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Indexing butterfly abundance whilst accounting for missing counts and variability in seasonal pattern

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Summary

1. Volunteer-based 'citizen science' schemes now play a valuable role in deriving biodiversity indicators, both aiding the development of conservation policies and measuring the success of management. We provide a new method for analysing such data based on counts of invertebrate species characterised by highly variable numbers within a season combined with a substantial proportion of proposed survey visits not made.
2. Using the UK Butterfly Monitoring Scheme (UKBMS) for illustration, we propose a two-stage model that makes more efficient use of the data than previous analyses, while accounting for missing values. Firstly, generalized additive models were applied separately to data from each year to estimate the annual seasonal flight patterns. The estimated daily values were then normalized to estimate a seasonal pattern that is the same across sites but differs between years. A model was then fitted to the full set of annual counts, with seasonal values as an offset, in order to estimate annual changes in abundance accounting for the varying seasonality.
3. The method was tested and compared against the current approach and a simple linear interpolation using simulated data, parameterised with values estimated from UKBMS data for three example species. The simulation study demonstrated accurate estimation of linear time trends, and improved power for detecting trends compared to the current model.
4. Comparison of indices for species covered by the UKBMS under the various model approaches showed similar predicted trends over time, but confidence intervals were generally narrower for the two-stage model.

5. In addition to creating more robust trend estimates, the new method allows all volunteer records to contribute to the indices and thus incorporates data from more populations within the geographic range of a species. On average, the current model only enables data from 60% of $10km^2$ grid squares with monitored sites to be included, whereas the two-stage model uses all available data and hence provides full coverage at least of the monitored area. As many invertebrate species exhibit similar patterns of emergence or voltinism, our two-stage method could be applied to other taxa.

Keywords: butterfly monitoring, citizen science; count data; generalized additive models; missing data

1. Introduction

The importance of biodiversity is widely recognised for its multifaceted role in controlling our ecosystems (Chapin *et al.* 2000; Díaz *et al.* 2006). Land-use change, climate change and other human-induced factors have been recognised as important causes of declines in biodiversity (Chapin *et al.* 2000; Rands *et al.* 2010). In 1993 the Convention on Biological Diversity (CBD; Glowka, Burhenne-Guilmin & Synge 1994) came into force as an international treaty which aimed for the conservation and sustainable use of biological resources. In response to the Convention the UK set up the UK Biodiversity Action Plan (UKBAP; Ruddock *et al.* 2007). At a UK and country level, biodiversity conservation efforts include maintaining protected areas, consideration in relevant policy and decision-making, action for declining species and habitats and conformity to international agreements. The use of biodiversity indicators was also recommended to measure and communicate progress in reaching biodiversity targets (CBD 2004). Species population data are required as a source for robust biodiversity indices and to answer both ecological and environmental questions.

Monitoring invertebrates presents a number of technical challenges, such as sampling frequency to cover seasonal patterns and the specialised expertise required for identification (Thomas, 2005). However, a growing number of participatory schemes for monitoring insects, predominantly butterflies, have been developed (Table 1). Improved statistical techniques are required to make the most efficient use of data collected by volunteer contributors to such schemes. Butterflies, as the most comprehensively monitored insect taxa, will be used to illustrate the methods of this paper. Butterflies are increasingly recognised as an environmental indicator for changes in biodiversity because they respond rapidly and sensitively to climatic and habitat changes and act as a representative for other species, particularly other insects (Roy & Sparks 2000; Maes & Van Dyck 2001; Roy *et al.* 2001; Thomas 2005; Pearman & Weber 2007). Abundance indices for butterflies form one of 18 indicators used to assess general trends in UK biodiversity (Defra 2011). Butterfly indicators for the UK and Europe are discussed further in van Swaay *et al.* (2008) and Brereton *et al.* (2011b).

Butterfly population data in the UK are principally gathered through an intensive, wide-scale monitoring system of weekly transect walks which form the UK Butterfly Monitoring Scheme (UKBMS). The main objective of the scheme is to provide data for assessment of the status and trends in the abundance of UK butterfly species for both conservation and research purposes. Abundance estimates derived from the UKBMS data play an important role in acting as indicators for trends in biodiversity, habitat change and climate change (Brereton *et al.* 2011b). In 2010, population trends could be calculated for 54 of the 59 butterfly species regularly found in the UK to demonstrate whether the overall population abundance of each species has changed over time (Botham *et al.* 2011).

A key element of such schemes is the high level of volunteer participation required to gather such a large dataset, who are often referred to as citizen scientists (Cooper *et al.* 2007; Greenwood 2007; Devictor, Whittaker & Beltrame 2010). Since its inception in 1976, a large network of recorders has contributed to the UKBMS, making around a quarter of a million weekly visits to almost 2000 different sites and counting over 16 million butterflies (Botham *et al.* 2011). Ideally, an annual index of abundance for each site can be calculated as the sum of the weekly counts; the scheme design is for a count to be made in each of 26 weeks of the year between April and October. Inevitably, some weeks of the transect season are missed due to unsuitable weather conditions or recorder unavailability, for example due to illness or holidays, and hence fewer than 26 counts per year are typically made at each site. In common with many invertebrates, UKBMS counts show pronounced patterns over the summer and each count taken certainly cannot be considered as a random variable with the same expectation. Appropriate modelling techniques are therefore required to enable the use of UKBMS data for monitoring changes in populations.

Initially, estimates of missing counts for butterfly monitoring schemes were obtained using linear interpolation of the counts either side of the missing value. The use of generalized additive models (GAM, Hastie & Tibshirani 1990; Wood 2006) as an alternative method was introduced by Rothery & Roy (2001), who applied models to both UKBMS and simulated data with varying flight periods, and this procedure is currently adopted by the UKBMS. A GAM is a generalized linear model (GLM) where part of the linear predictor contains one or more smooth functions of predictor variables (Wood 2006). It is therefore more flexible than the linear approach, but requires more data to avoid the potential for erratic behaviour. Under the current method, which fits a GAM to data on an individual site/year basis, where a high proportion of weeks or the peak of the flight period (defined where the maximum prediction of a missed count exceeds the maximum of the observed counts) is missed, data for that particular site and year are currently excluded from analysis.

Under these criteria, on average across the species monitored by the UKBMS 38% of transect visits made do not contribute to population indices. This represents a substantial quantity of data not utilised, and in the interest of the optimal use of the volunteer-collected records, the aim of this paper is to develop a more efficient method for analysing the UKBMS data and hence more robust estimates of changes in butterfly abundance. Current models for the estimation of missing counts are extended to allow for all incomplete series of recordings and annual variation in seasonal pattern, in order to make more efficient use of the data collected.

2. Materials and methods

We begin this section with an account of the UKBMS protocol. We then revisit the model currently employed, and introduce the novel method proposed in this paper. The procedure behind an extensive, simulation-based comparison of a linear interpolation approach and two GAM-based models, and an application of both GAM-based models to real data gathered for multiple species by the UKBMS, are then outlined.

2.1 Data - The UK Butterfly Monitoring Scheme

The UKBMS scheme began in 1976 with 34 sites but by 2010 the network had grown to over 1000 sites recorded each year (910 line transects as well as 117 sites applying other sampling methods not considered in this paper, such as larval web/timed counts (Botham *et al.* 2011)). The transect method employed is described in depth by Pollard & Yates (1993) and briefly here. So-called Pollard Walks have been shown to provide a good representation of large-scale trends in abundance for most species (Isaac *et al.* 2011). An observer records all butterflies observed within a set limit (an estimated distance of 5 metres ahead and to the sides of the recorder) along a fixed line transect route. Counts are taken weekly from the beginning of April until the end of September, within specified periods of the day and when weather conditions are suitable for butterfly activity. Transects are typically 2-4 km long and divided into a maximum of 15 sections which correspond to different habitat or management units, though in this paper we aggregate counts for all sections within a transect. The scheme design allows for counts to be made throughout the season for butterfly activity, during which abundance will vary according to different seasonal patterns of emergence.

2.2 Current method for calculating population indices

Currently, values for weeks with missing counts are imputed by fitting a GAM with Poisson distribution and a log link function to the observed counts at individual sites and years (Rothery & Roy 2001). If represents the count at a site on day in an example year then

$$E[y_t] = \mu_t = \exp[s(t; f)], \quad (1)$$

where the function $s(t; f)$ denotes a cubic regression spline with f degrees of freedom. Here, each represents a day in the monitoring season from April to

September. Thereafter, real counts are used where taken and the weeks with missing counts are allocated predicted values, , from the GAM for the middle day of that week. Annual site indices of abundance (an index value for each site and year recorded) are then calculated by an estimate of the area under the flight period curve. For a series of T counts $y_1, y_2, \ldots, y_T$ (real or imputed) at times $t_1, t_2, \ldots, t_T$, as in Rothery & Roy (2001), the trapezoidal rule is used to approximate the integral of the curve to give the index

$$\text{Index} = \frac{\qquad}{\qquad} \qquad (2)$$

Across-site, 'collated' indices are then derived by fitting a single log-linear regression model to the annual indices at all sites, with site and year as additive predictors (Roy, Rothery & Brereton 2007). This can be fitted using any of the widely-available software packages for GLM (van Strien, Pannekoek & Gibbons 2001). The model accounts for the fact that some years yield higher counts than others, and also that the population varies geographically, across sites.

2.3 <u>Proposed new method – a two-stage modelling approach</u>

A new method is proposed for interpolating the missing data. Whilst the current strategy involves fitting a GAM to counts on an individual site/year basis, here a GAM is applied across all sites within a year, to estimate the average annual seasonal flight curve.

A GAM with Poisson distribution and a log link function is used to estimate the annual seasonal pattern (constant across S sites). If represents the count at site $i = 1,\ldots,S$ on day , then

$$E[y_{it}] = \mu_{it} = \exp[\eta_i + s\,(t\,;f)], \qquad (3)$$

where η_i represents a site effect and $s\ (t; f)$ denotes a smoothing function with f degrees of freedom. This creates a curve representing the flight period which is common for all sites for that year, but varies (via η_i) in magnitude between sites with respect to varying abundance between sites. Estimation of an average seasonal pattern across sites for each year allows for even those with a high proportion of missing counts to be included in abundance estimation.

Studies of butterfly phenology confirm that butterfly flight periods vary from year-to-year (Roy & Sparks 2000). Therefore, due to an interaction between the day and the year, a single-stage extension of equation (3) for the full dataset with an additional simple year effect would be too restrictive, since this would only estimate a single flight period across all years. A direct comparison of total annual abundances, obtained by summing the expected values at all sites, which can each be estimated via equation 3, cannot be made due to the variation in the set of sites covered each year. Therefore an additional stage to the model is introduced.

If represents the count of a species at site =1,…,S in year =1,…,J on day ,
then the mean count is given by

$$E[y_{ijt}] = \mu_{ij}(t) = \exp[\alpha_i + \beta_j + \gamma_j(t)] \qquad (4)$$

where α_i and β_j represent effects for the i th site and the j th year respectively and $\gamma_j(t)$ allows for the seasonal pattern, which can vary between years, but not over sites. A site index, for year j, can be calculated as the sum of the expected counts for that season, which is given by summing equation 4 over t as follows

(5)

The annual effects, , provide an index proportional to total abundance provided that the sum to one. Since both the annual effects and seasonal effects in the model vary with respect to year, we constrain so that = 1. Hence equation (4) is fitted to the counts for all years as a Poisson GLM with the values of as an offset, where were obtained by scaling the output from the first stage (equation (3)) and represent the annual seasonal pattern. Missing values can also be estimated from equation 4 and thereafter the approach is the same as for the current model, as site indices are derived from formula (2). Collated indices can then be estimated, and β_j taken as an index of abundance, as before, via a further GLM with site and year as multi-level factors. GAMs were fitted throughout using the mgcv package in R (Wood 2000; Wood 2006; R Development Core Team 2012), which selects the level of smoothing internally using generalized cross-validation (GCV).

2.4 Simulation study

The two GAM-based models described above (current and two-stage) were applied to simulated count data to assess model performance. Estimation of missing values via simple interpolation was also tested. In order to create realistic simulation data, the expected counts were based on observed UKBMS data for three target species, which were chosen for their differences in voltinism (the number of generations per year). The Chalkhill Blue *Polyommatus coridon* is a univoltine species with a single brood per year. The Adonis Blue *Polyommatus bellargus* has a bimodal flight period in the UK, with two quite distinct generations per annum. The Speckled Wood *Pararge aegeria* has a more complex annual flight period, with up to three overlapping broods per year. Fig. 1 demonstrates example flight periods these three species.

Initially, to fill in the missing counts in these series prior to simulation, GAMs were fitted to each species' UKBMS data for individual years as in equation 3 (using data between 1990 and 2000) and the missing counts replaced by their predicted values. A GLM was then fitted to the complete dataset with day and site effects considered as factors and annual change modelled as a constant slope parameter. Normal random variables with mean and standard deviation equal to those of the estimated site effects from the GLM were used to generate 100 random site effects. Expected count values for the simulations were then produced for year 1 based on these random site effects and the estimated daily effects. In order to account for annual variability that exists in the seasonal pattern, we assume that the overall shape of the flight period is the same between years, but we shifted the values gradually backwards by 7 days over 10 years to reflect observed phenological changes (Roy & Sparks 2000). An annual trend was then imposed to simulate data exhibiting a constant rate of change in the expected annual total counts over 10 years, with declines of (i) 0%, (ii) 5%, (iii) 10% and (iv) 20%, thus generating a site × day × year matrix of expected values (100 sites × 182 days × 10 years) for scenarios (i)-(iv).

For each of 1000 simulations under (i)-(iv) in turn, random variables were taken from the Poisson distribution with expectation given by these values, as in Rothery & Roy (2001). In order to have a matrix of weekly values that portrays the UKBMS data, one of seven daily values for each week was randomly selected from the expected values. The day was selected at random since the UKBMS data did not show a particular tendency for counts to be made on certain days of the week. Thus 26 counts were retained for each site and year, i.e. a reduced site × day × year matrix (100 sites × 26 days × 10 years) consisting of only one day per week to reflect the scheme design.

To mimic the missing counts in the real data, a proportion of the simulated counts were removed. Analyses of cases where data are complete (26 counts made in the season) and where 30% of data are missing are both given, the latter in order to represent the observed pattern in the UKBMS data. On average, approximately 29% of counts across the UKBMS dataset are missed, equivalent to roughly 8 out of 26 weeks of the transect season.

In practice, a higher proportion of counts are missed at the beginning and end of the transect season. Therefore removal of counts for simulations was based on the average observed pattern of missing data in the UKBMS dataset. Although the percentage of counts missing will not be the same across sites and years, this approach should be sufficient to assess the model. The current and two-stage GAM-based models, as well as a linear interpolation approach, were applied to these sets of simulated data to determine the statistical power (percentage of simulations that detected a significant trend) and assess the statistical performance of the models (Elston *et al.* 2011). Model accuracy was also evaluated by comparing the mean estimated annual trend over ten years from all simulations against the 'true' value of change (the pre-specified declines of 0%, 5%, 10% or 20% over ten years). The standard error of the mean estimated trend from all 1000 simulations also provided information on the confidence of the precision of the trend estimates.

2.5 Application of the current and two-stage model to an example set of species

For comparison, collated indices were calculated from real data for a selection of butterfly species currently reported by the UKBMS, using both the current and two-stage models. To ascertain the precision of the derived indices, confidence intervals were generated via bootstrapping in order to account for all sources of uncertainty. This approach involves drawing a random sample, with replacement, from the set of sites, for a given number of replicates (for this study 100 replicates were obtained for each species, for each model). Collated indices were estimated for the sites in each bootstrap sample and then ordered to derive approximate 95% confidence intervals for each species (Fewster *et al.* 2000). This procedure naturally incorporates the uncertainty inherent in the imputing process as well as general overdispersion relative to the Poisson. Bootstraps were performed for a sample of UKBMS species; due to the high level of computational effort required, for widespread species the analysis was restricted to the last ten years and a random subsample of 300 sites.

3. Results

3.1 Simulations

Application of the two GAM-based models to simulated data shows that both approaches have virtually 100% power to detect 20% declines (over ten years) of the three example species (supplementary information, Table 1). With no change in abundance over ten years, the percentage of simulations that incorrectly predict significant trends lies reasonably around 5% in all cases.

Compared to the current model and the linear interpolation model, the two-stage model shows smaller standard errors for the trend estimation and performs better in the presence of missing data (Figure 2); with 30% of data missing, precision of trend estimation is reduced for the current or linear interpolation models, but not appreciably under the two-stage model. This is particularly demonstrated for smaller declines of 5% and 10% over ten years. For 30% missing data in the case of the Chalkhill Blue, although power under the two-stage model appears unaffected, that of the current model is reduced to 75.4% for a 5% decline. The accuracy of the trend estimates is also affected, with the declines of 5%, 10% and 20% estimated as approximately 4%, 9% and 19% respectively, accompanied by an increase in the associated standard errors.

Results for the simulated data based on a bivoltine species, the Adonis Blue, showed power to detect a negative trend in the presence of missing data to be markedly lower for the current and linear interpolation models, particularly for declines of 5% and 10% over ten years. Additionally, trend estimates from the two-stage model are generally more accurate and the associated standard errors are smaller.

For the Speckled Wood, differences between results for all models are less apparent, but the general performance of the two-stage model is still superior, with higher power to detect underlying trends and improved estimation of the trend in the presence of missing data.

3.2 Application for a wider set of species

We now apply the model to data for 46 species routinely monitored by the UKBMS. The mean number of sites (across years) that contribute to the two GAM-based models highlights the substantial improvement in data efficiency of the two-stage model (Fig. 3a). The two-stage model makes full use of the data available, whilst the current model discards a proportion of the data. For all species, fewer data were used under the current model and hence a reduced geographical coverage was represented, whereas results from the two-stage model are fully representative of the area for which data have been collected. The mean percentage of $10km^2$ monitored grid squares retained under the current model was approximately 63% (Fig. 3b), with a range from 31% (White-letter Hairstreak *Satyrium w-album*) to 91% (Heath Fritillary *Melitaea athalia*).

The collated indices for the 46 species under the two models are generally highly correlated and produce similar estimated linear trends in abundance (Fig. 4). The majority of points fall around the line of equality; although predictions from the two-stage model tend to be greater for the larger changes (i.e. estimation of large increases is more pronounced for the two-stage model). Results are given for each species in the Supplementary Information, Table 2. Confidence intervals derived from bootstrapping the set of sites are in general narrower for the two-stage model (Fig. 5). This is more pronounced for species recorded at fewer sites. A comparison of the indices over time (with corresponding bootstrapped confidence intervals) is given in Fig. 6 for selected species and shows the close correspondence between the collated indices. For the Marsh Fritillary *Euphydryas aurinia*, a localised species with few records, the confidence interval is considerably narrower under the two-stage model compared to the current model which shows particularly wide intervals for some years. However, alternative sampling methods not included here are utilised by the UKBMS to increase the sample size of monitoring sites for priorities species, such as Marsh Fritillary.

4 Discussion

Wild animal abundance typically fluctuates both within and between years. Invertebrates especially can show highly pronounced seasonal patterns, responding more directly to weather and some exhibiting multivoltine patterns of emergence. This provides particular problems in interpreting data from repeated visits within a season if some visits are missed, as simple measures of 'count per visit' may not be comparable. We have addressed the implications of this in documenting annual change via a new, 'two-stage' modelling approach, firstly estimating an annual seasonal pattern and then using this to adjust for incomplete series when modelling changes between years.

The UKBMS provides a large-scale source of butterfly population data for assessing the status and trends in abundance for species which serve as key indicators for change in biodiversity (Brereton *et al.* 2011b). Its full potential has not been realised because of limitations in previous analysis methods, particularly due to the substantial proportion of data gathered, but necessarily excluded from analysis (~38% visited sites per year).

When applied to simulated count data, the two-stage model performed substantially better than the current GAM approach. Standard errors were smaller, power to detect declines was greater (especially for small declines) and the trend estimates were more accurate. Standard errors were most similar between the two models for data matched to the Speckled Wood, which could be due to the complex seasonal pattern of overlapping broods. This may lead to a reduced effect of the missing data in the current model, compared to species which have more peaked-shaped seasonal patterns, where a single visit missed may have proportionately more impact. Power to predict declines was particularly low from the current model for the simulated bivoltine species. Estimation of missing values from separate GAM across sites may be poor for a bivoltine flight period shape with limited non-zero observations.

Standard errors are likely to be larger in the current model in part because fewer data are being used. When there were missing counts the current model tended to underestimate the decline in the simulation data. The performance of the two-stage model may also be superior as a consequence of the estimation of the annual seasonal pattern across sites, compared to estimation on an individual site and year basis under the current model.

Simulated data of course have the advantage that the true change is known and performance can be accurately assessed. Real data are however inevitably more complex. Application of the two models to the UKBMS data showed predictions of large changes in abundance were generally greater for the two-stage model, which may suggest that the current model underestimates the magnitude of the change in abundance for some such species. This could have implications for conclusions drawn from abundance indices for UKBMS data, for example in the classification of Red Lists (Fox *et al.* 2011). The difference in trend estimation from the two models is variable, but tends to be most notable for rare or elusive species, such as the Brown Hairstreak *Thecla betulae*, which may be benefitting from greater coverage under the two-stage model. However, national trend estimates published by the UKBMS for such species (Botham et al. 2011) incorporate data from larval web counts to estimate population size. Bootstrapped confidence intervals for the collated indices suggest estimates from the two-stage model have greater precision than the current model. The confidence intervals tend to be wider for earlier years in the dataset, probably due to the smaller number of sites available to sample from. The confidence intervals are particularly narrower from the two-stage model for species with fewer sites, which reinforces that such species may benefit from the greater usage of data. By applying all stages of each model to each bootstrap sample, error propagation is accounted for.

Further extensions for the two-stage model could be undertaken. It may be thought necessary to adopt a geographically varying approach to the model to improve missing count estimates, since for some species flight periods vary regionally. For example Common Blue *Polyommatus Icarus* populations are known to exhibit different levels of voltinism with latitude across the UK. Additionally, some species, especially those with a large latitudinal and altitudinal range, exhibit spatial variation in phenology, for example in their date of emergence (Roy & Asher 2003). Hence the seasonal pattern estimation may be over-simplified by the two-stage model, although variation will generally be greater from year to year than within years. We have considered seasonal patterns to be consistent at all sites (within a year) for ease of illustration, but as the correction of variation in species' flight periods at the site level is based upon a simple GAM, improved estimates of this may be obtained by incorporating covariates such as altitude and climatic zone.

The model may also be improved by accounting for weather conditions (Roy *et al.* 2001), which are recorded during each visit to a transect. Moreover, as the second stage is a GLM, various opportunities offered by this flexible family of models are available. If the Poisson fit is poor, the model could be reconsidered using negative binomial models (Hoef & Boveng 2007; Lindén & Mäntyniemi 2011). Alternatively, a Bayesian approach could be considered, for example using prior knowledge of the likely flight period. Both a Bayesian approach and parametric bootstrap were tested in Gross et al. (2007), who applied an alternative modelling method to transect data, using population dynamics to estimate abundance. A Bayesian approach has also been applied using hierarchical models for smoothing population indices (Amano *et al.* 2011). The use of Generalized Estimating Equations is considered by Brewer (2008).

The new model has the benefit of all volunteer input contributing to the abundance indices, thus providing confidence that their efforts are valuable and hence aiding the retention of volunteers, therefore allowing the scheme to continue at its current level (Lawrence 2005; Bell *et al.* 2008) and making further expansion more likely. The two-stage model also provides the estimation of site indices for data for which it was not previously possible, which could be beneficial for studying trends of individual sites, for example those of conservation concern. Additionally, with the two-stage model there is potential to include data from the Wider Countryside Butterfly Survey (WCBS), a recently established reduced-effort scheme, in order to reduce current bias from uneven sampling of wider countryside species (Roy, Rothery & Brereton 2007; Brereton *et al.* 2011a).

Adoption of the two-stage model will improve the estimation of indices and increase utilization of the data and thus benefit the calculation of UKBMS abundance indices, which have an important role as biodiversity indicators, and hence a role in management and policy. Given the large and increasing number of butterfly and other invertebrate schemes (Table 1), the two-stage model may also prove useful beyond the application to UKBMS data and has been shown to perform better than simple interpolation. Furthermore, some non-invertebrate based surveys can also have a seasonal component to them (Peach, Baillie & Balmer 1998; Atkinson *et al.* 2006). The sensitivity of insects to environmental changes compared to more widely monitored vertebrate taxa (Thomas et al. 2005), coupled with growth in monitoring schemes across much of Europe and North America, suggest that they are very good candidates to build biodiversity indicators. This paper demonstrates a novel analytical method that is both effective for assessing trends whilst making efficient use of the valuable contributions from citizen observers.

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Table 1. Monitoring schemes and research applications for (a) butterflies and (b) other seasonal insect taxa. Number of transects represents approximate number of transects currently recorded per year.

(a)

Location	Reference	Year Established	Number of transects
UK	http://www.ukbms.org/	1976	>1000
The Netherlands	http://www.vlinderstichting.nl/	1990	950
Switzerland	www.biodiversitymonitoring.ch	1998	500
Germany	http://www.tagfalter-monitoring.de/	2005	400
Ireland	http://butterflies.biodiversityireland.ie/	2007	150
Illinois, USA	http://www.ohiolepidopterists.org/bflymonitoring/instructions/introduction.htm	1987	130
Catalonia	http://www.catalanbms.org/	1994	115
France	http://www.bc-europe.org/subcategory.asp?catid=10&SubCatID=135	2002	100
Belgium	http://www.natuurpunt.be/nl/biodiversiteit/ongewervelden_291.aspx	1991	98
Finland	http://www.luomus.fi/nafi/	1991	548
Ohio, USA	http://www.ohiolepidopterists.org/bflymonitoring/	1995	60
Sweden	http://www.dagfjarilar.lu.se/	2010	59
Israel	http://www.butterfly.org.il/	2009	30
China	Not available	2010	28
Jersey	http://www.gov.je/ENVIRONMENT/LANDMARINEWILDLIFE/INSECTS/Pages/Butterflies.aspx	2004	25

(b)

Taxa	Reference	Location
Dragonflies	http://www.anisoptera.org/guideline.html http://www.british-dragonflies.org.uk/content/british-dragonfly-monitoring-scheme http://www.vlinderstichting.nl/libellen.php?id=92	US UK The Netherlands
Moths	http://www.rothamsted.ac.uk/insect-survey/ Spalding (1997) Grundy (2011) Conrad et al. (2006)	UK
Aphids	http://www.rothamsted.ac.uk/insect-survey/	UK
Bees	Westphal et al (2008) Kells, Holland & Goulson (2001)	Europe UK

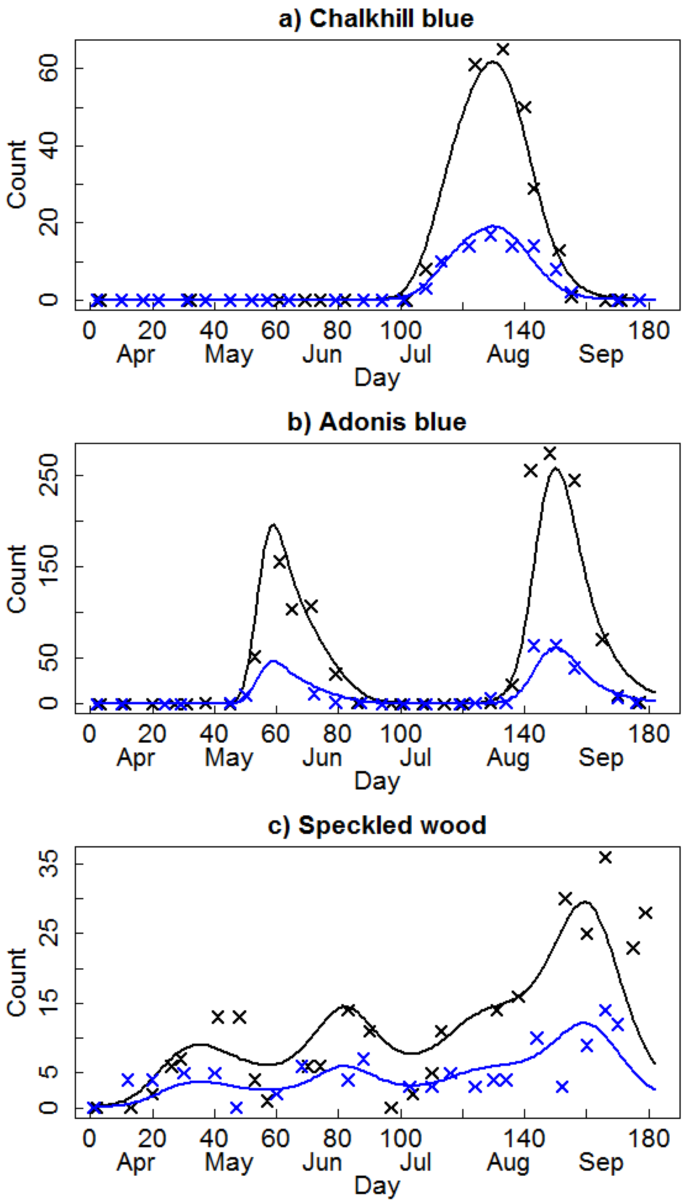


Fig. 1) Weekly counts at two example UKBMS sites with the corresponding GAM (equation 3) fitted with daily and site effects for 2005 (blue/black corresponding to different sites).

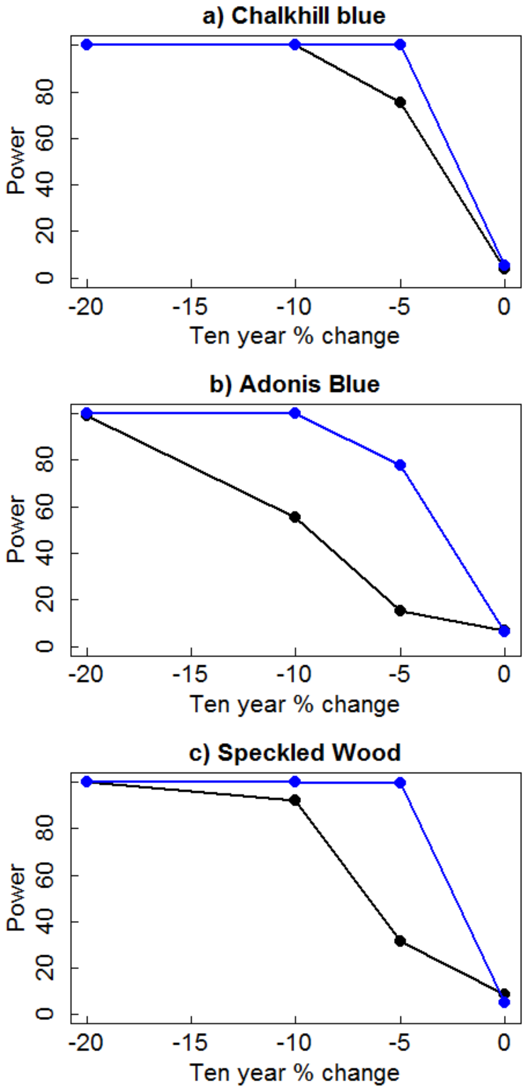
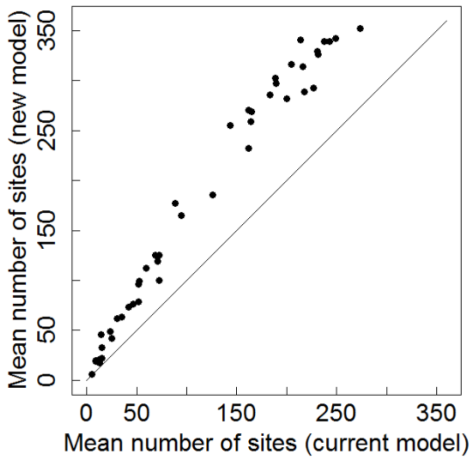


Fig. 2) Power to estimate simulated linear time trends from the current (black) and new (blue) method, applied to surveys of 100 sites over 10 years. 30% of observations are assumed missing.



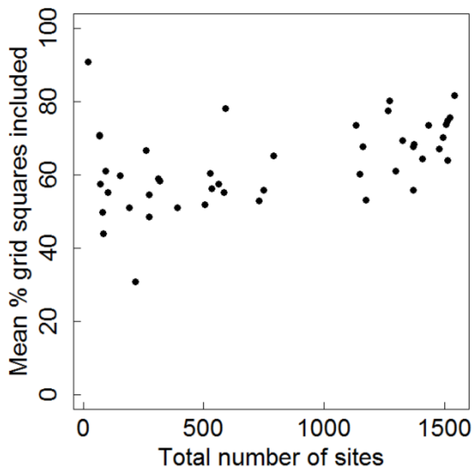


Fig. 3a) Comparison of the mean number of sites included (averaged by year) by each model for the set of UKBMS species.

Fig. 3b) Mean percentage of total monitored 10km^2 grid squares retained under the current model (across years) against the total number of sites for each species from the set of UKBMS species.

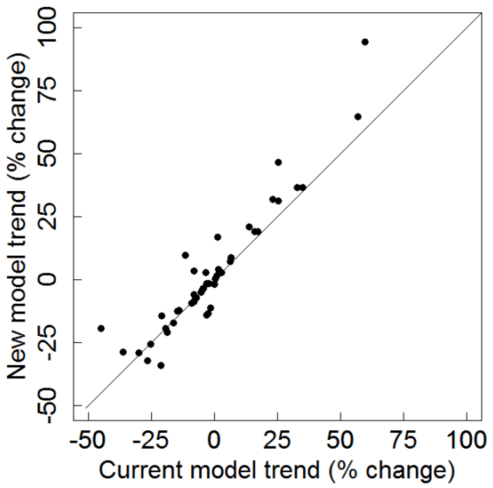


Fig. 4) Comparison of the estimated percentage trends of the collated indices for the two models for each UKBMS species (species and actual values listed in Supplementary Information).

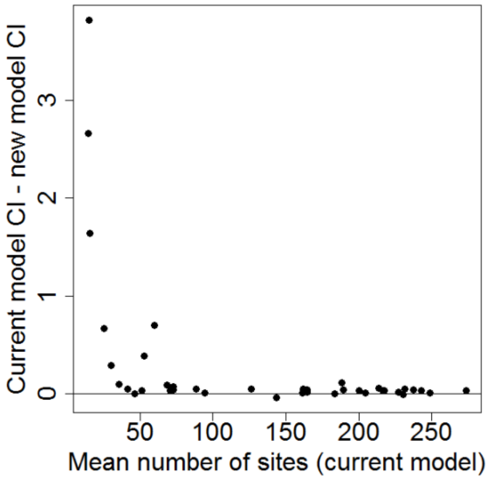


Fig. 5) Difference in the mean width (over years) of the bootstrapped confidence intervals for the current model and the two-stage model for a selection of UKBMS species compared to the mean number of sites (averaged by year) for each species (species listed in Supplementary Information).

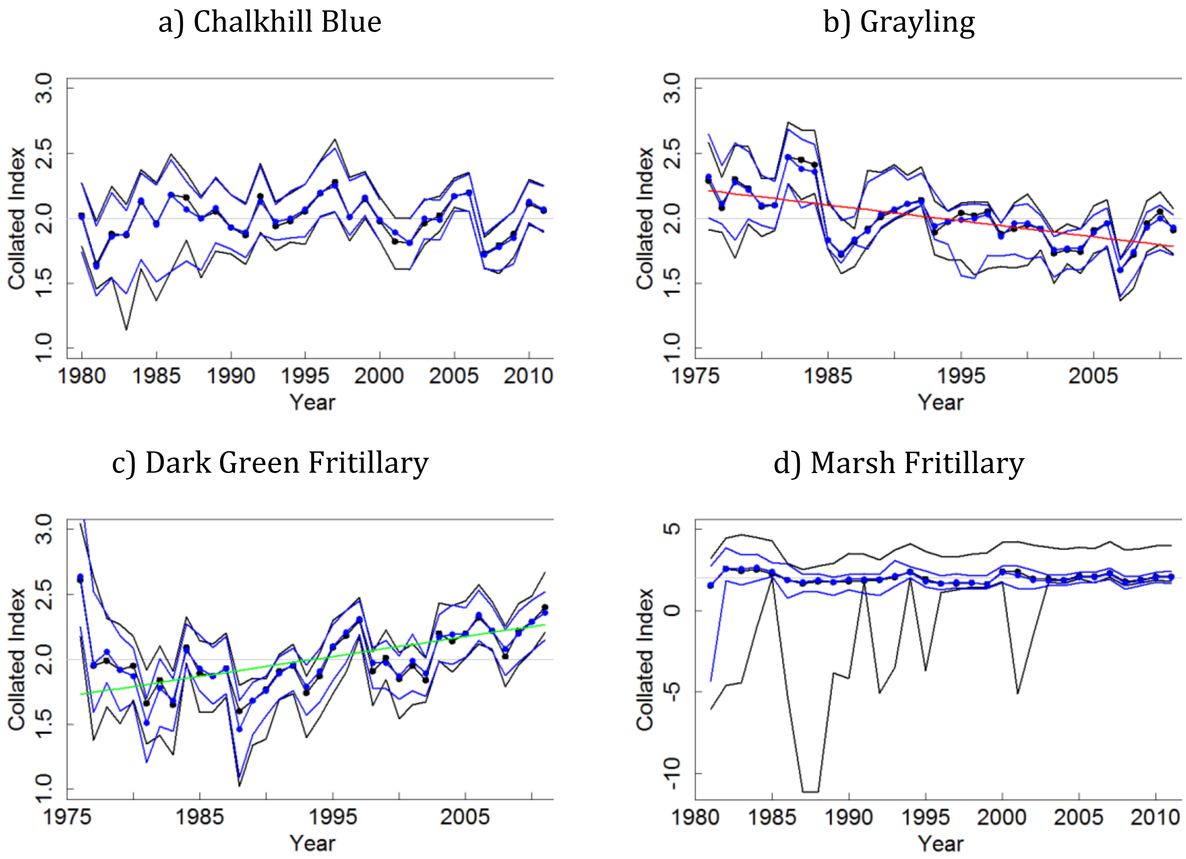


Fig. 6) Collated index plots for the current model (black) and two-stage model (blue) with corresponding bootstrapped confidence intervals (red/green line indicates significant linear decrease/increase), fitted to UKBMS data for four example species. Indices ($\log_{10}$(abundance)) are scaled relative to a value of 2.0 (100%) in the initial year.