted to an angle ( $a$ ) on the circular scale (16.1), where  $k$  is the total time units in the full cycle, we have then that:

$$a = \frac{(360^\circ)(X)}{k} \quad (16.1)$$

In terms of plant phenology applications, any date of observation (month, week or day) can be converted to an angle, and the frequency of observations at that angle or date is then plotted (Figs. 16.1 and 16.2). For instance, if we are considering monthly observations, these circular data divide the  $360^\circ$  range into 12 groups, corresponding to months of the year, where January is the first and December the last. The dates are conventions defined by the authors, who generally try to include a high number of complete phenological cycles (see Herrera 1988 for a good example). January as the lower degree makes angles easily comparable. Each sector or interval is  $30^\circ$  wide and, by convention, the midpoint of the sector is the angle representing a month, for example January being  $15^\circ$ , February  $45^\circ$  and December  $345^\circ$ . When dealing with circular distributions it is important to define the nature of the data used, that is delineate angles (0 to  $360^\circ$ ), compass direction (N, S, SE, etc), time (time in hours, day of week, month of year, day of year), or a date (the specific date when data were collected). As a time scale is naturally in intervals, this type of data is grouped in nature (see Fisher 1993), an aspect which may restrict the application of some circular statistical tests or may need some correction factor, depending on the nature of the grouped interval and the number of groups (Batschelet 1981, Fisher 1993). The correction for grouped data works only for variables exhibiting a unimodal distribution, or one mode or modal angle. The use of a correction factor is, however,



**Fig. 16.1** Circular histograms of the frequencies of species of each phenological variable for the semideciduous altitudinal forest data of Table 16.1. The vector line in the circle indicates the mean angle or direction and the sector outside the circle indicates the 95% confidence interval. Note that in histogram H there are no mean directions and the confidence limit is unreliable. For the purpose of this book, this was painted in black instead of the traditional red output given by Oriana. In each histogram the longest grey bar represents the main mode



**Fig. 16.2** Raw (a) and arrow data plots (b), and rose diagram (c) for the same frequencies of species for peak of leaf flush of the semideciduous altitudinal forest data of Table 16.1 and Fig. 16.1e. The bold arrow represents the  $r$  vector. (d) shows the bimodal data for leaf flush, where the bold arrow inside the circle indicates the nonsensical mean angle or direction calculated (as here the bimodality of the data has not been taken into account), and the tick line crossing the circle from July to January indicates the opposite angular directions of the bimodal distribution, calculated as in Zar (1999)

optional for more than 12 groups (Batschelet 1981), favouring the idea of increasing the frequency of observations (Chapter 5). For instance, biweekly intervals lead to 24 groups, and improves the application of the Watson-Williams  $F$  test (Batschelet 1981) for further comparisons. After overcoming the restriction of grouped data, we are then able to calculate the mean angle  $\bar{a}$  (a correlate but in a sense similar to the linear mean): the computations consider the sum of the sine and cosine of  $n$  angles  $a$ , and the rectangular coordinates and the length of the mean vector  $r$  is calculated, and the mean angle  $\bar{a}$  is thus defined (Table 16.1, Fig. 16.1). The resultant mean angle is obtained by calculating the inverse tangent. The mean angle can be back converted to a mean date (Table 16.1), based on the same formula (16.1) above, given the time of year around which the phenological activity is most concentrated. Definitions and formulations of sine, cosine and inverse tangent functions are given on the Wikipedia (2009) web link [http://en.wikipedia.org/wiki/Trigonometric\\_functions](http://en.wikipedia.org/wiki/Trigonometric_functions).



**Table 16.1** Results summarizing the main descriptive variables of a circular statistics analysis and the basic tests for uniformity of distribution, applied to the data extracted from Chapter 5 (Table 5.1), for the phenology transect (% of trees) and traps (dry weight), in the semideciduous altitudinal forest of Serra do Japi, Southeastern Brazil. NS = non significant values. Shaded lines: tests completed considering the data as not grouped. Calculations were performed using the Oriana 2.0 program

	First flower	Peak flower	First fruit	Peak fruit	Peak leaf flush	Peak leaf fall	Peak flower trap	Peak fruit trap
Number of observations	24	27	17	20	28	14	13	13
Group width (& number of groups)	30° (12)	30° (12)	30° (12)	30° (12)	30° (12)	30° (12)	30° (12)	30° (12)
Mean angle ( $\bar{\alpha}$ ) [mean vector ( $\mu$ ) Oriana's nomenclature]	175.51°	195°	187.68°	201.34°	254.44°	219.05°	117.84°	113.79°
Mean date	25/June	15/July	08/July	21/July	-	09/July	27/April	-
Mean group	June	July	July	July	September	August	April	April
Length of mean vector ( $r$ )	0.72	0.86	0.87	0.92	0.35	0.70	0.73	0.32
Median	195°	195°	195°	195°	255°	225°	135°	105°
Median group	July	July	July	July	September	August	May	April
Concentration	2.165	3.923	4.147	6.234	0.753	1.989	1.734	0.456
Circular variance	0.276	0.138	0.13	0.084	0.648	0.303	0.274	0.677
Circular standard deviation	46.04°	31.27°	30.25°	24.01°	82.77°	48.66°	45.87°	86.18°
Standard error of mean	9.34°	6.00°	7.32°	5.36°	20.66°	9.19°	13.65°	41.42° <sup>a</sup>
95% Confidence interval (-/+)	157.12° 193.82°	183.24° 206.76°	173.32° 202.01°	190.83° 211.85°	213.94° 294.95°	201.03° 237.08°	91.08° 144.60°	32.60° <sup>a</sup> 194.99° <sup>a</sup>

**Table 16.1** (continued)

	First flower	Peak flower	First fruit	Peak fruit	Peak leaf flush	Peak leaf fall	Peak flower trap	Peak fruit trap
99% Confidence interval (-/+ ) for $\mu$	151.45°	179.55°	168.82°	187.53°	201.21°	195.37°	82.68°	7.09°a
Rayleigh test (Z)	199.57°	210.45°	206.51°	215.15°	307.68°	242.74°	153.00°	220.50°a
Rayleigh test (P)	12.58	20.05	12.86	16.78	3.60	13.61	7.38	1.35
Rao's Spacing test (U)	$6.32 \times 10^{-7}$	$3.75 \times 10^{-9}$	$5.72 \times 10^{-7}$	$6.69 \times 10^{-8}$	0.026	$2.64 \times 10^{-7}$	$2.18 \times 10^{-4}$	0.263NS
Rao's Spacing test (P)	255	270	275.29	315	248.28	270	257.14	166.15
Rao's Spacing test (U)	< 0.01	< 0.01	< 0.01	< 0.01	< 0.01	< 0.01	< 0.01	NS
Watson's $U^2$ test (Uniform, $U^2$ )	0.911	1.314	0.75	1.179	0.289	0.869	0.472	0.104
Watson's $U^2$ test (P)	< 0.005	< 0.005	< 0.005	< 0.005	< 0.01	< 0.005	< 0.005	NS
Kuiper's test (Uniform, V)	3.615	3.857	3.316	4.04	2.375	3.269	2.735	1.423
Kuiper's test (P)	< 0.01	< 0.01	< 0.01	< 0.01	< 0.01	< 0.01	< 0.01	NS
Chi-Squared test (Uniform, $\chi^2$ )	75	230.33	b	b	31.83	86	b	b
Chi-Squared test (P)	$1.36 \times 10^{-11}$	0	b	b	$8.13 \times 10^{-4}$	0	b	b

a – value may be unreliable because of low concentration (uniform distribution)

b – indicates that a result could not be calculated

We refer the reader particularly to the unit-circle definitions of the sine, cosine and inverse tangent trigonometric functions and the unit-circle figure shown in [http://en.wikipedia.org/wiki/Trigonometric\\_functions](http://en.wikipedia.org/wiki/Trigonometric_functions).

It is important to remember that the angle of the mean vector (and the corresponding date) do not necessarily point to the time of peak activity, as can be seen in Fig. 16.1g, but indicates the central tendency of the data. The peak of activity is given by the modal angle, defined afterwards. Here  $r$  is the length of the mean vector, a measure of concentration of frequencies around the estimated mean angle  $\bar{a}$  (Table 16.1). The value of  $r$  has no units and varies proportionally with the amount of concentration in the data, from zero (when there is so much dispersion that a mean angle cannot be described) to one (when all the data are concentrated at the same direction or angle). Although not used in most phenological applications to date, one could calculate the circular deviation around the mean angle (in degrees), and additional estimators of angular dispersal, such as the circular variance  $S^2$ , angular variance  $s^2$  and standard variance, the angular deviation and the circular standard deviation, as well as the confidence limits for the population mean angles (Table 16.1, see Zar 1999), which can also assist in the detection of deviations from a unimodal distribution. Circular distributions can thus well represent varying amounts of concentration, corresponding to the values of  $r$  (Table 16.1 and Fig. 16.1)

Underpinning this approach is the assumption that the equivalent in circular statistics, to the Gaussian or normal distribution in conventional statistics, is the von Mises distribution (Fisher 1993). This distribution on the circle is probably the best known distribution in the field of directional statistics. The von Mises distribution is widely used to model the type of angular data described above, where an angle is represented here by a two-dimensional unit vector (that is, a point on the circle).

More frequently used to estimate phenological variables for plants is the median angle, to represent the centre of phenophase duration for a given species and, the modal angle, meaning the phenophase peak (Fig. 16.1). The median angle is defined in two steps: first one determines which diameter of the circle divides the data into two equal sized groups; then the diameter's radius, near to the majority of the data points, is taken to be the median angle. The modal angle is defined in the same way as for the linear scale and, as with linear data, there may be more than one mode or in fact no mode. The median angle may coincide, or not, with the mean angle (Table 16.1 see peak flower and first fruit, respectively).

There are cases of bimodal or multimodal distributions that may restrict the application of some circular tests (Batschelet 1981). A bimodal distribution occurs when, for instance, there are two peaks (modes) on the opposite sides of the circumference (see Morellato et al. 1989, Zimmerman et al. 2007). For example, the results of Rayleigh test for leaf flush data on Table 16.1, although significant, are unreliable due to low concentration of data, indicating a tendency to uniform or multimodal distribution. If we add eight records in January for the data from Table 16.1 on peak leaf flush, and Fig. 16.1e, we produce the distribution depicted on Fig. 16.2d,

with two modes, one in January and the other in July. The new mean vector is then smaller ( $r = 0.25$ ) than the previous from a unimodal distribution ( $r = 0.39$ ). If one applies the Rayleigh test (Batschelet 1981) we again would not reject the null hypotheses of a uniform distribution. Note, however, here we should reject the null hypotheses, since the distribution is bimodal (a type II error). In this case, after detecting, by visual inspection, a bimodal distribution (Fisher 1993), a specific procedure has to be adopted (Zar 1999), as follows: the bimodal distribution has to be converted to a unimodal variant, this by reducing the angles to one side of the circle (Zar 1999): then the Rayleigh test can be applied, and the mean angular direction re-calculated, and thus converted to give the two mean directions of the data (Fig. 16.2d). In this case no  $r$  value is estimated in the case of bimodal distributions.

As advised by Fisher (1993), it is always important first to look carefully at your data when analyzing circular distributions; this should occur before the interpretation of and performing of any circular tests. In the case of peak leaf flush in Table 16.1, although the Rayleigh test was significant, an examination of the circular diagram (Fig. 16.1e) shows a multimodal distribution, supported by the low  $r$  value, low concentration values and by the wide confidence limits (Fig. 16.1e). Hence the results are unreliable due to the low concentration of the data. However, the distribution of leaf flush peak is not uniform around the year (Table 16.1 peak leaf flush).

### ***16.2.2 Graphing and Describing Phenology Using Circular Distributions***

The best graphical representation of phenological data is a circular histogram, with the length of each bar representing the relative frequency of a given phenological variable observed at a given date or angle (Fig. 16.1a-h). We can add information to the circular diagram, such as the direction of the mean angle and 95% confidence intervals (Fig. 16.1a-h), the circular variance, or vector  $r$ . When plotting the  $r$  vector, the vector length should correspond to its value, and it also should point to the mean angle. Other representations exist, such as the raw data plot, arrow data plot and the rose diagram (Fig. 16.2a-c, respectively), which are very well discussed by Batschelet (1981) and Fisher (1993) in their chapters on circular data types and its representation (see also Oriana 2.0 software). The arrow data plot makes the modal angle more visible, while rose diagrams may misrepresent the importance of each angle frequency (Fig. 16.2b, c). The box-plot is an alternative representation for unimodal data (Fisher 1993). Some authors have used lines to connect the frequency value at each angle, demarcating an area inside the circle (Batalha and Martins 2004): this should be avoided as it gives the impression of dependence amongst the angles.

## 16.3 Applications of Circular Statistics to Phenological Data

Here we present a dozen examples, based on the current literature, of the application of circular statistics to plant phenology. We hope in this context to provide a practical approach, aiming to encourage phenologists to consider circular statistics as a viable and user-friendly tool by which to analyse phenological data.

### 16.3.1 *The Estimation of Phenological Variables Using Descriptive Circular Statistics and the Vector $\mathbf{r}$*

The definition of mean time of occurrence of a given phenophases, as the angle of the mean vector  $\bar{a}$ , is among the most widespread uses of vector algebra to plant phenological variables. Its application to phenological data from litter traps, instead of direct observation, is very well exemplified by Wright and Calderon (1995), Wright et al. (1999) and Zimmerman et al. (2007). Boulter et al. (2006) also employed the angle of mean vector to estimate the mean flower time or flower midpoint for herbarium data (over 36,774 records), and used the length of the mean vector  $r$  as a measure of the concentration of phenological activity. The daily concentration of airborne pollen for several species has also been estimated by circular statistical methods and its resultant parameterization (Kasprzyk 2006).

### 16.3.2 *Synchrony and Aggregation of Phenological Activity*

Descriptive statistics for circular distributions have been used to quantitatively characterize plant phenology at the individual and the species level. The length of the mean vector  $r$  has been used as a measure of the temporal concentration of phenological activity, with high  $r$  values, indicating aggregate phenological activity. For instance, Herrera (1988) analyzed the individual variations on fruit phenology of *Osyris quadripartita* using the mean angle as the centre of fruit period and the range and mean of the individual values of vector  $r$  as an indicator of the level of seasonality. To assess the annual variation in fruit phenology, Herrera (1988) calculated the  $\bar{a}$  and  $r$  for individual plants in each of the four annual cycle studies and compared the resulting  $r$  values. Herrera was able to detect differences of phenological patterns and the degree of seasonality among individuals and among years, demonstrating how an unusual year affects the mean fruiting date. In a similar way, Davies and Ashton (1999) applied the mean angle and vector length  $r$  at the individual and population level to indicate time of temporal aggregation or synchrony of reproductive activity of *Macaranga* species from Borneo forest. They found, for instance, a large population  $r$  indicating a high degree of intraspecific reproductive synchrony, while the elevated individual values for  $r$  reveal a reasonably short reproductive duration (Davis and Ashton 1999). In another application Pico and Retana (2001) calculated

the mean angle and  $r$  for each individual of *Lobularia maritima* over five flowering seasons, using the proportion of flowering stems per month in each individual plant as a circular frequency distribution (with data grouped at  $30^\circ$ ). The mean angle calculated by Pico and Retana (2001) represents the average date of phenological activity and  $r$  the degree of temporal aggregation or synchrony of reproductive activity for an individual or species. They determine differences among years in the flowering mean dates, comparing the mean angles using a Kruskal-Wallis ANOVA (Pico and Retana 2001), since the  $r$  values were too low to allow a circular test, as described below.

### ***16.3.3 Testing Hypotheses for Circular Distributions and Comparing Phenological Patterns***

Hypothesis testing for circular distributions is a valuable tool for phenology (see Morellato et al. 2000). The choice of the statistical test should depend on the previous assumptions based on exploratory analysis, such as a graphical display of the data (Fisher 1993).

The most straightforward circular test of hypotheses is the test for circular uniformity or significance of the estimated mean angle called the Rayleigh test. This test shows how large a sample  $r$  must be to indicate a nonrandom population distribution. The “Rayleigh’s  $z$ ” is utilized for testing the null hypothesis of no population mean direction. The null hypotheses  $H_0$ : states that the population samples are uniformly (or randomly) distributed around the circle; the alternative hypothesis  $H_A$ : the population samples do not show a uniform (or random) circular distribution. If the null hypothesis is rejected, we conclude that there is a significant mean population direction or angle (or date); otherwise we conclude the distribution to be uniform around the circle.

The length of the mean vector  $r$  gives some indication of unimodality; if  $r$  is sufficiently large, usually more than 0.5, the hypotheses of randomness can be rejected. Rayleigh’s test assumes a unimodal distribution or that the population does not have more than one mode. If a unimodal population distribution is assumed from the beginning, a significant Rayleigh test indicates a concentration around the mean angle or direction, or a preferred direction (Batschelet 1981). Note that there are some restrictions when employing conventional circular statistics calculations and tests to grouped data (Batschelet 1981, Fisher 1993); but the correction of Rayleigh is easy to apply. Both tests lead to the same results (Table 16.1), probably due to the robustness of the Watson-Williams test (Anderson-Cook 1999, Zar 1999).

An alternative to the Rayleigh test for uniformity is the V test (Batschelet 1981) applicable if a specific direction or date is expected. If for some reason one can assume a direction for the distribution of the data (for instance, if the fruit season of wind dispersed fruits is expected to fall in the dry season) we can test against a specified angle. In the example of Table 16.1, we could assume an expected mean

angle based on the previous phenological work from Morellato et al. (1989) at the very same forest site. Based on this work, testing considers a  $H_0$  = flowering population dates are uniformly (or randomly) distributed around the circle or year, and  $H_A$  = flowering population dates are not uniformly distributed around the year, but have a mean angle of  $225^\circ$  (August, 15). The resultant  $V$  (expected mean  $225^\circ$ ) = 0.74 and the  $V$  test ( $u$ ) = 5.42,  $P < 1 \times 10^{-5}$ , hence we reject  $H_0$ . The same test procedure could be performed for leaf fall, the expected mean based on Morellato et al. (1989) is  $164^\circ$  (June, 14); the resultant  $V$  (expected mean  $164^\circ$ ) = 0.39, the  $V$  test ( $u$ ) = 2.95,  $P < 0.001$ , again we reject  $H_0$ . The  $V$  test is sufficiently powerful to detect clustering around a predicted date, but the Rayleigh test remains powerful for aggregation on any part of the circle (Batschelet 1972).

Therefore, the Rayleigh test allows, as proposed by Morellato et al. (2000), for the detection of significant seasonal patterns (significant mean direction), the definition of a degree of seasonality ( $r$ ), and the further application of a two or multiple sample test (see details below) to test hypotheses regarding the comparison of phenological patterns (mean angles or dates). Comparisons can be performed among phenophases, sites, life forms, and vegetation types (Morellato et al. 1989, 2000, Talora and Morellato 2000, Batalha and Martins 2004, Zimmerman et al. 2007), species (Cruz et al. 2006) or populations (Osada et al. 2002, Brando et al. 2006, Castro et al. 2007). For instance, while Castro et al. (2007) compared the reproductive phenology of *Euterpe edulis* (Arecaceae) at three contiguous sites of Atlantic rain forest, Brando et al. (2006) tested for variations in the fruit phenology of *Coussarea racemosa* (Rubiaceae) under different experimental drought conditions across years. Cruz et al. (2006) employed the test for nonrandom flowering phenology as well as displaying flower visitors' seasonality. Whilst the mean vector  $r$  has been interpreted as a measure of aggregation or synchrony, different interpretations may be found in the literature (Hamrann 2004). ter Steege and Persaud (1991) have applied circular statistics to define uni- or multimodality of flowering for Guianese timber species. They demonstrated that unimodal species have a high  $z$ -value for the Rayleigh test and multimodal species a low  $z$ -value, and calculated an index of modality (ter Steege and Persaud 1991). The problem of multimodal and bimodal data distributions (sub-annual patterns) is still a challenge to implementing rigorous seasonal data analysis (Wolda 1988), but an excellent approach has been presented recently by Zimmerman et al. (2007).

Working with the phenology of tropical forest trees, Morellato et al. (2000), have proposed a test for the occurrence (or absence) of seasonal phenological patterns within sites using the Rayleigh test; and compared patterns among four different forest sites by applying the Watson-Williams test ( $F$ ) statistics (Anderson-Cook 1999, Zar 1999), detailed below. For all sites, based on monthly observations, they calculated reproductive and vegetative phenological variables to characterize the phenology of each species, such as date of first flowering, date of first fruiting, date of peak flowering, date of peak fruiting, date of peak leaf flushing, and date of peak leaf fall. This procedure is important since, under the assumptions of circular statistics, data around the circle are independent. If we just calculate the frequency of species or the frequency of individuals to each month or angle, the same species

may be considered in more than one month, since the duration of each phenophase, for instance flowering, is usually longer than the sample interval (month).

To calculate circular statistics based parameters, months were converted to angles, from  $0^\circ$  = January to  $330^\circ$  (December) at intervals of  $30^\circ$ . The frequency of occurrence of species of each phenological variable within each angle was calculated and the circular parameters estimated for each study site (mean angle  $\bar{a}$ , angular dispersion, confidence limits of the frequency distribution for each phenological variable and vector  $r$ ). To test for the occurrence of seasonality Morellato et al. (2000) rephrased the hypotheses tested as follows:  $H_0$  = dates are uniformly (or randomly) distributed around the circle or year (i.e. there is circular uniformity or no mean direction and consequently no seasonality);  $H_A$  = dates are not uniformly distributed around the year (i.e. there is a significant mean angle or mean direction and consequently, there is some seasonality). The Rayleigh Z test was applied and if  $H_0$  was rejected, the intensity of concentration around the mean angle, denoted by the vector  $r$ , was considered as a measure of the degree of seasonality, ranging from zero (when phenological activity is uniformly distributed through the year) to one (when phenological activity is concentrated around one single date or time of the year). If  $H_0$  was accepted, then  $r = 0$  and if no bimodal or multimodal distribution was detected it's possible to conclude that the data do not exhibit significant seasonality as reported in Morellato et al. (2000) using Zar (1999)

To compare seasonal phenological patterns within and among sites, when the mean angle  $\bar{a}$  was significant, Morellato et al. (2000) performed the two-sample Watson-Williams test ( $F$ ): to (a) compare the mean angles  $\bar{a}$  among the phenological variables within sites (so as to determine whether they exhibit similar seasonal patterns); and (b) compare the mean angle  $\bar{a}$  of each phenological variable among sites, to determine if the different sites exhibit a similar seasonal pattern or mean angle  $\bar{a}$  (Zar 1999). The hypotheses tested were:  $H_0$  = the samples are from populations with the same mean angle;  $H_A$  = the samples are not from populations with the same angle. The Watson-Williams test ( $F$ ) was utilized in Chapter 5 to compare the mean phenological patterns between traps and direct observation.

Castro et al. (2007) follow the same procedure to test if the reproductive phenology of *Euterpe edulis* (Arecaceae) differed among years and among three contiguous sites of Atlantic rain forest, while Cruz et al. (2006) used the same procedure to test if flowering patterns differed between species of Bromeliaceae. The same comparison was performed by Herrera (1988) to investigate possible differences among the study years regarding the mean fruiting angle in a population of *Osyris quadripartita*. Herrera (1988) was the first to apply the Watson-Williams test to study whether the mean fructification angle differed among populations of *Osyris quadripartita*, demonstrating that the population's phenology changed according to variations in rainfall. At the community level, Batalha and Martins (2004) employed the Watson-Williams test to evaluate if mean flowering times were significantly different between herbaceous and woody components of a savanna community and if mean fruiting patterns were different among seed dispersal modes. It is important to remember that the Watson-Williams test assumes that the samples are independent



(Batschelet 1981). In the examples above this translates to the time of occurrence of phenophases assumed to be independent.

Circular statistics can also be applied to test specifically for non-random temporal patterns (Batschelet 1981). For these analyses, year is represented by a circle divided into the number of segments that represent the interval of observations (12 months or  $30^\circ$  in the example on Table 16.1 and Fig. 16.1). The mean angle is back-converted to a mean calendar date representing the average date of phenological activity. The Rayleigh test is thus applied to determine if the distribution of phenological activity is not uniform or nonrandom (Davies and Ashton 1999, Osada et al. 2002, Batalha and Martins 2004). It should be used only in the case of unimodal distributions (Batschelet 1981). The Hodges and Ajne sign test is a valid option if the alternative is a unimodal distribution (Batschelet 1972).

If the objective is to detect any departure from a uniform or random distribution, other tests may be more appropriate. For example Kuiper's goodness-of-fit test, the circular version of the Kolmogorov-Smirnov test for one sample (Batschelet 1981), was used by Milton (1991) to detect whether or not the timing of phenological events for each Moraceae tree was randomly distributed around the year. The null hypothesis states that the phenological data are drawn from a uniform distribution. Note that Kuiper's test, although not recommended for groups larger than  $5^\circ$ , is more sensitive to departures from uniform and multimodal distributions than is the Rayleigh test (Batschelet 1972), but the latter is stronger if we assume a unimodal distribution. A test powerful for both unimodal and multimodal distributions is Rao's Spacing test (Jammalamadaka and SenGupta 2001). If the data is grouped and the expected frequencies are larger than four, the chi-square test ( $X^2$ ) is a best option (Batschelet 1981).

In summary, it is important to keep in mind that the examples of Figs. 16.1 and 16.2d and Table 16.1 are illustrative. As is the case for traditional statistics, a low sample size, usually below 25 can be problematic. Circular tests would then work better if one applied bootstrapping techniques (Fisher 1993). A very large sample size, on the other hand, may lead us to consider as significant very low  $r$  values. It is fundamental that we keep in mind the biological meaning of your interpretations.

## 16.4 Further Circular Methods: a Quick Overview

Calculating confidence intervals on the parameters of circular data, though not discussed here, can be approached using resampling methods (Manly 1991, Crowley 1992). Heideman and Utzurrum (2003) used randomization methods with circular statistics to test for synchrony and seasonality of reproduction in three species of nectarivorous bats on the Negros Island in the central Philippines. Stark and Abeles (2005) gave a unified framework for the use of resampling methods to construct specific tests for placing confidence limits on parameters of circular data, and specific procedures for testing hypotheses on circular data, in the context of neurophysiological data analysis, via an illustration with real data from monkey behaviour

experiments. Aspects covered by Stark and Abeles (2005) were also non-parametric confidence limits of circular parameters; testing circular distributions for equality and circular permutation tests.

Tests for synchrony are also discussed in chapter 15 of this book, and tests for seasonality in the chapter on singular spectrum analysis. Circular cross correlation (see Oppenheim et al. 1999, Zimmerman et al. 2007) is one advancement not discussed in detail in this chapter. However, the method is now available in Matlab 7.5 (use the CXCORR command). Note that  $CXCORR(a,b)$ , for  $a$  and  $b$  represent samples taken over time interval, which is assumed to be a common period of two corresponding periodic signals (phenological series) each of length  $M$  row vectors. Then the Matlab command  $[x,c]=CXCORR(a,b)$  returns the length  $M-1$  circular cross correlation sequence  $c$ , with corresponding lags  $x$ . For the calculation of a circular covariance between  $a$  and  $b$  use  $CXCOV(a,b)$  (see <http://www.mathworks.com/matlabcentral/>). Wavelet cross correlation methods for bivariate time series are also discussed in Chapter 17 of this book when relating either bivariate phenological-series or say one phenological-series with climate time series indicators. See also the cross correlation methods based on the SSA reconstructions of both phenological and climate time series in this book (Chapter 18).

The detection of change points is also one advancement in circular statistics that is not given here in detail. Change point problems on a circle for directional data (see Jammalamadaka and SenGupta (2001) can now be applied using the “change.point” command in Circular statistics in R (see <http://rss.acs.unt.edu/Rdoc/library/circular/html/00Index.html>). Change point methods for linear scaled data are discussed in other chapters of this book (Chapter 11, Chapter 19).

Other circular procedures not discussed here involve analysis of variance for circular data (Harrison and Kanji 1988) and circular-circular and circular-linear regression. There is a novel suite of graphical representations of circular data available in Oriana 2.0 and in Matlab. These include rose plots, plots for kernel density estimation for circular data, plots of circular empirical distribution functions, and fitting a two dimensional circle to bivariate  $(x,y)$  data. Milton (1991) was one of the first to use circular correlation in phenology, Wright et al. (1999) and Ting et al. (2008) are other examples of its application in phenology. Ting et al. (2008) present innovative solutions for the analysis of phenological data applying circular correlations.

## 16.5 Circular Statistics or Time Series Analyses? A Brief Comment

Phenological seasonal series are easily analysed applying circular statistics when considering one year cycle or few cycles. Those data are difficult to analyse using time series since we need a long time series to model data tendency, and the period and frequency of cycles. However, extended phenological time series, for instance, of 15 years, may not fulfil the premises of circularity, and would not be properly

analysed by application of parametric circular statistics. Within a 15 year time series there may be 16 cycles of 11 months each; where these cycles are not going to match the one year circle, and indeed may originate from multimodal distributions that mask the seasonality or the mean date (see Herrera 1988).

Therefore, as the number of cycles increases it seems more likely that conventional time series will describe the data better than circular statistics. Time series analysis is divided into frequency and time domain approaches - and the classic reference is Box and Jenkins (1976). In the frequency domain the spectral analysis attempts to describe patterns, somewhat similar to some circular techniques, although the spectral analytic approach summarizes the information across several years. In the time domain the main models used are the autoregressive models (AR), the autoregressive moving average models (ARMA), and the integrated ARMA or ARIMA, which not only investigate patterns, but also make predictions or forecasts. A subfamily of such ARIMA are the interrupted time series models (ITS) which, as far as we now, have never been applied to phenological data. Such models can evaluate the significance and make predictions of future changes due to a storm or a twister (McDowall et al. 1980). The ITS approach has been applied to medical science, and presents an unexplored potential in ecology (Britt et al. 1996, Hsieh et al. 2008).

Time series methods are still under-utilized in phenology, especially in the tropics, perhaps due to the lack of long phenological time series. However, in recent years there has been a growth in the analysis of phenological data through time series, as the phenological data can be bio-indicators of climate change (Menzel 2002, Hudson et al. 2003, 2004, 2009, Dose and Menzel 2004, 2006, Schleip et al 2009). Some applications of time series are illustrated in Chapter 18 of this book.

## **16.6 Concluding Remarks and Perspectives on the Application of Circular Statistics**

Our examples highlight important applications of circular statistics to the science of phenology. These applications, in summary entail:

1. calculation of phenological variables (mean date, concentration, distribution, duration)
2. estimating synchrony (asynchrony) or aggregation
3. testing hypotheses about: the distribution of a phenophase (divergence from a random or uniform pattern), testing whether phenological patterns differ between or among individuals, species or entire communities (by comparing angles, mean angles, or mean vectors), testing the predictability of occurrence of a specified phenophase, given an expected date or mean angle. These applications represent the most common applications of circular statistics in the phenological arena.

It is important to note that the circular statistics applies to any level (hierarchy) of analysis, from individuals to communities, and that the descriptive measures calculated are easily compared statistically by means of a variety of two or multi-sample tests.

Differences among species and among years in (budding, flowering, fruiting, reproductive) seasonality (namely, the tendency for clusters of events to fall at approximately the same point in each year) and synchrony (amount of clustering of events within a year) characterize much of plant phenology. Such questions can be approached using circular statistics. We conclude that circular statistics is an emergent field of analysis for plant phenology and its application is highly recommended for anyone wanting to investigate and better interpret phenological patterns. Circular statistics also has particular value and application when flowering onset (or fruiting) occurs almost continuously in an annual cycle and importantly in southern climates, where flowering time may not have a logical starting point, such as mid-winter dormancy. Circular statistics applies well to phenological research, where we may want to test for relationships between flowering time and other phenological traits (e.g. shoot growth), or with functional traits such as plant height. Circular statistics allows us to group species into annual, supra-annual, irregular, and continuous reproducers; to study seasonality in reproduction, and to assess synchronization of species. We advocate that while the theory underlying circular statistics is not new, the recent availability of mainstream statistical packages to implement this technique makes directional statistical methods clearly accessible to plant and animal phenologists, ecologists, biologists and evolutionary researchers.

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# Chapter 17

## Wavelet Analysis of Flowering and Climatic Niche Identification

Irene L. Hudson, In Kang, and Marie R. Keatley

**Abstract** This chapter discusses wavelet analysis which is a robust statistical method capable of handling noisy and non-stationary data which phenological time series often are.

We used a maximal overlap discrete wavelet transform (MODWT) analysis to examine the flowering records (1940–1970) of *E. leucoxylo*n and *Eucalyptus tricarpa*, *E. microcarpa* and *E. polyanthem*os. We identified four subcomponents in each flowering series: characterised as a non-flowering phase, duration, annual and intensity cycles. A decreasing overall trend in flowering was identified by the MODWT smoothed series.

Wavelet correlation found the same contemporaneous effects of climate on flow-ering for *E. leucoxylo*n and *Eucalyptus tricarpa*, and for *E. microcarpa* and *E. polyanthem*os.

Wavelet cross-correlation analysis identified the cyclical influence of temperature and rainfall on peak flowering intensity. For each species there are 6 months of the annual cycle in which any given climate variable positively influences flowering intensity and 6 months of negative influence. For all species, rainfall exerts a negative influence when temperature is positive.

**Keywords** Climate · Cycles · Flowering · Wavelet analysis · Wavelet cross correlation

### 17.1 Introduction

Phenology has contributed significantly to agriculture (Aitken 1974, Hodges 1991), to understanding the ecology and conservation of individual species (Ashton 1956, Baumgärtner and Hartmann 2000), and communities (Rabinowitz et al. 1981, Bawa

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et al. 2003). Some work also combines plant phenology in relation to animal phenology, for example the study on species composition and abundance of birds in relation to fruit and flower abundance in subtropical Argentinian forests (Malizia 2001) and the amount of leaf beetle damage to a herbaceous perennial plant with differential growth according to a high altitude site versus a low altitude site (Suzuki 1998). The wealth of these studies indicates the emergence of phenology as an important focus for ecological research (Schwartz 1999). Importantly, also is that phenological data have of late emerged as highly effective in the study of the impact of climate change on both plants and animals (Menzel 2002, Sparks and Menzel 2002, Chambers et al. 2005). During the last 14 years or so, studies using historical phenological observations mainly from the Northern Hemisphere: Europe (e.g. Fitter et al. 1995, Sparks and Carey 1995, Sparks et al. 2000, Ahas et al. 2002, Menzel et al. 2006), North America (e.g. Bradley et al. 1999, Beaubien and Freeland 2000, Schwartz and Reiter 2000, Abu-Asab et al. 2001, Miller-Rushing and Primack 2008) and Asia (e.g. Lu et al. 2006, Zheng et al. 2006, Miller-Rushing et al. 2007, Aono and Kazui 2008) have shown that the onset of flowering times of many plant species occurs significantly earlier (3–55 days) currently, than 35–150 years ago.

Most phenological data rely on observations from individuals who record a phenostage – frequently first bloom being the datum of choice (Hänninen 1995, Wielgolaski 1999, Chuine 2000) at a particular location over a long period. Other phenostages such as fruit production, first bird arrival are also used. At a global level, representation of these long time series, where long is considered to be of length (>20 yr) are rare (Lavoie and Lachance 2006). Whilst such long records often combined with dense phenological observational networks exist in Europe (see Chapter 2) and facilitate the monitoring of flowering dates (e.g. Menzel et al. 2001, Ahas et al. 2002); the scenario is very different elsewhere, with phenological records usually of short duration, highly dispersed and often limited to a small number of species (Schwartz and Reiter 2000). Indeed there are as yet few phenological data sets in the Southern hemisphere (Hudson et al. 2003, Keatley and Fletcher 2003, Morellato 2003). Some of the better known records across the northern hemisphere cover several decades (e.g. the International Phenological Gardens (Chmielewski and Rötzer 2001)) to several centuries (e.g. the flowering of cherry blossom in Japan (Arakawa 1955)). Their early purposes were: development of calendars to determine when crops should be planted (Aitken 1974, Ahas 1999), to judge whether a particular year was hotter or colder, compared to other years, prior to the invention of the thermometer (Pfister 1980), to understand the seasons within a year (Abbot 1863 in Winter 1972), and to understand the “natural” world (White 1912).

However, because the foundations of phenology rest in observation, monitoring and natural history (see Chapter 2), it has not been generally regarded as a real nor robust science (Sparks and Menzel 2002). This is despite many significant scientific contributions to phenological methods over an extended period (Bassett et al. 1961, Idso et al. 1978, Linkosalo et al. 1996, Schaber and Badeck 2002, Dose and Menzel 2004, Hudson et al. 2004, Kang et al. 2004). This view began to change in the mid 1990s (Schwartz 2003, Chapter 1 of this book) with the recognition that phenology can assist in delineating the impacts of climate change (Sparks and Carey

1995, IPCC 2001, Root et al. 2003, Parmesan and Yohe 2003, Parmesan 2007). However, phenological analytical methods which have been used to date, primarily regression and correlation, whilst useful and robust (de Vries 1980, Pfister 1980, Parmesan 2006) have their limitations (Sparks and Menzel 2002, Hudson et al. 2005, Sparks and Tryjanowski 2005). For example, the slopes of resultant regression lines are influenced by when the given series commences and finishes and, also by the length of the given series (Sparks and Tryjanowski 2005, Chapter 6). Statistical techniques used in phenology also need to accommodate for the inherent complexity of phenological records, which is often ignored. Complexity, such as their time series (correlated) nature, their often discrete and non-stationary properties, and the presence of excess zeros (non occurrence of a phenostage of interest). Additional methods for examining phenological time series are thus needed, these include Bayesian techniques (Dose and Menzel 2004, Chapter 11), sophisticated decomposition methods for time series (Hudson et al. 2005, Chapter 18); or for methods for combining time series (Häkkinen et al. 1995, Linkosalo et al. 1996, Schaber and Badeck 2002, Chapter 7) and for change point methods (Dose and Menzel 2004, Schleip et al. 2006, 2008, Keatley and Hudson 2008, Chapter 11). Wavelets analysis is one such method.

## 17.2 General Motivation for Wavelets Analysis

Over the last 30 years, wavelets have emerged as a mathematical tool for the analysis of complex datasets. Indeed, since their introduction in the geophysical literature by Goupillaud et al. 1984, the application of wavelets to time series (Percival and Walden 2000, Kang et al. 2005) and spatial data (White et al. 2005) has increased. Wavelets are well suited to signal processing, particularly the analysis of biological signals and images (e.g. human brain imaging and EEG data) which often possess fractal or scale invariant properties (Bullmore et al. 2003). Wavelets allow the decomposition of a time series with respect to two independent variables, namely, time and scale, and also the decomposition of an image with respect to location and extent. A review of the historical development of wavelets is provided by Jaffard et al. (2001). A detailed exposition on wavelets can also be found in Burrus et al. (1998). Wavelet analysis has also been used in an examination of European spring temperatures (Paluš et al. 2005) and rainfall (Koch and Marković 2007) and changes in vegetation cover (Lu et al. 2007). Some key papers that have applied wavelets in vegetation ecology and related fields include Bradshaw and Spies (1992), Dale (1999), Lark and Webster (1999), Katul et al. (2001), Csillag and Kabos (2002) and Dale et al. (2002).

Whitcher et al. (2000) were the first to propose a multi-scale analysis of covariance between two time series using the discrete wavelet transform (DWT). In atmospheric science for example, the bivariate relationship between two time series is paramount (see for example Whitcher et al. (2000) who identified the Madden-Julian oscillation (MJO) using bivariate spectral analysis (between the station

pressure and zonal wind components at Canton Island)). Whitcher's et al. (2000) novel technique for bivariate Gaussian time series utilized the maximal overlap DWT (MODWT). The MODWT is a non-decimated version of the orthonormal DWT, shown to be valuable in the analysis of geophysical processes (Percival and Guttorp 1994, Percival and Mofjeld 1997). Whitcher et al. (2000) introduced and defined the wavelet correlation and wavelet cross-correlation and performed an analysis of El-Nino (Southern Oscillation events and the Madden-Julian oscillation (MJO) using a 35+ year record), thus demonstrating his method to be an excellent alternative to traditional cross-spectrum (Fourier) analysis. Whitcher et al. (2000) showed how the wavelet cross-correlation between ENSO events and the MJO both quantifies and also visually displays how the association between the two processes changes with scale. Conventional time and frequency domain techniques had to that time, and still, provided results, difficult to interpret (see Foufoula-Georgiou and Kumar (1994) and Kumar (1996) for descriptions of time-frequency/time-scale analysis).

More recently Percival et al. (2004) illustrated the use of the DWT in the analysis on time series related to vegetation coverage in the Arctic region. Percival et al. (2004) showed how, given the DWT coefficients, the vegetation time series could be reconstructed perfectly by a multi-resolution analysis (MRA). In the MRA the series is re-expressed as the sum of a new set of time series (details and a smooth), each of which is associated with variations at a particular scale. Percival et al. (2004) illustrated how MRA allowed for the identification of certain decades (in the series for the boreal group) for which the year-to-year variations were smaller than usual. Whitcher et al. (2000), Katul et al. (2001) and Percival et al. (2004) all showed how potentially complicated patterns of cross-correlation are easily decomposed using the wavelet cross-correlation on a scale by scale basis, where each wavelet cross-correlation series is associated with a *specific physical time scale*. This scale by scale interpretation is possible as the energy in a time series is preserved in its DWT coefficients (Whitcher et al. 2000, Percival and Walden 2000, Bullmore et al. 2003). Wavelets thereby provide a decomposition of the sample variance (of a time series) into components that may be associated with different temporal scales.

Some phenological studies cover areas as large as Europe or North America using data-banks built up over decades from individual data collecting sites or remote sensing. Wavelets have had particular application for phenology via remote sensing (see White et al. 2003). Finally, some of the most interesting recent work combines plant phenology in relation to animal phenology. Examples of this work include a study on the species composition and abundance of birds in relation to fruit and flower abundance in subtropical Argentinean forests (Malizia 2001) and the amount of leaf beetle damage to a herbaceous perennial plant growing differently in a high altitude site than a low altitude site (Suzuki 1998).

This wide application is due to wavelet analysis being able to cope with non-stationary data: capable of deconstructing a time series into its subcomponents and removing noise; able to handle multi-scale information, and its ability to minimize correlation and time-dependency in data (Percival and Walden 2000, Gencay et al. 2001, Cornish et al. 2006). As phenological time series are often non-stationary and

noisy, wavelets would seem to be a useful analytic method (Hudson et al. 2005) for phenological records and for the determination of possibly changing climatic impacts on flowering, at an annual (and across years) basis.

The aim of this chapter is to demonstrate the utility of wavelet analysis for phenological records by using the flowering time series of four eucalypt species as a case study. Additionally, this study contributes to the much needed understanding of the interplay between climate and *Eucalyptus* flowering – a major southern hemisphere genus.

## 17.3 Methods

### 17.3.1 Continuous vs Discrete Wavelet Transform (CWT vs DWT)

In the earlier development of wavelet analysis the so-called wavelet transform (WT) was usually considered to be the continuous wavelet transform (CWT) (Percival and Walden 2000), as it was often applied to a function  $f(\cdot)$  defined over the entire real axis, say over time  $t$ . The CWT is a function of two variables  $\Psi(\tau, \lambda)$  and is obtained by projecting the function  $f(t)$  onto a particular wavelet  $\psi$  via

$$\begin{aligned} \text{CWT}_x^\Psi(\tau, \lambda) &= \Psi_x^\Psi(\tau, \lambda) = \frac{1}{\sqrt{\lambda}} \int f(t) \psi\left(\frac{t-\tau}{\lambda}\right) dt \\ &= \int_{-\infty}^{\infty} f(t) \psi_{\lambda, \tau}(t) dt, \end{aligned} \quad (17.1)$$

where

$$\psi_{\lambda, \tau}(t) = \frac{1}{\sqrt{\lambda}} \psi\left(\frac{t-\tau}{\lambda}\right), \quad (17.2)$$

and  $\tau$  is a translation parameter which measures time, while  $\lambda$  is a scaling parameter (Percival and Walden 2000). The translation of a wavelet function  $\psi(t-\tau)$  shifts its range,  $\tau$  units to the right, while a dilation of the function  $\psi(t/\lambda)$ , expands its range by a multiplicative factor. Hence, it is possible to break down the complicated structure, present in the function,  $f(t)$ , into its simpler components: signals at various scales or resolution and shifts. This is called *decomposing* the function.

### 17.3.2 The Discrete Wavelet Transform (DWT)

For most practical applications, the discrete wavelet transform (DWT), which analyses signals over a discrete set of scales, that are usually sampled at dyadic sequence ( $\lambda_j = 2^{j-1}, j = 1, 2, 3, \dots$ ), is sufficiently accurate and can recover signals perfectly

(Mallat 1989). In the dyadic form, the wavelet function corresponding to Eq. (17.2), with  $\lambda = \lambda_j = 2^{j-1}$  and  $\tau = k\lambda_j$  can be written as:

$$\psi_{\lambda_j, k\lambda_j}(t) = \frac{1}{\sqrt{\lambda_j}} \Psi \left( \frac{t - k\lambda_j}{\lambda_j} \right) = 2^{-(j-1)/2} \psi(t2^{-(j-1)} - k), \quad (17.3)$$

where  $j$  is the  $j$  th decomposition level or scale and  $k$  is the  $k$ th wavelet coefficient. By contrast to Eq. (17.1) we now have  $\lambda = 1, 2, 4, 8, \dots, 2^j$ .

Some details on the DWT decomposition and reconstruction follow. We assume that  $\mathbf{x}$  denotes a dyadic length column vector containing a sequence  $\mathbf{x}_1, \mathbf{x}_2, \dots, \mathbf{x}_{N-1}$ , of  $N=2^J$  observations of a real-valued time series. The length  $N$  vector of discrete wavelet coefficients  $\mathbf{w}$  is obtained via

$$\mathbf{w} = W\mathbf{x},$$

where  $W$  is an  $N \times N$  orthonormal matrix defining the DWT. The vector of wavelet coefficients may then be organised into  $J + 1$  vectors,

$$\mathbf{w} = [w_1, w_2, \dots, w_j, v_j]^T \quad (17.4)$$

where  $\mathbf{w}_j$  is a length  $N/2^j$  vector of wavelet coefficients associated with changes on a scale of length  $\lambda_j = 2^{j-1}$  and  $\mathbf{v}_j$  is a length  $N/2^j$  vector scaling coefficients associated with averages on a scale of length  $2^j = 2\lambda_j$ .

The matrix  $W$  is composed of wavelet and scaling filter coefficients arranged on a row-by-row basis. Let

$$\mathbf{h}_1 = [h_{1,N-1}, h_{1,N-2}, \dots, h_{1,1}, h_{1,0}]^T \quad (17.5)$$

be the vector of zero-padded unit scale wavelet filter coefficients in reverse order. That is, the coefficients  $h_{1,0}, \dots, h_{1,L-1}$  are taken from an appropriate orthonormal wavelet family of length  $L$ , and all values, such that  $L < t < N$ , are defined to be zero. Now we circularly shift  $\mathbf{h}_1$  by factors of two, so that

$$\mathbf{h}_1^{(2)} = [h_{1,1}, h_{1,0}, h_{1,N-1}, h_{1,N-2}, \dots, h_{1,3}, h_{1,2}]^T,$$

$$\mathbf{h}_1^{(4)} = [h_{1,3}, \dots, h_{1,0}, h_{1,N-1}, h_{1,N-2}, \dots, h_{1,5}, h_{1,4}]^T, \text{ and so on.}$$

Define the  $N/2 \times N$  dimensional matrix  $W_1$  to be the collection of  $N/2$  circularly shifted versions of  $\mathbf{h}_1$ , that is,

$$W_1 = [\mathbf{h}_1^{(2)}, \mathbf{h}_1^{(4)}, \dots, \mathbf{h}_1^{(N/2-1)}, \mathbf{h}_1]^T$$

Let  $\mathbf{h}_2$  be the vector of zero-padded, scale 2, wavelet filter coefficients defined similarly to Eq. (17.5). Now construct the matrix  $W_2$  by circularly shifting the vector  $\mathbf{h}_2$

by factors of four. Repeat this to construct the matrices  $W_j$  by circularly shifting the vector  $h_j$  (the vector of zero-padded scale  $j$  wavelet filter coefficients) by factors of  $2^j$ . The matrix  $V_j$  is simply a column vector whose elements are all equal to  $1/\sqrt{N}$  (Percival and Walden 2000). The structure of the  $N \times N$  dimensional matrix  $W$  is seen through the sub-matrices  $W_1, \dots, W_J$  and  $V_J$  via

$$W = [W_1, W_2, \dots, W_J, V_J]^T \tag{17.6}$$

To complete the construction of the orthonormal matrix  $W$ , we must be able to explicitly compute the wavelet filter coefficients for scales  $1, \dots, J$ . The wavelet filter  $h_j$  is associated with scale. Given the transfer functions of unit scale and scaling filters, define the wavelet filter  $h_{j,l}$ , for scale  $\lambda_j = 2^{j-1}$ , as the inverse discrete Fourier transform (DFT) of

$$H_{j,k} = H_{1,2^{j-1}k \bmod N} \prod_{l=0}^{j-2} G_{1,2^l k \bmod N}, \quad k = 0, \dots, N - 1.$$

Define the scaling filter  $g_j$  for scale  $\lambda_j$  as the inverse DFT of

$$G_{j,k} = \prod_{l=0}^{j-1} G_{1,2^l k \bmod N}, \quad k = 0, \dots, N - 1 \tag{17.7}$$

**17.3.2.1 Implementation of the DWT: Pyramid Algorithm**

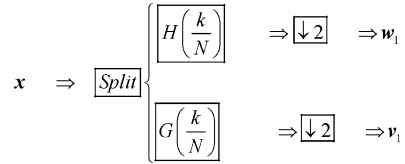
Decomposition

Implementation of the DWT via the pyramid algorithm (Mallat 1989) is detailed below. Let  $h = (h_0, \dots, h_{L-1})$  be the vector of wavelet (high-pass) filter coefficients and  $g = (g_0, \dots, g_{L-1})$  be the vector of scaling (low-pass) filter coefficients (Daubechies 1992). The length  $N$  vector of  $X$  is convolved with the filter  $h$ , whose discrete Fourier transform is  $H(f)$ , and downsampled by two in order to produce a new vector  $W$  of length  $N/2$  (similarly for  $G$ ).

Graphical representation of the DWT as applied to a dyadic length vector  $X$  is given in Fig. 17.1, which shows that wavelet decomposition is achieved by a combination of high and low pass filters,  $H$  and  $G$ , respectively. This decomposition essentially identifies high, medium and low scales in the function.

In practice the DWT is implemented via a pyramid algorithm (Mallat 1989) that starts with the data  $x_t$ , filters a series  $h_1$  and  $g_1$ , subsamples both filter outputs to half their original lengths, keeps the sub-sampled output from the  $h_1$  filter as wavelet coefficients and then repeats the above filtering operations on the subsampled output from the  $g_1$  filter. A flow diagram (Fig. 17.1) shows the first stage of the pyramid algorithm. The symbol  $\lfloor \downarrow 2 \rfloor$ , downsampling by 2, means that every other value of the input vector is removed.

**Fig. 17.1** First stage of the pyramid algorithm

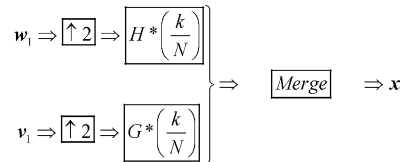


**Reconstruction**

Reconstruction moves from coarse to a fine approximation, while decomposition moves in the opposite direction. The one level reconstruction process is schematically shown in Fig. 17.2.

Inverting the DWT is achieved through upsampling the final level wavelet and scaling coefficients, convolving them with their respective filters (wavelet for wavelet and scaling for scaling) and adding up the two filtered vectors. A flow diagram (Fig. 17.2) depicts the reconstruction of  $x$  from the first level wavelet and scaling coefficient vectors. The symbol means  $\boxed{\uparrow 2}$  that a zero is inserted before each observation in  $w_1$  and  $v_1$ . The flow diagram in Fig. 17.2 shows the reconstruction of  $x$  from the unit scale wavelet coefficients  $w_1$  and from the unit scale, scaling coefficients  $v_1$ .

**Fig. 17.2** Reconstruction of  $x$  from the unit scale wavelet coefficients  $w_1$  and from the unit scale, scaling coefficients  $v_1$



**17.3.3 Maximal Overlap DWT (MODWT)**

The discrete wavelet transform (DWT) as applied here, following Percival and Walden (2000), requires a discretisation of the continuous time variable. For most practical applications, the DWT, which analyses signals over a discrete set of scales, that are usually sampled at dyadic sequence ( $\lambda_j = 2^{j-1}, j = 1, 2, 3, \dots$ ), is sufficiently accurate and can recover signals perfectly (Mallat 1989). The maximal overlap DWT (MODWT) is one discretisation choice which gives  $N$  wavelet coefficients for each scale (Percival and Guttorp 1994). The MODWT is a non-decimated variation of the DWT (Percival and Mofjeld 1997). It is also equivalent to the original time series, in the sense that, given the MODWT coefficients,  $Y$ , can be constructed as an additive decomposition, which is known as a multiresolution analysis (MRA) (Hernández and Weiss 1996, Gencay et al. 2001, Bratteli and Jorgensen 2002).

### 17.3.4 Multiresolution Analysis Using DWT

The MRA decomposition is as follows:

Using the DWT, we may formulate an additive decomposition of a series of observations. Let  $\mathbf{d}_j = W_j^T \mathbf{w}_j$  for  $j = 1, \dots, J$ . For example, the second detail series,  $d_2$ , represents the cross product of  $W_2$  where  $W_2$  is the scale  $\lambda_2$  MODWT coefficients. Define the  $j$  th level *wavelet detail* associated with changes in  $\mathbf{x}$  at scale  $\lambda_j$ . The wavelet coefficients  $\mathbf{w}_j = W_j \mathbf{x}$  represent the portion of the wavelet analysis attributable to scale  $\lambda_j$ , while  $W_j^T \mathbf{w}_j$  is the portion of the wavelet synthesis attributable to scale  $\lambda_j$ . For a length  $N = 2^J$  vector of observations, the final wavelet detail  $d_{J+1} = V_J^T \cdot V_J$  is equal to the sample mean of the observations.

A multiresolution analysis (MRA) may now be defined via

$$x_t = \sum_{j=1}^{J+1} d_{j,t} \quad (t = 0, k \dots N - 1) \tag{17.8}$$

that is, each observation  $x_t$  is a linear combination of wavelet detail coefficients  $\{d_{j,t}\}$ .

Let  $s_j = \sum_{k=j+1}^{J+1} \mathbf{d}_k$  define the  $j$  th level wavelet smooth for  $0 \leq j \leq J$ , where  $s_{J+1}$  is defined to be a vector of zeros. Note that, whereas the wavelet detail  $\mathbf{d}_j$  is associated with variations at a particular scale,  $s_j$  is a cumulative sum of these variations and will be smoother and smoother as  $j$  increases. In fact  $\mathbf{x} - s_j = \sum_{k=1}^j \mathbf{d}_k$  so that only lower-scale details (high-frequency features) will be apparent. The vector,  $s_j$ , is called the “smooth series” since it is associated with averages over scales  $2\lambda_{j_0}$  and longer; it thereby captures the slowly varying portion of the original time series, and is often considered to be the overall trend. The  $j$  th level wavelet rough,  $\mathbf{r}_j = \sum_{k=1}^j \mathbf{d}_k$  for  $0 \leq j \leq J + 1$ , characterises the remaining lower-scale details. Note  $\mathbf{r}_0$  is defined to be a vector of zeros. A vector of observations may then be decomposed through a wavelet smooth and rough via  $\mathbf{x}_j = s_j + \mathbf{r}_j$ , for all  $j$ .

### 17.3.5 Wavelet Cross – Correlation and Correlation

The above section considers decomposing the original time series into  $J+1$  subcomponents. However, the scale  $\lambda_j$  MODWT coefficients may also be used to examine the wavelet correlation and wavelet cross-correlation of bivariate time series  $X_t$  and  $Y_t$  (Serroukh and Walden 2000, Whitcher et al. 2000, Gencay et al. 2001), as described below.

The wavelet correlation (WCORR) of  $(X_t, Y_t)$  at scale  $\lambda_j=2^{j-1}$  is defined as

$$\rho_{XY,\tau=0}(\lambda_j) = \frac{\text{Cov} \left\{ \overline{W}_{j,t}^X, \overline{W}_{j,t}^Y \right\}}{\sigma_X(\lambda_j) \cdot \sigma_Y(\lambda_j)} = \frac{\gamma_{XY,\tau=0}(\lambda_j)}{\sigma_X(\lambda_j) \cdot \sigma_Y(\lambda_j)} \tag{17.9}$$



where  $\sigma_X^2(\lambda_j) = \text{var} \left\{ \overline{W}_{j,t}^X \right\}$  is the wavelet variance with scale  $\lambda_j$ .  $\overline{W}_{j,t}^X$  and  $\overline{W}_{j,t}^Y$  are the scale  $\lambda_j$  MODWT coefficients for  $X_t$  and  $Y_t$ , respectively (Percival 1995). Note that Eq. (17.9) is a theoretical quantity that is well-defined under an assumption of stationarity. For a time lag  $\tau$ , between the two series,  $X_t$  and  $Y_t$ , the wavelet cross-covariance and wavelet cross-correlation (denoted by WCCORR) (Gencay et al. 2001), for scale  $\lambda_j=2^{j-1}$  and time lag  $\tau$  is

$$\gamma_{XY,\tau}(\lambda_j) \equiv \text{Cov} \left\{ \overline{W}_{j,t}^X \overline{W}_{j,t+\tau}^Y \right\} \tag{17.10}$$

where  $\overline{W}_{j,t}^X$  and  $\overline{W}_{j,t}^Y$  are the scale  $\lambda_j$  MODWT coefficients for  $\{X_t\}$  and  $\{Y_t\}$ , respectively (Whitcher et al. 2000, Gencay et al. 2001), and the associated wavelet variances  $\sigma_X^2(\lambda_j)$  and  $\sigma_Y^2(\lambda_j)$  are unity. By setting  $\tau = 0$ ,  $\gamma_{XY,0}(\lambda_j)$  reduces to the wavelet variance for  $X_t$  or  $Y_t$  denoted by  $\sigma_X^2(\lambda_j)$  or  $\sigma_Y^2(\lambda_j)$ , respectively.

The wavelet cross-correlation in Eq. (17.10) is thus able to provide the lead or lag relationship on a scale-by-scale basis (Gencay et al. 2001), just as is the case for conventional cross-correlations, which can determine lead or lag relationships between two series. When the time lag  $\tau = 0$ , the corresponding MODWT estimator of the wavelet correlation (WCORR) between the two series  $X_t$  and  $Y_t$  (Percival et al. 2000) is derived.

### 17.3.5.1 Confidence Interval Determination

Construction of the 95% two-sided confidence interval (CI) of WCORR and WCCORR follows the development of Gencay et al. 2001. To produce CIs for the cross-correlation coefficient, the Fisher’s nonlinear z-transformation  $h(\rho)$  (Dépué 2003), as follows,  $h(\rho) = \frac{1}{2} \log \left( \frac{1+\rho}{1-\rho} \right) = \tanh^{-1}(\rho)$ , is required. For  $\hat{\rho}_X$ , an unbiased estimator of WCORR based on the MODWT, the following asymptotic normal distribution holds

$$\sqrt{N-3} [h(\hat{\rho}) - h(\rho)] \sim N(0,1) \tag{17.11}$$

Applying the transformation  $\tanh$  maps the confidence interval back to  $[-1,1]$  to produce an approximate 95% CI for  $\rho_X(\lambda_j)$  as follows (Whitcher et al. 2000, Gencay et al. 2001)

$$\tanh \left\{ h[\hat{\rho}_X(\lambda_j)] \pm 1.96 \left( \frac{1}{\overline{N}_j - 3} \right)^{1/2} \right\} \tag{17.12}$$

The quantity  $\overline{N}_j$  in Eq. (17.11) is the number of DWT coefficients associated with scale  $\lambda_j$ .

## 17.4 Data Analyses

DWT, MODWT and MODWT-MRA analyses were performed using code based on the wavelet methods developed by Percival and Walden (2000) and Gencay et al. (2001).

### 17.4.1 Phenological Data

The phenological data, used here as a case study, was collected between 1940 and 1970 and comprises the flowering intensity profiles of four eucalypts species growing in the region of Havelock, Victoria, Australia. Observations on the timing, quantity and distribution of flowering of these species were collected on a monthly basis (Keatley et al. 1999).

Flowering intensity of each of the species was quantified by assigning a rank value to these descriptions (Keatley and Hudson 2007) producing a discrete, small counts time series (Fig. 17.3 wherein only the period January 1945–December 1955 is shown for visual clarity). Flowering intensity (ranging from 0 to 5) was calculated, based on the sum of the quantity and distribution rank values. A score of 0 indicates that no flowering occurred, in the given month, whilst a score of 5 indicates that flowering was heavy and distributed throughout the observation area (Keatley and Hudson 2007).

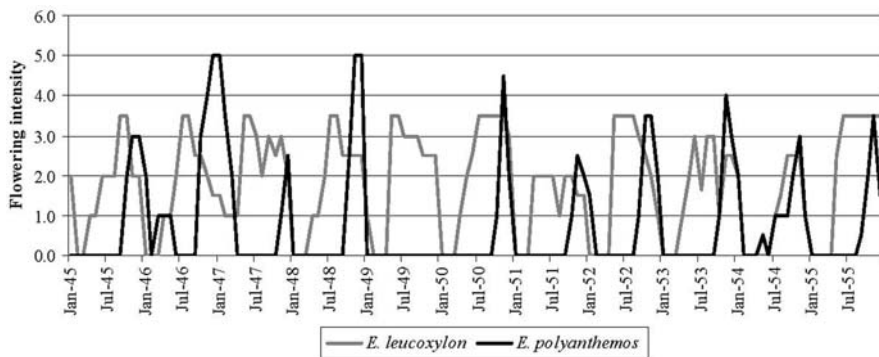


Fig. 17.3 Time series of *E. leucoxyton* and *E. polyanthemos* between 1945 and 1955

The four species examined in this study commonly occur together and, flowering between them may overlap (Keatley et al. 2004) (Table 17.1):

- *Eucalyptus leucoxyton* ssp *pruinosa* (F. Muell. ex Miq.) Boland,
- *E. tricarpa* (LAS Johnson) LAS Johnson and KD Hill,
- *E. microcarpa* (Maiden) Maiden,
- *E. polyanthemos* ssp *vestita* LAS Johnson and KD Hill.

**Table 17.1** Likelihood flowering characteristics of species at Havelock

Species	Commencement		Finishing month	Mean flowering duration (month) $\pm$ SD
	month	Peak month		
<i>E. leucoxydon</i>	May	September	December	9.7 $\pm$ 4.2
<i>E. tricarpa</i>	April	July	September	6.2 $\pm$ 2.1
<i>E. microcarpa</i>	February	March	May	4.0 $\pm$ 1.0
<i>E. polyanthemos</i>	October	November	December	3.6 $\pm$ 1.5

Daily minimum and maximum temperature along with daily rainfall were obtained from the Bureau of Meteorology, for the closest weather station (approximately 3.5 km away); Maryborough, Victoria (37' 03"S, 143' 44"E, 249.3 m elevation). The temperature dataset had some missing data. When only one day was missing, the average of the temperature either side of the missing date was used. If two or more days were not recorded, then the mean minimum or maximum temperature for that month was substituted. Daily mean temperature was calculated as the average of daily minimum and maximum temperature. Monthly means for minimum, maximum, diurnal temperature and rainfall were used in the analyses.

## 17.5 Results

### 17.5.1 MODWT-MRA

Maximal overlap discrete wavelet transform – multi-resolution analysis (MODWT-MRA) with  $J = 3$  (17.8) provided the subcomponents of the flowering signal within each species (see Fig. 17.4). The raw series is given by  $X$ ,  $d1$ – $d4$  are the different subcomponents (detail) of the original series  $X$ . Traditionally,  $d1$ – $d4$  are associated with changes in averages over 1, 2, 4 and 8 months, respectively (Fig. 17.4). Also  $s4$ , which is the smoothed series associated with averages over 16 months, is also provided by MODWT-MRA (see Fig. 17.4 for *E. tricarpa*).

Each of the subcomponents,  $d1$ – $d4$ , can be interpreted similarly across the four species as follows:  $d1$  shows the interval when flowering is absent – a non-flowering interval;  $d2$  reflects duration and the overall pattern of the original flowering data.  $d1$  and  $d2$  appear similar in their profiles (see Fig. 17.5 for *E. polyanthemos*), however,  $d1$  contains subcycles per year (in a flowering year) but it is unclear as to what these cycles are related. The annual cycle is delineated by  $d3$ , and  $d4$  relates to the annual or biennial cycling of intensity of flowering years.  $s4$  is the smoothed series and indicative of the overall trend.

$d3$  not only delineates the annual cycle of flowering, but reveals (by its peaks), in the majority of cases, the month of peak flowering in a flowering year (or within the month on either side) (Fig. 17.6). Note that for *E. leucoxydon* 73% of the peak months are thus selected, for *E. microcarpa* 72%, for *E. polyanthemos* 69% and for

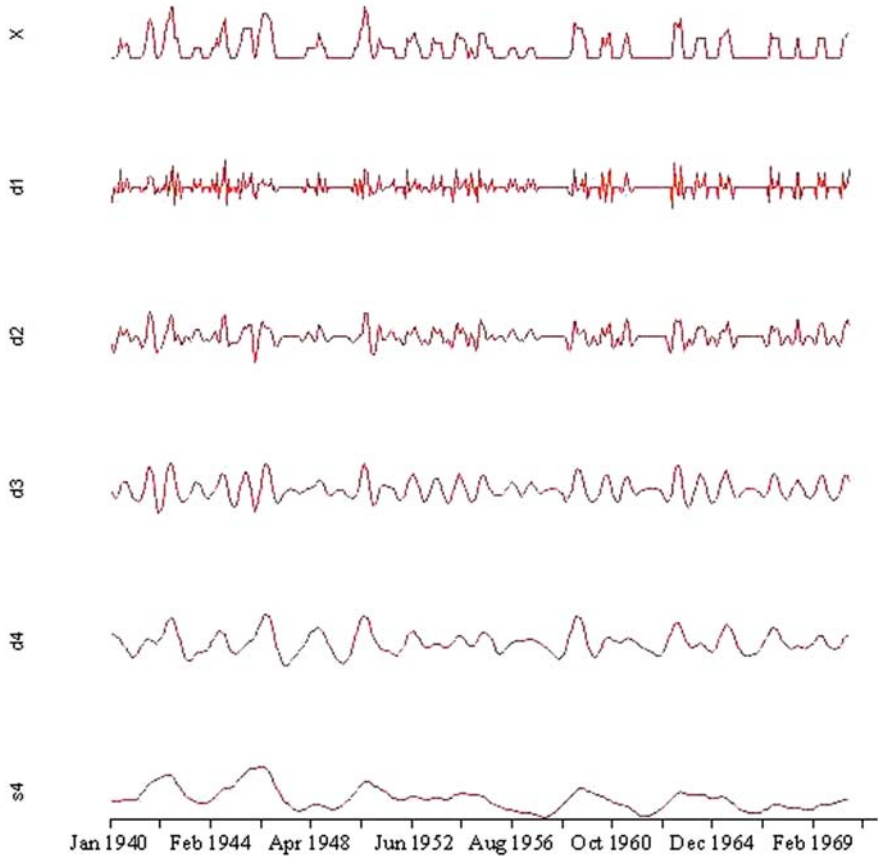


Fig. 17.4 Example of MODWT-MRA output using *E. tricarpa*. X = the raw data, d1–d4 different subcomponents (details) of the original series X, and s4 = the smooth series

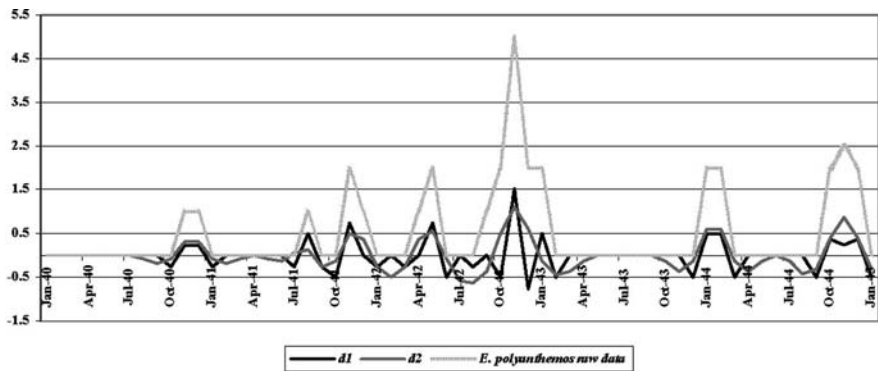


Fig. 17.5 d1, d2 and raw data of *E. polyanthemus* between January 1940 and March 1945

*E. tricarpa* 65%. Additionally, d3 highlights years when flowering does not occur – this is seen in Fig. 17.5 when d3 is zero. Per species, these years of non flowering are: 1943, 1958, 1962, 1968 and 1969 for *E. microcarpa*; 1949, 1956, 1958 and 1961 for *E. polyanthemos* and 1947, 1949, 1958, 1962 and 1966 for *E. tricarpa*. Note 1958 and 1962 are predominantly non-flowering years.

d4 outlines annual and biennial cycles of flowering intensity for each species (Fig. 17.7). For three of the four species, namely *E. microcarpa*, *E. polyanthemos* and *E. tricarpa*, the biennial cycle is associated with years of low flowering intensity ( $< 2$ ) and also includes years of no flowering (i.e. flowering intensity = 0).

Flowering alternates between a quasi-biennial (1950–1952, 1955–1963) and an annual cycle in *E. leucoxydon*. It is the only species where a biennial cycle is associated solely with low flowering intensity ( $< 2$ ) and/or late commencement with short duration. Flowering usually commences in May (Table 17.1), however, in some years (e.g. 1958 and 1962) flowering did not commence until September or October and then flowered only for approximately 3.5 months compared to the usual duration of 9.7 months (Table 17.1).

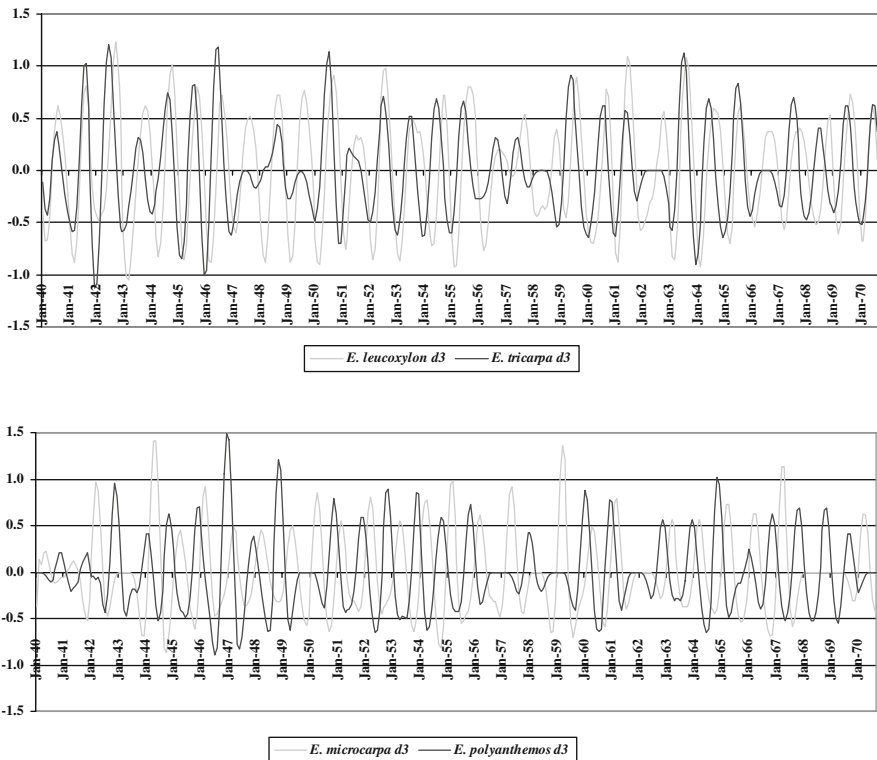


Fig. 17.6 d3 subcomponent for each of the species

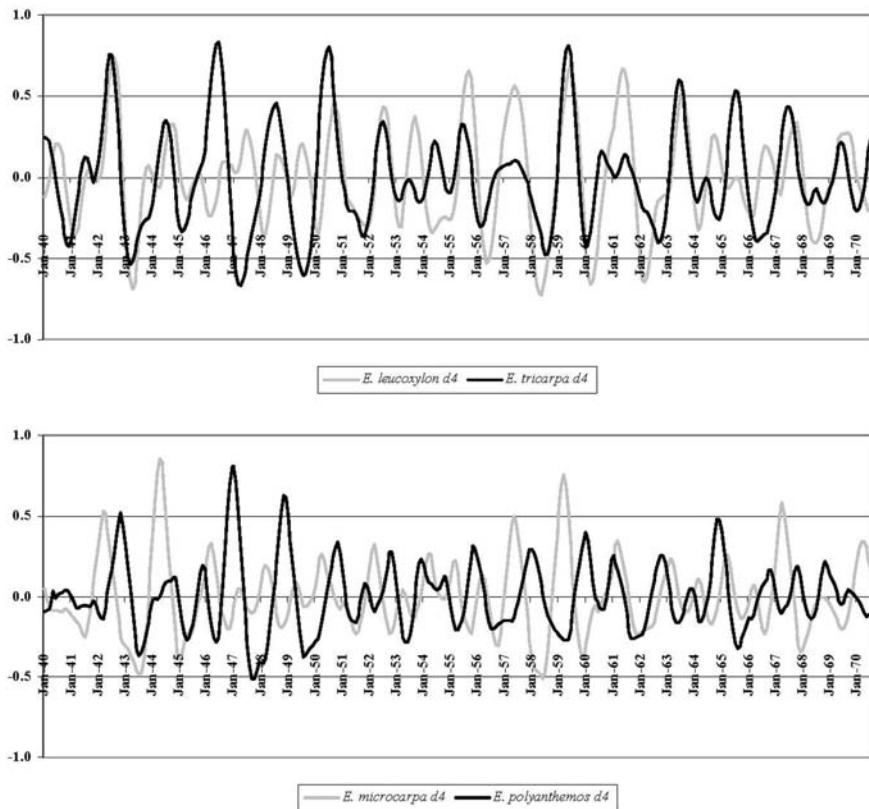


Fig. 17.7 d4 subcomponent of each species

Although s4 is the smoothed series it is also reflective of the trend and variation in flowering intensity. s4 indicates that flowering has become less intense from 1940 to 1970 for all four species (Fig. 17.8). *Eucalyptus leucoxydon* on average (mean intensity 1.63) flowers more intensely than the other 3 species except for a brief period, between June 1945 and July 1946, when *E. tricarpa* flowered most (Fig. 17.8). *Eucalyptus tricarpa* is the next most intense flowering species (mean intensity = 0.89). The remaining two species have flowered as intensely as each other (*E. microcarpa* mean = 0.59 and *E. polyanthemus* mean = 0.57) over time, but alternate between periods of heightened intensity (Fig. 17.8). A trough indicating lower flowering intensity overlapped only once in all species (i.e. between April and June 1962 (Fig. 17.8)). The most intense flowering period for all species occurred prior to 1958. Hudson et al. 2005 noted wetter years than average years in the mid 1940s to the end of the 1950s; and maximum temperature at Maryborough increasing until late 1967/early 1968 (also reflected by the Southern Oscillation Index (Ghil et al. 2002)).

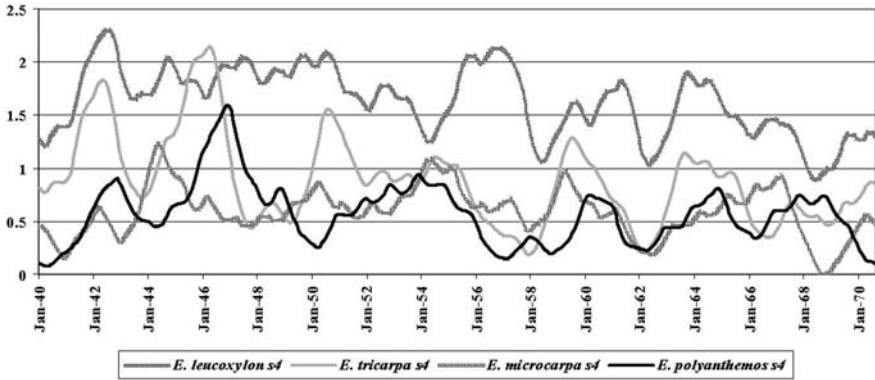


Fig. 17.8 s4 subcomponents for each species

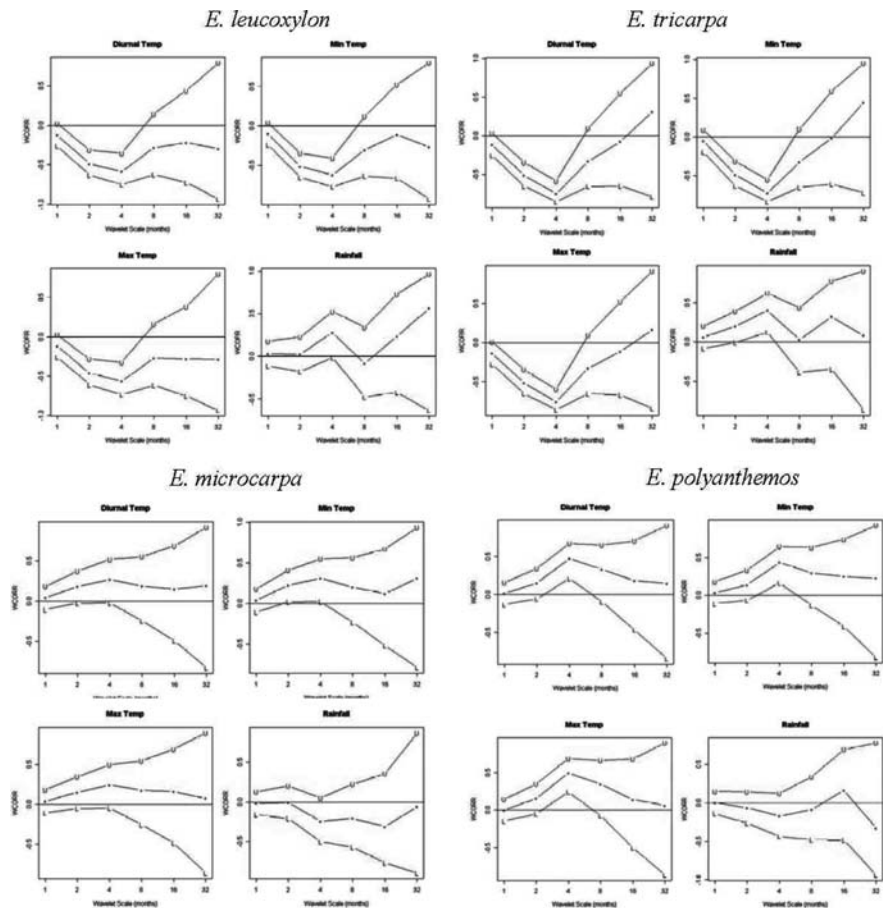
### 17.5.2 Correlation with Temperature and Rainfall

The wavelet correlations between temperature (minimum, maximum and diurnal) and rainfall with peak flowering intensity at different wavelet levels or scales (1, 2, 4, 8, 16 and 32 months) were examined. See Fig. 17.9, where significant ( $P < 0.05$ ) wavelet correlations are those where the upper (U) and lower (L) confidence limits are on the same side of the zero line. It can be seen that there are more correlations at scale 3 ( $2^{3-1} = 4$  months) which are significant than as scale 2, whereas, correlations at 1, 8, 16 and 32 months were not significant (Fig. 17.9).

For *E. tricarpa* minimum, maximum and diurnal temperatures have a significant negative relationship at 2 and 4 months (Fig. 17.9 and Table 17.2). *Eucalyptus tricarpa* was the only species for which rainfall had a significant, positive relationship with flowering at the 4 month scale (Fig. 17.9). This indicates that warmer, wetter periods lead to greater flowering intensity for *E. tricarpa*. The relationship for *E. leucoxyloides* and rainfall was positive but was not significant. For *E. microcarpa* and *E. polyanthemoides* a negative correlation (although not significant) with rainfall was indicated.

The temperature variables (mean, minimum and maximum) at 2 and 4 months (or wavelet scales) were also significant for *E. leucoxyloides*. At peak flowering intensity both *E. leucoxyloides* and *E. tricarpa* have a negative relationship with each of the temperature variables, indicating increased intensity of flowering with decreasing temperature. However, there is a slight difference in the strength of the relationship of flowering across the temperature variants (Table 17.2) indicating that for *E. leucoxyloides* the main relationship with flowering intensity is with minimum temperature and for *E. tricarpa* it is with maximum temperature (Table 17.2), both significant at the 4 month scale.

An inverse relationship between flowering and the temperature variants was found for *E. microcarpa* and *E. polyanthemoides*; with an increase in peak flowering intensity with increasing temperature. However, the only temperature variable



**Fig. 17.9** Wavelet correlations (WCORR – zero lag) of the four species with temperature variables and rainfall with 95% confidence intervals indicated by U and L

**Table 17.2** Wavelet (scale 3) correlation of peak flowering intensity and temperature and rainfall variables

Period (months)	Diurnal temp		Minimum temp		Maximum temp		Rainfall	
	2	4	2	4	2	4	2	4
<i>E. leucoxylo</i>	-0.49*	-0.59*	-0.52*	-0.62*	-0.46*	-0.56*	0.03	0.29
<i>E. tricarpa</i>	-0.51*	-0.75*	-0.49*	-0.72*	-0.51*	-0.76*	0.20	0.40*
<i>E. microcarpa</i>	0.18	0.27	0.23*	0.31*	0.15	0.25	-0.01	-0.24
<i>E. polyanthemos</i>	0.15	0.48*	0.14	0.43*	0.16	0.50*	-0.06	-0.17

\*P< 0.05



which impacts significantly on the flowering of *E. microcarpa* was minimum temperature (at 2 and 4 months), indicating that it may be the primary climatic driver of flowering intensity. In contrast, for *E. polyanthemos*, there was a significant positive relationship with all three temperature variables (at 4 months) with maximum temperature being identified as having a slightly greater influence on flowering (Table 17.2). This is in agreement with a recent Generalised additive model for location, scale and shape (GAMLSS) analysis of the data studied here (Hudson et al. 2009).

### 17.5.3 Wavelet Cross-Correlation with Temperature and Rainfall Variables

Wavelet cross-correlations were examined for all wavelet scales (1–32 months). Significant relationships ( $P \leq 0.05$ ) were found only at 4 months (level 3) for rainfall; but at 2, 4 and 8 months (levels 2–4) for the temperature variants (Fig. 17.10a, b). The strongest (highest absolute value of the correlation profile) and most significant relationship for all species with temperature was at 4 months (level 3) (Fig. 17.10a, b). This mirrors the correlation results (Table 17.2), where level 3 correlations were significant. Note that correlations are the equivalent of cross-correlations at lag zero.

### 17.5.4 Level 3 Wavelet Cross-Correlations

Cross-correlations between peak flowering intensity and the temperature variants and rainfall are lagged from 0 to 12 months prior to the species specific peak flowering month. An illustration of these cross-correlation profiles between mean diurnal temperature and flowering is given in Fig. 17.11 for each species. This sinusoidal profile shows that there are positive and negative relationships of 6 months duration and as a consequence there are seasonal change points (CPs) from positive to negative cross-correlation and vice-versa (see Table 17.3, where the season specific to each CP month is given).

**Table 17.3** Species specific change points (month, season) for diurnal temperature

Species	Positive to negative		Negative to positive	
	Month	Season	Month	Season
<i>E. leucoxydon</i>	August	Winter	February	Summer
<i>E. tricarpa</i>	March	Autumn	September	Spring
<i>E. microcarpa</i>	August	Winter	February	Summer
<i>E. polyanthemos</i>	December	Summer	June	Winter

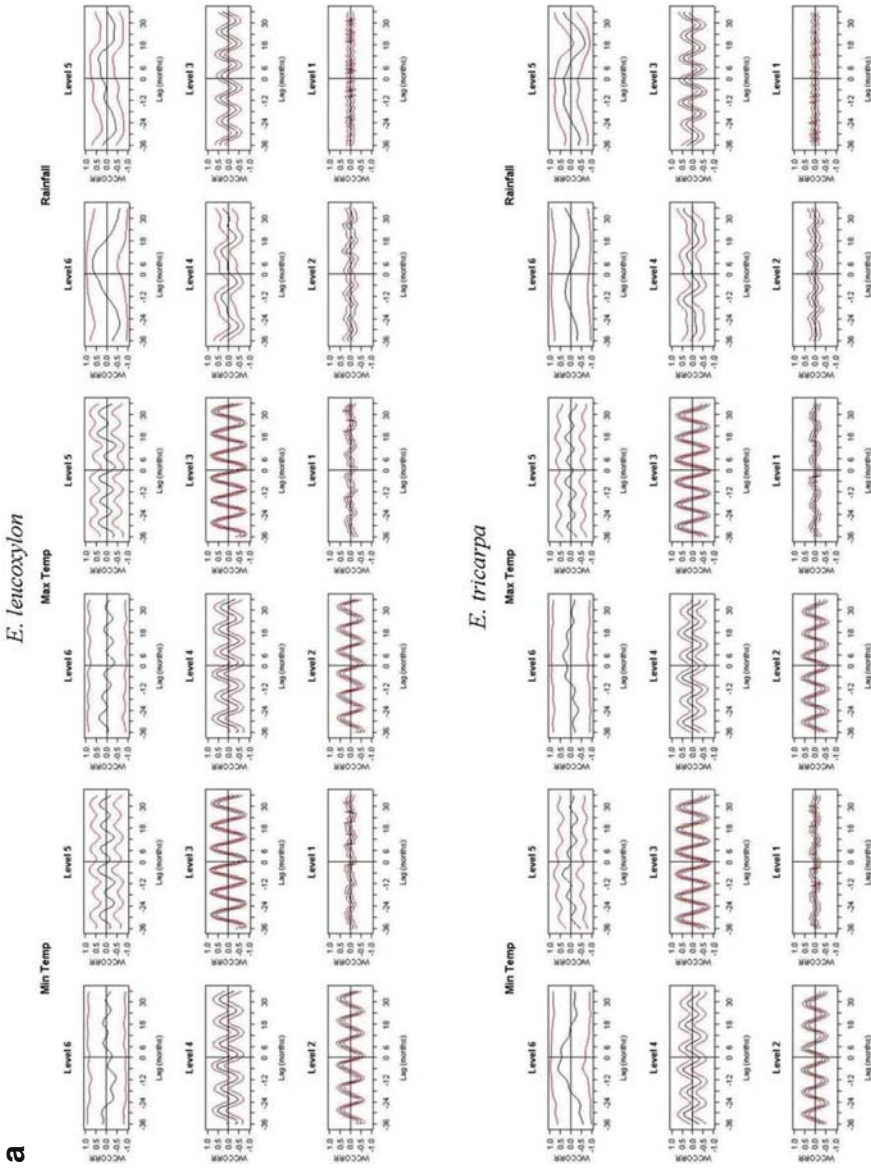


Fig. 17.10 (a) Minimum and maximum temperature and rainfall cross-correlations plots for each species for *E. leucoxylon* and *E. tricarpa*

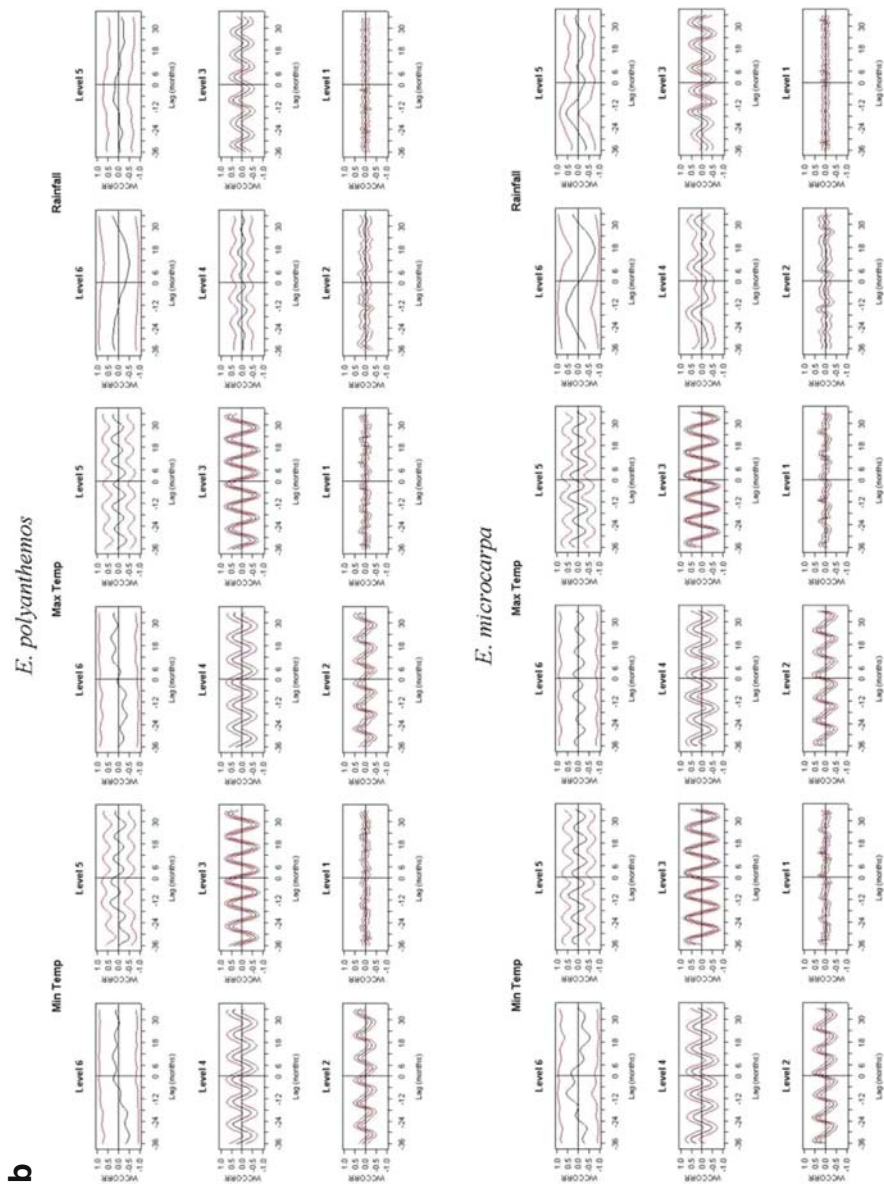
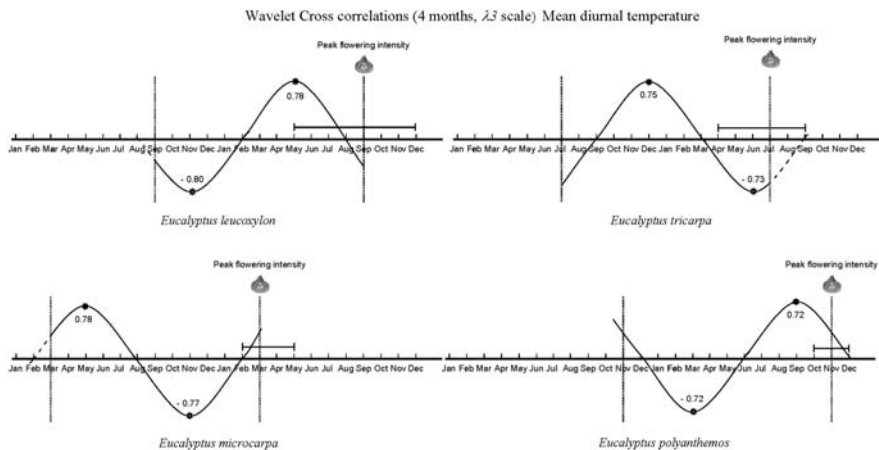


Fig. 17.10 (b) Minimum and maximum temperature and rainfall cross-correlations plots for each species for *E. microcarpa* and *E. polyanthemus*



**Fig. 17.11** Individual wavelet cross-correlations plots for daily mean temperature and flowering intensity. Vertical lines encapsulate the 12 months prior to peak flowering. The small horizontal interval indicates the annual flowering period

The cross-correlation profiles also show there is a maximum positive and negative cross-correlation, and these occur systematically 6 months apart for each species (Fig. 17.11 and delta values ( $\Delta$ ) in Table 17.4). These cross-correlations can be viewed as the highest absolute value of the wavelet cross-correlations, for lags either in the short term ( $\leq 6$  months prior to peak flowering intensity), or the long term ( $> 6$  months). The number of months at which either lag, occurs prior to peak flowering intensity, differs for each species (Fig. 17.11 and Table 17.4). Note that *E. polyanthemos*'s maximum short term lag is positive (0.72) and occurs in September, which is 2 months before peak flowering intensity, whereas *E. tricarpa*'s short term lag is negative ( $-0.73$ ) and occurs in June, this being 1 month prior to peak flowering intensity. The long term lag for *E. polyanthemos* is in March, which is 8 months before peak flowering intensity and negative ( $-0.72$ ), compared to the December positive (0.75), long term lag for *E. tricarpa*, which occurs 7 months before its peak flowering intensity in July (Fig. 17.11 and Table 17.4).

According to these wavelet cross-correlations, a similar relationship between flowering with temperature and between flowering and rainfall occurs in *E. leucoxylon* and *E. polyanthemos*. The strongest correlations with temperature are positive (0.78 and 0.72, respectively) in the short-term ( $\leq 6$  months) and negative ( $-0.80$  and  $-0.72$ , respectively) in the long-term ( $> 6$  months). With rainfall, the strongest wavelet cross-correlations are negative ( $-0.41$  and  $-0.32$ , respectively) in the short-term and positive (0.35 and 0.39, respectively) in the long-term. The reverse relationship between flowering and temperature and with rainfall is observed in *E. tricarpa* and *E. microcarpa*.

The cross-correlations also show, as did correlations, that for all species temperature and rainfall variables do not act in concert. That is, within a given species, if the cross-correlation with temperature is positive, at a particular time of year,

**Table 17.4** Significant ( $P < 0.0001$ ) wavelet cross correlations (4 months,  $\lambda_3$  scale) between species and climate: shorter [ $\leq 6$  months] and longer lags [ $> 6$  months] prior to peak flowering intensity

Species	Diurnal temp	Minimum temp	Maximum temp	Rainfall
<i>E. leucoxydon</i>	0.78 [-4]	0.78 [-5]	0.79 [-4]	-0.41 [-5]
Peak: September	May	April	May	April
Start: May	-0.80 [-11]	-0.81 [-11]	-0.80 [-10]	0.35 [-11]
End: December	October $\Delta = 7$	October $\Delta = 6$	November $\Delta = 6$	October $\Delta = 6$
<i>E. tricarpa</i>	-0.73 [-1]	-0.73 [-1]	-0.73 [-1]	0.46 [-1]
Peak: July	June	June	June	June
Start: April	0.75 [-7]	0.75 [-7]	0.74 [-7]	-0.45 [-7]
End: September	December $\Delta = 6$	December $\Delta = 6$	December $\Delta = 6$	December $\Delta = 6$
<i>E. microcarpa</i>	-0.77 [-4]	-0.76 [-4]	-0.77 [-4]	0.48 [-4]
Peak: March	November	November	November	November
Start: February	0.78 [-10]	0.78 [-10]	0.78 [-10]	-0.44 [-10]
End: May	May $\Delta = 6$	May $\Delta = 6$	May $\Delta = 6$	May $\Delta = 6$
<i>E. polyanthemos</i>	0.72 [-2]	0.72 [-2]	0.72 [-2]	-0.32 [-2]
Peak: November	September	September	September	September
Start: October	-0.72 [-8]	-0.73 [-8]	-0.72 [-8]	0.39 [-8]
End: December	March $\Delta = 6$	March $\Delta = 6$	March $\Delta = 6$	March $\Delta = 6$

$\Delta$  signifies the difference in months between shorter and longer lags

then the relationship with rainfall is negative (Figs. 17.10a, b and 17.11, Table 17.4) and vice versa. For example, each of *E. microcarpa*'s short term lags for temperature is positive and occurs in November. Its short term rainfall lag also occurs in November, but is negative. Additionally, cross-correlations provide further insight into the dynamic relationship between climate and peak flowering intensity for each species. For example, although at zero lag *E. tricarpa* and *E. leucoxydon* have a similar relationship with climate (somewhat intuitive as their flowering overlaps (Table 17.4)); their relationship over the 12 months differs, with an opposite sinusoidal profile of peaks and troughs (Fig. 17.11 and Table 17.4).

## 17.6 Discussion

### 17.6.1 Subcomponents

Wavelets multiresolution analysis (MRA) has delineated four subcomponents in the flowering series: non-flowering phase, duration, annual cycle, flowering intensity, as well as the overall trend for each species. d1 is the non-flowering phase per species. These "off phases" are coincident with other reproductive phases (e.g. budding, seeding) in eucalypts (Ashton 1975, Bassett 1995, Murray and Lutze 2004). This phenomenon has also been noted specifically in *E. tricarpa* (Keatley and Murray 2006). The second sub-component, d2, reflects both the duration and pattern of the original flowering record, for a given species.

The annual cycle has been clearly delineated by d3, with the mean month of peak intensity, so identified, being in agreement (i.e. *E. leucoxyton*: September, *E. tricarpa*: July, March: *E. microcarpa*, November: *E. polyanthemos*) with that identified by other analytic methods (the mean flowering intensity in a flowering year (Keatley and Hudson 2007)) and singular spectrum analysis (SSA) (Hudson et al. 2004).

d4 relates to the annual or biennial cycling of the intensity of flowering years. In three of the four species (*E. microcarpa*, *E. polyanthemos* and *E. tricarpa*) the biennial cycle is associated with years of low flowering intensity ( $< 2$ ). Note that in these three species low flowering intensity also includes years of no flowering (i.e. flowering intensity = 0).

In *E. leucoxyton* flowering alternates between a quasi-biennial (1950–1952, 1955–1963) and an annual cycle. It is the only species, where the biennial cycle is associated solely with low ( $< 2$ ) intensity, and/or late commencement with short duration (commencing in September or October compared to the most probable month of commencement in April). Variation in flowering intensity, in general, as well as cycling has long been reported in eucalypts (Chambers 1893). Flowering intensity exhibiting two year cycles in these species has also been previously reported, based on the opinion of apiarists (Goodman 1973, Somerville and Campbell 1997, Paton et al. 2004); the collection of reproductive components (Keatley and Murray 2006) and more recently confirmed by autocorrelogram analysis and SSA (Wells 2000, Hudson et al. 2004). However, there are also some differences between wavelet and SSA based results. For example, a 4 year cycle, previously detected by SSA for *E. tricarpa* (Hudson et al. 2004, Chapter 18), was not demonstrated by wavelet analysis. A four year cycle for this species has, however, been delineated using autocorrelograms (Wells 2000). Wells's study and that by Somerville and Campbell (1997) have also reported a four year cycle in *E. microcarpa*. It is worth noting that whilst SSA is a global analysis (see Hudson et al. 2005) wavelets provide a localised analysis. Yiou et al. (2000) note that SSA can be made more wavelet-like with the use of a specific windowing technique. Some comparisons between wavelets analysis and SSA are given in Chapter 18 but see also Yiou et al. (2000).

s4 is the smoothed series that captures the slowly varying portion of the flowering signal, effectively an estimate of the trend. Again the results of wavelet analysis, namely a decreasing trend in flowering intensity, align with SSA results (Hudson et al. 2004, 2005, Chapter 18). The so-called trend reconstructed component is usually the first reconstructed component in a SSA (Elsner and Tsonis 1996) and mirrors the smoothed overall trend S4.

### ***17.6.2 Temperature and Rainfall Correlations***

At the time of peak intensity both *E. leucoxyton* and *E. tricarpa* have a significant negative relationship with the temperature variants. This indicates that for both these species, flowering intensity is increased if cooler temperatures are present.

However, there is a slight difference in the strength of this relationship, possibly indicating that for *E. leucoxyton*, it is cooler minimum temperatures, and in *E. tricarpa* cooler maximum temperatures which have more of an influence on peak flowering time/intensity. *Eucalyptus leucoxyton* and *E. tricarpa* have a positive relationship with rainfall, but it is only *E. tricarpa*, where the correlation with rainfall is statistically significant, indicating that wetter conditions would tend to increase flowering intensity for this species. This strong evidence of a significant negative wavelet correlation between flowering and temperature variants for *Eucalyptus tricarpa* and *E. leucoxyton*, supports the earlier finding of an upper threshold temperature (of 18°C) above which flowering intensity reduces or ceases for *E. leucoxyton* (Hudson et al. 2003) and the recent GAMLSS modelling of Hudson et al. (2009) (see Chapter 10) which identified an upper threshold of 21.3°C for maximum temperature above which flowering intensity reduces or ceases for *E. tricarpa*.

*Eucalyptus microcarpa* and *E. polyanthemos* share a similar relationship with temperature (positive) and rainfall (negative). Note, however, that their flowering durations do not generally overlap (Keatley et al. 2004) and their months of peak flowering intensity are separated by four months. However, the mean diurnal temperature and mean monthly rainfall over their respective flowering duration is similar, 16.2°C and 38.7 mm for *E. microcarpa* and 16.3°C and 42.0 mm for *E. polyanthemos*. Rainfall did not have a significant influence in either of these species. In *E. microcarpa* flowering intensity is only significantly correlated with minimum temperature indicating warmer minimum temperatures are associated with more intense flowering. Minimum temperature has previously been nominated as the primary driver for *E. microcarpa* (Hudson et al. 2004). Other studies of these species (Porter 1978, Keatley and Hudson 2000, Hudson et al. 2004, 2009, Kim et al. 2009) have also identified similar relationships between temperature and/or rainfall with flowering commencement (or flowering intensity). The recent GAMLSS modelling of Hudson et al. (2009) (see also Chapter 10) identified a lower threshold of 16.1°C (mean temperature) for *E. microcarpa* and 17.5°C (maximum temperature) for *E. polyanthemos* above which flowering commences. This supports the results of this study: a significant positive wavelet correlation between flowering and temperature variants.

### 17.6.3 Temperature and Rainfall Cross-Correlations

Relationships delineated between phenophases and climatic variables, may be considered physiologically and/or statistically based (Yang et al. 1995, Spano et al. 1999). In this case, for each of the species examined, the relationships between peak flowering intensity and the temperature and rainfall variables could partly be reflecting the time of year these species flower. For example, *E. tricarpa*'s peak flowering intensity occurs in winter, and this species has a negative relationship with temperature, indicating increased flowering with decreasing temperature. Previously, this

scenario has been suggested for explaining at least some of the relationship between flowering commencement and climate in three (*E. leucoxylo*n and *E. tricarpa* and *E. polyanthemos*) species (Keatley and Hudson 2000). However, cross-correlations add further insight into and detail about the changing relationship between climate and peak flowering intensity (over an annual cycle). They show that whilst the pairing of *E. leucoxylo*n and *E. tricarpa*, and the pairing of *E. microcarpa* and *E. polyanthemos*, respectively, have similar relationships at zero lag with the climate variables; the relationship between peak flowering intensity and climate during the 12 months prior to each species' peak flowering is individual or species specific; and therefore not a reflection of the time of year in which the species flowers. Note that, four months prior to peak flowering intensity, *E. leucoxylo*n is most strongly and positively influenced by temperature, whereas the influence on *E. tricarpa* is not significant. Also the influence of temperature on each of these species switches from negative to positive and back again in different seasons pointing to a physiological basis for this interplay.

Additionally, it has been found that when rainfall and temperature have been accounted for, there is no significant remaining trend in flowering intensity in *E. leucoxylo*n (Hudson et al. 2003), indicating that there is a physiological basis to this relationship. Previous work (Porter 1978, Keatley and Hudson 2000, Keatley et al. 2002, Hudson et al. 2003, 2004) examining the influence of temperature and rainfall on flowering intensity of these species have found similar results, but have used different analytical methods (singular spectrum analysis, generalized additive models (GAMs) and Bayesian hierarchical models (BHM)s and regression).

In very broad terms, more intense peak flowering is likely to occur in *E. leucoxylo*n when cool, wet conditions coincide with peak flowering. However, peak flowering would be furthered enhanced if the preceding autumn and winter were warm and dry, and the previous spring and summer cool and wet. This endorses the upper threshold temperature of 18.5°C found for this species by Hudson et al. (2003). *Eucalyptus tricarpa* requires the same conditions at peak flowering intensity (i.e. cool and wet) but almost the opposite conditions to *E. leucoxylo*n in the months leading up to flowering: namely a cool, wet autumn and winter, with a warm, dry spring and summer. A warm, dry autumn and winter with a cooler, wet spring, and summer with warm, dry conditions at peak flowering, favours more intense flowering in *E. microcarpa*. Flowering is enhanced in *E. polyanthemos* with warm, dry conditions coinciding with peak flowering, preceded by a warm, dry winter and spring and cool, wet summer and autumn, in contrast to *E. microcarpa*.

Wavelets also clearly identify the cyclical influence on peak flowering intensity of climate (temperature and rainfall). There are 6 months of an annual cycle in which any given climate variable positively influences flowering intensity and 6 months of negative influence, within a given species which results in distinct seasonal change points.

Previous authors have also observed this 6 month cycling phenomenon in the reported tables and/or figures of various published studies; namely in an



examination of flowering commencement between 1954 and 1989 (by multiple regression) and the effect of mean monthly temperature by Fitter et al. (1995, Fig. 4); in a study using *P*-splines by Roberts (2008, Fig. 3) on flowering commencement, from 1978 to 2001, with respect to mean daily maximum temperature being an approximately 6 month period in which the sign of the smoothed regression coefficients changed from negative to positive. Finally, in Sparks and Carey (1995, Table 2) there is evidence of this cycling in correlation between flowering in wood anemone and turnip and monthly temperature in central England, for the months preceding mean observed date, over a 212 year period (1736–1947). Further investigation of this cycling phenomenon is required. Until now this phenomenon of 6 monthly cycling has not been commented on, nor formalised quantitatively as in this present study (via wavelets).

## 17.7 Conclusion

MODWT-MRA identified the sub-components (annual cycle, duration, non-flowering and trend) within each flowering series. Wavelet correlation found the same contemporaneous effects of climate on flowering for *Eucalyptus tricarpa* and *E. leucoxylon*, and for *E. microcarpa* and *E. polyanthemus*. There is strong evidence of a significant negative wavelet correlation between flowering and temperature variants for *E. tricarpa* and *E. leucoxylon*, which supports the earlier finding of an upper threshold temperature above which flowering intensity reduces or ceases for these species. There is also strong evidence of a significant positive wavelet correlation between flowering and temperature variants for *Eucalyptus microcarpa* and *E. polyanthemus*, which supports recent identification of lower temperature thresholds below which flowering intensity reduces or ceases. Wavelets cross-correlational analysis determined the relationship between temperature and rainfall identifying the primary climatic drivers at peak flowering intensity. Cross-correlations demonstrated the changing dynamics of the relationship between peak flowering and climate, and point to a physiological basis for this interplay. Specifically, wavelet cross-correlation analysis identified the cyclical influence of temperature and rainfall on peak flowering intensity ( $P < 0.05$ ). For each species there are 6 months of the annual cycle in which any given climate variable positively influences flowering intensity and 6 months of negative influence. For all species, rainfall exerts a negative influence when temperature is positive. In doing so, wavelet analyses add credibility to the use of phenological records to detect and understand local climatic impacts on phenological phases and possibly global climate change per se. This study shows that the discrete wavelet transform (DWT) and the maximal overlap DWT (MODWT), with multiresolution analysis are ideally suited for analysing the inter-correlations between climate and phenological time series which may exhibit non-stationarity. Whilst conventional time frequency domain techniques (such as the Fast Fourier Transform (FFT)) provide results that are difficult to interpret, the wavelet cross-correlation succinctly displays how the association between the two processes, climate with flowering, change with scale.

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# Chapter 18

## Singular Spectrum Analysis: Climatic Niche Identification

Irene L. Hudson and Marie R. Keatley

**Abstract** This chapter discusses singular spectrum analysis (SSA) and uses a 32 year record (1940–1971) of flowering of four eucalypt species (*Eucalyptus leucoxylon*, *E. microcarpa*, *E. tricarpa* and *E. polyanthemos*) to illustrate its use.

SSA delineated the trend, annual and biennial cycle in all four species. Additionally a 4 year cycle was detected in *E. tricarpa*. The trend and annual cycle were identified by SSA decomposition of the underlying climate profile (rainfall and mean, minimum, maximum temperatures).

An examination of the correlation between the reconstructed flowering series and lagged climatic components found that for *E. leucoxylon* and *E. tricarpa* there was a similar relationship to climate. These two species exhibit a significant negative relationship with the temperature variables and a positive relationship with rainfall. The strongest relationship for *E. leucoxylon* was with minimum temperature ( $\rho = -0.742$ ). In *E. tricarpa* maximum temperature was the marginally stronger driver ( $\rho = -0.895$ ). Both *E. microcarpa* and *E. polyanthemos* also share a similar relationship to climate but this differs to that of *E. leucoxylon* and *E. tricarpa*; in that these species were positively influenced at flowering by temperature and negatively by rainfall. For *E. microcarpa* minimum temperature is the main but weak influence ( $\rho = 0.383$ ) and *E. polyanthemos* maximum temperature is the stronger influence ( $\rho = 0.674$ ).

**Keywords** Cyclicity · Eigentriples · Singular value decomposition · Singular spectrum analysis · Time series subcomponents

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## 18.1 Introduction

Recent phenological literature has highlighted the need for additional mathematical and statistical methods for examining time series (Dose and Menzel 2004, 2006, Gordo and Sanz 2005, Hudson et al. 2005a, Doi 2007).

Singular spectrum analysis (SSA) was introduced in oceanographic research by Colebrook (1978) and developed for nonlinear dynamical systems by Broomhead and King (1986) and Fraedrich (1986). At present, the books, book chapters and papers dealing with the methodological aspects and the applications of SSA number several hundred (see, for example, Allen and Smith 1986, Vautard et al. 1992, Danilov and Zhiglyavsky 1997, Ghil and Taricco 1997, Yiou et al. 2000 and references therein) particularly within the field of digital processing, and the examination of geophysical and climatic data (e.g. Kumaresan and Tufts 1980, Pike et al. 1984, Vautard and Ghil 1989, Elsner and Tsonis 1991, 1996, Ghil and Vautard 1991, Allen et al. 1994, Ghil et al. 2002, Yiou et al. 2000). In the life sciences, SSA has been applied to the possible connections between ENSO and cholera (Rodó et al. 2002), and to neurophysiological problems (Mineva et al. 1996), among others. Loeuille and Ghil (2004) applied principal component analysis and SSA (as a spectral analytic technique) to study intrinsic and climatic factors in animal population dynamics. See also Salmerón et al. (2002), Weedon (2003) and Grigorov (2006) for diverse applications of SSA.

SSA is a nonparametric method. It attempts to overcome the problems of finite sample length and noisiness of sampled time series, not by fitting an assumed model to the available time series, but by using a data-adaptive basis set; this is instead of the more traditional fixed sine and cosine method of the Blackman-Tukey correlogram (Blackman and Tukey 1958), which constructs an estimate of the power spectrum using windowed fast Fourier transforms of the autocorrelation function of the time series under investigation.

The potential value of SSA in phenology and climate change research was detailed by Hudson et al. (2005a). SSA is essentially a linear approach which can decompose a time series into its underlying components (e.g. trends, oscillatory modes or seasonalities, change-points and noise) and is useful for short, noisy time series (Vautard et al. 1992, Allen and Smith 1996, 1997, Elsner and Tsonis 1996, Golyandina et al. 2001), of which many phenological datasets are. SSA is as yet not very widely applied to phenological data (D'Odorico et al. 2002, Hudson et al. 2004, Studer et al. 2005, 2007).

The problem of establishing the statistical linkages between large-scale and local-scale processes has been investigated through noise reduction by combining SSA (or Empirical Orthogonal Function [EOF] analysis), and spatial principal component analysis (Jolliffe 1986) with the aim of constructing appropriate statistical models for estimating the local-scale variables from large-scale processes (Tatli et al. 2005, Studer et al. 2007). This approach is viable as in statistics and signal processing, the method of EOF analysis is essentially a decomposition of a signal or data set in terms of orthogonal basis functions which are determined from the data. The basis functions are typically found by computing the eigenvectors of the



covariance matrix of the data set. Thus SSA (or equivalently EOF) is analogous to performing a principal component analysis on the data, except that the EOF method finds both time series and spatial patterns. EOF is extensively employed in climate research to identify dominant patterns of variability and to reduce the dimensionality of the data (Hannachi et al. 2005). SSA was used by Tatli et al. (2005) in a study of surface air temperature variability over Turkey and its connection to large-scale upper air circulation; and by Aban and Tateishi (2004) for the reconstruction of annual phenological profiles from Normalized Difference Vegetation Index (NDVI) time series data.

Recently Studer et al. (2007) used EOF analyses to link ground-based phenological observations with those obtained from satellite remote sensing. Long time series of ground-based plant phenology, in addition to more than 20 years of satellite-derived phenological metrics are currently accessible to evaluate the impacts of climate variability and trends on terrestrial vegetation (Schwartz and Reiter 2000, Schwarz et al. 2002, Schwartz 2003). Use of remote sensing data assimilation for phenology model development was recently investigated by Stöckli et al. (2008). It is well recognised that traditional plant phenology provides very accurate information on individual plant species, but with limited spatial coverage. Remote sensing phenology allows monitoring of terrestrial vegetation on a global scale and provides an integrative view at the landscape level (Schwartz 2003). Studer et al. (2007) compared a multispecies index (derived in Studer et al. 2005) from ground-observed spring phases with two types (maximum slope and threshold approach) of satellite-derived start-of-season (SOS) metrics (Zhang et al. 2004, White et al. 2005). Studer et al. (2007) concluded that there is good correspondence between the traditional observed ground-level phenology and the satellite approach to phenology, thereby satellite-derived phenology can assist in interpreting ground data of low coverage.

Caterpillar SSA (Golyandina et al. 2001) was successfully adapted and applied to epidemiological data to investigate the relationship between climate, pollution and Sudden Infant Death Syndrome (SIDS) (Hudson et al. 2005b) and to a case study of the impact of notable global and local weather events on the level of air pollution in Christchurch, New Zealand (Fukuda 2004, Fukuda et al. 2004, Fukuda and Hudson 2005a, b).

### ***18.1.1 SSA vs SSA MTM***

SSA is based on eigenvalue-eigenvector decomposition of a time series' lag-covariance matrix (Broomhead and King 1986, Fraedrich 1986). Given a series of length  $T$ , and a maximum lag  $L$ , the eigenvectors are data-adaptive basis functions for the representation of the series and are called empirical orthogonal functions (EOFs), by analogy with conventional principal component analysis. The eigenvalues are the associated variances  $\lambda_k$ , of each EOF ordered from largest to smallest. When two eigenvalues are nearly equal, and the corresponding pair of (odd and even) EOFs are in phase quadrature, they may capture, subject to statistical significance tests, an anharmonic (i.e. not sinusoidal) oscillation of possibly nonlinear origin (Ghil and Vautard 1991, Vautard et al. 1992).

Specifically, Broomhead and King (1986) applied the “method of delays” of dynamical systems theory to estimate the dimension of, and reconstruct series, using singular-value decomposition (SVD) on the trajectory matrix formed by lagged copies of a single series obtained from the system. Vautard and Ghil (1989) realised the formal similarity between classical lagged-covariance analysis and the method of delays, and called the SSA derived eigenvectors, *empirical orthogonal functions* (EOFs). The projection of the time series onto an EOF yields the corresponding principal component of length  $T-L+1$ . Reconstructed components are series of length  $T$  that are obtained by the least-square fitting of their lagged copies, at lag  $0, 1, \dots, L-1$  to the projection of the original series and its copies onto a given EOF or a set of EOFs (Ghil et al. 2002, Vautard et al. 1992) (see the mathematics method in Section 18.2 below). In summary, the SSA procedure then selects the subsets of eigen elements and principal components to facilitate three algorithms – noise-reduction, detrending and identification of oscillatory components – for constructing so-called new components, “reconstructed components” (Vautard et al. 1992).

The SSA-MTM Toolkit developed by the Theoretical Climate Dynamics group at the University of California, Los Angeles (Dettinger et al. 1995) and further improved in collaboration with researchers in Europe and North America (Ghil et al. 2002 and <http://www.atmos.ucla.edu/tcd/ssa>). The SSA-MTM Toolkit supports four different spectral methods: classical Fourier analysis, SSA, the multi-taper method (MTM), and the maximum entropy method (MEM). MTM is designed to reduce the variance of spectral estimates by using a small set of tapers rather than the unique data taper or spectral window used by Blackman-Tukey methods (Thompson 1982). MTM as In MTM a set of independent estimates of the power spectrum is computed, by pre-multiplying the data by orthogonal tapers which are constructed to minimize the spectral leakage due to the finite length of the data set. The optimal tapers or “eigentapers” belong to a family of functions known as discrete prolate spheroidal sequences and defined as the eigenvectors of a suitable Rayleigh-Ritz minimisation problem (Slepian 1978). Averaging over this set of spectra yields a better and more stable estimate – (i.e. one with lower variance – than do single-taper methods).

The foundation of SSA-MTM is to examine and expand the lagged-covariance matrix, that allows study over space and/or time (Shun and Duffy 1999). The SSA-MTM toolkit provides a battery of statistical significance tests for each method, as well as important visualisation tools that facilitate comparison of results between the methods. More complete descriptions of all four methods, as well as comparisons of their features and performance can be found in Ghil et al. (2002). The entire SSA-MTM Toolkit, along with the User Guide, is available as freeware (SSA-MTM Toolkit User’s Guide see <http://www.atmos.ucla.edu/tcd/ssa>). Further references on advanced spectral methods and their diverse applications are also listed therein (see also Vautard et al. 1992, Allen and Smith 1996, Mann and Lees 1996).

The key idea and procedures of SSA are similar between the two research groups, namely SSA-MTM (Vautard and Ghil 1989) and Caterpillar SSA (Golyandina et al. 2001). Both SSA-MTM and Caterpillar SSA can be applied without any a priori knowledge about the underlying system. The procedures then select the subsets

of eigen elements and principal components to facilitate three algorithms – noise-reduction, detrending and identification of oscillatory components – for constructing so-called new components, denoted as reconstructed components (RCs) (Vautard et al. 1992, Fukuda 2004). The main tasks of Caterpillar SSA are introduced in Section 18.2.

There are, however, some theoretical and mathematical differences between the two methods. SSA from the SSA-MTM group provides *three* steps with an appropriate selected window length; embedding the sampled time series, computing the lag-covariance matrix, and diagonalising the lag-covariance matrix (which includes decomposition via SVD). This lag-covariance matrix is a Toeplitz matrix, which is a square matrix with constant diagonal structure with negative slope. On completion of these three steps, the sum of the power spectra of the components (eigenvalues and associated principal components) then form the resultant reconstructed structures (recon). In contrast, Caterpillar SSA from Golyandina et al. (2001) has *four* steps: embedding, SVD, ET grouping (eigenvalues and principal components) and diagonal averaging. The summing of each decomposed structure is carried out prior to the diagonal averaging required to obtain the reconstructed structures. The lag-covariance matrix here is a Hankel matrix – a square matrix, with constant diagonal structure and a positive slope. Indeed the Hankel matrix is an upside-down Toeplitz. Detailed information on Caterpillar SSA is described in Section 18.2.1.1. For information on the mathematics of SSA-MTM, refer to Vautard and Ghil (1989), Dettinger et al. (1995) and Ghil et al. (2002) and for examples of applications Allen and Smith (1996) and Mann and Lees (1996).

Each SSA method also has their own statistical software available:

- “Caterpillar” SSA <http://www.gistatgroup.com/cat/> (Golyandina et al. 2001)
- SSA-MTM Toolkit which is freeware and can be found at <http://www.atmos.ucla.edu/tcd>
- kSpectra Toolkit software <http://www.spectraworks.com/> a commercial project which uses the same mathematics as SSA-MTM Toolkit.

### ***18.1.2 Examples of SSA-MTM and Monte Carlo SSA***

Loeuille and Ghil (2004) have applied multi-taper methods (MTM) and SSA (both spectral analytic techniques) to study intrinsic and climatic factors in animal population dynamics. In 2006, Grigorov (2006) used an extension of SSA, namely the Monte Carlo Singular Spectrum Analysis (as was introduced by Allen and Smith 1996) to test whether a given time series was generated from any well-defined process, including deterministic chaos. Chaos is an instance of dynamical nonlinearity and chaotic processes. See also the review papers of Ghil and You (1996) and Ghil and Taricco (1997). Monte Carlo SSA can be used to establish whether a given time series is linearly distinguishable from any well-defined

process, including the output of a deterministic chaotic system. “Red noise” is traditionally used to refer to any linear stochastic process in which spectral power declines monotonically with increasing frequency (see the SSA-MTM Group 2000; <http://www.atmos.ucla.edu/tcd/ssa/>). An enhanced Monte Carlo SSA was developed by Paluš and Novotná (2004). This enhanced Monte Carlo SSA was successfully applied in the detection of period 7.8 years oscillatory modes in records of monthly average near-surface air temperature from several European locations, as well as in the monthly North Atlantic Oscillation index (Paluš and Novotná 2004). Their method was based on evaluating and testing regularity of dynamics of the SSA modes against the so-called coloured noise null hypothesis, in addition to the test based on variance (eigenvalues, as in conventional SSA). The application of their regularity index, computed from a coarse-grained estimation of mutual information, enhances the test sensitivity and reliability in detection of relatively more regular dynamical modes than those obtained by decomposition of coloured noise components, in particular, in detection of irregular oscillations embedded in red noise (as in Monte Carlo SSA).

Earlier studies using Monte Carlo SSA or SSA-MTM are: Allen and Smith (1996) who used Monte Carlo SSA to detect trends in the Southern Oscillation Index (SOI) and El Niño/Southern Oscillation (ENSO) index; a coastal study (Rozynski et al. 2001); D’Odorico et al.’s (2002) phenological study; a pressure signal study in nuclear power plants (Paloma et al. 2003); the use of SSA in combination with principal component analysis and neural networks to derive a prediction model for ENSO by Hsieh and Tang (1998) and by Hsieh and Wu (2001, 2002); a combination of SSA and wavelets to detect the SOI/ENSO changes by Yiou et al. (2000) (see also Fukuda 2004 and the SSA-MTM ToolBox).

## 18.2 Methods

We follow part of the mathematical development of SSA by Hassani (2007) in addition to that of Golyandina et al. (2001) and provide a description of the methodology of SSA.

### 18.2.1 Stage 1 Decomposition

#### 18.2.1.1 First Step: Embedding

Embedding can be regarded as a mapping that transfers a one-dimensional time series  $Y_T = (y_1, \dots, y_T)$  into the multi-dimensional series  $X_1, \dots, X_K$  with vectors

$$X_i = (y_i, \dots, y_{i+L-1})' \in R^L, \quad (18.1)$$

where  $K = T - L + 1$ ;  $i=1, 2, \dots, K$ .

Vectors  $X_i$  are called *L-lagged vectors* (or, simply, *lagged vectors*). The single parameter of the embedding is the *window length*  $L$ , an integer such that  $2 \leq L < T$ , giving the trajectory matrix

$$X = [X_1, \dots, X_K] = (x_{ij})_{i,j=1}^{L,K}. \tag{18.2}$$

Note that the trajectory matrix  $X$  is a Hankel matrix, which means that all the elements along the diagonal  $i+j = \text{const}$  are equal. Embedding is a standard procedure in time series analysis. With the embedding performed, future analysis depends on the aim of the study.

**18.2.1.2 Second Step: Singular Value Decomposition (SVD)**

The second step, the singular value decomposition (SVD) step, performs a singular value decomposition of the trajectory matrix and represents it as a sum of rank-one bi-orthogonal elementary matrices. Denote by  $\lambda_1, \dots, \lambda_L$  the eigenvalues of  $XX'$  in decreasing order of magnitude ( $\lambda_1 \geq \dots \lambda_L \geq 0$ ) and by  $U_1, \dots, U_L$  the orthonormal system (that is,  $(U_i, U_j) = 0$  for  $i \neq j$  (the orthogonality property)) and  $\|U_i\| = 1$  (the unit norm property)) of the eigenvectors of the matrix  $XX'$  corresponding to these eigenvalues.  $(U_i, U_j)$  is the inner product of the vectors  $U_i$  and  $U_j$  and  $\|U_i\|$  is the norm of the vector  $U_i$ . Let

$$d = \max (i, \text{ such that } \lambda_i > 0) = \text{rank } X \tag{18.3}$$

If we denote  $V_i = X'U_i / \lambda_i$ , then the SVD of the trajectory matrix can be written as:

$$X_i = \sqrt{\lambda_i} U_i V'_i (i = 1, \dots, d) \tag{18.4}$$

where  $X_i = \sqrt{\lambda_i} U_i V'_i (i = 1, \dots, d)$ .

The matrices  $X_i$  have rank 1; therefore they are elementary matrices,  $U_i$ . In SSA literature they are called “factor empirical orthogonal functions” or simply EOFs and  $V_i$  often called “principal components” which represent the left and right eigenvectors of the trajectory matrix. The collection  $(\lambda_i, U_i, V_i)$  is called the  $i$ -th eigentriple of the matrix  $X$ ,  $\lambda_i (i = 1, \dots, d)$  are the singular values of the matrix  $X$  and the set  $\{\lambda_i\}$  is called the spectrum of the matrix  $X$ . If all the eigenvalues have multiplicity one, then the expansion (18.4) is uniquely defined.

SVD (18.4) is optimal in the sense that among all the matrices  $X^{(r)}$  of rank  $r < d$ , the matrix  $\sum_{i=1}^r X_i$  provides the optimal approximation to the trajectory matrix  $X$ , so that  $\|X - X^{(r)}\|$  is minimum. Note that  $\|X\|^2 = \sum_{i=1}^d \lambda_i$  and  $\|X_i\|^2 = \lambda_i$  for  $i=1, \dots, d$ . Thus we can consider the ratio  $\lambda_i / \sum_{i=1}^d \lambda_i$  as the characteristic of the

contribution of the matrix  $X_i$  to expansion (18.4). Consequently,  $\sum_{i=1}^r \lambda_i / \sum_{i=1}^d \lambda_i$ , the sum of the first  $r$  ratios, is the characteristic of the optimal approximation of the trajectory matrix by the matrices of rank  $r$ .

## 18.2.2 Stage 2 Reconstruction

### 18.2.2.1 First Step: Grouping

The grouping step corresponds to splitting the elementary matrices  $X_i$  into several groups and summing the matrices within each group. Let  $I = \{i_1, \dots, i_p\}$  be a group of indices  $i_1, \dots, i_p$ . Then the matrix  $X_I$  corresponding to group  $I$  is defined as  $X_I = X_{i_1} + \dots + X_{i_p}$ . The split of the set of indices  $J = 1, \dots, d$  into the disjoint subsets  $I_1, \dots, I_m$  corresponds to the representation:

$$X = X_{I_1} + \dots + X_{I_m} \quad (18.5)$$

The procedure of choosing the sets  $I_1, \dots, I_m$  is called the eigentriple grouping. For a given group  $I$  the contribution of the component  $X_I$  into the expansion (18.4) is measured by the share of the corresponding eigenvalues:  $\sum_{i \in I} \lambda_i / \sum_{i=1}^d \lambda_i$ .

### 18.2.2.2 Second Step: Diagonal Averaging

Diagonal averaging transfers each matrix  $I$  into a time series, which is an additive component of the initial series,  $Y_T$ . If  $z_{ij}$  stands for an element of a matrix  $Z$ , then the  $k$ -th term of the resulting series is obtained by averaging  $z_{ij}$  over all  $i, j$  such that  $i + j = k + 2$ . This procedure is called *diagonal averaging*, or Hankelization of the matrix  $Z$ . The result of the Hankelization of a matrix  $Z$  is the Hankel matrix  $HZ$ , which is the trajectory matrix corresponding to the series via the diagonal averaging. Note that Hankelization is an optimal procedure in the sense that the matrix  $HZ$  is the nearest to  $Z$  (with respect to the matrix norm) among all Hankel matrices of the corresponding size (for more information see Golyandina et al. (2001, Chapter 6, Section 2)). In its turn, the Hankel matrix  $HZ$  uniquely defines the series by relating the value on the diagonals to the values in the series. By applying the Hankelization procedure to all matrix components of (18.5), we obtain the following:

$$X = \bar{X}_{I_1} + \dots + \bar{X}_{I_m} \quad (18.6)$$

where  $\bar{X}_{I_1} = HX$ . This is equivalent to the decomposition of the initial series  $Y_T = (y_1, \dots, y_T)$  into a sum of  $m$  series:

$$y_t = \sum_{k=1}^m \bar{y}_t^{(k)} \quad (18.7)$$

where  $\bar{Y}_T^{(k)} = (\bar{y}_1^{(k)}, \dots, \bar{y}_T^{(k)})$  corresponds to the matrix  $X_{Ik}$ .

### 18.2.3 ET Groupings

The first step of stage 2, the reconstruction stage, is to separate the additive components of the time series that are constructed from the previous step – ETs – into groups. The procedure of selecting each possible group is called ET grouping. To understand the mechanism of the grouping, one needs to consider the concept of separability, as the grouping of similar components, from the group of additive components, can also be considered as partitioning, or separating the components from one another.

#### 18.2.3.1 Mathematical Description

The first part is the grouping procedure. Consider step 2 (Section 18.2.1.2), where the SVD was used to decompose the trajectory matrix,  $X$ , into the following:

$$X = X_1 + \dots + X_d \quad (18.8)$$

The grouping procedure partitions the set of indices  $\{J = 1, \dots, d\}$  into  $m$  disjoint subsets (ET groups),  $I_1, \dots, I_m$  (see equation 18.5).

Let  $I = \{i_1, \dots, i_p\}$ . The *resultant matrix*  $X_I$  corresponding to the group  $I$  is defined as:

$$X_I = X_{i_1} + \dots + X_{i_p} \quad (18.9)$$

The grouping parameters that combine the decomposed structures (see Equation 18.5) selecting the sets of  $I_1, \dots, I_m$  are called the ET grouping.

Separability is the key to achieving a successful ET grouping. If the original time series is constructed of separable components, it is said to possess *strong separability*. The original time series is described as  $F$ , and  $F$  is considered to be a sum of two time series,  $F^{(1)}$  and  $F^{(2)}$ :  $F = F^{(1)} + F^{(2)}$ . The idea is that matrix terms of the SVD of the trajectory matrix  $X$  can be split into two different groups –  $X^{(1)}$  and  $X^{(2)}$  – of the original time series  $F^{(1)}$  and  $F^{(2)}$ . This condition is critical for the SSA method to work. A description of the mathematical conditions of separability follows.

The original time series  $F$  is a sum of two time series  $F^{(1)}$  and  $F^{(2)}$ , such that:

$$f_i = f_i^{(1)} + f_i^{(2)} \text{ where } (i = 0, \dots, T - 1) \tag{18.10}$$

Details of conditions for separability follow, as do four methods to assess separability.

**18.2.3.2 Conditions for Separability**

Fix a window length  $L$ , thus  $K=T-L+1$ . The  $L$ -trajectory matrices of the components of  $F$ ,  $F^{(1)}$  and  $F^{(2)}$ , are respectively labelled  $X^{(1)}$  and  $X^{(2)}$ . Each row and each column of the trajectory matrix  $X^{(1)}$  of  $F^{(1)}$  is orthogonal to each row of the trajectory matrix  $X^{(2)}$  of  $F^{(2)}$ . Then orthogonality of the subspaces for the series  $F^{(1)}$  and  $F^{(2)}$  is necessary: If the subspace  $(L, 1)$  is spanned by the columns of the  $X^{(1)}$ , it must be orthogonal to the subspace  $(L, 2)$  spanned by the columns of  $X^{(2)}$ . At the same time, the subspaces  $(K, 1)$  and  $(K, 2)$  spanned by the rows of  $X^{(1)}$  and  $X^{(2)}$  must also be orthogonal.

Assessment of Separability

1. When the orthogonal condition above holds for  $X^{(1)}$  and  $X^{(2)}$ , (weak) separability is achieved for the series  $F$  by decomposition of  $X$ .

The following definition exists to satisfy (weak) separability:

If a collection of indices  $I \subset \{1, \dots, d\}$  exists, such that:

$$X^{(1)} = \sum_{i \in I} X_i \tag{18.11}$$

and

$$X^{(2)} = \sum_{i \notin I} X_i \tag{18.12}$$

then the series  $F^{(1)}$  and  $F^{(2)}$  are said to be (weakly) separable.

2. Assume that the singular values corresponding to  $X_k^{(1)}$  and  $X_m^{(2)}$  are the same, then the SVD of the matrix  $X$  is:

$$X = \sum_k X_k^{(1)} + \sum_m X_m^{(2)} \tag{18.13}$$

Thus the terms of  $X^{(1)}$  and  $X^{(2)}$  cannot be identified uniquely in the sum of  $X^{(1)}$  and  $X^{(2)}$  for this specific  $k$  and  $m$ , (i.e. they are not completely separable). This state is called weak separability.



3. Besides the condition of weak separability of  $F^{(1)}$  and  $F^{(2)}$  from 1 above and equations 18.11 and 18.12, if the collections of the SVD of the trajectory matrices  $X^{(1)}$  and  $X^{(2)}$  are disjoint as follows,

$$X^{(1)} = \sum_k X_k^{(1)} \quad (18.14)$$

and

$$X^{(2)} = \sum_k X_k^{(2)} \quad (18.15)$$

then it is said that  $F^{(1)}$  and  $F^{(2)}$  are strongly separable.

4. When the set of indices is fixed as  $I=I_1$ , the resultant matrices,  $X_{I_1}$  and  $X_{I_2}$ , are Hankel matrices. If  $X_{I_2} = X - X_{I_1}$ , then the trajectory matrix  $X$  is separable by the expansion of  $X$ . At the same time, if the matrices  $X_{I_1}$ , and  $X_{I_2}$  are thought to be Hankel matrices, then  $F^{(1)}$  and  $F^{(2)}$  as well as the corresponding trajectory matrices  $X^{(1)}$  and  $X^{(2)}$  are thought to be Hankel matrices. Then it is said that the sequence is “approximately separable” for two series;  $F^{(1)}$  and  $F^{(2)}$ . This can be assessed by the correlation coefficient  $\rho^{(L,K)}$  between the rows and the columns of the trajectory matrices of  $X^{(1)}$  and  $X^{(2)}$ , and all the correlations of these are close to zero.

The concept of separability (either weak or strong separability) is satisfied if condition 1 is true; basically, the corresponding  $X^{(1)}$  and  $X^{(2)}$  from each  $F^{(1)}$  and  $F^{(2)}$  are separable. The difference of weak and strong separability can be illustrated by examining whether the sum of the SVDs of the trajectory matrices of the series  $F^{(1)}$  and  $F^{(2)}$  coincide with one of the SVDs of the trajectory matrix of the series  $F = F^{(1)} + F^{(2)}$ , or more practically, whether it is possible to group the matrix terms of any SVD of the trajectory matrix  $X$  of the series  $F = F^{(1)} + F^{(2)}$ , to obtain the trajectory matrices of the series  $F^{(1)}$  and  $F^{(2)}$  (Golyandina et al. 2001). If the answer to these questions is yes, then it is said to be strongly separable, and condition 3 is satisfied. However, if the either or both answers are no, then condition 2 is satisfied, and the structure has weak separability.

In real life, exact separability is not often obtained, so that proving that the correlations between the rows and between the columns of the trajectory matrices of  $X^{(1)}$  and  $X^{(2)}$ , corresponding to each  $F^{(1)}$  and  $F^{(2)}$ , are close to zero is enough to conclude approximate separability, as in condition 4. Actual observations for the cross correlation coefficient  $\rho X_{1,2}^{(\omega)}$  can also be examined from the  $w$ -correlation analysis below (see equation 18.9).

### 18.2.3.3 Concept of $w$ -Correlation

The value of  $\rho$  from the  $w$ -correlation analysis is obtained from each selected ET group. Therefore separability is assessed by the cross correlation value of  $\rho$ , and

the quality of separability, called the weighted correlation or  $w$ -correlation is a natural measure of deviation of two series  $F^{(1)}$  and  $F^{(2)}$  from  $w$ -orthogonality and in the case of exact separability, the orthogonality of rows and columns of the trajectory matrices  $X^{(1)}$  and  $X^{(2)}$  means that all pairwise inner products of their rows and columns are “zero” (Golyandina et al. 2001). The  $w$ -correlation matrix is defined below.

Consider a  $w$ -correlation analysis for  $F^{(1)}$  and  $F^{(2)}$ , then the  $w$ -correlation is derived as follows:

Let  $L^* = \min(L, K)$  and  $K^* = \max(L, K)$ , then

$$\omega_i = \begin{cases} i + 1 & \text{for } 0 \leq i \leq L^* - 1, \\ L^* & \text{for } L^* \leq i \leq K^*, \\ T - i & \text{for } K^* \leq i \leq T - 1. \end{cases} \tag{18.16}$$

The inner product of series  $F^{(1)}$  and  $F^{(2)}$  of length  $T$  given by

$$(F^{(1)}, F^{(2)})_\omega = \sum_{i=0}^{def\ T-1} \omega_i f_i^{(1)} f_i^{(2)}. \tag{18.12}$$

Then, if  $(F^{(1)}, F^{(2)})_\omega = 0$ , the relationship between  $F^{(1)}$  and  $F^{(2)}$  is  $w$ -orthogonal.

The weighted correlation, or  $w$ -correlation, is a value that quantifies the separability of two series  $F^{(1)}$  and  $F^{(2)}$  as follows:

$$\rho_{12}^{(\omega)} = \frac{(F^{(1)}, F^{(2)})_\omega}{\|F^{(1)}\|_\omega \|F^{(2)}\|_\omega} \tag{18.18}$$

for

$$\|F^{(i)}\|_\omega = \sqrt{(F^{(1)}, F^{(2)})_\omega}, \quad i = 1, 2. \tag{18.19}$$

where from Equation 18.16, the absolute value of the  $w$ -correlation is obtain.

If this value is small (close to zero), then the two time series are said to be almost  $w$ -orthogonal, and they are approximately separable. However it is important to mention that when two time series are large (i.e. infinitely long), this assumption is no longer true, because the series are not likely to be  $w$ -orthogonal, thus providing poor separability, whereby  $F^{(1)}$  and  $F^{(2)}$  are called asymptotically separable, when the correlation coefficients tend to zero, while  $T \rightarrow \infty$  (with the condition of the window length  $L=L(T)$ ) (Golyandina et al. 2001).

An examination of the correlation coefficient  $\rho$  is certainly helpful in confirming separability in the series and this information is used subsequently to group the ETs into the appropriate groupings to derive requisite separability.

### 18.2.4 Assessment of Any ET Groups by the $w$ -Correlation Plot

Graphical interpretation of separability is examined by observing the  $w$ -correlation plot (provided automatically by Caterpillar SSA). The  $w$ -correlation plot for *E. leucoxylo*n is shown Fig. 18.1. It shows how all ETs are grouped together and how the resultant groups are successfully separated.

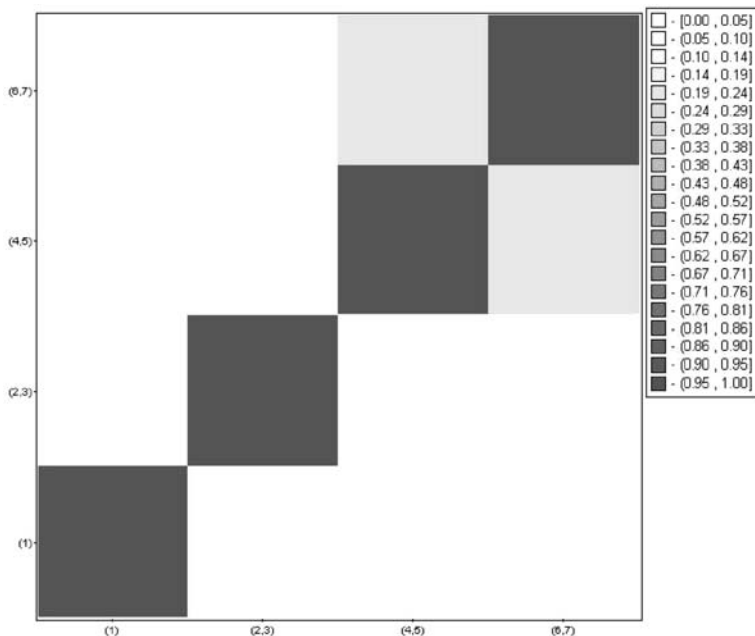


Fig. 18.1  $w$ -correlation plot for *E. leucoxylo*n

### 18.2.5 Considerations

There are three issues to consider when using SSA (regardless of the package used) these are:

- the data are assumed to be complete (i.e. there is no missing data),
- the appropriate window length,
- the number of, and which eigentriples to group (see Fig. 18.1 the  $w$ -correlation plot).

#### 18.2.5.1 Missing Data

Missing data are common in datasets and phenological data are no different. Any standard spectral analysis requires data to be complete (Kondrashov and Ghil

2006). Hence methods for filling in missing data have been developed (Schneider 2001, Schollhamer 2001, Kondrashov et al. 2005, Kondrashov and Ghil 2006, Golyandina and Osipov 2007). Each of these methods has different underlying mathematics which is explained in detail in the individual papers and compared in various of the following papers (Ghil et al. 2002, Kondrashov and Ghil 2006, 2007, Schneider 2007). The missing value algorithms of Golyandina and Osipov (2007) can now be performed by the CatMV 1.0 (2007) software (see <http://www.gistatgroup.com/cat/>).

### 18.2.5.2 Window Length

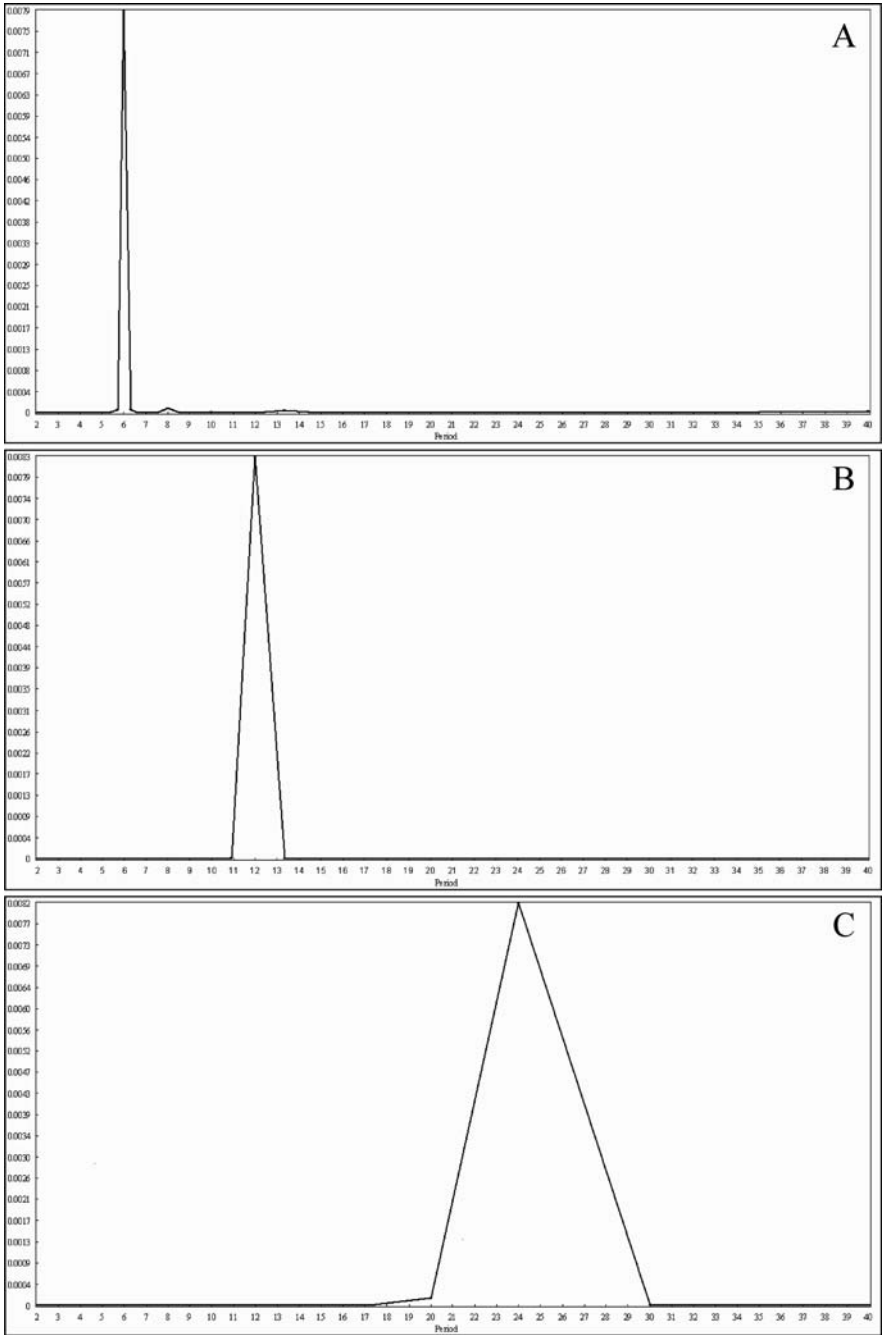
The selection of window length  $L$  is undertaken by the user. In choosing the window length the user needs to consider the question they are asking and balance the amount of information extracted versus the degree of confidence in that information. There is greater statistical confidence in smaller window lengths (Elsner and Tsonis 1996, Ghil et al. 2002).

The ultimate choice of  $L$  depends on what kind of structural changes one is looking for. If one is only interested in the low-frequency components of the limited (finite) available variance in the time series, then  $L$  need to be very large. On the contrary, with a larger window length, the strictly, high-frequency components can be resolved (Golyandina et al. 2001). Moreover, Results cannot be very sensitive to  $L$  as long as  $L$  is considerably small. According to Golyandina et al. (2001), there are several general principles for the selection of  $L$ , which are summarized as follows:

1. The value of  $L$  should be reasonably large to separate the low-frequency component from the high-frequency component, but not greater than a half of series length  $N_t/2$ .
2. The larger  $L$  is the more detailed is the decomposition of the time series. The most detailed decomposition is achieved when  $L$  is approximately equal to half of the length of time series, that is,  $N_t/2$ , its maximized possible value.
3. For specific series and tasks, choice of a small  $L$  may be optimal than a large  $L$ , and may perform better than the large  $L$ . It is worthwhile trailing several window lengths.
4. When a series contains an obvious or known periodic component, say with an integer period  $T$ , set  $L$  proportional to  $T$ .
5. For a long series, it is better to choose  $L$  close to  $N_t/2$  and such that  $L/T$  is an integer. This is a combination of principles (2) and (4) above.

Indeed, the selection of window length  $L$  is determined by the time series itself. Often the shape of the graph of the series can be an effective visible indicator (of a trend or of underlying harmonics). Using a periodogram of the series may also help determine the periods of possible harmonic components in the series and as such in the selection of window length (see Fig. 18.2).

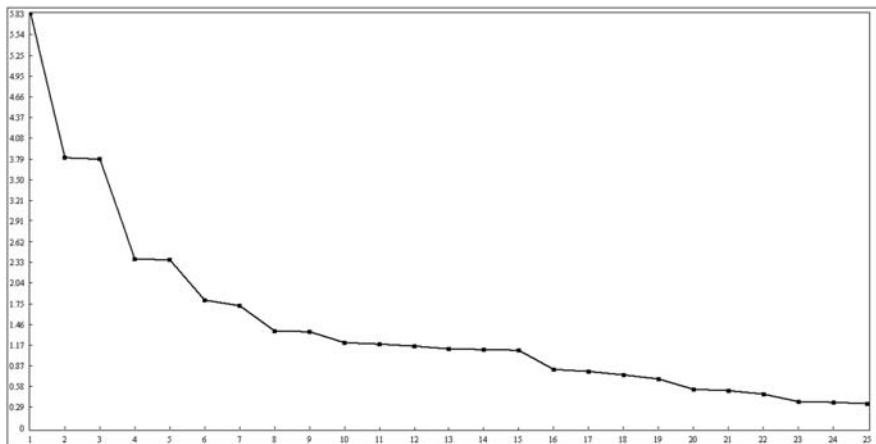
Differences in window length may result in differences in trend.



**Fig. 18.2** Periodograms for *E. leucoxyton*: (a) 6 month cycle, (b) 12 month cycle and (c) 24 month cycle

### 18.2.5.3 Choice of Number and Eigentriples (ETs) to Group

The use of a scree diagram (eigenvalues  $\lambda_k$  plotted against  $k$ ) assists in determining which of the principal components should be considered (Vautard and Ghil 1989, Ghil et al. 2002). Eigenvalues which have the same amplitude and are harmonic (or almost) (Golyandina et al. 2001) are considered oscillatory pairs and may be grouped (Fig. 18.3, Tables 18.1 and 18.2). The principal components which are above the noise floor are those which are considered “significant” (Vautard and Ghil 1989, Shun and Duffy 1999, D’Odorico et al. 2002) (Fig. 18.3).



**Fig. 18.3** Scree diagram of first 25 eigenvalues. Four eigentriple pairs are indicated 2–3, 4–5, 6–7 and 8–9

**Table 18.1** Reconstructed series, characteristics and variance accounted for in climate

Variable	Principal components (#indicates grouped RSs)	Characteristic	Variance (%)	Total variance
Minimum temperature	1	Trend	83.7	98.4
	2–3#	Annual	14.5	
	4–5#	6 monthly	0.2	
	6–7#	~Biennial	0.04	
Maximum temperature	1	Trend	91.6	99.2
	2–3#	Annual	7.5	
	4–5#	6 monthly	0.10	
	6–7#	~Biennial	0.04	
Mean temperature	1	Trend	90.0	99.4
	2–3#	Annual	9.3	
	4–5#	6 monthly	0.1	
	6–7#	~Biennial	0.04	
Rainfall	1	Trend	69.9	72.6
	2–3#	Annual	2.7	

**Table 18.2** Reconstructed series, characteristics and variance accounted for in phenological data

Variable	Principal components (#indicates grouped RSs)	Characteristic	Variance (%)	Total variance
<i>E. leucoxylo</i>	1	Trend	62.5	86.4
	2–3#	Annual	16.3	
	4–5#	~ Biennial	4.0	
	6–7#	20 months	2.2	
	8–9	6 monthly	1.4	
<i>E. tricarpa</i>	1	Trend	36.6	75.4
	2–3#	Annual	20.4	
	4–5#	~Biennial	11.2	
<i>E. microcarpa</i>	6–7#	~ 4 year	7.2	65.0
	1	Trend	23.5	
	2–3#	Annual	29.3	
	4–5#	6 monthly	7.5	
<i>E. polyanthemos</i>	6–7#	~ Biennial	4.7	68.4
	1	Trend	21.7	
	2–3#	Annual	24.6	
	4–5#	6 monthly	8.0	
	6–7#	~Biennial	4.1	

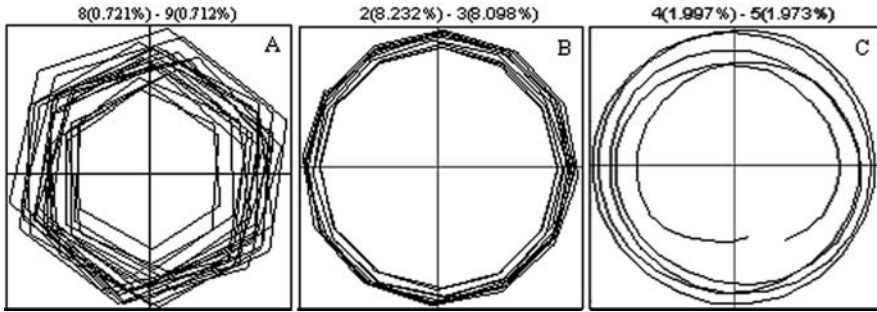
There are several principles for grouping to best achieve separation and identification of the underlying additive components of a time series.

- Collect and combine all the slowly varying (low-frequency) singular vectors to extract the major trend of a time series.
- A single periodicity component of the series produces a pair of principle components with approximately equal eigenvalues. Therefore eigenvalues close in value can indicate a seasonal component of the series.
- Although eigenvalues are important for eigentriple grouping, plots of both the grouping eigenfunctions and principle components can be more informative. For example, scatterplots of the eigenfunctions of sines and cosines with equal frequencies, amplitudes and phases, turn out to be increasing circular with increasing period (see Fig. 18.4).

## 18.2.6 Methods

### 18.2.6.1 Climate Data

Daily rainfall, along with daily minimum and maximum temperature records, were obtained from the Bureau of Meteorology, for the closest weather station (approximately 3.5 km away); Maryborough, Victoria (37' 03"S, 143' 44"E, 249.3 m elevation).



**Fig. 18.4** Scatter plots of three of *E. leucoxyton*'s eigentriple pairs: (a) 8–9 with a harmonic corresponding to a period of 6, (b) 2–3 with a harmonic corresponding to a period of 12, (c) 4–5 with a harmonic corresponding to a period of 24

### 18.2.6.2 Phenological Data

The records used in these analyses come from Havelock, Victoria, Australia and cover the years 1940–1971. Over this observation period there were two observers. The first observer covered the period 1940 until 1962, and the second 1962 until the 1971.

The timing and distribution of flowering of eight species of *Eucalyptus* were collected on a monthly basis. The observations were undertaken on a regular basis, on the 15th (and sometimes 16th) of each month. Whilst the monthly basis of the data limits the sensitivity of the analysis, no data of greater temporal resolution are currently known to be available in Australia for this period. It should also be noted that the mean flowering for each of the species studied is greater than 3 months. Observations were undertaken within plots. This study concentrates only on the four species that commonly occur together (Muir et al. 1995).

- *Eucalyptus leucoxyton* – Yellow gum
- *E. microcarpa* – Grey Box
- *E. polyanthemus* – Red Box
- *E. tricarpa* – Red Ironbark.

### 18.2.6.3 Analyses

In this study Caterpillar 3.30 SSA was used to examine the eucalypt data with a window length of 120 (equivalent to 10 years). The modifications based on the eigentriple (ET) grouping method of Fukuda (2004) used in the study of the impact of global and local weather events on air pollution in Christchurch, New Zealand (Fukuda et al. 2004) was employed. This ET grouping method, called an enhanced Fourier expansion method (EFE) was based on the Fourier expansion criteria for ET separability from Golyandina et al. (2001) and FastGrouping software, which allowed for the detection of small frequency changes.

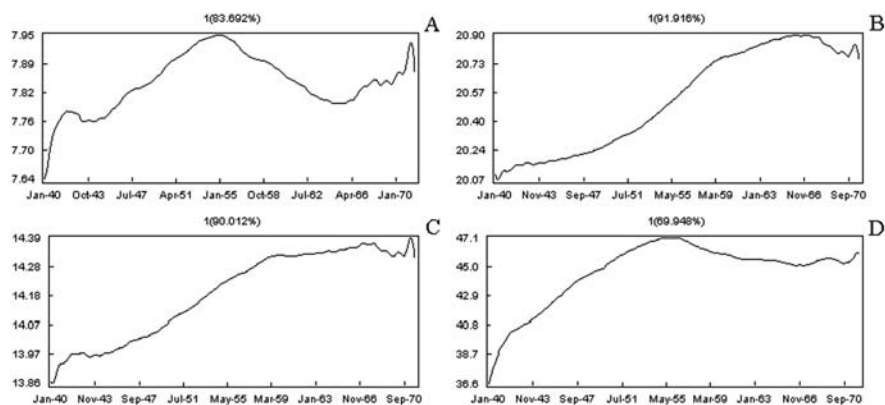


## 18.3 Results

### 18.3.1 Climate

The first reconstructed series (RS) (Fig. 18.5a–c) for minimum, maximum and mean daily temperature 1940–1971 for Maryborough account for 83.7, 91.3 and 90.0% of the signal (Table 18.1), respectively. It is typical for trends to be indicated in the first component and this is the case here. Minimum temperatures (Fig. 18.5a) increased until approximately September 1954 and were stable for a short period until early March 1955; after this date there is a downwards trend in minimum temperature until September 1964; after this minimum temperatures began to increase again in September 1955. Maximum temperature at Maryborough was increasing until November 1965, stable until March 1967 and then decreased until July 1970.

The mean temperature at Maryborough is driven by the maximum temperature (Fig. 18.5c). It increases until February 1967. There appears to be an agreement in the trends between rainfall and minimum temperature (Fig. 18.5a, d). The first RS in rainfall accounts for 69.9% of the signal (trend); rainfall increases until early 1955 (January) and is stable through to mid 1956 (June 1956) and then trends downwards.

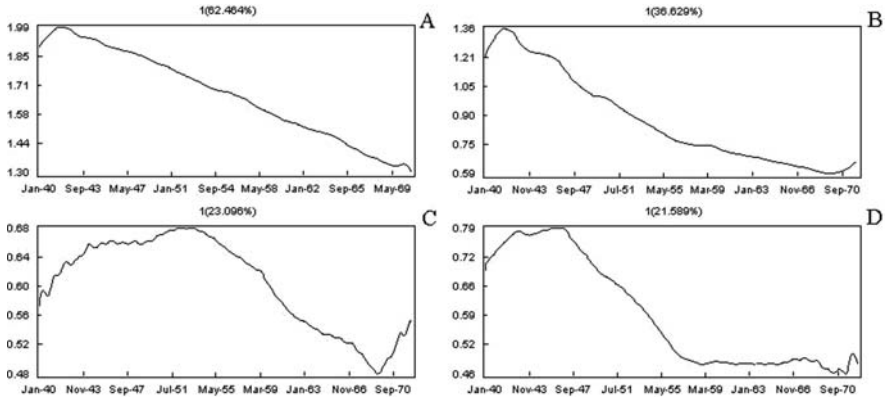


**Fig. 18.5** First reconstructed series for (a) minimum, (b) maximum, (c) mean temperature and (d) rainfall

### 18.3.2 Phenological Data

The first reconstructed series (RS) also account for the maximum amount of variation in two of the species examined *E. leucoxydon* (62.5%) and *E. tricarpa* (36.6%) (Table 18.2, Fig. 18.6a, b). In both *E. microcarpa* and *E. polyanthemus* the second RS (annual cycle) accounts for the majority of the variance (29.3 and 24.6%, respectively) compared to 23.5 and 21.7% for the trend (Table 18.2, Figs. 18.6c, d and 18.7c, d).

As with the climate RSs, the first RSs of the eucalypt species reflects the trend. There is a clear decrease in flowering intensity in all species – although this occurs



**Fig. 18.6** First reconstructed series for (a) *E. leucoxyton*, (b) *E. tricarpa*, (c) *E. microcarpa* and (d) *E. polyanthemus*

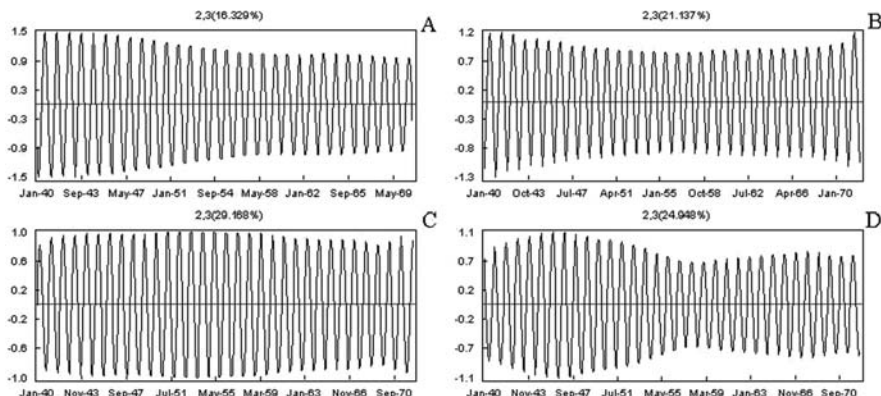
at different times across the species. For *E. leucoxyton* this commences in early 1942 February (Fig. 18.6a) and *E. tricarpa* a decrease is evident from September 1942 (Fig. 18.6b). *Eucalyptus microcarpa* increases in flowering until June 1952 and remains stable for about a year (May 1953), and then decreases to April 1969 followed by a sharp increase (Fig. 18.6c). In *E. polyanthemus* there is a sharp decrease from November 1946 until September 1958, after which flowering intensity stabilises (Fig. 18.6d).

The general decrease in flowering in each species indicates that flowering has become less intense over time. Another possible explanation for the downward trend is that the observers of flowering have changed their interpretation of intensity over time. The latter explanation does not seem to be as likely given the trends observed in *E. microcarpa* which as already indicated increased for the first 11 years.

### 18.3.3 Reconstructed Series 2 and 3

For all species (Fig. 18.7a–d) and for each of the weather variables examined these RSs represent the annual cycle. The peaks in the RS2 and 3 for each of the species indicate the time of peak flowering. For *E. leucoxyton* this is the month of September, for *E. microcarpa* it is March, *E. polyanthemus* peaks in November and *E. tricarpa* peaks in July.

As already mentioned, for *E. microcarpa* and *E. polyanthemus* these RSs accounted for the greatest amount of variation. In all species there is an overall decrease in amplitude of flowering over time. This decrease is least pronounced in *E. microcarpa* whose amplitude is constant until late 1960 thereafter there is a slight decrease (Fig. 18.7c). There is a general decrease in amplitude in *E. leucoxyton* flowering until approximately 1957 when the amplitude seems to be “even” until 1966 and then decreases again (Fig. 18.7a). *Eucalyptus tricarpa* which flowers in the cooler months, as does *E. leucoxyton*, decreases, until early 1953 (Fig. 18.7b).



**Fig. 18.7** Second and third reconstructed series for (a) *E. leucoxyton*, (b) *E. tricarpa*, (c) *E. microcarpa* and (d) *E. polyanthemus*

Flowering of *E. polyanthemus* increases from the beginning of the time series until late 1945 and then decreases until late 1957/early 1958 (Fig. 18.7d).

### 18.3.4 Correlation and Cross-Correlations Between Species and Weather Reconstructed Series 2 and 3

The relationship between the annual cycle (reconstructed series 2 and 3) of flowering and the climate variables were examined (Table 18.3) via correlational analysis. For, *E. leucoxyton* and *E. tricarpa* there were negative correlations (no lags) between each of the temperature variables and a positive relationship with rainfall. These relationships are reversed in the remaining species.

At peak flowering, the most influential temperature variable for *E. leucoxyton* is minimum temperature ( $\rho = -0.742$ ) and for *E. tricarpa* it is maximum temperature ( $\rho = -0.895$ ). This in contrast to the positive correlations for *E. microcarpa* and *E. polyanthemus*: minimum temperature ( $\rho = 0.383$ ) and maximum temperature ( $\rho = 0.674$ ), respectively.

Broadly speaking, at the time of peak flowering a negative relationship between temperature implies that as these temperature variants increase during the observation period flowering intensity decreased with the positive influence of rainfall moderating flowering in wetter periods. For *E. microcarpa* and *E. polyanthemus* increased temperatures in dry conditions Results in greatest flowering intensity.

**Table 18.3** Correlations between climate parameters and species (no lag)

Species	Minimum temp	Maximum temp	Mean temp	Rainfall
<i>E. leucoxyton</i>	-0.742	-0.693	-0.711	0.642
<i>E. tricarpa</i>	-0.857	-0.895	-0.882	0.539
<i>E. microcarpa</i>	0.383	0.297	0.328	-0.494
<i>E. polyanthemus</i>	0.626	0.674	0.658	-0.405

**Table 18.4** Cross correlations of the reconstructed series between species and climate: shorter [ $\leq 5$  months] and longer lags [ $> 5$  months] prior to peak flowering intensity

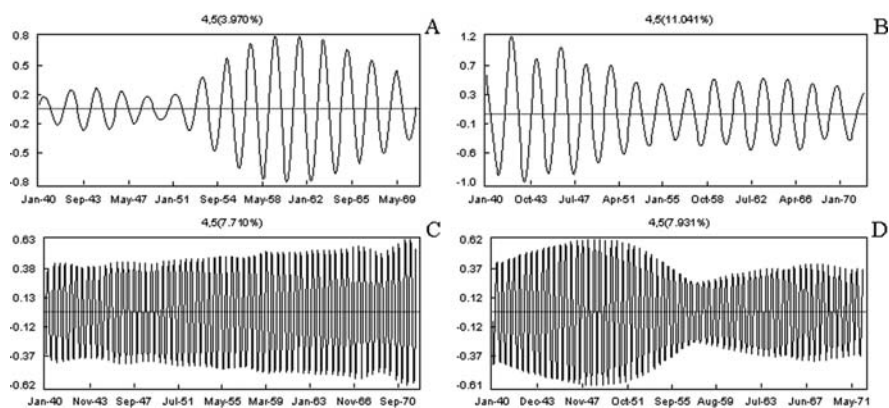
Species	Minimum temp	Maximum temp	Mean temp	Rainfall
<i>E. leucoxylon</i> Peak: September	0.94 [-5] April	0.91 [-5] April	0.92 [-5] April	-0.78 [-5] April
Start: May End: December	-0.89 [-10] October $\Delta = 5$	-0.92 [-10] October $\Delta = 5$	-0.91 [-10] October $\Delta = 5$	0.72 [-11] November $\Delta = 6$
<i>E. tricarpa</i> Peak: July Start: April	-0.92 [-1] June	-0.91 [-1] June	-0.92 [-1] June	0.68 [-1] June
End: September	0.90 [-7] December $\Delta = 6$	0.87 [-7] December $\Delta = 6$	0.89 [-7] December $\Delta = 6$	-0.83 [-7] December $\Delta = 6$
<i>E. microcarpa</i> Peak: March Start:	-0.97 [-4] November	-0.96 [-4] November	-0.96 [-4] November	0.82 [-4] November
February End: May	0.91 [-9] June $\Delta = 5$	0.93 [-9] June $\Delta = 5$	0.97 [-10] May $\Delta = 6$	-0.77 [-10] May $\Delta = 6$
<i>E. polyanthemus</i> Peak: November	0.90 [-1] October	0.90 [-2] September	0.90 [-2] September	-0.79 [-2] September
Start: October End: December	-0.93 [-8] March $\Delta = 7$	-0.92 [-7] April $\Delta = 5$	-0.92 [-8] March $\Delta = 6$	0.72 [-8] March $\Delta = 6$

Cross-correlation analysis revealed that although *E. leucoxylo*n and *E. tricarpa* are similarly influenced at the time of peak flowering by temperature and rainfall (Table 18.4) they are, overall, influenced differently throughout the year (Table 18.4). That is for approximately 4 months before peak flowering the influence of any temperature variable is positive for *E. leucoxylo*n; which would favour increased flowering intensity but would be moderated by the negative influence of rain. However, for *E. tricarpa* 5 months prior to, and including peak flowering the influence of temperature is negative. This would result in a lower flowering intensity with the positive influence of rain once again being a moderating factor.

For all four species there is on average, 5.7 months, when temperature positively influences flowering and 5.7 months when the influence of temperature is negative. Additionally, the influence of rainfall is always opposite to that of temperature (for example, *E. tricarpa* is positively influenced by temperature and negatively influenced by rain between October and March, and negatively influenced by temperature and positively influenced by rain between April and September. This relationship with temperature is illustrated in Fig. 17.11).

### 18.3.5 Reconstructed Series 4 and 5

This is the first difference in the flowering signal between the four species (i.e. the previous RSs were similar across all four species). *Eucalyptus leucoxylo*n and *E. tricarpa* exhibit a quasi-biennial cycle (Fig. 18.8a, b), whereas *E. microcarpa* and *E. polyanthem*os exhibit a 6 monthly cycle (Fig. 18.8c, d). The intensity of flowering in *E. leucoxylo*n and *E. tricarpa* is, however, reversed. The shift in the amplitude of flowering in *E. leucoxylo*n from less intense to more intense occurs in approximately mid April 1952, the shift from more intense to less intense in *E. tricarpa* also occurs in 1952, approximately August.



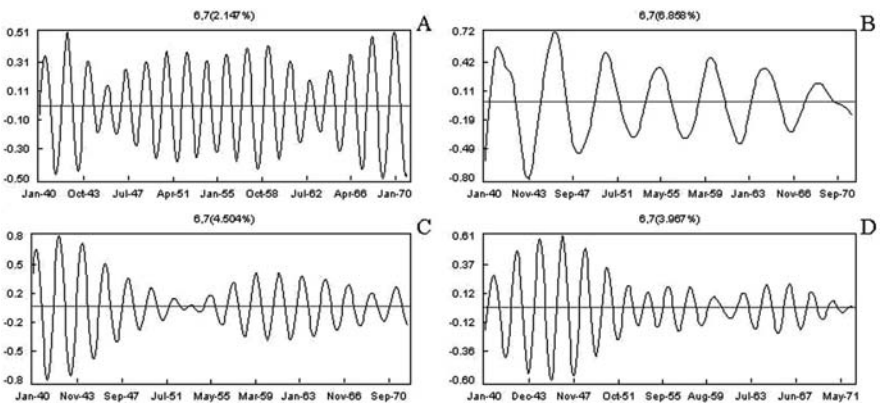
**Fig. 18.8** Fourth and fifth reconstructed series for (a) *E. leucoxylo*n, (b) *E. tricarpa*, (c) *E. microcarpa* and (d) *E. polyanthem*os

The half yearly cycles evident in *E. microcarpa* and *E. polyanthemus* are out-of-phase with each other by approximately 7 weeks. *Eucalyptus microcarpa*'s peaks are usually in late March and the middle of September, whereas *E. polyanthemus*' peaks occur in May and November (Fig. 18.8c, d). It is difficult to determine what these peaks relate to in a biological sense. In each species one of the peaks coincides with their average month of peak flowering (e.g. March is the month of peak flowering in *E. microcarpa*). There is an increase in the flowering intensity of *E. microcarpa* from early 1944 until the beginning of 1968. In *E. polyanthemus* there is a clear decrease in flowering intensity in 1956.

### 18.3.6 Reconstructed Series 6 and 7

This set of RSs exhibits the first occurrence of a significant difference between the species pair of *E. leucoxyton* and *E. tricarpa* (Fig. 18.9a, b). *Eucalyptus leucoxyton* has an average cycle of 20.5 months with a range of 23 months (1940–1942) to 18 months (1945–1947). The RSs 6 and 7 (Fig. 18.9a) account for a small amount of the variation (2.1%) in the flowering of *E. leucoxyton* but based on the values of the eigenvalues this is considered “significant”. There are two changes evident in flowering intensity one which occurs in early 1945 and one in late 1963. *Eucalyptus tricarpa* has an average cycle of 4 years 8 months but ranges from 4.5 years (between 1950 and 1955) to 5 years (between 1941 and 1946) (Fig. 18.9b).

Both *E. microcarpa* and *E. polyanthemus* exhibit a quasi-biennial cycle (mean 22.9 and 23.8 months, respectively) (Fig. 18.9c, d). *Eucalyptus microcarpa*'s cycle has a range of 17 months (between 1952 and 1953) to 24 months (which occur on multiple occasions). The cycle in *E. polyanthemus* has a range of 20 months (between 1952 and 1954) to 32 months (between 1960 and 1962). These differing



**Fig. 18.9** Sixth and seventh reconstructed series for (a) *E. leucoxyton*, (b) *E. tricarpa*, (c) *E. microcarpa* and (d) *E. polyanthemus*

periods in the individual species cycles correspond to change points in overall RSs (Fig. 18.9c, d). The period of 32 months could be detecting a phase of non flowering; as *E. polyanthemos* did not flower between February 1960 and September 1962.

## 18.4 Discussion

### 18.4.1 Cycles

SSA has separated out the trend and annual cycle in the climate variables. It has also delineated the trend, annual and biennial cycle in flowering intensity all four species. In defining the annual cycle the average peak intensity month for each species was generally delineated. For example, the peak flowering month for *E. microcarpa* is March (Keatley and Hudson 2007, Chapter 17) and the Results of SSA were in agreement with these other analytic methods (e.g. Keatley and Hudson 2007, Chapter 17).

Biennial cycling in flowering in these species has been commonly reported by bee keepers based on their experience (Beuhne 1914, Goodman 1973, Somerville and Campbell 1997) and mathematically quantified by Wells (2000). Variation in the intensity of flowering occurs within other species of eucalypts (Beuhne 1914, Goodman 1973, Ashton 1975, Setterfield and Williams 1996, Wilson 2002) and other species (e.g. Banksias (Copland and Whelan 1989)). These years of “good” and “poor” flowering in eucalypts have been attributed to climatic factors (Hudson et al. 2004, Flint and Fagg 2007) such as rainfall deficits resulting in soil moisture stress which in turns increases the abscission rate of buds and flowers (Ashton 1975, Wilson 2002, Flint and Fagg 2007). Other factors such as insect and fungal attack and the carry-over of buds to the following season are also believed to contribute to this apparent cyclicity of flowering (Ashton 1975, Davis 1969, Bassett 2002).

*Eucalyptus tricarpa* was the only species to have an extended cycle of 4 years and 8 months cycle detected. A four cycle has been detected using autocorrelograms (Wells 2002) but not by wavelet analysis (Chapter 17). Four year cycles have been detected in other eucalypt species: *E. regnans*, *E. diversifolia*, *E. dumosa*, *E. fasciculosa*, *E. incrassata* and for one of the other species in this study, *E. leucoxylon* (Ashton 1975, Paton et al. 2004).

With the exception of *E. tricarpa*, each species was found to have an approximately 6 month cycle. Determining the biological significance of this cycle is difficult. It is tempting to suggest that this cycle is related to the periods of flowering and non flowering through out the year. However, this does not seem to hold for any of these species as their mean flowering period ranges from  $3.6 \pm 1.5$  months for *E. polyanthemos* to  $9.7 \pm 4.2$  months for *E. leucoxylon* (Keatley and Hudson 2007). Additionally, if there were the case it would be expected that this cycle was present in *E. tricarpa*. It is possible that the 6 month cycle is within the eigentriples which were not considered significant. Clearly, further work on this aspect of the cycles is required.

### 18.4.2 Temperature and Rainfall Correlations

An examination of the correlations between the reconstructed flowering series and climatic components found that for *E. leucoxyton* and *E. tricarpa* there was a similar relationship with climate. Each is negatively influenced by temperature: be that mean, minimum or maximum temperature and each is positively influence by rainfall. For *E. leucoxyton* the main influence on flowering is minimum temperature and *E. tricarpa* it is maximum temperature. Rainfall has a slightly greater influence on flowering in *E. leucoxyton* than *E. tricarpa*. Hence, overall flowering intensity is enhanced by cooler, wetter conditions for each of these species. Both *E. microcarpa* and *E. polyanthemus* also share a similar relationship to climate but this is the opposite direction to that of *E. leucoxyton* and *E. tricarpa*. Flowering intensity in *E. microcarpa* and *E. polyanthemus* is enhanced by warmer, drier conditions.

The main temperature driver of flowering for three of these species: *E. leucoxyton*, *E. tricarpa* and *E. polyanthemus* is now established: in that linear regression (Keatley and Hudson 2000), GAMLSS (Hudson et al. 2009, Chapter 10), Wavelets (Chapter 17) and SSA (Hudson et al. 2004, this chapter) have nominated the same temperature variable for each of these species (e.g. *E. polyanthemus*'s main driver is maximum temperature which positively influences flowering intensity).

Stepwise regression (Keatley and Hudson 2000) also nominated the same main drivers for each of these species but highlighted that the influences on flowering are not simple: that is although there is a dominant climatic variable which influences flowering there are others which contribute. Using *E. tricarpa* as an example stepwise regression found that growing degree days and minimum temperature also contribute significantly to flowering. GAMLSS analysis (Hudson et al. 2009, Chapter 10) also found that minimum temperature positively influences flowering in this species therefore minimum moderates the influence of maximum temperature.

The main influence on the flowering of *E. microcarpa* is less clear. This is because two methods, Wavelets and SSA, have suggested minimum temperature influencing flowering and GAMLSS has indicated mean temperature as the main driver of flowering. Both contending variables have a positive influence.

The effect of rain has been shown to range from none (Porter 1978, Keatley and Hudson 2000) to a significant but minor effect (i.e. temperature has a much greater influence) (Wells 2000, Keatley et al. 2002); to significant with a major influence (Wilson and Bennett 1999, Kim et al. 2005). Therefore the role of rain on the flowering of these species needs further work.

*E. leucoxyton* and *E. tricarpa* commonly occur together (Muir et al. 1995) and have overlapping flowering periods (Wilson 2002, Keatley et al. 2004) both flower in the cooler, wetter months and these are precisely the conditions which enhance flowering. This might be regarded as just reflecting the climatic season in which these species flower. However, with the use of lags and cross correlation we demonstrated that there is an underlying physiological basis to the influence of climate and that these species avoid competition by occupying a different annual climate niche. These two species, as well as *E. microcarpa* and *E. polyanthemus*, are differently influenced by climate in the months preceding flowering. There is approximately



6 months of the annual cycle in which, any given climate variable, positively influences flowering intensity and 6 months of negative influence.

This 6 monthly cycle has also been delineated and statistically confirmed by wavelets analysis (Chapter 17) and has been illustrated in the Results, but not commented on, in the examination of the relationship between temperature and flowering of various species in the United Kingdom by regression, correlation and *P*-splines (Fitter et al. 1995, Sparks and Carey 1995, Roberts 2008).

So clearly the flowering of these species is influenced by climate. Their flowering period will change in response to climate change (Keatley et al. 2002) as will their peak flowering intensity and therefore nectar production (Porter 1978) as well as how often they flower (Mac Nally et al. 2009). The consequences of these responses to climate have been recently and dramatically demonstrated by a crash in the population of the birds which depend on the nectar these species (Mac Nally et al. 2009).

### ***18.4.3 Advantages and Limitations of SSA***

The advantages that SSA has over simple linear regression (SLR) are that it makes no specific distributional assumptions and can cope with non-stationary data. SSA also overcomes the enforced linearity that SLR imposes. Additionally, in a study of 3 datasets of global surface air temperature which varied in length between 90 and 130 years Elsner and Tsonis (1991), found that the trends of the air temperature were very similar regardless of the length of the series. A known limitation of SLR is that the slopes of the resultant regression lines are influenced by when the series commences and finishes and, also by the actual length of the series in the case of phenological data (Sparks and Menzel 2002, Menzel 2003, Sparks and Tryjanowski 2005).

As shown, a reconstructed phenological series may also be cross-correlated with climate variables so as to determine whether there is significant contemporaneous or lagged relationship. SSA also allows for forecasting and detection of change points in a time series (Golyandina et al. 2001); not discussed here. See SSA based change point analysis of herbarium records in Chapter 19.

As with all analytic methods there are limitations and restrictions: for SSA datasets are assumed to be complete (i.e. that there are no missing data) but methods are available to fill in the gaps (Schneider 2001, Schollhamer 2001, Kondrashov et al. 2005, Kondrashov and Ghil 2006, Golyandina and Osipov 2007). Also the grouping of eigentriples is currently determined by the user, however, AutoSSA is being developed to accommodate and allow automated ET grouping procedures (see <http://www.pdmi.ras.ru/~theo/autosssa/>). The window length is also required to be determined by the user, and as to which window length is optimal to use is a balance between the amount of information extracted versus the degree of confidence in that information. Smaller window lengths provide greater confidence. Differences in window length may result in significant differences in trend.

## 18.5 Conclusions

SSA has been shown to be a useful technique in the analysis of a phenological time series. It can, as with wavelet analysis, deconstruct a series into its major underlying components: trend and cycles (annual, biennial etc.).

At an individual species level SSA identified which of the climate variables were the main drivers of flowering. Cross-correlation has established that each species is uniquely influenced by climate through out the year. Cross correlation analysis of the resultant SSA reconstructed series demonstrate that there is an underlying physiological basis to the influence of climate and that these species avoid competition by occupying a different annual climate niche. *Eucalyptus leucoxylon* and *E. tricarpa* as a species pair; and *E. microcarpa* and *E. polyanthemus* as the other species pairing, are differently influenced by climate in the months preceding flowering. There is approximately 6 months of the annual cycle in which, any given climate variable, positively influences flowering intensity and 6 months of negative influence. Future work will entail the analysis and forecasting of the four eucalypt species jointly via SSA-based approaches to multidimensional time series.

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# Chapter 19

## Herbarium Collections and Photographic Images: Alternative Data Sources for Phenological Research

Fran MacGillivray, Irene L. Hudson, and Andrew J. Lowe

**Abstract** Irrefutable evidence is emerging from the scientific literature of universal shifts in phenology as a consequence of climate change. The intimate relationship which exists between seasonal flowering and climatic conditions, coupled with ease of observation, makes the monitoring of flowering events a reliable and cost effective method for the early detection of change in biological systems and an important tool in global change research. However, the long-term data sets required to determine the nature and magnitude of climatic impacts are very limited in Australia, and current research incorporates an interrogation of archival records to redress this important issue. Herbarium collections and photographic images have been found to provide robust estimates broadly in keeping with those published in the literature. This chapter is specifically focussed on accessing long term phenological data from the alternative data sources residing in herbarium and photographic collections. We outline the constraints to be considered when linking phenological changes with climatic fluctuations and long-term trends, offer some cautionary principles for analysis and interpretation and finally offer two case studies where phenological data have been successfully extracted from herbarium records. We investigate the value of less traditional methods such as Generalised Additive Models for Location, Scale and Shape (GAMLSS) adapted for time series data to accommodate possible non-linearities between herbarium records and year and/or climate; and suggest a model-free method of change-point detection. How best, if possible, to infer first flowering dates and actual stage of flowering from snap records is also an issue for inference and interpretation.

**Keywords** Analysis of time series · Climate change · Herbaria · Generalised additive model for location · Scale and shape (GAMLSS) · Photographic images

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## 19.1 Introduction

In the past, as now, an intimate knowledge of the timing of seasonal events was of great cultural and economic importance (Bolmgren and Lonnberg 2005). Before the advent of scientifically based weather forecasting, people's survival and well-being depended to a large extent on accumulated knowledge from generations of careful, detailed observations (Sparks et al. 2000, Bolmgren and Lonnberg 2005). Memorable events sometimes came to have cultural and religious significance, such as the flowering of cherry trees in Japan for which records from Kyoto date back to the ninth century (Arakawa 1955, 1956) and constitute the oldest known series (Koch et al. 2007). Dedicated amateur natural historians such as the Marsham family in the U.K. from 1786 to 1947, Henry Thoreau from 1837 to 1861 and, more recently, Mrs. Anderson from 1960 to 2002 in Massachusetts USA (Thoreau 2000, Ledneva et al. 2004, Miller-Rushing and Primack 2008) have provided a further legacy of valuable long-term data sets which are now providing evidence that many aspects of the world's physical and biological systems are changing in concert with current enhanced global warming. Consequently, phenological research has taken on a new significance and urgency. Answers are being sought to fundamental questions about the implications of climate change for species survival and ecosystem function in which phenology is now recognised as a driver of dynamic ecological processes as opposed to merely a passive response to environmental change (Primack et al. 2007, Post and Inouye 2008).

In most cases however, long-term historical observations of phenology are the exception rather than the rule, and information needs to be acquired from alternative data sources. This chapter is specifically focussed on accessing long-term phenological data from specimens residing in herbarium collections and photographic images. We outline the constraints in linking phenological changes with climatic fluctuations and long term trends, make some specific observations about herbaria and photographic data, offer some cautionary principles for analysis and interpretation and finally offer two case studies where phenological data have been successfully extracted from herbarium records. In contrast to northern hemisphere regions, where long-term biological data sets are frequent and diverse (Europe, USA, Japan), southern hemisphere records are an order of magnitude less frequent. The potential to access phenological information from alternative data sources such as herbaria and photographs therefore represents a very useful resource for South America and Africa, and particularly for Australia where more than six million herbarium specimens exist. <http://www.anbg.gov.au/chah/avh/avh.html>

## 19.2 Constraints to Linking Phenology with Climate

Phenology encompasses a wide range of vegetative and reproductive responses to local environmental conditions. However, consistencies have long been observed which indicate that phenological patterns are intrinsic and relatively stable properties of taxon groups (Clarke 1893, Kochmer and Handel 1986, Boulter et al. 2006).



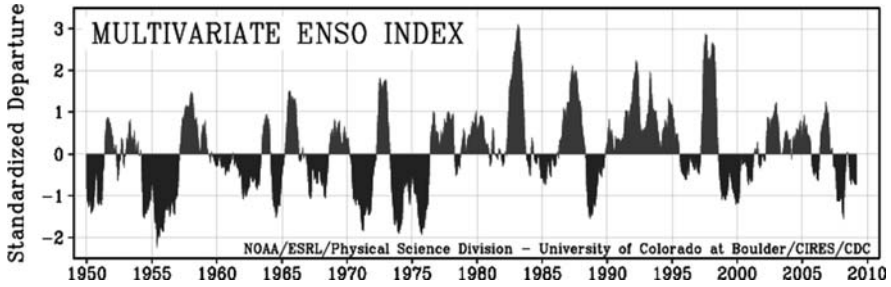
Phylogenetic constraints have been defined as those “properties shared by members of a monophyletic group by virtue of their common ancestry which limit the response of these taxa to directional selection” (Kochmer and Handel 1986). One of the first to suggest and document this, in relation to flowering time, was Clarke (1893) who wrote more than a century ago “The truth is forced upon us that the various groups of flowering plants are not scattered indiscriminately from one end of the season to the other, but are regulated by definite systematic principles” (Clarke 1893) p 770, and it has indeed proven to be the case. However, within the constraints imposed by past evolutionary adaptations and shared through lineage relationships, there is a great diversity and complexity of phenological responses (Colasanti and Coneva 2009).

The synchronization of a plant’s vegetative and reproductive biology with local environmental conditions is essential for maximisation of its chance of reproductive success. To this end, plants need to detect and respond to environmental cues that indicate incipient seasonal changes, both favourable and hostile to their ongoing development. The most reliable indicator of seasonal progression is photoperiod. As seasonality and changing day length are dependent upon distance from the equator, photoperiod monitoring is imperative for daylength dependent transition to flowering at higher latitudes (Simpson and Dean 2002). Plant species have evolved distinct reproductive strategies by which they can respond very precisely to relatively small changes in the ratio of daylight to darkness (Rivera and Borchert 2001, Simpson and Dean 2002, Yanovsky and Kay 2003). However, despite its fundamental importance, the influence of photoperiod is independent of climate and environmental conditions, and alone is insufficient to determine the procession of plant phenological responses.

### 19.3 Weather and Climate

Superimposed on the seasonal regularity of photoperiodism are more highly variable and unpredictable climatic factors such as temperature and precipitation (Spano et al. 1999, Lechowicz 2001, Brearley et al. 2007, IPCC 2007). Temperature has a major influence on plant developmental responses. Accumulated temperature above a certain threshold value, usually expressed as degree-days from the first of January, is a major trigger for the onset of flowering (Spano et al. 1999, Beaubien and Freeland 2000), and accumulating evidence from the northern hemisphere links the timing of phenological events to the onset of spring warming (Spano et al. 1999, Wielgolaski 1999, Beaubien and Freeland 2000, van Vliet and Schwartz 2002, Walther et al. 2002). Temperate and cold zones are particularly sensitive to changes in climate (Ahas et al. 2002, Sparks and Menzel 2002, Rutishauser et al. 2007) and shifts towards the earlier onset of spring phenophases have been more pronounced in these regions than nearer the equator (Parmesan 2007, Rutishauser et al. 2007).

Global patterns of change have been attributed to changes in large-scale climatic processes such as the North Atlantic Oscillation (NAO) (Scheifinger et al.



**Fig. 19.1** Multivariate ENSO Index. Positive MEI values indicate the warm El Niño phase; negative values the cold La Niña phase. The El Niño events of 1982–1983 and 1997–1998 which rank as the highest of the century (Wolter and Timlin 1998) fall within a period (1976–1998) during which there is a noticeable reduction of La Niña events. Sourced from <http://www.cdc.noaa.gov/people/klaus.wolter/MEI/> (5/5/2009)

2002), the Arctic Oscillation (AO) (Min et al. 2008) and the El Niño Southern Oscillation (ENSO) (Wolter and Timlin 1993, 1998, Beaubien and Freeland 2000, Schaubert et al. 2002, Walther et al. 2002, Brearley et al. 2007) (Fig. 19.1). There were two main periods of warming during the twentieth century; the first between 1910 and 1945, and the second from 1976, marking the beginning of an extended warm El Niño phase (Wolter and Timlin 1993, 1998, IPCC 2007) (Fig. 19.1). Records from the Australian Bureau of Meteorology show that the period since 1980 includes many of the warmest years on record for Australia, with considerable increases in both annual maximum and annual minimum temperatures <http://www.bom.gov.au/climate/change/amtemp.shtml>. The rate of warming during this period has been approximately double that of earlier in the century, and the rate has continued to increase (IPCC 2007).

Paleoclimatic data indicates that the rate of warming since 1950 has been the highest for at least the last 1300 years (van Vliet and Schwartz 2002, IPCC 2007). Estimates of projected future climate change (IPCC 2007) indicate that, by 2030, rates of global warming could very likely be at least double that observed for the twentieth century, manifesting as more frequent and extreme heat waves, and heavy precipitation events brought on by the increasing frequency and intensity of El Niño events (Walther et al. 2002) as have occurred after 1976 (Wolter and Timlin 1993, 1998) (Fig. 19.1).

Regional precipitation is more erratic and less dependable than temperature, with years of good rainfall interspersed with sometimes extended periods of drought. Various aspects of both temperature and precipitation need to be considered both separately and in combination to unravel the synergistic interactions among these parameters (Keatley and Hudson 2007a), and careful analysis required to tease out signals from within this complex system. Temperature and rainfall interact to impact on processes such as evapotranspiration with very serious consequences in regions where rainfall is unreliable; and severe water deficit tends to coincide with high temperature extremes. These interactions will have particular impact in areas such

as southern Australia, where a year round growing season and high maximum temperatures coincide with periods of low precipitation and drought, both of which are predicted to increase in frequency and intensity (IPCC 2007, Chambers 2008, CSIRO 2008) and must be given overriding consideration.

Broad-based multi-taxon analyses have indicated a mean response to recent warming with advances of spring events, estimated at between 2.3 and 2.8 days/decade (Parmesan and Yohe 2003, Root et al. 2003, Parmesan 2007), reflecting the current enhanced warming trend. With regard to the higher northern latitudes where cold winters, often augmented by snow and ice cover, restrict the growing season (Rutishauser et al. 2007), research focus has been on minimum temperatures. While plants do not experience temperature or any other aspect of weather in isolation, other climatic parameters such as rainfall and periods of drought, while influential, are not considered to be major drivers of phenology in these northern regions (Wielgolaski 1999, Rutishauser et al. 2007). However, they do take on much greater relative importance for rainfall limited ecosystems, such as occur in Africa and Australia.

Opportunely, Australia's endemic plant species have had the benefit of millennia to evolve effective responses to the climatic extremes and irregularities typical of the continental weather systems. A good example can be seen in the reproductive ecology of some species of *Eucalyptus*. Unencumbered by an urgency imposed by a restricted growing season, these trees have adapted instead to cope with a continuous growing season plagued by uncertainty. Thus, while initiation of flower buds in some species may be in response to quite precise and predictable photoperiodic signals (Fitter et al. 1995, House 1997, Law et al. 2000, Renner 2007), the onset of flowering can be withheld, sometimes for many months, until conditions become suitable (Fitter et al. 1995, Lechowicz 2001, Keatley et al. 2002). Keatley et al. (2002) found that the combined effect of temperature and rainfall had more explanatory power in relation to the flowering commencement of four eucalypts species than either factor showed when considered separately.

By comparison, the species *E. regnans*, when growing at elevations above 600 metres, with adequate water supply, exhibits a more stable reproductive cycle with relatively specific budding and flowering periods influenced predominantly by summer and autumn temperatures, and photoperiod (Ashton 1975). Flower buds, first detected in late spring to late summer, swell during the following November and December and finally come into full flower more than two years later during the shortening days of autumn when three generations of buds may be present on the same branch. Flowering tends to be earlier at lower altitudes and on younger trees, but considerable variation is found among individual plants. A considerable variability in flowering abundance, which conforms to a more or less regular two or four-yearly pattern may, however, be disrupted during periods of drought.

Generally, however, satisfactory explanations for the coincidental timing of climatic and biological events have been difficult to ascertain, and details of the mechanisms regulating ecosystem processes in general remain unknown. At the same time, our dependence upon the consequences of such processes has become an issue of utmost importance. Throughout the world native plants may be well

adapted to the vagaries of their regional climates, but they now must face increased challenges while coping with adversity imposed by habitat loss and destruction, the introduction of pests, and other human related activities. Thus, after millennia of remarkable and successful adaptations, the future of many endemic species is now uncertain.

## **19.4 Using Phenology to Assess Complex Relationships Between Species and Climate Through Time**

Irrefutable evidence is emerging from the scientific literature of universal shifts in phenology as a consequence of climate change, now widely expected to have a number of major impacts on biological systems around the globe. Mediterranean systems such as occur in southern Australia are especially vulnerable (Bardsley 2006). The intimate relationship which exists between seasonal flowering and climatic conditions, coupled with ease of observation, makes phenological monitoring of flowering events a reliable and cost effective method for the early detection of change in biological systems and an important tool in global change research (Keatley et al. 2002, 2008, Menzel 2002, Keatley and Hudson 2007a).

Even when rapid, climate change is a relatively long-term process and observations on decadal timescales are insufficient to place phenological shifts in perspective. Short-term phenological studies provide important snapshots in time, but cannot be used to determine the magnitude or nature of impacts on the large temporal and spatial scales of the processes themselves. Much of what we know about the influence of climate on phenology comes from investigations of archival records undertaken in the northern hemisphere. For these we are indebted to the dedication of amateur naturalists (Marshall 1789, Thoreau 2000, Dean 2008, Post and Inouye 2008) whose observations and collections were made at a time when environmental concern was directed at the newly arrived railroads and their trains steaming across their landscapes (Fender 1997); heralding the arrival of the industrial revolution and enhanced input of greenhouse gases into the atmosphere.

## **19.5 Historical Data Sets**

While not always conforming to modern, systematic standards and often highly subjective, many historical recordings made by these motivated, knowledgeable and extremely precise observers, now provide us with a valuable source of reliable phenological information (Rutishauser et al. 2007, Dean 2008, Miller-Rushing and Primack 2008). Although such records are by nature variable, discontinuous, and incomplete, they have been shown to furnish comparable results to those obtained from field investigations (Primack et al. 2004, Miller-Rushing et al. 2006) and provide supporting evidence that flowering times are indeed responding to current

warming trends. Some species in Massachusetts are now flowering seven days earlier than they did 150 years ago in Thoreau's day (Miller-Rushing et al. 2006, Dean 2008).

In many countries, particularly those of the southern hemisphere, no long-term data equivalents are available: Marsham was making the first of his recordings more than 50 years before the first fleet sailed out of Portsmouth bound for Botany Bay, Australia. As it is inappropriate to extrapolate from findings derived from northern hemisphere data sets, however sound they may be, researchers in the southern hemisphere must turn to alternative, local sources for urgently needed information on a comprehensive selection of plant species. Collections held in national herbaria satisfy these criteria, and the immediate future of phenological studies in the southern hemisphere, particularly Australia, rests to a large extent on this resource.

### ***19.5.1 Herbarium Collections***

The application of herbarium vouchered specimens to comparative phenological studies is a relatively recent approach, but initial explorations have produced convincing evidence of their suitability and led the way to their wider application (Borchert 1996, Primack et al. 2004, Bolmgren and Lonnberg 2005, Lavoie and Lachance 2006, Gallagher et al. 2009) (Table 19.1).

Collections comprise a broad temporal, geographic and phylogenetic representation of their regional flora which are conveniently available independent of season. In particular, they have been found to provide a reliable estimate of the peak flowering date, a convenient measure of flowering time as it is relatively independent of population size (Primack and Miller-Rushing 2009). Indeed vouchered specimens, used either alone or in combination with field observations, can show that flowering times respond to changes in temperature and reveal intraspecific variations in flowering phenology relative to seasonal conditions throughout a species' entire range (Borchert 1996). They thereby offer a reliable data source (Primack et al. 2004, Bolmgren and Lonnberg 2005) with the potential to provide valuable supporting evidence of phenological changes in response to global warming (Miller-Rushing et al. 2006, Sparks 2007).

In Australia, herbaria collectively house in excess of six million vouchered specimens dating from the earliest days of European settlement; an historical record of over two hundred years. By its nature, a large component of this data source is prone to error, especially in relation to spatial positioning and scientific naming, and the process of digitization has incorporated careful revision. While a very time consuming, and therefore expensive process, the end product with errors minimized, is highly reliable, comprehensive and readily accessible.

Australia's Virtual Herbarium, a collaborative project of Australian State, Territory and Commonwealth herbaria, delivers its product via an electronic Australian Flora on-line with data storage and retrieval via the world wide web: <http://www.anbg.gov.au/chah/avh/avh.html>. It provides a wealth of botanical data

**Table 19.1** An overview of studies investigating the suitability of herbarium collections for the detection of climate-change impacts on flowering phenology

Reference	Data source	Investigation	Main measure: Analysis	Region	Taxa investigated
Borchert 1996	Missouri Botanical Garden herbarium collections	Comparison of flowering information obtained from collections and field data	Month of flowering: Graphical comparisons	Central and South America N.H/S.H	18 Neotropical dry forest species
Rivera and Borchert 2001	Herbario Nacional, San José, Costa Rica, Missouri Botanical Garden, St. Louis, Mo.	Inter-annual variation in flowering periodicity	Flowering period: Graphic representation of flowering period and other phenophases	Costa Rica Central Americas N.H/S.H	> 25 tree species; herbs
Bolmgren and Lönnberg 2005	Swedish Natural History Museum	Evaluation: herbarium flowering-time data	Collection dates: Product-moment correlations Wilcoxon matched-pairs test	Uppland, Sweden N.H	77 species
Lavoie and Lachance 2006	Canadian herbaria	Phenology reconstruction	Flowering dates: Linear regression	Quebec, Canada N.H. N.H/S.H	Tussilago farfara Multi-taxon
Buggs 2007	Review of herbarium data	Historical evidence of hybrid zone movement	First flowering date: Linear regression	Victoria Australia S.H.	79 coastal species.
Rumpff et al. 2008	3 Australian herbaria	Determination of indicator species	Presence of flowers: maximum entropy models	Bolivia, Ecuador S.H	323,711 voucher specimens of 76 species
Lavoie and Lachance 2006	Missouri Botanical Garden's TROPICOS data base	Predicting species distributions	Flowering dates: Linear regression	Australian alpine zone S.H	7 families, 20 species
Gallagher et al. 2009	3 Australian herbaria electronic data	Phenological trends			

N.H = Northern hemisphere, S.H = southern hemisphere

**Fig. 19.2** Photograph of vouchered specimen *Diuris pardina* BS128-3730, record number AD176137, held at the State Herbarium of South Australia, Plant Biodiversity Centre, Adelaide. See Table 19.2 for the information provided by Australia’s Virtual Herbarium (AVH) for this specimen



associated with scientific plant specimens held in these major Australian herbaria (Fig. 19.2), many enhanced by images, descriptive text and identification tools. It has the advantage of including records from multiple sources without the duplication which arises when the same data is obtained independently from each of the contributing institutions. A global equivalent, the Index Herbariorum, comprises a detailed directory of the public herbaria of the world; This joint project of the International Association for Plant Taxonomy and the New York Botanical Garden lists above 3300 herbaria and includes a photographic archive and is available at <http://sciweb.nybg.org/science2/IndexHerbariorum.asp> (Holmgren and Holmgren 1998).

**Table 19.2** Information relating to vouchered specimen of *D. pardina* BS128-3730, #AD 176137, as obtained from the AVH data base. See Fig. 19.2 for photograph of the actual specimen held at the State Herbarium of South Australia. N.B. Collection date as formatted does not specify century of collection. This particular specimen was collected in 2004

Family	Angiosp.
Genus	<i>Diuris</i>
Species	<i>Pardina</i>
Scientific Name	<i>Diuris pardina</i> Lindl.
Herbarium Source	AD
Record Suffix	176137
Latitude	-34.54861
Longitude	135.71833
Nearest named place	Wanilla
State	South Australia
Country	Australia
Collection Date	3 September 2004
Collector	Lang, P.J.
Collecting number	BS128-3730
Additional collectors	
Geocode Precision	150
Coordinate Error Method	GPS
Date Last Edited	11 December 2006

However, the archival record available to us today has not arisen from an interest in, or concern about, climate change. Its value in this respect has only become evident in retrospect, and analysts investigating these collections, made by someone else for purposes other than those being analysed (Miller-Rushing and Primack 2008), must deal with the restrictions this imposes upon them. Those who work directly from original sources find that old records do not always give up their secrets easily, and as with all valuable collections, care needs to be taken. Until relatively recently, field naturalists did not have the convenience of the world-wide-web or word processors to keep them updated on the latest taxonomic developments or to redress their messy handwriting and, without the strict guidelines imposed on the collectors of today, many otherwise valuable early records lack collection date and/or location details and therefore cannot be considered in this type of scientific analysis (see case study 2 below). Leopold and Jones (1947) demonstrate the benefits to be derived from the careful and systematic organization of data, a practice not made obsolete by the advent of the computer. While they did not consider the impacts of climate change in their report covering the decade 1935–1945, they discuss many pertinent issues and possible sources of error including those arising from multiple observers and differing intensity of observations.

While dated vouchered specimens, collectively, may provide a good indication of peak flowering date, each individual specimen can provide only an approximation of that event. This is especially the case for plants with long flowering periods, when any one specimen could be collected several weeks earlier or later than the actual occurrence (Primack and Miller-Rushing 2009). Relatively large sample sizes are



needed for this assumption to be valid. When compared with field data, flowering times derived from herbarium specimens also tend to be later for early spring-flowering species, and earlier for late summer-flowering species (Bolmgren and Lonnberg 2005). This may be explained by the fact that early-flowering species are typically collected later, and late-flowering species, earlier, in their relative flowering periods. The length of a species flowering period gauged from herbarium collections is usually greater than that obtained from geographically restricted and time limited field investigations but shorter than that suggested by published floras (Bolmgren et al. 2003, Bolmgren and Lonnberg 2005).

### ***19.5.2 Collection Effort***

It is well recognised that collection efforts are not consistent over time, but may vary from species to species, location to location, and from year to year. Early records are sparse, as are those coincident with adverse periods in history, such as the two world wars. Short term anomalous increases may correspond to periods in which field investigators are employed or field naturalists with a special interest make a particular endeavour. Resulting bias may lead to a false interpretation of flowering time variation, reflecting collection effort rather than climate change. Concerns have also arisen in relation to possible roadside and other collection bias associated with geographic distribution and the different climatic conditions associated with sampling locations (Rumpff et al. 2008).

Loiselle et al. (2008) found that although climatic gradients were non-uniformly and poorly represented in herbarium collections, this did not detract from the overall value of the data set (Loiselle et al. 2008). Where necessary, correction procedures should be applied to account for these parameters when using herbarium specimens to reconstruct flowering dates (Kochmer and Handel 1986, Johnson 1992). Although elevation is now required for each vouchered specimen submitted to a herbarium, the AVH database does not provide information specifying elevation of collection location, and this must be obtained by other means if necessary. Spatial coordinates are generally, but not always, provided.

With such irregularities as these making it difficult to extract a clear signal from the data, recourse to expert opinion is always advisable (Walther et al. 2002, Rumpff et al. 2008). However, when allowances have been made and precautions taken, these data sets have the potential to make an outstanding contribution to studies in comparative phenology. Especially now, with many of the early specimens representing former distributions, species on the verge of extinction, or already extinct, these collections are beginning to take on a special significance. Recent searches for the plants recorded by Thoreau highlight the plight of many; of the 21 species of orchids Thoreau observed in Concord, only seven are known to exist in the area today (Dean 2008). Paradoxically, with herbarium records now accessible as never before, collection efforts appear to be on the decline (Prather et al. 2004, Watanabe et al. 2006). Alternative sources of information, however valuable, cannot replace

the need for the actual specimens, the “fundamental records of biodiversity” (Prather et al. 2004) p 216, which will continue to provide the crucial infrastructure and reference base upon which phenological and other floristic research depends. They may, however, fulfil other roles and provide opportunities for phenology studies to proceed in a new, and hitherto inaccessible, direction.

### ***19.5.3 Completing the Picture***

While we cannot return to the past to “fill in” the inevitable gaps in the record, statistical methods for the analyses of time series with missing values have been developed to compensate for this deficiency (Fornaciari et al. 2003, Golyandina and Osipov 2007). Furthermore, researchers are now exploring the potential of photographic images to supplement herbarium collections. Flowering phenology has always had popular appeal and attracted the attention of many photographers who, unsuspectingly, have bequeathed a rich resource of pictorial knowledge. These are less likely than specimens to have found their way into the major archives, and many undoubtedly still await discovery in wooden filing cabinets or on dusty shelves in local museums and private collections. Initial investigations have demonstrated the potential of dated photographs with referenced locations to reliably augment other sources used to assess shifts in flowering times (Table 19.3). They have been found to provide robust estimates comparable with those derived from field investigations and broadly in keeping with those published in the literature. As for herbarium specimens, assumptions of peak flowering have been validated, providing confidence in the evidence of change obtained from this metric, both in relation to time and to differences in past and present temperatures, (Bolmgren and Lonnberg 2005, Miller-Rushing et al. 2006, Sparks 2007). The visual record also provides information on plant size, a confounding factor in flowering phenology (Primack and Miller-Rushing 2009).

Additional information can be retrieved from photographic time series obtained by repeat or time-lapse photography at permanent monitoring sites; a process indispensable for capturing changes over time (Watanabe et al. 2006). Historical photo-point time-series, however, tend to be in black and white and are often restricted to an annual series which more generally captures a landscape perspective. They are, perhaps, more appropriate for the recording of phenophases other than flowering, such as leaf flushing or the emergence of winter grasses, along with indications of periods of drought and other seasonal and climatic changes (Sinclair 2004, 2005).

### ***19.5.4 Digital Photography***

But it is not only climate which is changing; advancing technology is also making an impact on our world and the methods by which we interpret it. A growing catalogue of digital images, accompanied by a wealth of pertinent and readily shared

**Table 19.3** An overview of studies investigating the suitability of photographic images for the detection of climate-change impacts on flowering phenology

Reference	Data	Investigation	Main measure: Analysis	Region	Taxa Investigated
Photography (archival) Sinclair 2004	fixed date, fixed subject photographs	landscape changes following exclusion of grazers	descriptive	Koonamore South Australia S.H	Arid zone vegetation including <i>Acacia</i> , <i>Casuarina</i> , <i>Myoporum</i> spp <i>Galanthus</i> , <i>Narcissus</i> , <i>Aesculus</i> , <i>Fagus</i> spp.
Sparks et al. 2006	fixed-date, fixed subject photographs: Weather-wise (Willis 1944)	influence of weather variables	plant development scores: ANOVA, Multiple regression	United Kingdom N.H	
Sparks 2007	photographs	Review			
Primack et al. 2007	archival collections: (1) Arnold Arboretum (2) Landscape photographer	Effects of climate change on flowering times	Flowering dates: Linear regression	(1) Boston Mass. USA (2) Concord Mass. USA N.H	(1) Various cultivated woody plants (2) Various wildflowers, trees and shrubs
Photography (digital) Crimmins and Crimmins 2008	repeat photography: Nikon D70 digital SLR camera	Phenological monitoring	Estimate of greenness; individual flower counts; Image analysis; mathematical algorithms	Tucson, AZ, USA N.H	Native wildflowers
Ahrends et al. 2008	standard digital 5-megapixel NIKON Coolpix 5400, CCD sensor	leaf unfolding	date of leaf emergence; image analysis based on RGB colour	Switzerland N.H	Mixed beech forest including Fraxinus, Fagus spp.

N.H = Northern hemisphere, S.H = southern hemisphere

**Fig. 19.3** Digital photograph of yellow form of *Diuris orientis* (Orchidaceae). Photographer Jennifer Skinner



information (Fig. 19.3, Table 19.4), is dramatically expanding the available phenological data base. Until now, the accurate capture of a key phenological event has necessitated regular, labour intensive monitoring, beginning some days prior to its expected occurrence (Rivera and Borchert 2001). Automatic digital repeat or time-lapse photography, freed from the restrictions imposed by a grey colour scale, the need for photographic film and constant human intervention, is ideally suited to these demands (Sparks et al. 2006). Resulting images reliably capture not only the actual phenological events, but also quantitative changes over time, such as shifts in the abundance of flower blooms, their pollinators and herbivores (Crimmins and Crimmins 2008, Faast and Facelli 2009).

More recent technological initiatives have led to the coupling of cameras with edaphic and meteorologic recording devices. Such integrated networks are capable of augmenting digital images with sufficient site-specific information to enable a precise determination of environmental triggers of the events observed (Sparks et al. 2006, Ahrends et al. 2008, Crimmins and Crimmins 2008). However, systems are still under trial, and reports to date have been limited to experimental plots.

**Table 19.4** Digitally recorded information relating to digital photograph (Fig. 19.3) of yellow form of *Diuris orientis* (Orchidaceae)

Date and Time	22/09/2008; 9.20am
Location	Belair National Park, South Australia
Camera	Pentax K10D
Image ID	IMGP7783.JPG
Image size	3.96 MB
Settings	ISO 100, f 32, exposure time 1/90, 80 mm focal length

Conversion for larger scale field investigations will require several important modifications, including weatherproof housing for camera and computer equipment, an external power source (electricity, battery or solar panel) and, in some locations, insulation from temperature extremes. However, they promise unprecedented opportunities to obtain the wealth of data needed to answer the wider questions about the implications of global climate change in relation to ecological processes and ecosystem function. To this end they can be archived as a permanent record readily available to future researchers.

## 19.6 Cautionary Points for Analysis and Interpretation

As always, the value of these data sets as a source of phenological information depends to a very large extent on the methods of analysis employed and the interpretation of the results obtained.

Some points for consideration include:

- the non-independence of data due to phylogenetic constraints, multiple collections on any one day at any one site
- the validity of assumptions that sampling has been random with respect to geography, climatic and environmental gradients, etc.
- natural variation across sites, including local microclimatic conditions, genetic differences and other non-climatic factors contributing to uncertainty
- geographical limits (latitude, longitude, elevation)
- bias resulting from inconsistent collection effort
- environmental changes throughout the period of collection such as deterioration and loss of habitat, conservation status of species, etc.
- increasing impact of urban heat island effects confounding climatic warming signals
- appropriate flowering time measure for the data set under consideration (date of first flowering, date of peak flowering, length of flowering time, changes in flowering abundance, etc.)
- non-linearities inherent in the time series

- non-uniform periods of warming which have occurred throughout the twentieth century and the particular challenge they pose when linear regression analysis is used for the reconstruction of trends
- error may be introduced through taxonomic issues, nomenclatural inconsistencies, inaccurate recording of spatial coordinates, etc.
- detection of signals indicative of earlier flowering need to be very strong to be discerned above noise in the data
- ways of improving the accuracy and reducing the uncertainty in analyses, and the limitations assumptions and uncertainty impose on the interpretation of the results.

## 19.7 Two Australian Case Studies

### *19.7.1 Phenological Trends Among Australian Alpine Species: Using Herbarium Records to Identify Climate-Change Indicators*

Until recently, the major investigations into flowering phenology of plants in southern Australia have been obtained from State Forest Commission records of *Eucalyptus* species (Keatley et al. 2002, 2004, Barbour et al. 2006, Keatley and Hudson 2007b). The recent study by Gallagher et al. (2009) represents a departure from this precedent with a multi-taxon study exploring the strengths and limitations of herbarium voucher specimens for the detection of changes in flowering phenology of Australian alpine plants in the vicinity of Mt. Kosciuszko. This region has a unique climate for the Australian mainland, but is comparable to many regions in the northern hemisphere where an intimate link between the timing of snowmelt and flowering plant phenology is well established (Lavoie and Lachance 2006, Rutishauser et al. 2007, Inouye 2008). Temperature sensitivity in relation to flowering time in these alpine regions is likely to be more pronounced than elsewhere on the Australian continent, and rising temperatures, accompanied by a 40% reduction in snow cover since the 1960s, have special significance (Green and Pickering 2002, Pickering et al. 2004, Gallagher et al. 2009).

This study entailed a search for suitable indicator species and potential locations for proposed monitoring sites. A preliminary list of 171 potential candidates representing the flora of the alpine region and the Victorian Alps at elevations above 1500 m was selected from Kosciuszko Alpine Flora (Costin et al. 2000). Data for these species were then obtained from three of Australia's major herbaria: the National Herbarium of NSW, the National Herbarium of Victoria and the Australian National Herbarium in Canberra. Duplicate records were removed from the combined data sets, as were:

- records with insufficient, or incorrect, collection date or location information
- multiple observations of a species in any one year (the first observation only was retained)

- all observations not falling within the period 1950–2007 inclusive (to correspond with the temperature data used in the analysis)
- species for which records indicated a flowering season longer than three months
- species represented by ten or less independent specimen records.

This process of elimination reduced the original 171 to a working list of 20 species representing 7 families. The metric chosen for analysis was the onset of flowering and referred to as “flowering observation.” This approximation was extracted from the data by discarding all but the earliest collection date for any one species in any one flowering season. For analysis, flowering observation was expressed as a Julian date (January 1st = day #1), adjusted to overcome the difficulty of dealing with plants whose flowering season spanned the transition from one year to the next.

Data obtained from the Bureau of Meteorology provided evidence of an increase in the mean annual temperature of 0.74°C over the 1950–2007 period, and by matching spatial locations of herbarium specimens to the temperature data and using ordinary least-squares linear regression models, eight of the 20 species were identified for which flowering response showed a significant negative relationship with mean annual temperature (i.e. a temperature increase at the point of collection corresponded with earlier flowering observations for these species). One of these species was *Prasophyllum tadgellianum* ( $R^2 = 0.63$ ,  $P < 0.0001$ ;  $y = -8.99x + 447.62$ ), one of two orchids whose sister species *P. suttonii*, was the only species to show a positive correlation ( $R^2 = 0.17$ ;  $P = 0.06$ ;  $y = -3.73x + 375.56$ ). Simultaneous convergence/divergence in flowering times between these two closely related species in response to the same changing conditions may have long-term implications for hybridization (see also case study 2 below). Of the eight species, only one, *Senecio pectinatus* var. *major*, was deemed suitable for use as an indicator species for environmental monitoring.

With only one potentially suitable species selected from an original 171 candidates, the attrition rate was high, and it becomes clear that the search for a range of site-specific indicator species requires interrogation of large data bases. This would hardly be possible without the availability and convenience of the rich resources provided by herbaria. With a realization of the emerging importance of their role in climate change research, it is to be hoped that increased funding is forthcoming for the continued collection and curation of the voucher specimens upon which these data sets are based. Gallagher et al. (2009) concluded that “the real utility of herbarium specimens lies in providing a complementary historical baseline of data to which new field-based observational records can be compared” p 7.

### ***19.7.2 Tracking Phenological Shifts and Evolutionary Impacts Relating to Climate Change***

Shifts in phenology impact on community-level interactions and other evolutionary processes, and have the potential to induce ecosystem compositional turnover as

the synchrony between developmental times of co-evolved and dependent species is disrupted (Beaubien and Freeland 2000). For plants such as orchids these shifts may impinge on the finely tuned relationships with their pollinators providing opportunities for interspecific hybridization.

The present case study (Section 19.7.2) case study investigation has two aspects. As for the previous study, the first component incorporates an examination of herbarium collections in a search for evidence of recent shifts in flowering phenology in line with recent climate change. The species chosen for the study belong to the genus *Diuris* Sm. (donkey orchids), a genus of 64 Australian species and four named hybrids, as listed by Jones (2006). The flowers have a structural resemblance to those of the pea family (Fabaceae), considered by many to be a mimicry associated with the deceptive attraction of native bee pollinators (Indsto et al. 2007). Natural hybridization is common within this genus. In South Australia, co-occurring local populations of *D. orientis* (Fig. 19.3), *D. behrii* and *D. pardina* readily form hybrids exhibiting considerable variation in floral colour patterns. *Diuris* X *palachila*, a fertile, natural hybrid between *D. pardina* and *D. behrii* is capable of producing further crosses between either parent and the hybrid species itself, resulting in a confusing array of morphologically different forms (Jones 2006). Orchid plants arise from underground tubers towards the end of winter, and flowering finishes before hot summer temperatures becomes established. The flowering period is relatively short and compact thus making it easier to detect shifts over time (Rumpff et al. 2008). Spotting and photographing orchid flowers is a very popular pastime, and many dedicated and knowledgeable observers have amassed valuable photographic collections to supplement the considerable collection held in the state herbarium.

Presented in this section is an initial exploratory analysis of the data extracted from the AVH electronic database, using simple linear regression (SLR). This amounted to 388 individual South Australia collections of the study species, *D. orientis*, *D. behrii* and *D. pardina*, from a total of 6,395 Australian *Diuris* records. All specimens are represented by one and only one record eliminating the need to check for, and remove, duplicates. Converting the collection date format to yyyy/mm/dd makes for easier sorting and eliminates the problematic issue of mistaken century of collection. Of the 388 records, 72 were discarded because collection date was not provided, leaving 316 usable records available for analysis. Two hundred and nine of the total data set had no information on their spatial coordinates, but as many of these were also undated this omission did not necessitate further reduction. The following analysis discussed in this chapter has been restricted to the two species, *D. orientis* and *D. behrii*.

An assumption was made that collection date was a reliable surrogate for peak flowering, and where multiple records existed for any one flowering season, the median value was chosen as the most appropriate measure for peak flowering. For analysis, date of peak flowering was converted to the number of days following the winter solstice, and calculated from June 22 (day #1). This not only keeps the metric within a reasonable numerical range, but also conveniently differentiates lengthening day from shortening day (with negative values) flowering responses. For these species flowering occurs during the noticeably lengthening days from late winter to late spring.



## 19.8 Initial Exploratory Data Analysis

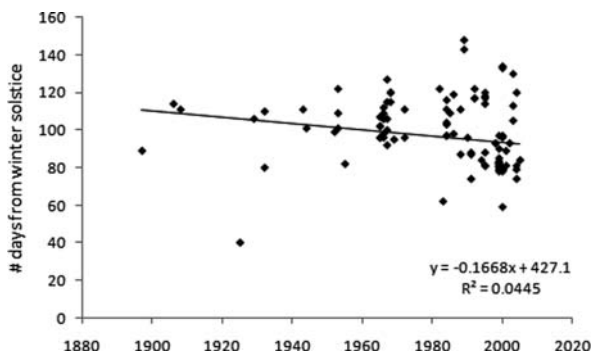
### 19.8.1 Simple Linear Regression

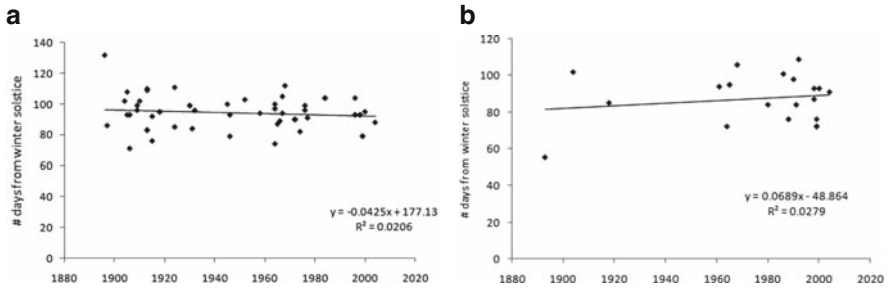
Methodologically, the detection of trends in time series is frequently performed via the classical statistical methods using slopes of linear regression models where phenological dates (less frequently temperatures) are plotted against time (Bradley et al. 1999, Menzel and Fabian 1999, Schwartz and Reiter 2000, Defila and Clot 2001, Menzel et al. 2001, Ahas et al. 2002, Penuelas et al. 2002, Menzel 2003) and, more rarely, by other curve fitting methods (Ahas 1999, Sagarin and Micheli 2001). For herbarium applications see Table 19.1 and for general phenology applications see Menzel and Fabian (1999), Walther et al. (2002), Parmesan and Yohe (2003), Root et al. (2003), and Menzel et al. (2006).

The slope of the linear regression equation then indicates the average rate of change in phenology given as days per annum (days/a), or temperature expressed as degrees per annum ( $^{\circ}\text{C}/\text{a}$ ). The major disadvantages of this least squares approach (SLR) is its limitation to time series with a comparatively linear trend, possible poor extrapolation properties, and sensitivity to outliers (or so-called extremes (Schlittgen and Streitberg 1999)) and to boundary values. As noted by von Storch and Zwiers (2001), one or two outliers can seriously distort the results of a least squares analysis (NIST/SEMATECH, e-Handbook of Statistical Methods, 2006, available at <http://www.itl.nist.gov/div898/handbook/index2.htm>).

A plot of the entire data set for *D. orientis* spanning a 98 year period from 1897–2005 (Fig. 19.4) supplies provisional evidence of a shift to earlier flowering of between one to two days per decade, or approximately 16 days over the entire period. This figure also clearly illustrates the non-uniform nature of the data series and identifies possible collection bias with a concentration of points for the period 1965–1969 and again around 2000. This recent increase in collection effort does not appear to substantiate the claims made by (Prather et al. 2004, Lavoie and Lachance 2006) of a growing decline in collection activity. However, orchids species have popular appeal and have been the focus of many recent surveys. A closer investigation of the data reveals that the orchid specialist and author, D.L. Jones, collected

**Fig. 19.4** Plot of all data points for *D. orientis* spanning the period 1897–2005. The concentration of collection points around 1965–1969 and around 2000 may introduce collection bias





**Fig. 19.5** (a) Number of days to peak flowering for *D. behrii* for  $S34.5 < \text{latitudes} < S35.5$ ; average of 94 days to flowering over the period. The negative slope indicates slight evidence of a trend to earlier flowering. (b) Number of days to peak flowering for *D. behrii* north of latitude  $S34.5$ ; average of 87 days to flowering over the period. The positive slope provides evidence of a trend to later flowering

all 24 specimens recorded for the period between 7th and 14th September 1999, confirming dependence and necessitating their exclusion from the final analysis. Following substitution of all multiple data points for any one season by their median value, and discarding the outlier in 1925, former evidence of a negative trend (i.e. towards earlier flowering) diminished ( $y = -0.1058x + 308.76$ ,  $R^2 = 0.0397$ ), and the mean number of days to peak flowering across all latitudes increased from 96 to 100 days.

Because changes are not consistent across the entire range of a species (Lavoie and Lachance 2006) the possible effect of latitude was investigated for *D. behrii*. When regions are considered separately as central (Fig. 19.5a) and northern (Fig. 19.5b) populations, there emerges some evidence of a difference in mean peak flowering date and tendency for an opposite trend in flowering time shifts over this period. Southerly populations have flowered on average seven days later than more northerly populations, where hotter and drier conditions are more likely to induce earlier flowering. However, these regional differences appear to be diminishing as a result of the contrary shifts. See Gallagher et al. (2009) above for further evidence of opposite shifts in flowering time for *Prasophyllum* species.

## 19.9 Limitations of Standard Methods to Detect Trend

### 19.9.1 Non-Linearity of Trends

As noted by Hudson et al. (2005), Sparks et al. (2000), Dose and Menzel (2004) and Parmesan (2007), this commonly used method of searching for signals in phenological time series presents problems. Indeed it will be difficult to find a linear model that fits the data well for essentially non-linear processes. This is true particularly as the range of the data increases (Schleip et al. 2008b). Importantly, Menzel et al. (2008) noted that when utilising SLR, the length of a time series and its start and end

dates are crucial in correct detection of changes, and in estimating their magnitude. This is particularly so when highly variable, multi-decadal, phenological time series are analysed (Dose and Menzel 2004). We show this also for the three herbarium data sets analysed here.

How can we accommodate for non-linear responses of phenology to time (year) and/or to climatic factors? In the Chapter 20 on meta analysis this question is addressed by the illustration of three approaches to modelling phenological time series assuming possible non-linear trends, namely:

1. The Generalised Additive Model for Location, Scale and Shape (GAMLSS) approach (Rigby and Stasinopoulos 2005, Stasinopoulos and Rigby 2007) applied recently to flowering records of four Eucalypts (*Eucalyptus leucoxylon*, *E. microcarpa*, *E. polyanthemos* and *E. tricarpa*), from Maryborough, Victoria, Australia, for the period 1940–1971 (Hudson et al. 2008, Hudson et al. 2009); see also Chapter 10.
2. Penalised spline (*P*-spline) signal regression (PSR) (Marx and Eilers 1999, 2005) applied recently to a dataset of 208 species compiled from the 1978 to 2001 flowering records of the Last family (Last et al. 2003, Roberts 2008), and
3. The Bayesian nonparametric function estimation approach of Dose and Menzel (2004) applied to blossom (onset) time series of *Prunus avium* L., *Galanthus nivalis* L. and *Tilia platyphyllos* SCOP (1896–2002) in Germany, in an analysis of the variations of the onset of phenological phases in the twentieth century.

In this chapter we present the GAMLSS approach to show its greater accuracy and relevance to the assessment of non-linear trends over time (year) for the herbarium records. We clearly establish the existence of non-linear trends in days to peak flowering of herbarium records. A short introduction to GAMLSS follows, as does a brief cautionary point on change points in time series analysis and detection.

It is noteworthy that GAMLSS models often provide the researcher with a visual indication of points of change in a given time series. However, formal tests of significance for change points should be carried out in addition to fitting GAMLSS models to phenological time series. We explore the use of both non-linear methods (GAMLSS) and change points methods in combination in this analysis of herbarium records. It is important to note (as evidenced in the *D. behrii* for S34.5 < latitudes < S35.5 data) that whereas GAMLSS modelling of a cubic spline or non-linear effect of year (time) may show statistically non-significant effects of year; formal change point detection tools can point to significant and abrupt change points.

### ***19.9.2 Need for Formal Change Point Analyses***

Rapid shifts in climate can lead to, or be contemporaneous with, abrupt phenological changes. Although it has been appreciated for some time that these change points cannot be detected satisfactorily (if at all) by either regression or correlation

methods, they continue to be used for the detection of temporal changes in phenology (Keatley et al. 2002, Hudson et al. 2005, Cleland et al. 2006, 2007). However, new techniques for change point analysis which enable a quantitative representation of non-linear phenological responses and associated (abrupt and non-abrupt) rates of change have been reported (Hudson et al. 2003, Sparks and Tryjanowski 2005, Keatley and Hudson 2008). See also Bayesian change point techniques (Hasselmann 1998, Dose and Menzel 2004, Menzel and Dose 2005, Menzel et al. 2008, Schleip et al. 2008a,b). These allow for the analysis of so-called change-point probabilities which provide the researcher with the ability to both visualize and quantify major changes (shifts) in long-term time series. It is anticipated that future developments in change point analysis will address the assessment of increasingly complex time series models such as multiple change-point models.

In this chapter a model-free method of change-point detection has been used to establish the existence, or otherwise, of significant change points in time series of days to peak flowering of herbarium records (Moskvina and Zhigljavsky 2003). This method is based on the sequential application of singular-spectrum analysis (SSA) (Chapter 19) to subseries of the original series, and the monitoring of quality of approximation of the other parts of the series by suitable approximates (Moskvina and Schmidt 2003). The three test data sets obtained from AVH, namely flowering dates of South Australian orchid species *Diuris behrii* (S34.5 <latitude<S35.5), *D. behrii* (latitudes < S34.5) and *D. orientis* (all latitudes) are used as exemplars. We show that significant change points exist for two of the three herbarium series; change points which could not be detected using traditional linear regression analysis.

## 19.10 Introduction on GAMLSS

The Generalised additive model for location, scale and shape (GAMLSS) is part of the Generalized Linear Model (GLM) (Nelder and Wedderburn 1972) and the Generalized Additive Model (GAM) “family” (Hastie and Tibshirani 1999, Hastie 2008). GAMLSS was introduced by Rigby and Stasinopoulos (2001) and Akantziliotou et al. (2002), and further developed by Rigby and Stasinopoulos (2005) to overcome various limitations of the popular GLM and GAMs. For example, GAMLSS can deal with non-normally distributed data (e.g. highly skewed, or kurtotic continuous and discrete distributions). Current updates of GAMLSS can deal with up to 50 different types of distributions (Stasinopoulos and Rigby 2007). See Chapter 10 for mathematical theory and details on the implementation of GAMLSS.

Importantly, the GAMLSS family extends linear regression to a non-linear form by allowing each regression variable to have a non-linear relationship with the dependent variable. The type of non-linearity is not pre-specified a priori, but is calculated and tested for in the modelling process. GAMLSS models are thereby a general framework for univariate regression analysis which allow for testing of

semi-parametric models. By semi-parametric, we mean they need a parametric distribution for the response variable, although they can cope with a wide range of distributions such as the Poisson, negative binomial, log normal, Weibull etc. These GAMLSS models are thus “semi” in the sense that the modelling of the actual parameters, such as the mean or location (as functions of the explanatory variables), may involve using non-parametric smoothing functions, such as for example cubic smoothing splines [cs()]. For a discussion on cubic splines see Chapter 12.

The benefits of GAMLSS for phenological and herbarium time series data are that they:

1. can identify the main drivers of the event of interest from a multiplicity of predictors such as climate and food sources etc.,
2. allow for non-linear impacts of time and/or the explanatory variables or predictors,
3. can statistically detect thresholds; for example, the lowest temperature for the commencement of flowering and
4. can model and/or account for the auto-correlated nature of the phenological series; for example by incorporating lag effects, such as autoregressive AR( $k$ ) lags ( $k=1,2,..$ ).

Recent applications of GAMLSS have involved modelling climate with Sudden Infant Death Syndrome counts (Hudson et al. 2008) and in the establishment of the world standard child growth curves by the World Health Organisation (Borghini et al. 2006). Further examples are given in Rigby and Stasinopoulos (2005) and Stasinopoulos and Rigby (2007). As far as the authors are aware, GAMLSS have not been applied to phenological research to date, apart from a forthcoming paper by Hudson et al. (2009). It should also be noted that Hudson et al. (2003) used GAMs (the precursor to GAMLSS) and Bayesian methods to model *E. leucoxylo*n flowering, and found that the estimated effects of mean temperature were smoothly non-linear on flowering intensity. The work of Roberts (2008) (Chapter 12) on penalized splines (*P*-splines) (Eilers and Marx 1996) illustrates a method that also has some inter-relatedness with GAMLSS in that spline functionals are used in the modelling (the term “spline” refers to a wide class of functions that are used in applications requiring both data interpolation and/or smoothing).

### 19.10.1 GAMLSS Methods

The GAMLSS framework of statistical modelling is implemented in a series of packages in R (R Development Core Team 2007), a free software (see URL <http://www.R-project.org>). The packages can be downloaded from the R library, CRAN, or from <http://www.gamlss.com>. For this study the GAMLSS procedure was used with a cubic spline smoothing function (Stasinopoulos and Rigby 2007). Each model assumes that the flowering series represents normally distributed data

and the RS algorithm, a generalization of the algorithm of Rigby and Stasinopoulos (1996) used to obtain the estimates of the year (time) effect.

### 19.10.2 GAMLSS and Change Point Results

Table 19.5 shows GAMLSS modelling of the effect of year (time) on the number of days to peak flowering of *D. orientis* spanning the period 1897–2005. The significant and negative cubic spline effect of year (cs(year)) of  $-0.1668$ , with an associated non-linear P value of 0.0009, indicates a highly significant non-linear and overall negative trend with year for *D. orientis*. Figure 19.6 indicates the curvilinear nature of change in days to peak flowering for *D. orientis* (1897–2005). A significant change point in the time series in 1925, marks the end of a period of decreasing trend (to earlier flowering). This is followed by a period of increasing trend to 1972, after which a slow negative trend till 1984 becomes increasingly negative (significant change point or deviation starting about 1985) and most negative, indicating significantly earlier flowering, after the change point in 1995.

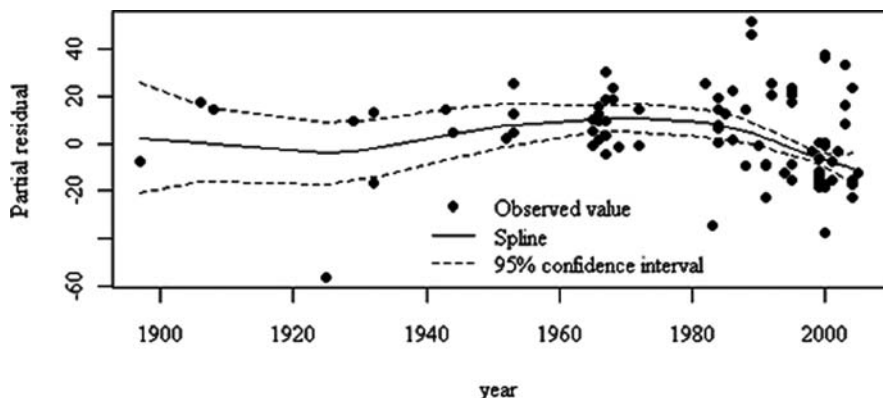
Note that the precursor to GAMLSS, namely GAMs, gave a  $R^2$  for the model of 17.63% (compared to the  $R^2$  of 4.45% obtained by the earlier simple linear regression (SLR) analysis (Fig. 19.4)), indicating that the non-linear cubic spline model fits the data significantly better than that achieved by SLR. The scaled deviance statistics (Stasinopoulos and Rigby 2007), the Akaike information criterion (AIC) (Akaike 1983) and the Schwarz Bayesian Criterion (SBC) (Stasinopoulos and Rigby 2007) goodness of fit statistics are also shown for the resultant GAMLSS model in Table 19.6. The sparsity of data prior to 1925 may, however, be biasing the GAMLSS analysis prior to 1925.

Table 19.7 shows the GAMLSS model for the effect of year (cs(year)) on the number of days to peak flowering of *D. behrii* between the latitudes S35.5 and S34.5 for the period 1986–2004. The cubic spline effect of year (cs(year)) of  $-0.0425$  is, however, not statistically significant. Figure 19.7 indicates the relatively flat profile of the days to peak flowering for *D. behrii* after 1924; with a slight increase in 1964 and then a negative trend after 1984 (as for *D. orientis*) and increased earlier time to peak flowering date after 1999.

It is noteworthy that whilst the GAMLSS cubic spline effect for year (cs(year)) is not statistically significant, a formal change point detection analysis gives three years of significant change (Table 19.8).

**Table 19.5** Intercept and year effects via GAMLSS modelling of the number of days to peak flowering of *D. orientis* spanning the period 1897–2005

	GAMLSS				GAMLSS			Non	GAMs
	intercept	S.E.	t value	P value	cs(year)	S.E.	t value	linear	100( $R^2$ )%
<i>D. orientis</i>	427.10	134.520	3.175	0.001	-0.167	0.068	-2.459	0.0009	17.63



**Fig. 19.6** Variant of Fig. 19.4: GAMLSS term plot of all data points for *D. orientis* spanning the period 1897–2005; showing the cubic spline effect of year ( $cs(year)$ ) and its associated 95% confidence interval. (Spline line and 95% confidence band for effect of year flowering day number for *D. orientis*)

**Table 19.6** Significant change points in the time series of the number of days to peak flowering of *D. orientis* spanning the period 1897–2005; with GAMLSS goodness of fit statistics (GD, AIC and SBC) shown

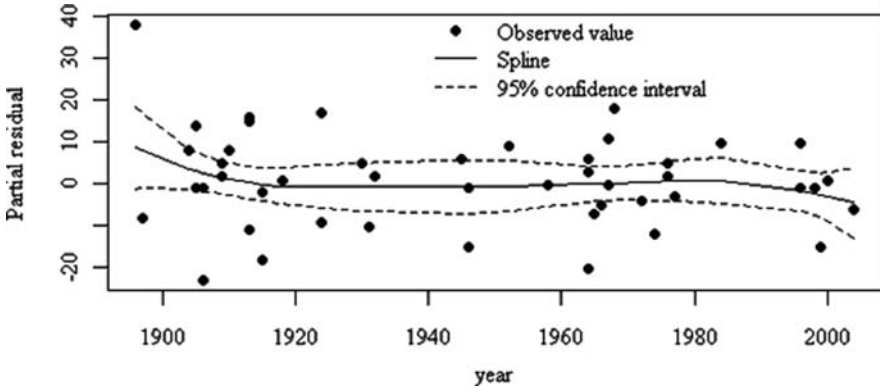
	Change point years: Moskvina & Zhigljavsky (2003)	Global Deviance(GD) <sup>φ</sup>	AIC <sup>φ</sup>	SBC <sup>φ</sup>
<i>D. orientis</i>	1925, 1972, 1984, 1995	967.2	979.2	995.6

<sup>φ</sup> GD denotes the scaled deviance statistic (Stasinopoulos and Rigby 2007); AIC denotes the Akaike information criterion (Akaike 1983) and SBC denotes the Schwarz Bayesian Criterion (Stasinopoulos and Rigby 2007) goodness of fit statistics.

**Table 19.7** Intercept and year effects via GAMLSS modelling of number of days to peak flowering for *D. behrii* for  $S34.5 < \text{latitudes} < S35.5$ ; mean over the period of 94 days spanning the period 1896–2004

	GAMLSS		GAMLSS		GAMLSS		Non	GAMs	
	intercept	S.E.	t value	P value	cs(year)	S.E.	t value	linear	100(R <sup>2</sup> )%
<i>D. behrii</i> (all)	177.131	71.485	2.478	0.0163	-0.0425	0.037	-1.149	NS*	7.11

\*NS = not significant



**Fig. 19.7** Variant of Fig. 19.5a: GAMLSS term plot of data points for *D. behrii* number of days to peak flowering for *D. behrii* for  $S34.5 < \text{latitudes} < S35.5$ ; mean over the period of 94 days; showing the cubic spline effect of year ( $cs(\text{year})$ ) and its associated 95% confidence interval. (Spline line and 95% confidence band for effect of year flowering day number for *D. behrii*)

In summary, from Table 19.8 and following the change point detection methods of Moskvina and Zhigljavsky (2003), significant change points in the *D. behrii* for  $S34.5 < \text{latitudes} < S35.5$  time series were found at 1924 (a decrease), 1964 (increase) and at 1999 (decreased trend). Recall that there was a change point (decrease) in 1925 for the days to peak flowering of *D. orientis* (1897–2005), similar to the *D. behrii* for  $S34.5 < \text{latitudes} < S35.5$  time series. The years 1999 and 1995 mark the beginning of an increased negative trend for the *D. behrii* (for  $S34.5 < \text{latitudes} < S35.5$ ) and the *D. orientis* time series, respectively (an earlier point of decrease could not be detected for the *D. behrii* data, due to lack of records after 1984 and 1998).

GAMs gave a  $R^2$  for the model of 7.11% (in contrast to the  $R^2$  of 2.06% obtained by the earlier SLR (see Fig. 19.5a)). GD, AIC and SBC goodness of fit statistics are shown for the resultant GAMLSS model in Table 19.8.

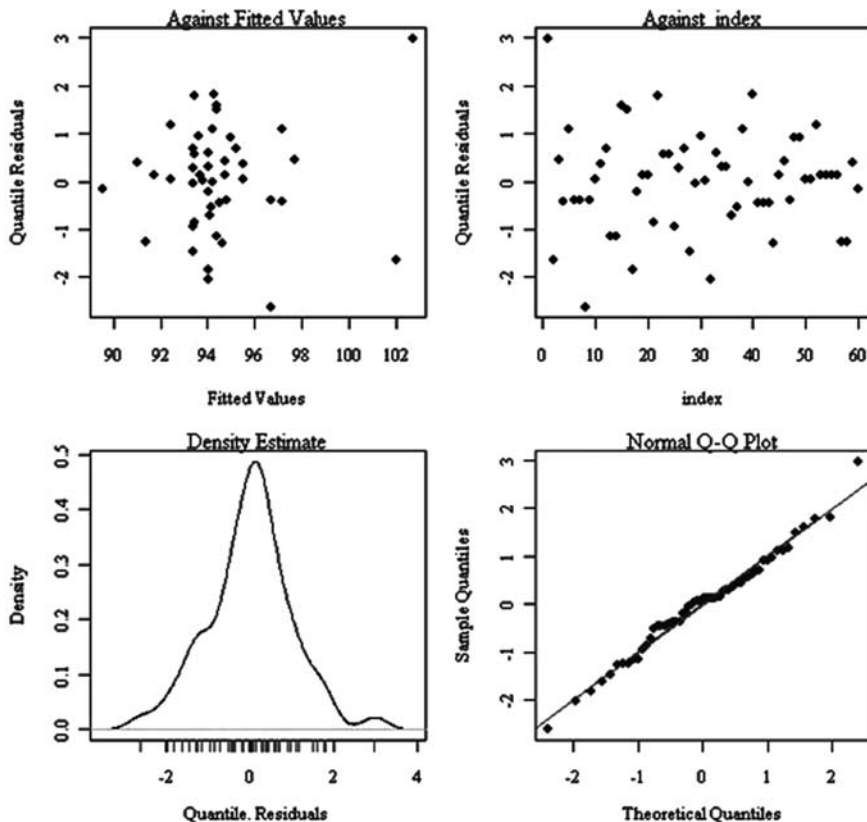
Diagnostic plots (Fig. 19.8) of quantile residual diagnostics and a normal Q-Q plot of the theoretical quantiles show that the GAMLSS intercept and cubic spline

**Table 19.8** Significant change points in the time series of number of days to peak flowering of *D. behrii* for  $S34.5 < \text{latitudes} < S35.5$ ; mean over the period of 94 days spanning the period 1896–2004; with GAMLSS goodness of fit statistics (GD, AIC and SBC) shown

	Change point years: Moskvina & Zhigljavsky (2003)	Global Deviance(GD) <sup>ϕ</sup>	AIC <sup>ϕ</sup>	SBC <sup>ϕ</sup>
<i>D. behrii</i> (all)	1924, 1964, 1999	444.5	456.5	469.1

<sup>ϕ</sup> GD denotes the scaled deviance statistic (Stasinopoulos and Rigby 2007); AIC denotes the Akaike information criterion (Akaike 1983) and SBC denotes the Schwarz Bayesian Criterion (Stasinopoulos and Rigby 2007) goodness of fit statistics.





**Fig. 19.8** Diagnostic plots of GAMLSS analysis of the number of days to peak flowering for *D. behrii* for  $S34.5 < \text{latitudes} < S35.5$ ; mean over the period of 94 days; showing quantile residual diagnostics, and normal Q-Q plot of the theoretical quantiles. A straight 1:1 line (plot on RHS bottom) indicates a good fit of the GAMLSS model

year (time) effect model fits the data well. This is indicated by the straight 1:1 line for the sample versus theoretical quantile plot (RHS bottom). For brevity we show only this model’s diagnostic plots.

Table 19.9 shows GAMLSS modelling of the number of days to peak flowering of *D. behrii* north of latitude S34.5 for the period 1893–2004. Interestingly the cubic spline effect of year ( $cs(\text{year})$ ) is positive with a value of 0.0689; but this is not a statistically significant positive trend. Figure 19.5b indicates a relatively flat profile for the days to peak flowering for *D. behrii* after 1918; with slightly later peak flowering day after 1964; but earlier time to peak flowering after 1999 (but this trend is non-significant). Here the GAMLSS cubic spline effect for year ( $cs(\text{year})$ ) is not statistically significant and likewise a formal change point detection found no significant points of change (Table 19.10, Fig. 19.9).

**Table 19.9** Intercept and year effects via GAMLSS modelling of number of days to peak flowering for *D. behrii* north of latitude S34.5; mean 87 days (1893–2004)

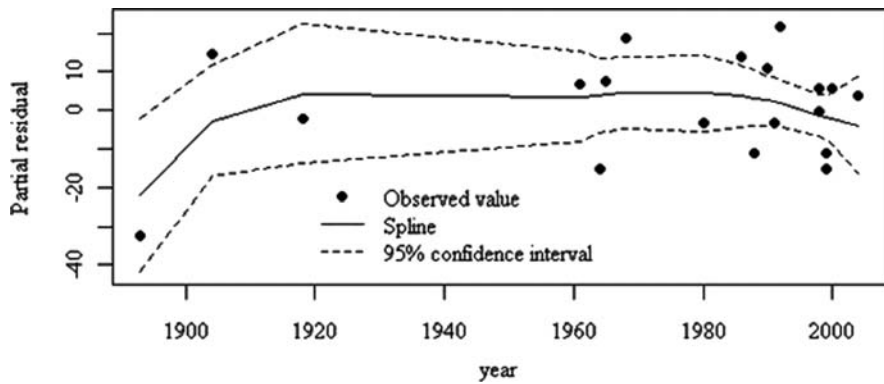
	GAMLSS			GAMLSS			Non linear		GAMs
	intercept	S.E.	<i>t</i> value	P value	cs(year)	S.E.	<i>t</i> value	P value	100( <i>R</i> <sup>2</sup> )%
<i>D. behrii</i>	-48.864	154.050	-0.317	NS*	0.069	0.078	0.884	NS*	25.71

\*NS = not significant

**Table 19.10** Significant change points in the time series of number of days to peak flowering of *D. behrii* north of latitude S34.5; mean 87 days; with GAMLSS goodness of fit statistics (GD, AIC and SBC) shown

	Change point years: Moskvina & Zhigljavsky (2003)	Global Deviance(GD) <sup>φ</sup>	AIC <sup>φ</sup>	SBC <sup>φ</sup>
<i>D. behrii</i>	No significant change points	153.6	156.5	171.6

<sup>φ</sup> GD denotes the scaled deviance statistic (Stasinopoulos and Rigby 2007); AIC denotes the Akaike information criterion (Akaike 1983) and SBC denotes the Schwarz Bayesian Criterion (Stasinopoulos and Rigby 2007) goodness of fit statistics.



**Fig. 19.9** Variant of Fig. 19.5b: GAMLSS term plot of number of days to peak flowering for *D. behrii* north of latitude S34.5; mean 87 days; showing the cubic spline effect of year (cs(year)) and its associated 95% confidence interval. (Spline line and 95% confidence band for effect of year flowering day number for *D. behrii*.)

GAMs gave a high *R*<sup>2</sup> for the model of 25.71% (in contrast to the *R*<sup>2</sup> of 2.79% obtained the earlier SLR analysis (see Fig. 19.5b)). GD, AIC and SBC goodness of fit statistics are shown for the resultant GAMLSS model in Table 19.8.

## 19.11 Discussion

GAMLSS modelling has shown a significant curvilinear change in days to peak flowering for the *D. orientis* records covering the period 1897–2005. The change point year of 1972 coincides with an abrupt change in the El Niño Southern Oscillation (ENSO), from an extended cold La Niña phase to one dominated by El Niño (Wolter and Timlin 1993, 1998) (Fig. 19.1). The negative trend beginning around 1972 (Fig. 19.6) coincides with the warm El Niño phase and the period of significant warming in Australia from the mid 1980s when some of the warmest years on record were experienced <http://www.bom.gov.au/climate/change/amtemp.shtml>. The change point years of 1984 and 1995 come at the end of the most extreme (1982–1983), and the most protracted (1990–1995), El Niño events on record (Fig. 19.1).

It is noteworthy that a change point or deviation starting about 1985 was also shown in the study of Dose and Menzel (2004). These authors developed non-parametric regression from a Bayesian viewpoint to explore the possible non-linear functional behaviour of blossom onset time series of *Prunus avium* L., *Galanthus nivalis* L. and *Tilia platyphyllos* SCOP (1896–2002) in Germany, and thereby analysed the variations of the onset of phenological phases in the twentieth century. The period covered in their study is similar in to that represented by the herbarium records for *Diuris* (1896–2005) analysed here.

Dose and Menzel (2004) trialled three different models: a constant model, a linear model (though more complex than SLR) and a one change point model, to represent the functional behaviour of their blossom onset time series. See Dose and Menzel (2004, 2006) for details on the relevant computational and mathematical formulae. Further discussion appears in the Chapter 11. However, the change point methods used here, following the development of Moskvina and Zhigljavsky (2003), allow for multiple change points in a given time series, not just one change point as in Dose and Menzel (2004).

Dose and Menzel (2004) calculated the rates of change (days per year) as well as the so-called average functional behaviour with its associated uncertainty range. This model average for the rate of change was calculated from the mean rates of change of the three models, weighted by their respective probabilities. The rate of change was shown to be essentially zero over most of the century, with a significant and abrupt change point or deviation starting around 1985 (Dose and Menzel 2004), and a current rate of change of  $-0.6$  days per year (Dose and Menzel 2004). In Dose and Menzel (2004) this negative curvilinear slope and associated rate of change was associated with an uncertainty of  $-0.5$  days per year. Likewise, GAMLSS modelling and change point analysis of the days to peak flowering for *D. behrii* indicate a relatively flat profile from 1924 to 1984, and an estimated rate of change of  $-0.7$  days per year for *D. orientis* and  $-0.8$  days per year for *D. behrii*, obtained from SLR slopes for the same current period, thus comparing favourably with the Dose and Menzel (2004) estimates.

The non-uniform periods of change that typify the climate of the twentieth century (Dose and Menzel 2004, Rutishauser et al. 2007, CSIRO 2008) pose a particular

challenge when linear regression analysis is used for the reconstruction of trends. To properly address the question of change, periods of no change must be considered as an important part of the overall picture. While it is obviously necessary to determine changes in phenology with respect to corresponding changes in climate, it is likewise, but maybe less obviously, important to determine events throughout periods of reasonably stable conditions.

Schleip et al. (2008b) also applied linear trend analysis and Bayesian model comparison to an investigation of three unique, 250-year phenological time series from Switzerland and France, spanning the years from 1753 to the present (Chuine et al. 2004, Schleip et al. 2006, Meier et al. 2007). Schleip et al. (2008b) detected major changes in both long-term phenological and temperature time series at the end of the twentieth century, as we do here for the herbarium flowering records. It is noteworthy that Schleip et al. (2008b) showed that the functional description of the change-point model exhibited a sharp decline at the end of the twentieth century for all the phenological time series studied. In this chapter we also report change points of increased decline near the end of the twentieth century, namely near 1995 and 1999/2000 for *D. orientis* and *D. behrii* respectively. Analysis of change incorporating temperature is a topic of further investigation.

Whilst GAMLSS splines often give the researcher a visual indication of points of change in a time series, formal tests of significance of change points should be carried out in addition to fitting GAMLSS (splines or polynomials approaches) to phenological time series. We advocate the combined use of both non-linear methods (GAMLSS) and change points methods in the analysis of herbarium records. It is important to note that whereas GAMLSS modelling of a cubic spline or non-linear effect of year (time) may show statistically non-significant effects of year, formal change point detection tools can point to significant abrupt change points, as evidenced in the *D. behrii* for  $S34.5 < \text{latitudes} < S35.5$  data (Table 19.8). Linear regression methods cannot accommodate significant and abrupt change points; although piecewise linear regression methods may. Such an approach (but via Bayesian methods) was used in the seminal paper of Dose and Menzel (2004) in their linear model approach.

While climate change forecasts provided by the Bureau of Meteorology <http://www.bom.gov.au/climate/change/amtemp.shtml>, indicate that the current trend of persistent and substantial warming which began in 1950 will continue into the future, orchid species emerge at the end of a generally mild, and hopefully wet, winter and finish flowering before summer heat sets in. Future refinements to the GAMLSS modelling of these herbarium records will incorporate both temperature and rainfall as predictors, despite the inherent complexities of irregularly spaced time points, the inclusion of lagged dependencies of current with past climate and/or flowering days, for up to 12 months prior to the event; and the development of specific functionals for the herbarium flowering records. Sparsity of data and irregularity of records over time, as well as the need for more complex underlying distributions, remains an issue in the analysis of trends in herbarium records.

### ***19.11.1 Potential for Change in Hybridization Dynamics***

Understanding the impact of climate on the phenology of these orchids, in combination with knowledge of their genetic heritage, will help clarify their future prospects for survival, both as populations and species. Opportunities for pollination will be diminished if the synchrony between plants and their pollinators is disrupted, especially when the pollinators themselves are seasonal and impacted by climate change (Fitter and Fitter 2002). On the other hand, seed predation may be disrupted if the phenology of seed predators shift independently of the timing of seed production (Tarayre et al. 2007). Thus when sympatric species display divergent responses to change, the resulting mistiming of seasonal activities has the potential to disrupt existing biotic interactions (Walther et al. 2002, Visser and Both 2005).

The historical baseline data forthcoming from this investigation should be well suited to place the complementary phase of this study in perspective. This will entail field and molecular investigations to determine the genetic variation present within sympatric populations of these orchid species and the extent of natural hybridization occurring among them. Flowering time has a genetic basis incorporating levels of individual variation within populations as a form of bet-hedging against normal patterns of year to year variability.

Shifts in phenology as a consequence of climate change are expected to have a number of major impacts on biological systems, and successful evolutionary adaptation is more likely when high levels of genetic variance (Fox 1990, Franks et al. 2007) provide the resources for a species to cope with change in the short term, outcompete less resilient species and have better prospects for long term survival (Cavers et al. 2003, Burke 2004). Species which do not have sufficient capacity to respond to the conditions imposed by enhanced and rapid change will be prone to local extinction.

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# Chapter 20

## Meta-Analysis and Its Application in Phenological Research: a Review and New Statistical Approaches

Irene L. Hudson

**Abstract** Climate change is one of the greatest challenges to sustainable development. Results from many individual studies show significant variation in response to climate change and human activities. Given the scope and variability of these trends, global patterns may be much more important than individual studies in assessing the effects of global change. There is a need to synthesize quantitatively, existing results on ecosystems and their responses to global change, in order to reach a general consensus or summarize the differences. Meta-analysis provides such a quantitative synthetic method, in that it statistically integrates results from individual studies to find common trends and differences: so called fingerprints of change. Only a small number of studies to date have performed a formal statistical meta-analysis of species' responses or have synthesized independent studies to reveal emergent and globally coherent patterns of ecological changes in physical and in biological systems in the phenology and distribution of plants and animals. There are very few reports available on the use of meta-analysis to examine global climate change in Australia. The unequivocal conclusion across the global syntheses, to date, is that twentieth-century anthropogenic global warming has already impacted on the Earth's biota. This chapter reviews the general methodology of meta-analysis, assesses its advantages and disadvantages, synthesizes its use in global climate change phenology and discusses future directions and proposes new statistical methods, as yet not applied to phenological research, and only recently applied, only in part, in the health-climate epidemiological literature.

**Keywords** Bayesian hierarchical meta-analysis · B-,*P*-spline regression · Fractional polynomials · Meta-analysis · Nonlinear nonparametric functionals

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## 20.1 Introduction

### 20.1.1 Why Meta-Analysis in Global Climate Change Research?

Climate change is one of the greatest challenges to sustainable development (Sathaye et al. 2007). Climate change, human influences and ecosystem response have become more and more interrelated. Changes in phenology have been long regarded as sensitive indicators of climatic change (Hughes 2000, 2003, Walther et al. 2001, 2002, 2005, Badeck et al. 2004, Thomas et al. 2004, Pounds et al. 2006, Robinson et al. 2008, Morissette et al. 2009), where phenology has traditionally involved the study of the rhythm of biological phenomena primarily related to climate (Schwartz 2003). Phenology with its recording of dates provides high-temporal resolution of changes which are frequently reported as time series. The recording of phenological observations has a long history, for example the several centuries of records of cherry blossoming in Japan (Menzel and Dose 2005, Aono and Kazui 2008).

Global surface temperature has increased by an estimated  $0.74^{\circ}\text{C}$  over the past century, a change that is widely believed to result primarily from the effects of anthropogenic emissions of carbon dioxide and other greenhouse gases (IPCC 2007). Many physical changes have been attributed to this warming, including sea level rise, melting of glaciers and ice sheets, decreased snow and ice cover, changed depth to permafrost and changes in patterns of wind, temperature, and precipitation (IPCC 2007). Such changes are likely to have considerable biological effects and numerous studies have sought evidence of such biological effects in nature. Indeed several recent papers summarize the results of these studies and conclude that biological effects are already evident and have impacted on numerous taxa in different geographical areas (Peñuelas and Filella 2001, Walther et al. 2002, Parmesan and Yohe 2003, Root et al. 2003, Menzel et al. 2006, Parmesan 2006, Rosenzweig et al. 2008). Results from many individual studies show significant variation in response to climate change and human activities. Given the scope and variability of these trends, global patterns may be much more important than individual studies in assessing the effects of global change. There is a need to synthesize quantitatively, existing results on ecosystems and their responses to global change, in order to reach a general consensus or summarize the differences.

### 20.1.2 Definition

Meta-analysis is a quantitative research method that statistically integrates results from individual studies (Hedges and Olkin 1985, DerSimonian and Laird 1986, Borenstein et al. 2009) to find common trends and differences: so called *fingerprints of change*. Meta-analysis as such is also called a synthetic approach, as it synthesizes and integrates the results of many studies chosen a priori. Meta-analysis has been increasingly applied in *large scale global change research* in recent years

(Blenckner et al. 2007). Indeed, meta-analysis has become popular in large scale global change ecology of late and shows high value for studying the response of terrestrial ecosystem to elevated CO<sub>2</sub> and global warming. There are, however, few reports available on the use of meta-analysis to examine global climate change in the Southern Hemisphere (Australia, South American and Africa). Twenty years is considered to be the minimum time period needed for rigorous phenological study (Sparks and Menzel 2002). In Australia, this is currently being address with research locating data sets that are currently extant and of sufficient temporal length (e.g. NEMD <http://www.bom.gov.au/nemd> and PhenoArc; Chambers et al. 2007, Keatley et al. 2009). Networks fuel the need for combining data and results and thereby add impetus to governments' decision making on climate change. It is expected as such, that global meta-analysis will be more widely adopted in future climate change research, and in policy making (van Kooten et al. 2004).

### ***20.1.3 History of Meta-Analyses and Syntheses***

A number of studies to date have performed a formal statistical meta-analysis of species' responses or have synthesized independent studies to reveal emergent and globally coherent patterns of ecological changes in physical and in biological systems in the phenology and distribution of plants and animals (Parmesan and Yohe 2003, Root et al. 2003, 2005, Menzel et al. 2006, Parmesan 2006, Rosenzweig et al. 2008). The unequivocal conclusion across these global syntheses is that anthropogenic global warming has already impacted on the Earth's biota as noted by Peñuelas and Filella 2001, Walther et al. 2002, 2005, Root et al. 2003, Parmesan and Yohe 2003, Parmesan and Galbraith 2004, Parmesan 2005a, b, Root and Hughes 2005, Menzel et al. 2006, Pounds et al. 2006, Parmesan 2007 and Rosenzweig et al. 2008. In what follows meta-analytic case studies are reviewed followed by recommendations and future statistical methods and directions. Note that a meta-analysis on bird phenology by Lehikoinen et al. (2004) is not discussed here. Also not discussed in this review are early developments of meta-analysis in ecology (see Gurevitch and Hedges 1993, Arnqvist and Wooster 1995, Gurevitch et al. 2001).

## **20.2 Case Studies**

### ***20.2.1 Case Study 1: Meta-Analysis: Three Decades and 29,000 Natural Systems***

The climate change cause-effect, meta-analytic study of Rosenzweig et al. (2008) demonstrates the power of meta-analysis in global climate change research. This is the first study to date to formally link observed global changes in physical and biological systems to human-induced climate change, principally due to increasing

greenhouse gases. Their approach used joint attribution (Rosenzweig et al. 2007) across multiple biological and physical systems at both the global and continental scale. The joint attribution approach by these authors is as follows: (1) they first show that the observed correspondence between impacts and warming would be very unlikely to occur if patterns of temperature change were the result of natural climate variability; (2) then argue that human influence has a role because observed large-scale climate change can be attributed to human influence on the climate system (Zwiers and Hegerl 2008). As described “joint attribution,” delineates thus a two-step linkage: human activities contribute significantly to temperature changes and human-changed temperatures are associated with discernible changes in plant and animal traits. This approach to joint attribution was conducted on studies of 145 specific plant and animal species earlier by Root et al. (2005). Root’s et al. study involved linking climate models with process-based or statistical models to simulate changes in natural systems caused by different climate forcing factors, and comparing these directly with the observed changes in natural systems. When temperature data from the HadCM3 global climate model were used to examine the likely cause for changes in the timing of spring events of Northern Hemisphere wild animals and plants, results show the strongest agreement when the modelled temperatures were derived from simulations incorporating anthropogenic forcings (Root et al. 2005). Indeed Rosenzweig’s et al. (2008) synthesis is ground-breaking and pushes detection-and-attribution research into a much broader arena given the huge number (29,000) and range of natural systems investigated. It may permit us to better understand the mechanisms by which, and by how much, anthropogenic factors cause the observed impacts (Zwiers and Hegerl 2008).

### **20.2.1.1 Data**

Rosenzweig et al. (2008) examined 80 previous studies, the majority of which came from Europe, based on a single meta-analysis of a collaborative database of observations of annual natural events from Menzel et al. (2006). Several hundred others came from studies around the world. Australia, Africa and Latin America were, however, inadequately represented. Rosenzweig et al. (2008) monitored 29,000 natural systems between 1970 and 2004: most of the studies synthesized examined the impact of climate change on plants and animals: others focussed on its impact on land, water, and ice. The literature sampled by Rosenzweig et al. (2008) studied for example, the perturbation of polar bear behaviour: timing of peak stream flow, of grape harvests: and of spring flowering and bird migration: and variation in the freeze–thaw pattern in the tundra, in krill stocks and in glacier depletion. All of the phenomena were monitored for at least 20 years.

### **20.2.1.2 Methods and Results**

Rosenzweig et al. (2008) studied how many of the 29,000 natural systems had changed in ways consistent with warming. They developed a database of observed

changes in natural systems from peer reviewed papers, which had shown a statistically significant trend in change in either direction related to temperature and represented data for at least 20 years (between 1970 and 2004). Observations in the studies were characterized as a “change consistent with warming” or a “change not consistent with warming.” The databases of the observed significant changes in the natural systems were overlaid with two gridded observed temperature data sets and the spatial patterns of the observed system changes were compared with the observed temperature trends using pattern-comparison measures. The link between their binary indicators and climate change was assessed by means of techniques involving “spatial pattern congruence” statistics. Based on the conclusions of the original authors, 90% of the biological systems showed the effects of rising temperatures (e.g. penguins dying off), as did 95% of the physical systems (e.g. glaciers melting). The second part of the study plotted the location of every instance of ecological disruption and noted local temperature trends since 1970. Average temperatures were analysed against computer models which calculate the natural climate variability for any spot on the globe, for any year. Results showed that a system (physical, plant or animal) change occurred almost exclusively where highly elevated levels of warming were recorded in recent decades.

### ***20.2.2 Case Studies 2–4: Influences of Methods on Estimates of Phenological Response to Global Warming and the First Fingerprints of Global Warming***

A meta-analysis of 203 species performed on published datasets from the northern hemisphere by Parmesan (2007) demonstrated that data-sampling and inclusion criteria for the studies selected for meta-analysis and the methods used for analysis may significantly impact global (meta-analytic or synthetic) estimates of the magnitude of global warming response (Root et al. 2003, Parmesan and Yohe 2003). Other more general literature on how methods affect estimates of climate change impacts include considerations by many others about the effects of publication bias, differences across studies in time periods analyzed, non-random sampling within a species and non-random selection of species (Parmesan and Yohe 2003, Badeck et al. 2004, Parmesan and Galbraith 2004, Parmesan 2005a, b).

#### **20.2.2.1 Meta-Analytic Factors Affecting Response**

As Parmesan (2007) reported studies documenting responses of wild species to global warming show that responses deviate significantly from being homogeneous (Walther et al. 2002, Parmesan and Yohe 2003, Root et al. 2003, Parmesan 2006). Whilst there are only a few species, which are opposite in their direction of response (e.g. breeding later despite warming temperatures) the magnitude of response, however, in the expected direction, varies significantly across species. Many species



(20–70% of species at a given location) reveal no significant response, exhibiting steady phenological patterns over years despite warming (Parmesan and Yohe 2003). Parmesan (2007) makes a case for the inclusion of such stable (nonresponsive) species in meta-analytic studies, in the second study to date (after Menzel et al. 2006), to explicitly investigate the impact of publication bias, exclusion of stable processes, sampling methods, latitude, taxonomic representation and variation in time periods covered by studies synthesised: and test for these effects on quantitative estimates of species' responses. The phenological global climate change community has, as yet, no formal agreement upon choice on study design or on statistical methods for meta-analyses. The paper of Parmesan (2007) attempts to inform on the need for such a future consensus. Much work and an increased inter-disciplinary dialogue needs, as yet, to occur to achieve such a consensus.

### **20.2.2.2 Diagnostic Fingerprint**

To date there have been quantitative, globally inclusive datasets on strictly phenological responses to recent climate warming by Parmesan (2007), Rosenzweig et al (2008) and the two earlier studies of Root et al. (2003) and of Parmesan and Yohe (2003). Quantitative comparisons across broad taxonomic and functional groups have only been performed in the single meta-analytic study of Root et al. (2003). These two synthetic papers Root et al. (2003) and Parmesan and Yohe (2003) both used data published in peer-reviewed literature, but differed in their criteria for study inclusion due to the divergent aims of the two studies. Specifically Root et al. (2003) focussed on estimating the pervasiveness of a positive correlation between temperature trends and phenological trends (a sustained climate change and correlated system change; see Fig. 1 of Menzel et al. 2006) for species that were changing through time, whilst Parmesan and Yohe (2003) focused on estimation of the total response to climate change, by analysing the overall strength and consistency of response across all species, irrespective of whether or not they showed phenological change. Both these studies revealed the first consistent pattern across diverse species to global climate change, a so-called climate “diagnostic fingerprint” in biological changes that provide a causal link between anthropogenic global warming and biological impacts (Cleland et al. 2007, Dang et al. 2007, Rosenzweig et al. 2008). Since the publication of these two seminal meta-analytic studies, new data have been rapidly accumulating (Root et al. 2005, Parmesan 2006).

### **20.2.2.3 Differential Advance in the Timing of Spring Events**

Parmesan (2007) investigated causes for the more than two-fold difference in estimates of the mean magnitude of advance in the timing of spring events between the two studies: 2.3 days per decade advance found by Parmesan and Yohe (2003), and 5.1 days per decade by Root et al. (2003). Different latitudes, taxa, or different time periods could account for this discrepancy: Parmesan (2007) found the latter effect

significant, but importantly also the effect of differing inclusion criteria. A three-fold approach was used, which involved analysis of the Parmesan and Yohe (2003) dataset without modification. Base analyses were then conducted on the dataset of Root et al. (2003). The same set of analyses conducted on the unmodified (base) dataset was repeated with modified data sets: with and without the composite (mean) values from studies where species were not separated, and with and without replication of individual species in different studies. The combined data set was compiled such that each data point represented one unique species. Parmesan's (2007) analysis of a new expanded dataset produced an estimate of overall spring advancement across the northern hemisphere of 2.8 days per decade.

### ***20.2.3 Case Study 5: European Phenological Response to Climate Change***

The first meta-analytic study to examine for possible lack of evidence for changes or shifts at sites, where no temperature change is observed, was undertaken by Menzel et al. (2006). This was done to test whether there was bias in the previous literature towards principally reporting climate change-induced impacts. Meta-analyses, which included reanalyses of network data, for all available species, did not yet exist, to that date. Menzel et al. (2006) keenly observed, as did Parmesan (2007) somewhat later, that the two previous seminal synthetic studies (Parmesan and Yohe 2003, Root et al. 2003) had different inclusion criteria. The first included multispecies studies from any location that reported neutral, negative and positive results and analysed a total of 677 species or species functional groups' phenology (Parmesan and Yohe 2003). The results of one study site in the UK (Fitter and Fitter 2002), however, itself accounted for nearly half of its records, possibly affecting its generalisability. The second meta-analysis was restricted to publications reporting significant changes of one or many species (Root et al. 2003). Subsequently, the average spring advance revealed by the latter was higher (5.1 compared to 2.3 days per decade).

#### **20.2.3.1 Publication Bias**

The majority of published phenological-climate studies focus on the problem of whether changes in systems and sectors relate to altering regional climates. As a consequence of this, future reporting of phenological trends in peer-reviewed journals may become more and more difficult, especially when dealing with "no change" or "change opposite to the direction expected" (see Table 1 of Menzel et al. 2006), as commented by Hughes (2000) and others (Menzel 2002, Kozlov and Berlina 2002, Menzel et al. 2006). In principle, four combinations of system and climate changes are possible. "No change" in the tracking systems seems to be less likely to be reported, especially if it matches with "no change" in temperatures. (See Fig. 1 of Menzel et al. 2006)

### **20.2.3.2 Data and Results**

Menzel's et al. 2006 study was a comprehensive Europe-wide analysis of all observed changes in phenology (plants/animals) in the period 1971–2000. In total, more than 125,000 observational series were examined. Phenological trends of 542 plant species in 21 countries (125,628 time series) and of 19 animal species in three countries (301 time series) were analysed. Menzel et al. (2006) concluded that previously published results of phenological changes were not biased by reporting or publication predisposition: their study found a coherent signal of earlier spring (leaf unfolding and flowering) and summer (fruit ripening), the average advance of spring/summer was 2.5 days per decade in Europe. This analysis of 254 mean national time series indisputably demonstrated that species' phenology is responsive to temperature of the preceding months (mean advance of spring/summer by 2.5 days per 1°C, delay of leaf colouring and fall by 1.0 day per 1°C).

### ***20.2.4 Case Study 6. Human Modified Temperatures Induce Species Changes***

Can a signal of human-induced global warming be identified in the changing phenology of wild plants and animals? Until the meta-analytic study of Root et al. (2005) this question had not been answered, and indeed temperature-species associations had not been statistically attributed directly to anthropogenic climate change. This study performed a two-step linkage paradigm: human activities contribute significantly to temperature changes, and human-changed temperatures are linked with detectable changes in plant and animal traits. Subsequently, Rosenzweig et al. (2008) used the same approach to link both physical (and biological) systems changes with human-induced climate change.

#### **20.2.4.1 Joint Attribution**

The study of Root et al. (2005) modelled climatic variables and observed species data, traditionally independent of thermometer records and paleoclimatic proxies, to demonstrate statistically significant joint attribution, in that, (i) human activities involving injection of greenhouse gases and aerosols into the atmosphere were found, by modelling studies, to be changing the surface-air temperatures at a local and more regional scale, and (ii) some phenological changes in species, at various locations around the globe were highly likely to be caused by such a human-induced temperature increase. This approach specifically involved relating climate models with either process-based or statistical models to simulate changes in natural systems caused by different climate forcing factors, namely, natural climatic forcings (NF), anthropogenic forcings (AF), and a coupling of both natural and anthropogenic forcings (combined forcings (CF)) and comparing these directly with observed changes in natural systems.

#### 20.2.4.2 Species Data

The temporal scale covered by the synthesized studies ranged from 11 to 97 years: were gleaned from 29 published studies and also from Root et al.'s unpublished data: were distributed over 41 GCM grid boxes and included 145 species representing a variety of taxa (130 exhibiting statistically significant changes in spring phenology). Europe comprised the bulk of locations (62%) and North America most species (57%). Phenological changes were measured consistently in all studies (date of event), allowing calculation of the mean annual phenological change for sets of species in the Northern Hemisphere from 1969 to 1999.

#### 20.2.4.3 Analytic Methods

To facilitate comparisons among taxa and regions, species were divided into 7 overlapping groups, each of which contained at least 25 species: all species: species north of 45° latitude: North American species: European species: birds: herbaceous plants: and woody plants. Data only on species that exhibit a statistically significant trend in a phenological trait were analysed, and used in association with GCM modelled temperature values at both one- and nine-gridbox scales to test for joint attribution in three different ways.

Firstly, Pearson correlation was used to quantify the association between the annual phenological averages and each of the three time series of GCM-temperature data (i.e., temperatures modelled with NF, AF, and CF) at three spatial scales: (i) averaging only grid boxes covering study locations, (ii) averaging all grid boxes in the Northern Hemisphere (ocean and terrestrial), and (iii) grid boxes around the entire planet (ocean and terrestrial). Secondly joint attribution was tested by calculating individual correlation coefficients between the three temperature time series and species' data for each of the 145 species and then calculating the means of the correlation coefficients for species included in each of the regional and taxa-specific subsets described above. Monte Carlo simulations with one species chosen randomly from each of the 41 individual grid boxes containing the 42 site locations were performed to assess possible bias due to multiple-species observations being recorded at one location. Thirdly the frequency distribution of the species' correlation coefficients, were examined.

#### 20.2.4.4 Results

Using temperature data from the HadCM3 global climate model to examine the probable cause for changes in the timing of spring events (flowering, migration) of Northern Hemisphere wild animals and plants, results showed the strongest tracking, when the modelled temperatures, were derived from simulations incorporating anthropogenic forcings. The *species trends over time results* are of particular interest, in that whilst, as expected, the direction of change is negative (shift earlier in the season in response to warming), the estimated average number of days changed is

–3.2 day per decade for all 130 species. Despite some contention (on issues of inclusion methods), this is in fact not very different to the finding of Parmesan (2007), whose expanded analysis gave an estimate of overall spring advancement across the northern hemisphere of 2.8 days per decade. An advance of 3.2 days per decade is also not statistically different from Parmesan's (2007) re-calculation of the data of Root et al. (2003) – to permit the inclusion of stable species, which gave a value of mean advance in spring timing of 3.1 days per decade: the latter is not statistically different to the advance of 2.3 days per decade (Parmesan and Yohe 2003).

Root et al. 2005 do not suggest that plant-and-animal-climate-proxy data should replace archives of actual instrumental climatic records or the detection and attribution literature based on them. However, use of these species data, from varied locations and diverse taxa, potentially give independent confirmation of the many earlier attribution studies that utilise instrumental observations. Indeed, as Root et al. (2005) note by demonstrating significant correlations between biological records and the HadCM3, resultant modelled anthropogenic climatic changes increases our confidence in the ecological implications of GCM-based projections of climatic changes into the twenty-first century (Thomas et al. 2004).

## **20.3 Limitations and Future Directions**

### ***20.3.1 Scarcity of Global Data***

The largest gaps in meta-analytic studies are geographic rather than taxonomic (Parmesan 2006). A reason for this paucity may be that some areas, such as sub tropical or tropical regions in particular, have poorly marked temperature seasons, thus events such as the advance of spring phenology is less significant. Phenological information on lower latitude taxa is rather scarce, particularly in Australia, as noted by many authors (Hughes 2000, 2003, Stenseth et al. 2002, Chambers et al. 2005, Walther et al. 2005, Chambers 2006, Zwiers and Hegerl 2008). Phenological data and documentation of observed changes is also lacking in Africa and Latin America (Rosenzweig et al. 2008). Some specific examples of temperature sensitive phenologies in lower biomes, however, on which records exist, are the Australian Box-Ironbark eucalypt forests, the *E. regnans* eucalypt forests in southeast Australia and the Arizona-Sonora desert (see Ashton 1975, Keatley et al. 2002, Hudson et al. 2005, Bowers 2007, Bustamante and Búrquez 2008).

### ***20.3.2 Integrated Data Archiving and Phenological Networks***

In many European countries National Meteorological Services have organized phenological recordings since the second half of the twentieth century (Menzel 2003a, Schwartz 2003, Pfister and Dietrich-Felber 2006). Some networks were extant at

the beginning of the twentieth century (Menzel 2003a, Nekovář et al. 2008). The longest written phenological record is believed to be the record of the commencement of flowering of cherry at the Royal court of Kyoto, Japan, which dates back to AD 705 (Sekiguti 1969, Menzel 2002, Aono and Kazui 2008). One of the oldest and longest European time series of phenological observations is the Marsham family record in Norfolk, UK (1736–1947) (Sparks and Carey 1995). Europe also has many old and some still extant phenological networks (Nekovář et al. 2008)

### **20.3.3 Shortness of Records**

Does the relative shortness, as yet, of phenological records used in meta-analyses reduce our capacity to put biological changes in the context of past observed variations in climate (Zwiers and Hegerl 2008), especially when we consider studies spanning over a century (Parker et al. 1992, Rutishauser et al. 2007). The records mined by Rosenzweig et al. (2008), for example, were primarily from the period 1970 to 2004, with the rule that at least 20 years of data be available: the time series studied by Root et al. (2003) had to have at least 10 years of data from recent decades (1951–2001), whilst Parmesan and Yohe (2003) stipulated time series be of length 20 or more years, starting from the past decade and working back in time. Typically 50–100 year data sets are used to attribute and to detect change in basic climate variables such as temperature, rainfall and surface pressure (Hegerl et al. 2007, Zhang et al. 2004, Min et al. 2008).

There has, however, been one recent study by Schleip et al. (2008a) that evaluates plant phenological variability and temperature impacts over the last 250 years. Schleip et al. (2008a) reported coherence factors and temperature weights that indicate that spring phenological variability is not only influenced by forcing temperatures of the current year, but also by temperatures of particular months in the preceding year. This is the first study to date, to investigate the relationship of phenological records with temperatures of the previous year. The approach adopted by Schleip et al. (2008a) was a Bayesian analysis following the work of Dose and Menzel (2004, 2006) (see also Chapter 11).

Extending phenological records over time and particularly over geographical location is much needed (Chambers 2006, Sparks et al. 2006, Parmesan 2007, Sparks 2007, Bertin 2008). Herbarium specimens and photographs represent a possible new resource to extend the range of species and localities addressed in global-warming research (Miller-Rushing et al. 2006, Sparks 2007). The approach involves a comparison of current observational phenological records to older records documented by either photographs or herbarium specimens (Lavoie and Lachance 2006, Loiselle et al. 2008, Gallagher et al. 2009, Chapter 19). Herbarium and museum records are traditionally used in taxonomic, systematic and biogeographical studies as well as providing information on the distribution and habitat of organisms (Bolmgren and Lonnberg 2005, Rumpff et al. 2008). Commonly these

collections contain detailed information on collection date, location, habitat, life-form, abundance, co-occurring species and reproductive state. As noted by Rumpff et al. (2008) the relevance of such collections to a range of wider ecological conservation and biological studies has been, to date, largely under-appreciated (Rumpff et al. 2008, see also Chapter 19).

### **20.3.4 *Direct Attribution Studies***

Statistical analysis plays a major role in climate change detection and attribution studies (Lee et al. 2005), as it does for meta-analysis (Borenstein et al. 2009). Complexity with regard to methodological issues of detection (correctly detecting a real trend) and attribution (assigning causation) has been discussed by many authors (Hasselmann 1998, Parmesan et al. 2000, Parmesan 2002, 2005a, b, Root et al. 2003, Parmesan and Yohe 2003, Dose and Menzel 2004, Root and Hughes 2005, Hegerl et al. 2006, 2007, Shoo et al. 2006, Zwiers and Hegerl 2008). Indeed Zwiers and Hegerl (2008) pointed out that it would be difficult to quantify the climate–impact link with an analysis, as in Rosenzweig et al. (2008), as the approach adopted involves aggregation of results from distinctly different types of systems, both biological and physical. Two-step joint attribution studies are those in which an aspect of change in the climate system is first ascribed to an external influence, and alteration in a physical or biological system is subsequently attributed to climate change (Root et al. 2003, Parmesan and Yohe 2003). Estimation of the size of the anthropogenic contribution may, however, call for a so-called direct attribution approach. This involves an end-to-end modelling system that: (i) explicitly represents all the major climate and non-climatic processes which are possible components of the variation in the system (whether biological or physical): (ii) can simulate response (e.g. to greenhouse-gas changes, or to other factors affecting the observed impacts) (Hasselmann 1998, Stone and Allen 2005, Hegerl et al. 2006).

To date only a few end-to-end attribution (Stone and Allen 2005) studies exist (Rosenzweig et al. 2007, 2008, Zwiers and Hegerl 2008). These are usually restricted to scenarios where the affected system’s interaction with climate is either empirically described (Gillett et al. 2004) or somewhat well understood (Barnett et al. 2008). Recently, Zwiers and Hegerl (2008) noted that the undertaking of more end-to-end studies will assist much in the interpretation of less direct approaches to attribution, and also assist in the all important projections of future impacts. To better understand “end-to-end” attribution we refer to Stone and Allen (2005) who contextualize end-to-end attribution in the framework of cause and effect in the epidemiological arena. They state that “When a damaging extreme meteorological event occurs, the question often arises as to whether that event was caused by anthropogenic greenhouse gas emissions. The question is more than academic, since people affected by the event will be interested in recurring damages if they find that someone is at fault. However, since this extreme event could have occurred by chance in an unperturbed climate, we are currently unable to properly respond

to this question. A solution lies in recognising the similarity with the cause-effect issue in the epidemiological field. The approach there is to consider the changes in the risk of the event occurring as attributable, as against the occurrence of the event itself. Inherent in this approach is a recognition that knowledge of the change in risk as well as the amplitude of the forcing itself are uncertain. Consequently, the fraction of the risk attributable to the external forcing is a probabilistic quantity.” Stone and Allen (2005) develop and demonstrate this method in the context of the climate change problem.

### ***20.3.5 Publication Bias and Consensus***

Criticisms of meta-analysis are based on its misapplications and deficiencies (Rosenthal and Di Matteo 2001, Noble 2006); these include publication bias, possible partisanship in literature selection and non-independence among studies. Various methods, rarely used in the phenology community, exist to verify publication bias (Egger et al. 1997, Duval and Tweedie 2000a, b, Macaskill et al. 2001, Rothstein et al. 2005). When bias is detected, further analysis and interpretation should only be performed with care (Møller and Jennions 2001, Kotiaho and Tomkins 2002, Jennions et al. 2004). (See also Jennions et al. 2004). It behoves us also to update the results of meta-analysis on a given subject topic at regular intervals by inclusion of newly published literature. A consensus on inclusion criteria and sampling methods for meta-analytic studies must be reached by the phenological community. Publication bias in synthetic studies remains highly contentious, as underlined by a recent publication by Michaels (2008), which showed that a survey of *Science* and *Nature*, demonstrates that the likelihood that recent climate change literature is not biased in a positive or negative direction is less than one in  $5.2 \times 10^{-16}$ .<sup>1</sup> This has considerable implications as Michaels (2008) states “for the popular perception of global warming science, for the nature of ‘compendia’ of climate change research, such as the reports of the United Nations’ Intergovernmental Panel on Climate change, and for the political process that uses those compendia as the basis for policy.” See also Higgins et al. (2003) for a discussion on measuring inconsistency in meta-analyses.

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<sup>1</sup>The climate research community believes that published findings on global warming will have an equal probability of raising or lowering forecasts of climate change and its impact. This is a testable hypothesis based upon the recent literature and the assumption that extant forecasts are themselves unbiased. A survey of *Science* and *Nature* demonstrates that the likelihood that recent literature is not biased in a positive or negative direction is less than one in  $5.2 \times 10^{-16}$ . This has considerable implications for the popular perception of global warming science, for the nature of “compendia” of climate change research, such as the reports of the United Nations’ Intergovernmental Panel on Climate change, and for the political process that uses those compendia as the basis for policy.)



### ***20.3.6 Binary Indicators***

When biological impacts occur due to seasonal changes, non-local climate change or variation in temperature extremes, binary indicators of impacts (i.e. whether a given impact is consistent or inconsistent with warming), as used recently in spatial pattern congruence statistics by Rosenzweig et al. (2008), do not allow us to glean impact patterns perfectly correlated with annual mean warming (Easterling et al. 2000, Zwiers and Hegerl 2008). It is thus difficult to quantify the climate-impact link with such an approach. Zwiers and Hegerl (2008) noted that a “spatial pattern congruence” statistic, assumes that the effects of local climate change occur locally; as such this “measure will not fully capture connections where biological impacts result from remote climate changes, seasonal changes or changes in temperature extremes” (Zwiers and Hegerl 2008). Perhaps structural equation modelling and spatial regressions may offer some solution to this problem.

### ***20.3.7 Future Perspectives and Projections***

Increased empirical data is needed to create accurate future probabilistic projections of response to global change impacts. An essential component in achieving this is to gain a better understanding of the complex interdependencies between species. Implementation of long-term field observations and/or experiments is one way forward (Parmesan 2007). Apart from temperature, there is a need to consider other climate variables (e.g. rainfall) and particularly non-climatic drivers (e.g. soil moisture, CO<sub>2</sub>) of phenological change. Increased CO<sub>2</sub> may, for example, directly impact on plant phenology: though experimental evidence to date shows no consistent direction of response (either advance or delay) (Asshoff et al. 2006). Following the arguments and development of the Bayesian coherence approach of Dose and Menzel (2006), future analyses of the impact of temperature on phenology should include temperature forcing periods other than primarily calendar months: we should consider, as noted by Schleip et al. (2008a) a combination of precipitation and drought, say, by use of drought severity indices.

As Menzel et al. (2006) stated phenological studies also need to track the entirety of changes to rigorously answer questions of evidence of no change, change opposite to the direction expected, change not matching climate/temperature change.

### ***20.3.8 Change Point Analyses***

Rapid shifts in climate can lead to, or be contemporaneous with, abrupt phenological changes. These cannot be well detected by regression nor correlation, methods traditionally used to detect temporal changes in phenology (Keatley et al. 2002, Cleland et al. 2006, 2007). However, new techniques based on change point analysis enable a quantitative representation of such often non-linear phenological responses and associated rates of change as reported by others (Hudson et al. 2003, 2005,

Sparks and Tryjanowski 2005, Keatley and Hudson 2008; and for Bayesian techniques see Hasselmann 1998, Dose and Menzel 2004, Menzel and Dose 2005, Menzel et al. 2008, Schleip et al. 2008a, b). Analysis of the change-point probabilities via Bayesian methods provides the advantage of visualizing and quantifying major changes in long-term time series.

Specifically for the study of Schleip et al. (2008a) their change-point model allowed for nonlinearities in the description of functional behaviour and rates of change. The change-point model was formulated in terms of triangular functions consisting of two linear segments defined by the endpoints of the series and a change point in between. The variables of these triangular model functions were assumed to be the unknown functional values, both at the endpoints and at the change point as well (which delineates the temporal position of the change point). Bayesian probability theory estimates the probabilities of all possible change point positions by marginalization over the functional values at the endpoints and the change point of the series. Indeed these change-point probability distributions exhibit the change-point probabilities as a function of time for a temperature or a phenological time series. Future and ongoing work will address the assessment of increasingly complex time series models, such as multiple change-point models (see e.g. Keatley and Hudson 2008).

## **20.4 Increased Statistical Sophistication**

### ***20.4.1 Why We Need to Move Beyond Regression***

There is much need to update the fundamental statistical tools for research synthesis, so as to include rarely used methods in global climate change research. Methodologically, trends in time series are frequently analyzed using simple linear regression (SLR) where phenological dates or temperatures are plotted against time (for examples of phenology applications see Menzel and Fabian 1999, Walther et al. 2002, Parmesan and Yohe 2003, Root et al. 2003, and Menzel et al. 2006). The slope of the linear regression equation then indicates the average rate of change in phenology (days per year or days per °C). This method can be easily applied to a large number of sites to compare differences between species and sites, and thus be applied to synthetic studies. The major disadvantages of this least squares approach, are their restriction to time series exhibiting comparatively linear trend, possible poor extrapolation properties, and also sensitivity to outliers (or so-called extremes (Schlittgen and Streitberg 1999)), and sensitivity to boundary values. Indeed one or two outliers can seriously distort the results of a least squares analysis (von Storch and Zwiers 2001) (NIST/SEMATECH, e-Handbook of Statistical Methods 2006, available at <http://www.itl.nist.gov/div898/handbook/index2.htm>). For inherently non-linear processes it is difficult indeed to find a linear model that fits the data well. This is true particularly as the range of the data increases (Schleip et al. 2008a). Menzel et al. (2008) noted that, when utilising SLR, the length of a time series and its start and end dates are crucial in correct detection of changes and in estimating

their magnitude, particularly when highly variable phenological time series of a few decades are analysed (see also Dose and Menzel 2004).

### ***20.4.2 Non Linearity of Phenological Response: Implications to Modelling and Meta-Analysis***

Numerous studies have examined the relationship between phenological events and temperature over several seasons to derive predictive relationships between say temperature and the timing of a given phenophase. Such functions are typically used as the basis for predicting phenological changes (likely to be associated with future temperature changes) with a linear relationship generally assumed (Bertin 2008). Indeed many publications demonstrate the coherence of phenological spring phases and temperature, using classical statistical methods which assume linearity, such as correlation analysis, linear and multiple regression methods (Sparks and Carey 1995, Sparks et al. 2000, Menzel 2003b, Luterbacher et al. 2007, Rutishauser et al. 2008).

Experiments have shown the link between temperature and phenology to be causal in many plant species: in that, warmer temperatures generally lead to earlier spring phenology (Saxe et al. 2001). Plant phenophases may also respond to many other types of environmental and meteorological factors such as light, photoperiod, wind, humidity, rainfall and soil conditions (Menzel 2002, Schleip et al. 2008a, b, 2009). Sparks et al. (2000) noted that plant response to temperature, even if linear over a certain range, must inevitably taper off, though we do not know at what temperature this is likely to occur.

As noted by Sparks et al. (2000) and by Dose and Menzel (2004) the commonly used methods of searching for signals in phenological time series present problems. The detection of shifts is frequently performed via classical statistical methods, such as slopes of linear regression models (Bradley et al. 1999, Menzel and Fabian 1999, Jones and Davis 2000, Schwartz and Reiter 2000, Defila and Clot 2001, Ahas et al. 2002, Peñuelas et al. 2002, Menzel 2003b), rarely by other curve fitting methods (e.g. Ahas 1999, Sagarin and Micheli 2001, Sagarin 2001). Trends are traditionally reported in days per year or decade, or days of change over the study period.

### ***20.4.3 Generalised Additive Model for Location, Scale and Shape (GAMLSS), Penalised Spline Signal Regression and Bayesian Nonparametric Function Estimation: 3 Approaches to Non-Linear Response***

There are two pertinent questions here. How can we accommodate for non-linear responses of phenology to time (year) and/or to climatic factors? This shall be addressed by illustration of three approaches to modelling phenological time series assuming possible non-linear trends:

1. The Generalised Additive Model for Location, Scale and Shape (GAMLSS) approach (Rigby and Stasinopoulos 2005, Stasinopoulos and Rigby 2007) applied recently to flowering records of four eucalypts (*Eucalyptus leucoxydon*, *E. microcarpa*, *E. polyanthemos* and *E. tricarpa*), from Maryborough, Victoria, Australia, for the period 1940–1971 (Hudson et al. 2009, see also Chapter 10)
2. penalised spline (*P*-spline) signal regression (PSR) of Marx and Eilers (1999, 2005) applied recently to the flowering records from 1978 to 2001 of the Last family (Last et al. 2003) by Roberts (2008). From these records, a dataset of 208 species and cultivars has been compiled (see also Chapter 12 of Roberts)
3. The Bayesian nonparametric function estimation approach of Dose and Menzel (2004) applied to blossom (onset) time series of *Prunus avium*, *Galanthus nivalis* and *Tilia platyphyllos* (1896–2002) in Germany in an analysis of the variations of the onset of phenological phases in the twentieth century.

A handful of papers have used other methods to account for the possible non-linearity and for the complex interdependencies and for changing structure in phenological time series: namely dynamic factor analysis (Gordo and Sanz 2005) and chronological clustering (Doi 2007). See also Doi and Katano (2008). These methods prove valuable in separating out underlying components of a univariate (single) time series that show significantly different patterns: however, they are not discussed in this chapter. The issue of accounting for, modelling and detecting change points in phenological time series also remains an important issue (Dose and Menzel 2004, Keatley and Hudson 2008, Schleip et al. 2008a) and is briefly discussed in Section 20.6.6 of this chapter.

It is noteworthy that the Bayesian non-parametric function estimation methods (in the above list point (3)) were also recently applied by Menzel et al. (2008) to study four deciduous tree species: horse chestnut (*Aesculus hippocastanum* L.), silver birch (*Betula pendula* L.), common oak (*Quercus robur* L.), and European beech (*Fagus sylvatica* L.) from the phenological network data of the German (1951–2003) and the Slovenian meteorological service (1961–2004). Menzel et al. (2008) aimed to investigate the following:

1. whether changes in the length of the growing season are related to trends in leaf unfolding and/or leaf colouring dates,
2. the nature of the variation among different broad-leaved species,
3. possible confounding effects of an insect attack, and
4. how these changes are related to recent temperature changes.

Menzel et al. (2008) confirmed advanced leaf unfolding in both countries with the same species order (oak > horse chestnut, beech, and birch). However, this advance was non-linear over time and more apparent in Germany, with clear change-points in the late 1970s, followed by marked advances (on average 3.67 days per decade in the 2000s). In Slovenia, there was a more gradual advance of onset dates (on average 0.8 days per decade in the 2000s).

Recently Schleip et al. (2008a) also applied these Bayesian non-parametric function estimation methods (linear trend analysis and Bayesian model comparison) to an investigation of three unique, multidecadal, 250-year phenological time series from Switzerland and France from 1753 to the present (Chuine et al. 2004, Meier et al. 2007, Rutishauser and Studer 2007, Rutishauser et al. 2007). Schleip et al. (2008a) detected major changes in long-term phenological and temperature time series at the end of the twentieth century, especially for summer temperatures since the 1980s. Bayesian model-averaged trends revealed a warming rate that increased from an almost zero rate of change to an unprecedented rate of change of  $0.08^{\circ}\text{C}$  per annum in 2006. After 1900, temperature series of all seasons show positive model-averaged trends. In response to this temperature increase, the onset of phenology advanced significantly. See also Schleip et al. 2006, 2008b, 2009.

The second question is how best to accommodate for non-linearity between phenological response and time in meta-analytic studies aimed at determining possible fingerprints of change. Or in other words, when a phenological response or outcome is in fact non-linearly related to time (or temperature, say), how can one apply meta-analytic procedures to obtain a combined (pooled) estimate of effect of time (temperature) across studies? These pooled estimates usually assume linearity.

## **20.5 Epidemiological Perspectives and Relevant Studies**

### ***20.5.1 Dose-Response Functionals and Bayesian Hierarchical (BH) Meta-Analysis***

We advocate that meta-analytic methods used only recently to account for nonlinear “dose/exposure to response” functionals in epidemiology (Bagnardi et al. 2004, Gamborg et al. 2007) may be possibly adapted and apply well to phenological synthetic studies. Another focus of the discussion in this chapter will be on Bayesian hierarchical (BH) meta-analytic studies, to modelling so-called dose-response functionals. BH models were recently used to assess the impact of extreme heat events on hospitalizations for cardiovascular and respiratory admissions in 12 European cities (see Michelozzi et al. 2009): in what is now known as the PHEWE (Assessment and Prevention of acute Health Effects of Weather conditions in Europe) study: which enrolled 15 cities, about 30 million people on calendar years 1990–2001. The latter study aimed to investigate possible climate change impacts on human health. Indeed, under climate change scenarios, it has recently been hypothesised that the increase in extreme weather events and certain air pollutants, especially ozone (Confalonieri et al. 2007), are likely to further exacerbate chronic respiratory diseases (see also Bell et al. 2007, Analitis et al. 2008, Baccini et al. 2008, Mahmud et al. 2008) and cardiovascular mortality (Ren et al. 2008).

The interested reader should also note the following meta-analytic approaches: meta-regression (Berkey et al. 1995), which is an extension of meta-analysis to allow testing for heterogeneity of effects across studies, cumulative meta-analysis:

sensitivity analysis: and importantly as noted above, hierarchical Bayesian meta-analysis (widely used in health environmetrics) and discussed by numerous authors (Smith et al. 1995, Louis and Zelterman 2000, Stuhlmacher and Gillespie 2005, Barnett 2007, Michelozzi et al. 2007, Baccini et al. 2008, Ren et al. 2008, Zanobetti and Schwartz 2008).

### ***20.5.2 Bayesian Hierarchical Distributed Lag Models (BHDLMs)***

The recent study of Peng et al. (2009) that develops Bayesian hierarchical distributed lag models (BHDLMs) to relate particulate matter air pollution exposure to hospitalisations for cardiovascular and respiratory diseases (using a national US database on 3 million enrollees of the US Medicare system, living in 94 countries, and covering the period 1999–2002) will also be referred to in this chapter, again with a view to advancing more sophisticated meta-analytic approaches in phenological and climate change research.

### ***20.5.3 Approach and Justification of New Methods***

The three approaches and applications to the modelling of non-linear phenological response over time delineated above (GAMLSS, penalised spline regression and Bayesian nonparametric function estimation) will be reviewed, and will then be linked to the following recently developed epidemiological approaches (dose-response functionals, Bayesian hierarchical meta-analysis and BHDLMs). The meta-analytic methods proposed here for phenological studies are all essentially based on nonparametric regression (Green and Silverman 1994, Eubank 1999) or semiparametric regression (Chen and Ibrahim 2006, Ruppert et al. 2009), including Bayesian hierarchical models (Gelman et al. 2004), the latter of which can be cleverly reformulated in terms of a penalised spline model. This was only recently shown by Peng et al. (2009) in the context of Bayesian hierarchical distributed lag models (BHDLMs).

## **20.6 Modelling of Non-Linear Phenological Response over Time**

### ***20.6.1 Generalised Additive Model for Location, Scale and Shape (GAMLSS) Models for Non-Linear Response***

Hudson et al. (2009) (see also Chapter 10) represents the first attempt to apply the Generalised Additive Model for Location, Scale and Shape (GAMLSS) (Rigby and Stasinopoulos 2005, Stasinopoulos and Rigby 2007, Hudson et al. 2008), to study a phenological data set, with the aim, in part, of detecting non-linear responses to

climate change (contrasting earlier stepwise regression approaches). Regardless of the cyclicity of flowering over time, this study shows that each species' flowering is significantly influenced by temperature and that this effect is non-linear. Importantly from the view of phenological studies GAMLSS allows for the: (i) identification of lower and upper thresholds of temperature for flowering commencement and cessation: (ii) estimation of long and short-term non-linear effects of climate, and (iii) the identification of lagged cyclic effects of previous flowering.

### ***20.6.2 Non-Linear Functionals with Temperature: Slope – Threshold Forms from Cubic Splines***

GAMLSS is thus a possible way, not only to detect non-linear trends, but to actually establish at what temperature the plant response to temperature tapers off (Sparks et al. 2000). From the cubic splines analysis of GAMLSS, lower (maximum) temperature thresholds for (commencement of) flowering for *E. polyanthemos* were shown to be 17.5°C temperature then reaching cessation at 25.9°C (Hudson et al. 2009). In terms of meta-analytic studies, we believe that the smoothing cubic spline estimates of trend that GAMLSS provide per time series, could then be combined to obtain an overall effect measure, traditionally used in the meta-analytic approach. Alternatively these cubic spline estimates of trend from GAMLSS could be analysed using linear or non-linear Bayesian mixed models (meta regression) (see also Thompson and Higgins 2002). One could also potentially compare the temperatures at which the tapering off occurs across species and sites and obtain an overall estimate. These ideas need to be rigorously tested and demonstrated, and are the topic of future work.

### ***20.6.3 Regression Methods: from Simple Linear, Multiple Linear, Stepwise Regression to P-Spline Signal (PSR) Regression***

Linear regression is a commonly used method to determine rates of change in phenological data (Fitter and Fitter 2002). The limitations of linear regression have been highlighted in the phenological literature (Menzel 2003b). The slopes of the resultant regression lines are influenced by when a series commences and finishes and by the length of the series (Sparks and Menzel 2002, Sparks and Tryjanowski 2005). Given that temperature in the last 20 years encompasses the warmest period recorded to date, this will affect the slope of the resultant regression lines. The difference in rate of change has been illustrated by Menzel et al. (2003). The suggestion by Menzel et al. (2003) that trends should be reported in days per year along with the number of years analysed, in addition to the years study, should be taken up. Dose and Menzel (2004) (followed by Menzel et al. 2008 and Schleip et al. 2008a, b, 2009) have addressed the issue of estimating rates of change based on Bayesian nonparametric function estimation, (see Section 20.6.6). Their approach very much

addresses problems in estimating rate of change, determining change-points and importantly provides a rigorous analysis of uncertainties of the results. The provision of uncertainty analysis is much needed in climate-related research (see Katz 2002, Dose and Menzel 2004).

Multiple linear regression (MLR) or stepwise regression (Draper and Smith 1981) are regularly used to investigate the influence of temperature on the first day of flowering (Fitter et al. 1995, Sparks and Carey 1995, Keatley and Hudson 2000, Roberts 2008 etc), or to relate a phenological response to weather measurements. To date, MLR or stepwise methods have delineated similar results across different regions (Fitter and Fitter 2002, Roberts et al. 2004). Stepwise regression is a procedure that selects the subset of the regressors that best explains the variation in the phenological response. Stepwise regression however, has limitations in studies relating a phenological response to weather data. Firstly it does not accommodate for large numbers of highly correlated regressors (Roberts 2008). This is a real issue if daily or weekly climate measurements are used as regressors. In practice monthly aggregates of weather data are used and clearly information is lost. Stepwise regression also does not take into account the marked auto-correlated structure in the regressors. Indeed what has not often been highlighted in the phenological literature is that phenological series (or fine time scale weather series) are correlated by nature, an aspect not accounted for by linear, MLR, nor stepwise regression methods (see Hudson et al. 2005, Roberts 2008, Chapter 12 of Roberts and Chapter 13 of Kelly).

Recently Roberts (2008) suggested and tested an approach to account for the evident structure in the (daily weather) regressors (see also Chapter 12). Several regression methods aimed at accommodating many correlated regressors exist and are derived mainly in the field of chemometrics. These include ridge regression, principal components regression and partial least squares (Hastie et al. 2001, Frank and Friedman 1993). However, as Roberts (2008) noted none of these explicitly take advantage of the ordered structure inherent in regressors based on higher time resolution weather data. Roberts (2008) applied *P*-splines signal regression (PSR) (Marx and Eilers 1999) and ridge penalties (Eilers and Marx 2003) to the Last family bluebell data, with 730 daily temperatures for both the year of flowering and the preceding year as regressors. These results were compared to those from a partial least squares (PLS) stepwise regression analysis of the same bluebell flowering dates (from 1978 to 2001), using daily temperatures for both the year of flowering and the preceding year as regressors.

#### ***20.6.4 Smoothed Profile of Regression Coefficients in Current and Preceding Year***

To motivate and illustrate this approach consider a regression with daily temperatures as regressors. The effects of the temperature on two consecutive days might be expected to be similar. The penalised regression approach (Elston and Proe 1995)



utilises this information by steering the model towards a solution where consecutive regressors have similar regression coefficients. The penalised regression method illustrates the concept of penalising differences between regression coefficients so as to obtain a smooth profile. This so-called smoothed profile of regression coefficients is both intuitive and highly informative (see Fig. 2 of Roberts 2008).

In this chapter we point out that the form of this smoothed profile of regression coefficients bears a striking resemblance to curves, which can be drawn from the Pearson correlation analysis, between flowering and temperature in the current and preceding year, derived recently by Schleip et al. (2008a, Table 1). See also the form of the wavelet cross-correlation curves between flowering intensity and temperature (and rainfall) for the current flowering year (and back) for four species of Australian eucalypts, as developed and discussed by Hudson et al. in Chapter 18. We discuss the relevance of this finding later.

It is also noteworthy that there are various methods for smoothing, though they do not appear to be commonly used in plant phenology models; see e.g. running means (Schaber 2002) and LOWESS that have been applied (Crick and Sparks 1999, Roy and Sparks 2000, Gange et al. 2007). Splines, which smooth via applying polynomial regressions, appear to have been only recently applied to phenological data (Roberts et al. 2004) (see also Chapter 12, Roberts 2008, Chapter 10 and Hudson et al. 2009).

There are other approaches that have the same aim as penalised regression. The identical regression model can be re-expressed as a linear mixed model (Sims et al. 2007). Smoothing of the regression coefficients is then achieved by assuming the differences between adjacent regression coefficients to be random (non-fixed) effects with a common variance component. The smoothing parameter is estimated internally, as part of the procedure, being directly related to the latter common variance component. Roberts (2008) pointed out that similarly, the idea can be translated into a Bayesian context by placing a common prior distribution on the differences between adjacent regression coefficients: this would generally be a normal distribution with zero mean and variance  $\sigma^2$ . The degree of smoothing is estimated directly and can be found through the posterior distribution for  $\sigma^2$ . Marx and Eilers (1999) extended the usefulness of the penalised regression in a method termed *P*-spline signal regression (PSR), which allows for the use of many more regressors in a computationally efficient fashion (Roberts 2008). This allows for modelling long sequences of daily (say climatic) measurements as regressors. PSR also uses *P*-splines (Currie and Durban 2002) and smooth B-splines (Eilers and Marx 1996). In brief, the latter consist of polynomial pieces: the degree of the polynomial can be chosen by the user.

In his application Roberts (2008) showed that when stepwise regression was applied to the Last bluebell data, January and February were chosen as significant regressors, with regression coefficients of 3.4 and 4.4 days/°C respectively: thereby a uniform 1°C rise in temperature would be expected to advance flowering by 7.8 days. Using PLS and PSR Roberts (2008) showed that a uniform 1°C rise in temperature would be expected to advance flowering by 10.2 days. The time of year that had the greatest influence was in the period around 14 February, about a month

before the earliest date of first flowering. A clear relationship between the lateness (of onset) of a species and its phenological behaviour was discovered, in that later species tend to be affected by later temperatures. This has been noted by other authors (Fitter et al. 1995, Sparks et al. 2000). In addition Roberts (2008) observed that the influential temperatures may be nearer to flowering for earlier species than for later species.

Roberts (2008) showed that the application of both one-dimensional and two-dimensional forms of penalised regression to the Last family (Bluebell) records was successful, and noted that it was possible to build PSR models across species: this potentially via multivariate models. The number of flowering years available clearly has an influence on the quality of the results obtained. With smaller datasets, the complexity of the curve or surface that can be fitted is limited by the number of observations (Marx and Eilers 1999). In the Last family records, with 24 years, the degree of smoothing changed considerably between different responses, in some cases appearing to be under-smoothed. It is expected that, with the addition of more years, the choice of degree of smoothing should become more stable. Roberts (2008) pointed out that the number of years required to achieve this, will depend on the complexity of the underlying model, as well as on the precision of measurements and on the lack of fit. Both this problem and the possible link of these PSR models with biologically-based models (Chuine et al. 2003) need to be studied further. To what degree penalised regression can recover information about an underlying mechanistic process (Chuine et al. 2003) would be of particular interest (Roberts 2008) (see also Chapter 12 of Roberts).

### ***20.6.5 GAMLSS Interconnection with PSR and Splines in General: Computer Routines***

The work of Roberts (2008) (see also Chapter 12) on *P*-splines (Currie and Durban 2002) and on B-splines is a method that also has some strong inter-relatedness with the GAMLSS approach discussed here (see also Chapter 10) – in that for all approaches, spline functionals are used in the modelling procedures. The term “spline” is generally used to refer to a wide class of functions that are used in applications requiring data interpolation and/or smoothing. The data may be either one-dimensional or multi-dimensional. Spline functions for interpolation are normally determined as the minimizers of suitable measures of roughness which are subject to the certain interpolation constraints. Smoothing splines may be viewed as generalizations of interpolation splines, where the functions are determined to minimize a weighted combination of the average squared approximation error over observed data and the roughness measure. The smoothing spline is a method of smoothing (fitting a smooth curve to a set of noisy observations) using a spline function (Hastie and Tibshirani 1990). Smoothing splines are related to, but however distinct from, *P* splines (Penalized Splines) which combine the reduced knots of regression splines, with the roughness penalty of smoothing splines (Ruppert

et al. 2003) Indeed smoothing splines though related to, are distinct from: (1) Regression splines, wherein the data is fitted to a set of spline basis functions, with a reduced set of knots, typically by least squares, and no roughness penalty is used: (2) Penalized Splines, which combines the reduced knots of regression splines (e.g. Roberts 2008 used 100 knots) with a roughness penalty and a ridge penalty term (Eilers and Marx 2003). Computer routines for general smoothing splines and  $P$  splines for Generalized Additive Models (GAMs) (Hastie 2006) and Generalised Linear Models (GLMs) are given by Gu (2007) and Marx (2003), respectively. See also computer routines for GAMLSS in Stasinopoulos and Rigby (2007).

### ***20.6.6 Modelling the Functional Behaviour of Phenological Time Series: Bayesian Nonparametric Regression***

As noted by Dose and Menzel (2004) Bayesian analysis offers the possibility to overcome the pitfalls of linear regression models. Indeed Bayesian statistical methods have been applied to date in climate change detection, analysis and attribution (Hobbs 1997, Hasselmann 1998, Leroy 1998, Tol and De Vos 1998, Barnett et al. 1999, Berliner et al. 2000, Katz 2002), and also in climate reconstructions (Robertson et al. 1999, Schoelzel 2006). Recently various studies show that Bayesian analysis offers huge benefits in the analysis of varying changes, model probabilities and change-point probabilities of time series, when non-linear changes in phenological and climate time series exist. Along with these rates of change, rigorously calculated uncertainties of model-averaged rates of change and linear trends can be described by Bayesian statistics (Dose and Menzel 2004, Menzel et al. 2008, Schleip et al. 2008a; see also Chapter 11).

We shall now review the studies of Dose and Menzel (2004) and of Schleip et al. (2008a), with the aim of indicating how estimates of the resultant functional behaviour of the phenological time series (which allow for both linear non-linear change and abrupt change points) could be modelled and combined for pooled estimates of change, say over species and localities – a meta-analytic viewpoint, that can account for so-called non-linear climate exposure-response functionals. Finally, we show that the overarching paradigm for all the methods, is the area of semi-parametric regression (Chen and Ibrahim 2006, Ruppert et al. 2009), except for the Bayesian approach to modelling the non-linear functional relationship between flowering and time (of Dose and Menzel 2004). It is noteworthy however, that the latter work models nonparametric functionals via Bayesian methods.

Dose and Menzel (2004) developed nonparametric regression from a Bayesian viewpoint to describe the possibly non-linear functional behaviour of blossom (onset) time series and analysed the variations of the onset of phenological phases in the twentieth century. The functional behaviour of these series was represented by three different models: the constant model, the linear regression model and the one change point model. In addition to the functional behaviour, rates of change in terms of days per year were also calculated. Dose and Menzel (2004) also obtained the average functional behaviour with its associated uncertainty range. The three

models were compared for the trend of flowering time series, using the model comparison option of Bayesian theory, which relies on Ockham's razor (Garrett 1991); and ensures that the model of choice should be as complex as required to explain the data and as simple as necessary to avoid fitting the model to noise. The model average for the rate of change was calculated by averaging the rates of change of the three models weighted by their respective probabilities. The rate of change was shown to be essentially zero change over most of the century, with a significant and abrupt change point or deviation starting about 1985, with a current rate of change of  $-0.6$  days per year (Dose and Menzel 2004). This negative curvilinear slope and associated rate of change was associated with an uncertainty of  $-0.5$  days per year (Dose and Menzel 2004). We later argue that this plateau-threshold shape of the time series functional may lend itself to Bayesian hierarchical (BH) meta-analytic study, when obtained across sites: an approach that still requires rigorous testing.

Recently Schleip et al. (2008a) also applied the linear trend analysis and Bayesian model comparison discussed above, to an investigation of three unique, multi-decadal, 250-year phenological time series from Switzerland and France from 1753 to the present (Chuine et al. 2004, Meier et al. 2007, Rutishauser et al. 2007). Schleip et al. (2008a) detected major changes in long-term phenological and temperature time series at the end of the twentieth century. See Dose and Menzel (2004, 2006) for details on the relevant computational and mathematical formulae. Schleip et al. (2006, 2009) also demonstrated the flexibility of the Bayesian procedure on different climate change detection issues. Schleip et al. (2008a) showed that the model-averaged rates of change of the phenological phases demonstrated a significant advance of the onset of spring and harvest dates. Summer temperature time series showed an abrupt temperature increase at the end of the twentieth century. For all phenological time series the change-point model was the preferred model. Schleip et al. (2008a) noted that the linear model provided an adequate alternative for describing the temperature time series for winter and autumn. In the context of the last 250 years the end of the twentieth century represents a period with unique major increases in temperatures for all seasons and earlier grape harvest phenology as derived from model averaged trends Schleip et al. (2008a). The functional behaviour of the change-point model suggests a considerable increase in summer temperatures since 1978. Since the 1980s, and using Bayesian model-averaged trends, Schleip et al. (2008a) showed that the summer warming rate increased from an almost zero rate of change to an unprecedented rate of change of  $0.08^{\circ}\text{C}$  per annum in 2006. After 1900, temperature series of all seasons showed positive model-averaged trends. In response to this temperature increase, the onset of phenology advanced significantly.

### ***20.6.7 Understanding Long-Term Ecological Change: Modelling Current and Preceding Year Climate***

Importantly Schleip et al. (2008a) also used Bayesian correlation to compare the phenological records with independent Swiss instrumental temperature measurements (commencing in 1753), so as to assess the impact of monthly temperature

on phenological variability of the past three centuries. This was achieved by using the method developed by Schleip et al. (2009), which improved on the Bayesian correlation approach of Dose and Menzel (2006), in that the coherence of long term temperature and phenological time series was estimated to determine and weight single monthly and seasonal 3-monthly averaged temperature impacts: and a simulated annealing optimization algorithm was used to obtain a coherence factor and temperature weights (Schleip et al. 2008a).

### ***20.6.8 Cyclic Correlational and Regressor Profiles of Past Climate on Flowering: Links with PSR and Wavelets***

Whilst the earlier analyses of Dose and Menzel (2006) assumed that temperatures of the previous year (of the phenological event) could be neglected with regard to the phenological onset in the year of interest, the results of Schleip et al. (2008a) confirm that summer temperatures very likely influence, not only summer phases of the current year, but also spring phases of the following year as seen in the onset of the Swiss “spring plant,” Schleip et al. (2008a) noted that for “spring plant” phenology, temperatures during the spring season of the year of budburst, and temperatures during the summer season of the previous year, appeared particularly important, especially temperatures in the previous July and the following May. With simple linear approaches (e.g. Sparks and Carey 1995), this result is much less evident: but has been discussed to date, only in part, by Roberts (2008), who used a penalised spline regression (PSR) method, with 730 daily temperatures for both the year of flowering and the preceding year as regressors. See also the wavelet analytic, the singular spectrum analysis (SSA) and GAMLSS approaches investigating lagged dependencies between flowering and climate (of the current year and back) in Chapters 17, 18, and 10, respectively.

Schleip’s et al. (2008a) study represents a long term approach (see Cheke 2007) and is the first study to date to investigate the relationship of phenological records with temperatures of the previous year by Bayesian methods. Pearson correlation (Table 1 of Schleip et al. 2008a), coherence factors and temperature weights (Fig. 5a, b of Schleip et al. 2008a), indicated that spring phenological variability is not only influenced by forcing temperatures of the current year, but also by temperatures of the preceding June and October. It is noteworthy that the cyclic curve which can be drawn from the Pearson correlation analysis between flowering and temperature in the current and preceding year, as derived by Schleip et al. (2008a, Table 1), bears a striking resemblance to the cyclic form of the smoothed profile of regression coefficients of Roberts (2008). These are also comparable to the cyclic shape of the wavelet cross-correlation curves between flowering and temperature (and rainfall) for the current flowering year (and back) for four species of Australian eucalypts, as recently developed and discussed by in Chapter 17. Wavelets clearly identified the cyclical influence on peak flowering intensity of climate (temperature and rainfall).

There are 6 months of an annual cycle in which any given climate variable positively influences flowering intensity and 6 months of negative influence, within a given species which results in distinct seasonal change points (Chapter 18; see also similar profiles from the singular spectrum analytic approach of Chapter 17).

We now review three significant and recent meta-analytic approaches in epidemiological research, namely dose-response functionals, Bayesian hierarchical meta-analysis and BHDLMs, which we believe hold much promise to further meta-analytic studies in phenology. Proof of concept is an important area of future research. We also show their interconnectedness to the three modelling approaches discussed earlier, namely, GAMLSS, penalised spline regression (PSR) and Bayesian nonparametric function estimation, recently applied to non meta-analytic phenological studies of late (Dose and Menzel 2004, Roberts 2008, Schleip et al. 2008a, Menzel et al. 2008, Hudson et al. 2009).

## **20.7 Accounting for Non-Linearity in Meta-Analysis via Fractional Polynomials and Spline Regression – an Epidemiological Application**

Recently Bagnardi et al. (2004) described fractional polynomials (Greenland 1995) and spline regression (Royston 2000) (in particular random effects cubic splines) by which to represent smooth non-linear dose-response relations in summarizing meta-analytical aggregate data of 29 cohort studies, investigating alcohol consumption and all-cause mortality, for the period 1966–2000. This was the first study, to that date, to use so-called flexible meta-regression functions in a meta-analysis of dose-response aggregate data (for alcohol consumption and all-cause mortality). Specifically, curvilinear J-shaped curves between the logarithm of the relative risk of death versus alcohol “dose” (i.e. exposure) were consistently obtained via fractional polynomials and cubic splines (Bagnardi et al. 2004).

It is noteworthy that attempts to represent non-linearity in epidemiologic meta-analysis are traditionally made via polynomial models, typically quadratic models (Berlin et al. 1993, Friedenreich 1993). Such low-order polynomials, however, offer a limited suite of shapes for the dose-response functional, whilst high-order polynomials, on the other hand, may fit poorly at the extreme values of the exposure variable (McCullagh and Nelder 1989). Furthermore, polynomials do not have asymptotes and cannot fit data for which a threshold value is expected. This represents a major disadvantage to epidemiological applications and wider. We now delineate the rationale for the parametric approach of Bagnardi et al. (2004) (parametric versus nonparametric regression) and later suggest possible phenological applications and adaptations. These could possibly apply to modelling accumulated heat (temperature, growing degree days (GDD)) – phenological response curves (over time): or apply to modelling across location nonparametric functionals of phenological response (as in Dose and Menzel 2004, Menzel et al. 2008 and Schleip

et al. 2008a), but in this case by using random effects for the parameters of the functionals across locations (sites). This is the topic of future research.

### ***20.7.1 Nonparametric (Smoothing) Regression***

Whilst nonparametric regression methods (e.g. the GAMs family of Hastie and Tibshirani 1990: the GAMLSS family of Stasinopoulos and Rigby 2007, see also Green and Silverman 1994), are useful alternatives for avoiding strict assumptions about the form of the dose-response relation (asymptotes, thresholds, plateaus, polynomial order) a main impediment of this approach is the lack of widely known and standard software. Moreover, nonparametric regression is particularly useful when little or nothing may be assumed about the form of the exposure-disease relation. For most epidemiologic purposes, however, knowledge or strong prior evidence exists about the functional form of the exposure-response relationship. This is particularly true in meta-analysis, for which the shape of the relationship is indicated by the individual (say across locations) studies.

### ***20.7.2 Parametric Approaches***

Two alternative curve-fitting methods, fractional polynomial regression and spline regression, have been described by Greenland (1995) and Royston (2000). Fractional polynomials are a family of models considering, as covariates, power transformations of a continuous exposure variable restricted to a small predefined set of integer and non-integer exponents (Royston and Altman 1994). The family includes conventional polynomials, as a particular case, and therefore aligns with simple regression, though it offers important improvements (Royston et al. 1999).

Fractional polynomials ( $\text{fp}()$ )<sup>2</sup> can be invoked in the GAMLSS platform (see Chapter 10) as parametric additive terms. The main advantage of parametric regression models using fractional polynomials, rather than traditional ones, is that models containing as few as two power transformations are able to encompass a large range of shapes (Royston et al. 1999). This allows then for the accommodation of almost all known dose-response relationships. Indeed splines (de Boor 1978) are a family of smooth functions that can take on virtually any shape, and, as a consequence, they come close to nonparametric regression (Durrleman and Simon 1989). Noteworthy also is that the GAMLSS platform also accommodates for cubic splines (Green and Silverman 1994), *P*-splines (Eilers and Marx 1996) and varying coefficient models (Hastie and Tibshirani 1993). An advantage of such parametric approaches, namely

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<sup>2</sup>Originally the fractional polynomial ( $\text{fp}()$ ) function was an implementation of the fractional polynomials introduced by Royston and Altman (1994). The functions involved in  $\text{fp}()$  and  $\text{bfp}()$  are loosely based on the fractional polynomials function  $\text{fracpoly}()$  for S-PLUS given by Ambler (1999)

fractional polynomial and spline regression, is that they allow researchers to obtain interpretable, intuitive and communicable results.

## 20.8 Possible Phenological Applications

In considering phenological applications the statistical validity of any application depends on the nature of the response (e.g. date of first flowering (DOFF) (Roberts 2008), flowering intensity (Keatley et al. 2002, Keatley and Hudson 2007), harvest date (Schleip et al. 2008a, b), first (median or mean) arrival (birds), peak passage (migratory birds) (Jenni and Kéry 2003, Lehtikoinen et al. 2004)). We believe that the fractional polynomial or spline regression methods could well apply to meta-analytic studies, where one modelled, say, flowering versus accumulated heat (temperature exposure) over time, wherein a particular temperature threshold was found/assumed to lead to flowering. The resultant curve would potentially be flat and then curve upwards, opposite to the plateau followed by a negative rate of change of DOFF found by Dose and Menzel (2004). Recall that Dose and Menzel (2004) showed that the rate of change was essentially zero over most of the century with a significant and abrupt change point or deviation starting about 1985 and a current rate of change of  $-0.6$  days per year. This negative curvilinear slope and associated rate of change was associated with an uncertainty of  $-0.5$  days per year. Clearly temperature/heat thresholds as described above would need to be established (to be considered as a change-point in any so-called heat accumulation curve). These ideas need, however, to be rigorously tested and are the topic of future research.

### 20.8.1 *Bayesian Hierarchical Models (BHMs): a Climate Change and Health Meta-Analysis*

Bayesian hierarchical meta-analytic studies were recently used to assess the impact heat on mortality in 15 European cities (Baccini et al. 2008) and more recently assess the impact of extreme heat events on hospitalizations for cardiovascular and respiratory admissions in 12 European cities (Michelozzi et al. 2009): in what is now known as the PHEWE (Assessment and Prevention of acute Health Effects of Weather conditions in Europe) study, which enrolled 15 cities, about 30 million people on calendar years 1990–2001. These studies aimed to investigate possible climate change impacts on human health (Confalonieri et al. 2007, see also Chapter 4 by van Vliet). The impact of extreme heat events on respiratory admissions is expected to increase in European cities as a result of global warming and progressive population aging (see also Bell et al. 2007, Analitis et al. 2008, Mahmud et al. 2008). Epidemiologic studies show that high (and cold) temperatures may be related to mortality, but until 2008 little was known about the exposure-response function and the lagged effect of heat/cold, whether on mortality or morbidity. The foundational mathematical formulae used in these studies, namely Bayesian hierarchical



models (BHMs) is given in the work of Samoli et al. (2005) which earlier estimated the exposure-response relationships between particulate matter (pollution) and mortality of 22 European cities participating in the APHEA (Air Pollution and Health – A European Approach project) and also performed a meta-analysis.

Specifically in the study of Michelozzi et al. (2009) hospital admissions were related to the daily counts for cardiovascular, cerebrovascular and respiratory causes by age (all ages, 65–74 years age group, and >75 years age group) in the resident population for the period 1990–2001. Maximum apparent temperature (Tappmax), (see Fig. 2 of Michelozzi et al. 2009) was used as the exposure variable of interest. This is an index of thermal discomfort (“exposure”) based on air temperature and dew point temperature according to the work of Kalkstein and Valimont (1986) and of O’Neill et al. (2003). The analysis was restricted to the warm period of the year (April–September), as in Baccini et al. (2008). Note that Baccini et al. (2008) also used maximum apparent temperature (Tappmax) as the exposure variable.

### **20.8.1.1 First Stage Analysis**

In the study of Baccini et al. (2008), the first stage of the analysis involved estimation of the city-specific effects, and in the second stage, the results were combined to obtain pooled across cities effect (of exposure) estimates. The city-specific analyses were based on generalized estimating equations (GEEs) (Liang and Zeger 1986). Certain distributed lag models (DLMs) (Shiller 1973) were specified in studying the delayed effect of the exposure of interest. Time-varying coefficient models were used to check the assumption of a constant exposure (heat effect) over the warm season. Indeed on the basis of an exploratory analysis (Chiogna and Gaetan 2003, 2005, Michelozzi et al. 2009), Baccini et al. (2008) specified an autoregressive structure, that has a lag of 0–3 days (Schwartz and Dockery 1992) – where observations close in time, tend to be more correlated than more distant observations, so as to take into account the intrasummer correlation. Michelozzi et al. (2009) also used the model based variance estimator for the standard errors (recommended for use in the presence of few large clusters by Diggle et al. 2002). A common city-specific model was used. A Poisson distribution of the outcome variable was assumed (i.e. a daily time series Poisson regression was used): including potential confounders (e.g. in Michelozzi et al. 2009) such as holidays, day of the week and calendar month, linear terms for barometric pressure (lag 0–3) and wind speed, and linear and quadratic terms for time and maximum 1-hour daily value of nitrogen dioxide (NO<sub>2</sub>) (lag 0–1).

### ***20.8.2 Threshold-Slope Model – Large Variability Amongst the Cities***

In Baccini et al. (2008) regression cubic splines (Durrleman and Simon 1989) were used to estimate the exposure–response relationship for each city. The exposure–response curves of the relationship between maximum apparent temperature

(Tappmax) (exposure) and admissions/death (response) were highly heterogeneous between cities. In Baccini et al. (2008) exposure effects were modelled by cubic regression splines (with 1 knot every 8°C) and a straight line above a city-specific threshold was utilised. Baccini et al. (2008) showed that the city-specific exposure-response functions had a non-linear, in fact a V shape, with a change-point that varied significantly amongst the cities. These were interpreted and modelled as threshold-slope models, with a separate city-specific threshold temperature, after which the outcome (deaths) increased significantly (with generally a positive slope). The meta-analytic estimate of the threshold (maximum apparent) temperature was 29.4°C for Mediterranean cities and 23.3°C for north-continental cities. The estimated overall change (slope) in all natural mortality associated with a 1°C increase in maximum apparent temperature above the city-specific threshold was 3.12% (95% credibility interval = 0.60–5.72%) in the Mediterranean region and 1.84% (0.06–3.64%) in the north-continental region. We note that in some sense Dose and Menzel's (2004) relationships between flowering and year (years from 1896 to 2002) were thresholds with a subsequent negative slope (see also Schleip et al. 2008a and Chapter 11).

By contrast in Michelozzi et al. (2009), however, two models were used to describe the Tappmax–hospitals admission relationship. In the first model, a semiparametric approach, that includes penalised cubic regression splines for temperature, was applied to describe the exposure–response relationship. This approach allowed modelling of the data in a flexible way without imposing a specific shape for the exposure–response curve (Wypij 1996). The relationship was modelled using piecewise polynomials between equally spaced breakpoints. Because no significant threshold of Tappmax was identified in the exposure–response curves (aimed to estimate the impact of Tappmax on admissions) Michelozzi et al. (2009) applied a second model, assuming a log-linear increase in risk above the 90th percentile of the distribution of Tappmax (lag 0–3) in each city. The effect was expressed as a percent variation in daily hospital admissions for 18°C increase in Tappmax above this value.

### ***20.8.3 Second Stage: Bayesian Random Effects Meta-Analysis***

In the second stage, as mentioned above, city-specific results were combined via a Bayesian random effects meta-analysis using the method described by DerSimonian and Laird (1986). This essentially entails regressing the city-specific exposure effect estimates (say thresholds, slopes and other regression coefficients) produced from the first stage of the analysis, on city-specific covariates, to obtain the overall exposure–response curve and to explore potential heterogeneity in the city-specific curves (see also Berkey et al. 1995). Separate meta-analyses were performed for two a priori defined geographical regions Mediterranean versus North-continental cities: thereby providing summary estimates and reducing heterogeneity. Cities were grouped into “Mediterranean” (Barcelona, Ljubljana, Milan, Rome, Turin, and

Valencia) and “North-Continental” (Budapest, Dublin, London, Paris, Stockholm, and Zurich) according to geographical and climatic criteria. City-specific effect estimates were combined using random effects meta-analysis using the method described by DerSimonian and Laird (1986) (see also Egger et al. 1997, 2001). For phenological applications city can be clearly interpreted as a location (whether local or global): exposure can be interpreted as time and/or temperature: and response can be interpreted as phenophase etc. (Baccini et al. 2008).

## 20.9 Bayesian Hierarchical Distributed Lag Models – an Epidemiological Application

Multi-site studies, which combine information from many locations by using national or regional databases, have of late, obtained precise and consistent results which demonstrate an adverse health effect associated with short-term exposure to particulate matter (PM) and ozone (Peng et al. 2009). The National Morbidity, Mortality, and Air Pollution Study in the USA and the “Air pollution and health: a European approach” study in Europe are important exemplars of such multi-site time series studies (Samoli et al. 2003, Bell et al. 2004, Peng et al. 2005). Also more recently the Medicare Air Pollution Study (MCAPS) showed a strong association between fine particulate matter ( $< 2.5 \mu\text{m}$  in aerodynamic diameter) and hospitalization for cardiovascular and respiratory diseases in 204 US counties (Dominici et al. 2006, 2007). Most recently is the study of Peng et al. (2009) which develops Bayesian hierarchical distributed lag models (BHDLMs) to relate particulate matter air pollution exposure to hospitalisations for cardiovascular and respiratory diseases (using a national US database on 3 million enrollees of the US Medicare system living in 94 countries covering the period 1999–2002).

We believe that such newly developed BHDLMs, which Peng et al. (2009) proves can be reformulated as penalized spline models (see also Roberts 2008) have particular value for phenological multi-site (and multi-species) studies, where a meta-analytic approach is needed to obtain a so-called fingerprint (across locales, species) of change.

We briefly overview Peng et al.’s (2009) approach: showing how the Bayesian distributed lag models (DLMs), invoked by Baccini et al. (2008) and Michelozzi et al. (2009), extend to BHDLMs. In general DLMs are applicable where the association between an input (or exposure) and a response (health or phenological outcome) is anticipated to exist over multiple time points into the future. DLMs have been used for decades in economics (Almon 1965) and have been applied more recently in the area of environmental epidemiology. Schwartz (2000) for example used both unconstrained and constrained (polynomial) distributed lag functions to estimate the effects of PM on daily mortality. Zanobetti et al. (2000) extended this work and developed the generalized additive modelling (GAM) methodology (see Chapter 10). DLMs in air pollution and health studies have primarily been applied to time series data at an individual location such as a county or a city. Typically, a

DLM is fitted to the data and the estimated distributed lag function is then smoothed across lags by using a polynomial or a non-parametric smoother (e.g. Almon 1965).

In contrast Peng et al.'s (2009) BHDLM uses a prior distribution that constrains the time course of the short-term health effects of air pollution (exposure) and combines information from multiple locations (and then performs a meta-analysis). The model builds on the study of Welty et al. (2009), who proposed a Bayesian model for estimating the distributed lag function in a time series study using a single location. Welty et al. (2009) introduced a prior distribution that constrains the shape of the distributed lag function, by allowing effects corresponding to early lags to take a wide range of values, whilst effects at more distant lags are constrained to be near zero and are correlated with each other. Peng et al. (2009) likewise constrains the distributed lag function because the effects of air pollution at early lags are not well understood – this because of the lack of knowledge about biological mechanisms and the time course of the disease process within the population.

Competing hypotheses exist about the shape of the distributed lag function, however, all suggest that fewer constraints should be placed at early lags (Schwartz 2000, Zanobetti et al. 2002, Dominici et al. 2002b). At longer lags there are justifications for assuming that the effects of air pollution on the outcome should approach zero smoothly. Peng et al.'s (2009) BHDLMs also further the approach of Zanobetti et al. (2000) by smoothing distributed lag function estimates across lags and by providing a technique by which to combine these functions across locations. Importantly Peng et al.'s (2009) hierarchical model allows for the examination of a range of shapes in the location (county) – specific distributed lag functions. In summary Peng et al.'s (2009) BHDLM involves the description of a specific prior distribution for constraining the distributed lag function and proposes a hierarchical structure for combining information about the shape of the distributed lag function across multiple locations. A few details follow.

### ***20.9.1 Single-Location to Across Locations: a National Across County Averaged Distributed Lag Function $\mu$***

Peng et al.'s (2006) approach begins with a model for air pollution and hospitalization data in a single location such as a county. This model relates day-to-day changes in air pollution levels to day-to-day changes in rates of hospitalization for a given county; controlling for other time varying factors that might confound the relationship of interest. At the county level, Peng et al. (2009) used the log-linear Poisson model for the county-specific hospital admissions rates and air pollution data: where the length  $L$  vector of parameters  $\mu$  is the distributed lag function and parameters in  $\beta$  are nuisance parameters (see Eq. (2) Peng et al. 2009). In the county-specific model, the random effect part  $Z$  of the model (see Eq. (2) Peng et al. 2009), incorporates certain time varying factors that might confound the relationship between air pollution and hospitalization (Kelsall et al. 1997, Dominici et al. 2002a). In particular, Peng et al. (2009) include smooth functions of average daily temperature,

dewpoint temperature and indicators for the day of the week. They also include a smooth function of time to adjust for seasonal variation that is common to both the air pollution and the hospitalization time series. This smooth function of time is modelled by using natural splines and the natural spline basis is included in  $Z$  (see also Welty and Zeger 2005 and Peng et al. 2006).

A direct extension of the single-county model would assume a common association between air pollution and hospital admissions across counties. Rather than assume a common association, Peng et al. (2009) let each county have its own parameter  $\theta_c$ , so as to allow for heterogeneity between counties. Peng et al. (2009) assumed that each of the county-specific distributed lag functions  $\theta_c$  is normally distributed around a “national average” distributed lag function  $\mu$ , with variance covariance matrix constrained as described in Peng et al. (2009). The variance covariance matrix describes the unexplained variation or heterogeneity across counties of the county-specific distributed lag functions  $\theta_c$ . A priori it is assumed that there will be more variation across counties in the coefficients corresponding to early lags and less variation in the coefficients corresponding to longer lags.

Peng et al. (2006) assume that the prior distribution for the national-average-distributed lag function  $\mu$ : and importantly proved that the BHDLM can be reformulated as a penalized spline model, where the prior distributions (in expressions (5) and (6) of Peng et al. 2009) induce a special type of penalty for constraining the county-specific distributed lag functions and combining information across counties. This connection creates a basis for understanding the statistical properties of Peng et al.’s (2006) approach: but also adds credibility to a unified approach to meta-analysis for phenological studies (see the penalized spline regression approach of Roberts (2008) and Bagnardi et al. (2004) who described fractional polynomials and spline regression (Royston 2000), in particular random effects cubic splines, to model non-linear exposure-response curves). The principal benefit of the DLM is its ability to estimate the shape of the distributed lag function relating increases in exposure to outcomes in short periods of time after an extreme episode. The BHDLM provides a useful parameterization that can easily incorporate prior knowledge and be applied to large multi-site databases. The BHDLM has clear applicability to phenological climate change research and generally to environmental statistics. In general, with the increasing sophistication of data (networks) and collection systems, in health and now in phenology, which provide data from multiple locations, the applicability and relevance of the BHDLM model in phenology and climate change research is clear

## 20.10 Towards a Unified Approach: Semiparametric Regression

As noted earlier the three approaches and applications to the modelling of non-linear phenological response over time delineated above (GAMLSS, penalised spline regression (PSR) and Bayesian nonparametric function estimation) will be linked

to these recent epidemiological approaches (dose-response functionals, Bayesian hierarchical meta-analysis and BHDLMs).

The meta-analytic methods proposed here for phenological synthetic studies are all essentially based on nonparametric (Green and Silverman 1994, Eubank 1999) or semiparametric regression (Chen and Ibrahim 2006, Ruppert et al. 2009) methods, including the Bayesian hierarchical models (Gelman et al. 2004), the latter of which was recently reformulated in terms of a penalised spline model by Peng et al. (2009) (for Bayesian hierarchical distributed lag models (BHDLMs)).

Semiparametric regression (Ruppert et al. 2003, 2009) is an embellishment of parametric regression that uses penalised spline basis functions (Harezlak et al. 2005, Pearce and Wand 2006) to achieve greater flexibility, than can be achieved when linearity is assumed. The mixed model variants of semiparametric regression, and antecedents such as smoothing splines, have been firmly established and have a long history (Wahba 1978, Eubank 1999). All the approaches discussed here (spline penalized regression, fractional polynomials, spline regression. GAMLSS, BHM and BHDLMs), apart from the nonparametric function estimation of Dose and Menzel (2004), are so-called semiparametric regression techniques.

**20.10.1 Mixed Model Approach to Semiparametric Regression: Handling Nonparametric Functionals**

Semiparametric regression techniques allow for nonlinear nonparametric functionals, generalized scalar link functions, fixed ( $X\beta$ ) and random effects ( $Zu$ ) in that most semiparametric regression models are expressible as

$$E(y|u) = g(X\beta + Zu), u \sim (0, G) \tag{20.1}$$

In Eq. (20.1)  $g$  is a scalar “link” function. The fixed effects term,  $X\beta$ , handles covariates that enter the model linearly, whereas the random effects component  $Zu$ , with corresponding covariance matrix  $G$ , handles non-linear effects, random subject effects and other spatial correlation structure. There will often also be other parameters, for example, in the variance structure ( $R = cov(y|u)$ ), but we will ignore this in the current discussion.

The hierarchical Bayesian version of (20.1), which allows for meta-analytic approaches, takes the form

$$\begin{aligned} [y|\beta] &= f_1(y; X\beta + Zu), [u|G] = f_2(u; G) \\ [\beta] &= f_3(\beta; A_\beta), [G] = f_4(G; A_G) \end{aligned} \tag{20.2}$$

where  $A_\beta$  and  $A_G$  are hyper parameters  $f_1, \dots, f_4$  are fixed conditional density functions and  $f(v|w)$  denotes the conditional density of  $v$  given  $w$ . Inference is based on posterior densities for parameters of interest, in particular  $f(\beta|y)$ ,  $f(u|y)$  and  $f(G|y)$ .

Noteworthy is that in the mixed model approach to semiparametric regression, nonparametric functional relationships are handled through modelling mechanisms

such as delineated by Eq. (1) of Samoli et al. (2005). These involve functionals of the exposure-response relationship, so-called spline basis functions, the simplest being so-called knots. More sophisticated spline basis functions are given in Wood (2003), Welham et al. (2007) and Wand and Ormerod (2008). All the spline basis functions fall under what is generally known as smoothing splines (Wahba 1990).

Recall also the *P*-spline signal regression (PSR) approach of Roberts (2008) (see also Chapter 12). As noted by Roberts (2008) this approach is extendable to multivariate functions (time series or multiple regressors, say temperature and rainfall as predictors of phenological response, say DOFF) by using either radial basis functions (e.g. Ruppert et al. 2003, Wood 2003) or tensor products (e.g. Wood 2006). It is noteworthy that Dose and Menzel (2004) also modelled nonparametric functions using Bayesian theory. We believe that the *B*-splines approach as described in Roberts (2008) could well be adapted to meta-analytic scenarios where different vectors of climatic regressors of the preceding and current year are modelled in relation to phenological response, say across locations. This is the topic of future research. Multivariate adaptations of PSR are as mentioned above also plausible. This is the topic of future research.

BHMs and BHDLMs also have clear application to phenological time series (under the semiparametric regression paradigm) where one is interested in estimating non-linear functionals, say of a phenological response with climatic exposure variables. This, as yet, needs to be tested and developed rigorously, and would possibly require thresholds and functionals between phenological response and exposure (heat, rain) to be derived and modelled, such that time (year) can be accommodated, and such that random effects can be involved in the parameters delineating the so-called “exposure” effects across locations. Essentially here we are talking about the derivation of the pooled (across location estimates) (i.e. pooled trend, pooled thresholds, pooled slope, pooled lag dependency across locales/sites). This is the topic of future work.

## 20.11 Discussion on Increased Statistical Sophistication

It is advocated that meta-analytic methods used only recently to account for non-linear “dose/exposure to response” functionals in epidemiology (Bagnardi et al. 2004, Gamborg et al. 2007, Baccini et al. 2008, Peng et al. 2009) may be possibly adapted and apply well to phenological synthetic studies. The overarching paradigm for all the methods suggested here for modification and /or direct application to phenological meta-analytic studies (except for the Bayesian approach to modelling the nonlinear functional relationship between flowering and time of Dose and Menzel 2004) is the area of semiparametric regression. Three significant and recent meta-analytic approaches in epidemiological research, namely dose-response functionals, Bayesian hierarchical meta-analysis and BHDLMs, have been reviewed, which hold much promise to further meta-analytic studies in phenology. Proof of concept is

an important area of future research. We have also shown, via mathematical interpretation and example, their inter-connectedness to the three modelling approaches discussed earlier – GAMLSS, penalised spline regression (PSR) and Bayesian non-parametric function estimation, all of which have been recently applied to non meta-analytic phenological studies (Dose and Menzel 2004, Roberts 2004, Roberts et al. 2008, Menzel 2008, Schleip et al. 2008a). Fractional polynomial or spline regression methods could also well apply to meta-analytic studies where one modelled, say, flowering versus accumulated heat (temperature exposure) over time, where a particular temperature threshold was found or assumed. These ideas need, however, to be rigorously tested and are the topic of new research.

In terms of meta-analytic studies, the smoothing cubic spline estimates of trend that GAMLSS provide per time series, and of those of past regressors from PSR could be combined to obtain an overall effect measure, traditionally used in the meta-analytic approach. Alternatively these spline estimates could be analysed using linear or non-linear Bayesian mixed models (meta regression). It is also potentially possible to compare the temperatures at which the tapering off (say of flowering) occurs across species and sites and obtain an overall estimate. These ideas also need to be rigorously tested and demonstrated, and are the topic of future work.

All the methods, particularly the most recent and newly developed BHDLMs have particular value for phenological multi-site (and multi-species) studies, where a meta-analytic approach is needed to obtain a so-called fingerprint (across locales, species) of change. The principal benefit of the DLM is its ability to estimate the shape of the distributed lag function relating increases in exposure to outcomes in short periods of time after an extreme episode. The BHDLM provides a useful parameterization that can easily incorporate prior knowledge and be applied to large multi-site databases. The BHDLM has clear applicability to phenological climate change research and generally to environmental statistics per se. In general, the increasing sophistication of data (networks) collection systems in phenology, which provide multiple time series data from multiple locations, make the applicability and relevance of the both the BHM and the BHDLMs in phenology and climate change research clear.

## 20.12 Conclusions

We have reviewed the general methodology of meta-analysis, assessed its advantages and disadvantages, synthesized its use in global climate change phenology and discussed future directions and importantly proposed new statistical approaches, as yet not applied to phenological research, and only recently applied, only in part, in the epidemiological literature. These we believe offer much promise to phenology and climate change research. Documentation of observed changes in physical and biological systems in tropical and subtropical regions is still, however, sparse (Africa, South America, Australia, Southeast Asia, the Indian Ocean and some



regions of the Pacific). Data mining of historical documents and improved observation networks are urgently needed to develop data sets and to document sensitivity of physical and biological systems to warming in tropical and subtropical regions, where many developing countries are located. Thereby in 20 years (but hopefully less) we can perform meta-analytic studies to demonstrate as Rosenzweig et al. (2008) have found, a “statistical consistency of observed changes (which are very unlikely to be caused by natural internal variability of the systems themselves or other driving forces) in natural systems with warming and conduct spatial analyses that show that the agreement between the patterns of observed significant changes in natural systems and temperature changes is very unlikely to be caused by the natural variability of the climate.”

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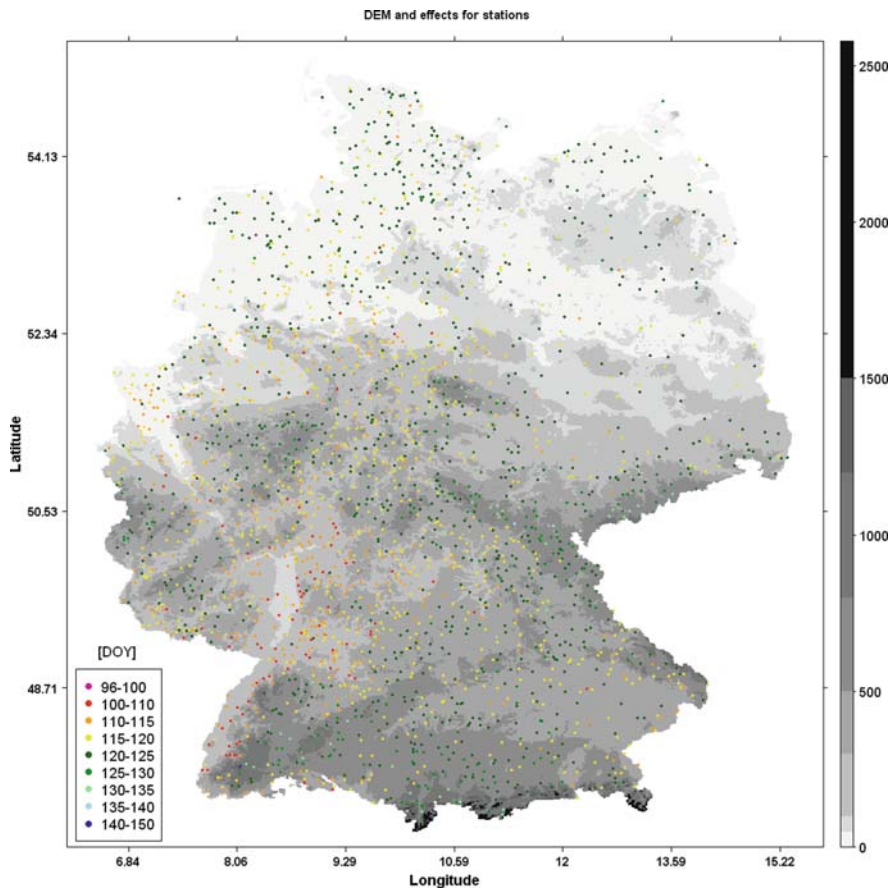
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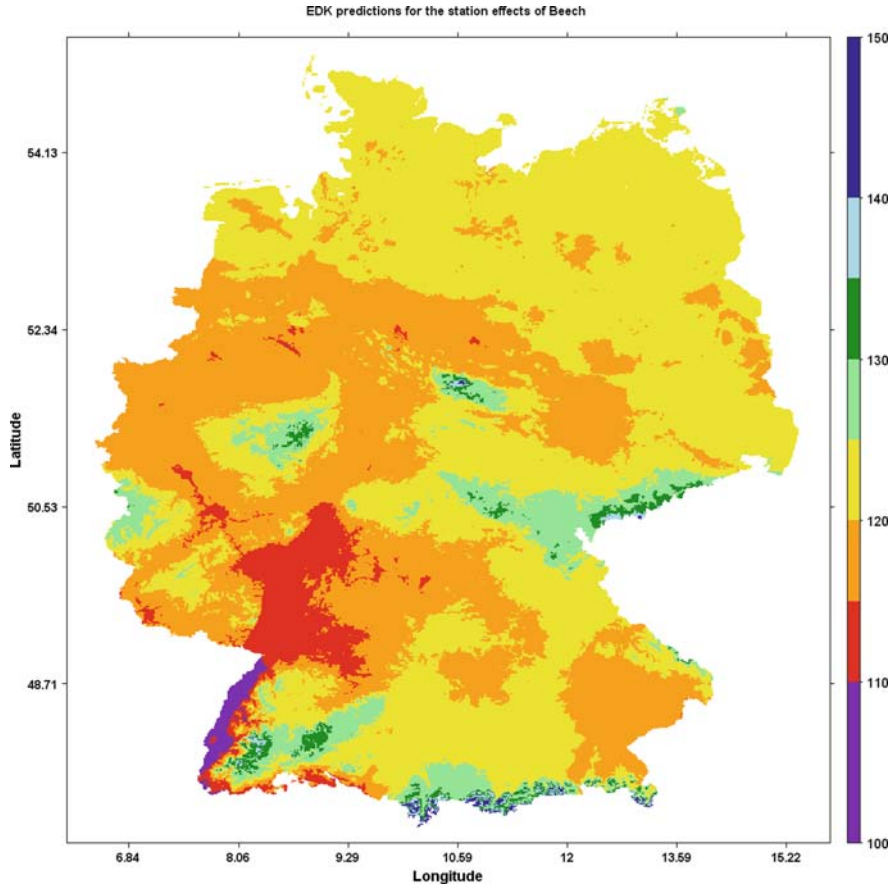
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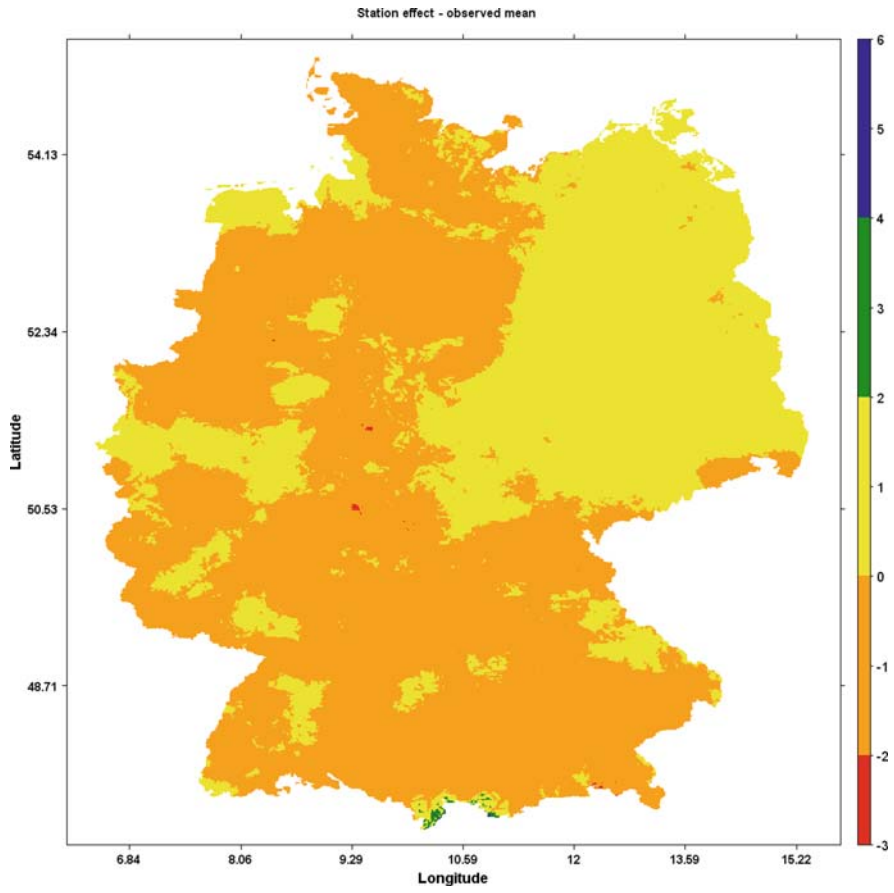
# Color Plates



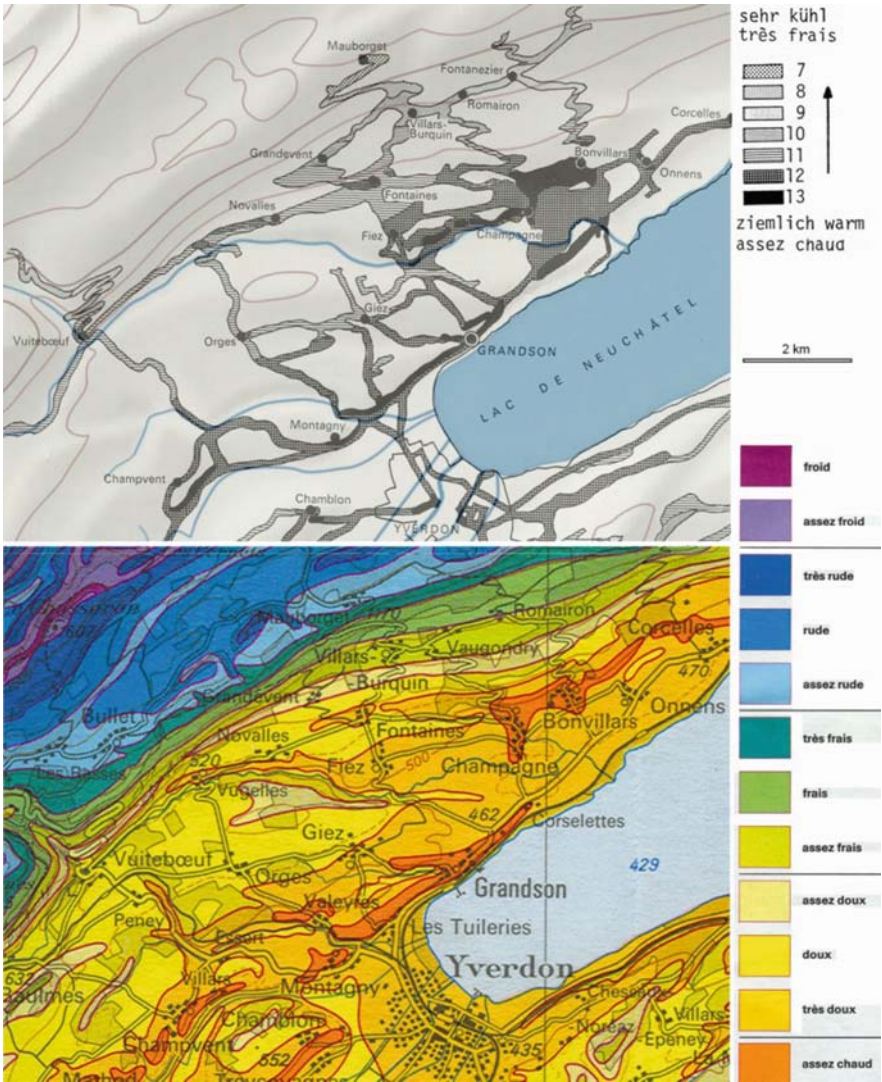
**Plate 1** Computed station effects + the general mean (day of year) based on observed budburst dates of Beech from 1951–2004 over Germany. A Digital Elevation Model (1\*1 km in meters) represents the topography, which considerably influences the timing of phenological phases in spring time. Observation stations are indicated as coloured points



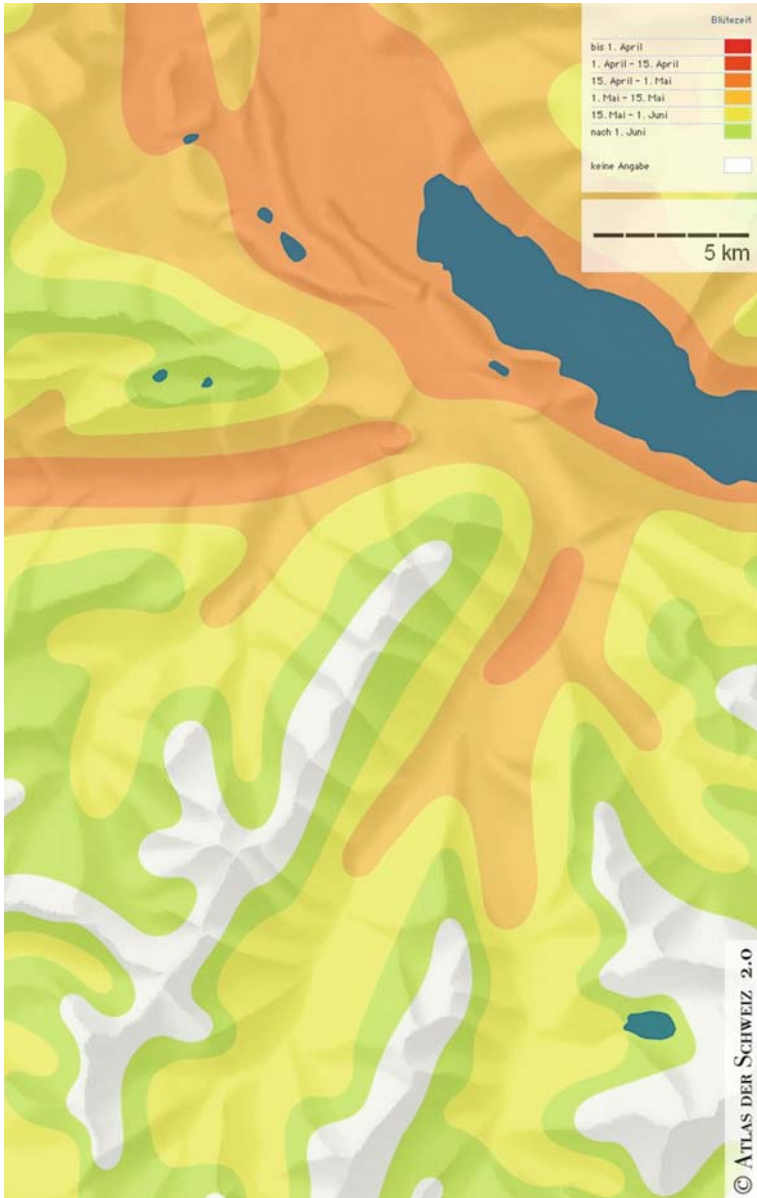
**Plate 2** Computed station effects + general mean (day of year) based on observed budburst dates of Beech interpolated using External Drift Kriging (EDK). The DEM of Germany (1\*1 km) provides the external variable.



**Plate 3** Difference of the interpolated maps: the computed station effects – observed mean budburst dates of the respective stations



**Plate 4** (a) Phenological map or thermal conditions at the Western end of Lake Neuchâtel and the Southern slopes of the Jura Mountains (Switzerland, from Schreiber et al. 1976). Examples of itineraries of the phenological campaign between 28th and 30th April 1962. From “7 froid” = cold to “13 assez chaud” = rather warm. The estimated observation density for this area is about 300 m per km<sup>2</sup>. (b) Resulting thermal map after 4 seasons (1969–1973). Base map by swisstopo. From Schreiber et al (1977), original scale 1:200,000. Reproduced by permission of swisstopo (BA081114)

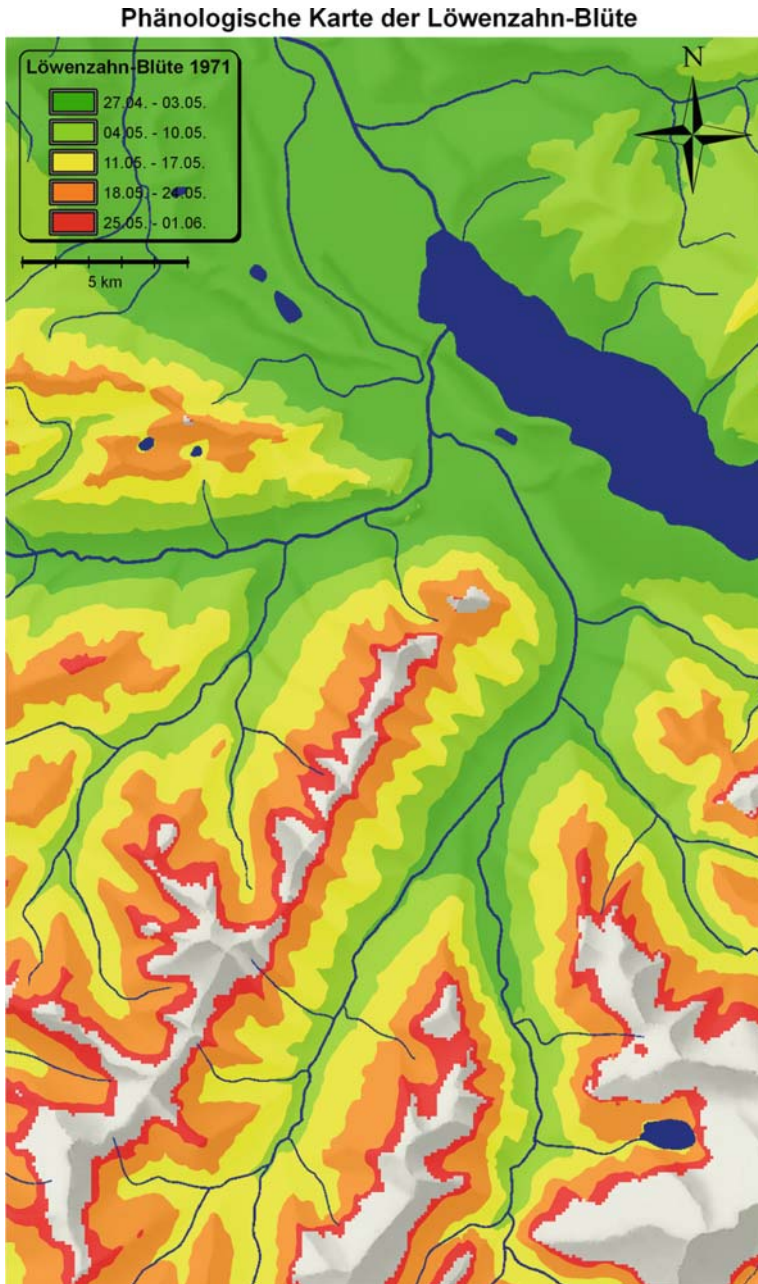


**Plate 5** Phenological map of the dandelion general bloom 1951–1990 of the same area as Plate 7 from the digital Atlas of Switzerland 2.0, Swisstopo (2003) based on conventional mapping of the isophanes (Primault 1984), two observation stations lie within and four in the vicinity of the map fragment. Reproduced by permission of swisstopo (BA081114)



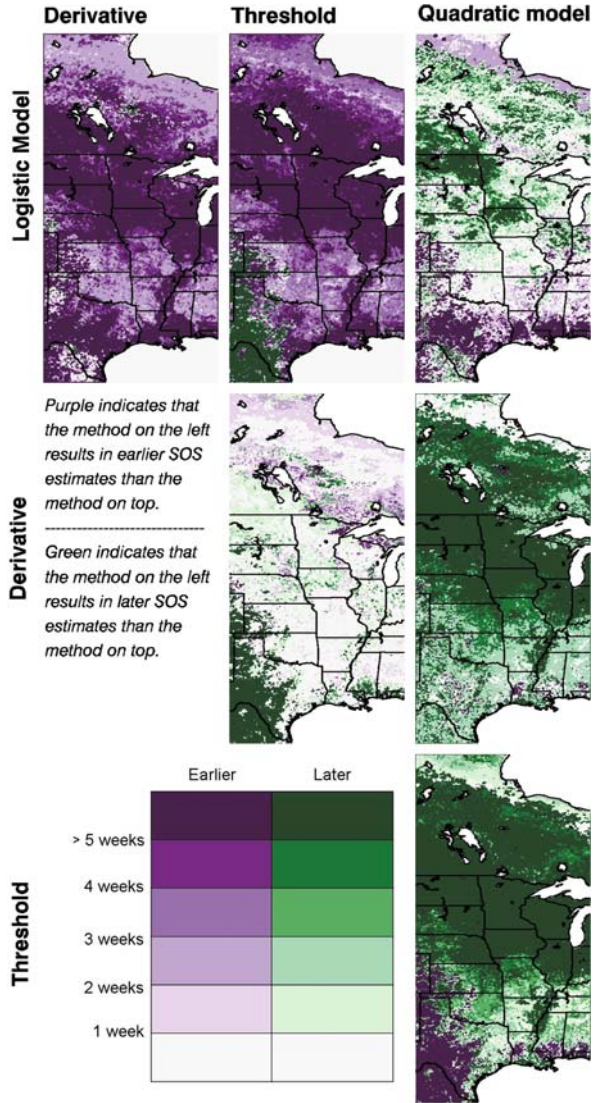
**Plate 6** Manually drawn map of the wheat harvest 1970 in the area of the Lake of Bière. (a) Details of map drawing of a South-Western part of the area. Full red dots mean wheat variety Probus, the empty ones other varieties. Isophanes indicate the date (DDMM) at 10 days interval, dashed lines indicated uncertainties. Original scale 1:25,000, vertical interval between contours 20 m, base map by swisstopo. (b) Generalized survey, published at the scale 1:300,000, green frame shows the area of map A. From Jeanneret 1971. Reproduced by permission of swisstopo (BA081114)





**Plate 7** Map of the general bloom of the dandelion 1971, in an area of the western Bernese Oberland, Switzerland (Lake of Thun and Kander valley, same area as Plate 5, top limit of the phenology mapping at 2100 m). The map was produced with a digital terrain model with 100 m raster distance and is based on 50 observations, mostly in valleys close to cities and villages. From Kottmann 2008, base map: Atlas of Switzerland 2.0. Reproduced by permission of swisstopo (BA081114)

**Plate 8** Difference matrix for the derivative method, the threshold 50% method, the logistic model and the quadratic model based on AGDD. The results fall in two groups with the logistic model and the quadratic model generally finding earlier SOS than the 50% threshold and derivative methods



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