ORIGINAL ARTICLE

Detecting population decline of birds using long-term monitoring data

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Abstract Abrupt population change in birds may be caused by various factors. When such events occur, it is important to understand the population-level impact on the species. We applied a change point analysis with Markov chain Monte Carlo using long-term population count data to address this question. We first investigated the method with a simple Poisson model using synthetic data sets for different population decline scenarios and number of observations. Estimated change points were particularly accurate when a large decline in counts occurred. Accuracy and precision of posterior change magnitude tended to increase when actual change magnitude became larger. We applied the method to two cases using data from the North American Breeding Bird Survey: epidemic mortality of Florida scrub-jays (*Aphelocoma coerulescens*) in central Florida and population decline of American crows (*Corvus brachyrhynchos*) in Maryland and Virginia after West Nile virus emergence. The Florida scrub-jay case study indicated that the estimated change point was accurate compared with that reported by local monitoring. A Poisson-log model that included observer and year variability resulted in better fit to the data than a simple Poisson model. The American crow case study showed that the method detected change points towards the end of observational data, but not all change point parameters converged, which may suggest that a population decline did not occur or was small for some survey routes we analyzed. Our study demonstrates the utility of change point analysis to examine abrupt population change. Data from systematic long-term monitoring can be a basis of such an analysis.

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Introduction

Acute mortality of birds due to epidemic infection may cause an abrupt reduction in population size of the species. Such events may occur locally or on a large scale. An example of the former case is an apparent epidemic mortality event in the Florida scrub-jay (*Aphelocoma coerulescens*), a threatened species, in central Florida between 1979 and 1980 (Woolfenden and Fitzpatrick 1984, 1990; Fitzpatrick et al. 1991; Woolfenden and Fitzpatrick 1991, 1996). Examples of the latter are *Myciokasma gallisepticum* infections in house finches (*Carpodacus mexicanus*) in the mid 1990s that spread from eastern USA, and recent West Nile virus (WNV) infections in corvids in North America (Steel et al. 2000; McLean 2006; LaDeau et al. 2007). When such population incidents happen, understanding the magnitude of population decline may be important in conservation efforts for the species.

Examining the impact of an event on population size of birds requires monitoring data before and after the occurrence of the event. Data from systematic long-term bird population survey programs, such as the National Audubon Society's Christmas Bird Count (CBC) (Butcher 1990) and North America Breeding Bird Survey (BBS) (Robbins et al. 1989), have proven useful in examining population change in birds. These annual surveys are systematically conducted over a large geographic range which allows researchers to retrospectively examine the data in an area of interest.

While long-term bird population monitoring data have often been analyzed to examine overall increasing and decreasing trends over time using continuous models such as linear regression on log counts (Geissler and Sauer 1990) and loess (James et al. 1996), abrupt population change may cause a shift of a population parameter at a point in time when the causal event occurred. This can be modeled as a discontinuity of model parameters. One approach to this problem is to fit the data to distinct models before and after the change if the point in time that the population decline occurred is known exactly. However, uncertainty may exist as to the timing of such an event. For example, West Nile virus was first introduced in New York in 1999, but years when mortality of birds associated with this virus was found varied between states (McLean 2006). Change point analyses have been used to model abrupt shifts of parameters at unknown time (Raftery and Akman 1986). Although the method is rarely applied to population monitoring of birds, it is potentially useful to examine the impact of population incidences: when the change occurred, whether the change significant, and the magnitude of the change.

Here, we apply change point analysis to examine population decline in birds using long-term monitoring data. We examine cases of abrupt population decline, that is, a downward shift of relatively stable population counts at a point in time. One challenge in modeling long-term bird population counts is to account for variability associated with data such as observer difference and year-by-year variability. Long-term bird monitoring data are often analyzed in a Bayesian framework in which such variability is accounted for as random variables in a hierarchical model (Link and Sauer 2002; LaDeau et al. 2007). Our primary objective is to investigate utility of change point analysis in population monitoring of birds using data from a long-term monitoring program. However, since the accuracy and precision of this method of analysis relative to actual change magnitude and number of observations were uncertain, we first apply the method of analysis to synthetic data to investigate how well it detects a change of an actual model parameter and estimates the magnitude of the change. We include these preliminary analyses using the synthetic data in this paper for illustrative purposes. Then, we apply the method to two cases using BBS data: Florida scrub-jay in central Florida and American crow (*Corvus brachyrhynchos*), which are known to be susceptible to WNV, in Maryland and Virginia. In the Florida scrub-jay case study, we examine if the method can accurately detect the time when the acute mortality of Florida scrub-jays was observed and estimate the magnitude of the change. In the American crow case study, we examine data from multiple survey routes.

A simulation study with synthetic data

Data

Synthetic integer vectors with lengths of 20, 30, and 40 were generated as random Poisson variable with a parameter λ which decreases by 20, 40, 60, and 80% at a known change point t. We generated t from normal distributions centered at the middle of each vector length, so change points are around the center of each series. The vector length, percentage decrease, and t mimic the number of observations in sequential monitoring (e.g., year), magnitude of population decline, and time when population decline occurred, respectively. Since we are interested in applying the method using the BBS data, we selected parameters and vector length (number of observations) within the range as BBS data. The initial λ (λ_1) was 30 for all scenarios and the λ after the change point (λ_2) were 24, 28, 12, and 6 for each of 20, 40, 60, and 80% decline scenarios.

Model

We used a Poisson model with a change point (Raftery and Akman 1986). The distribution of the annual counts of bird (denoted by x) is assumed to be Poisson with a parameter λ. Without change in λ, the probability of bird occurrence is

$$p(X = x|\lambda) = e^{-\lambda} \frac{\lambda^x}{x!}, \quad x = 0, 1, 2\ldots, \text{ and } \quad \lambda > 0.$$

In the change point model, the rate of occurrence at time i is λ_1 if $0 \leq i < t$ and λ_2 if $t \leq i$, where t is the change point. We used a simple Poisson model with a single change point to analyze the synthetic data. Let x_i denote the number of counts in year i, then

$$x_i \sim \text{Poisson}(\lambda_j) \, i = 1, \ldots, n,$$

where $\lambda_j = \lambda_1$ for $i = 1, \ldots, t - 1$, and $\lambda_j = \lambda_2$ for $i = t, \ldots, n$. We used uninformative priors as

$t \quad \sim$ discrete uniform on $\{1, 2, \ldots, n\}$ n = number of observations,

$\lambda_j \sim$ gamma (a, b) $j = 1, 2$ (before and after the change), and

$\varepsilon_i \sim$ normal $(0, \delta)$.

Parameters of our interest are the change point (t), the rate of count before and after the change point $(\lambda_1$ and $\lambda_2)$, and the percentage change or change magnitude (Δ). We also fit the data to the null model in which λ is constant across each series. We used deviance information criteria (DIC) to compare models (Spiegelhalter et al. 2002). The parameters were estimated from Gibbs sampling of Markov chain Monte Carlo (MCMC) using WinBUGS 1.4 (Gilks et al. 1996). A sample code for the change point analysis is available in the WinBUGS online examples (http://www.mrc-bsu.cam.ac.uk/bugs/welcome.shtml). For each data set, parameters were estimated from 10,000 iterations after burn-in of 5,000 iterations. Iterations were started from two distinct initial values and convergences were inspected with Gelman–Rubin diagnostics with the convergence diagnostics and output analysis (CODA) package of R (Gelman and Rubin 1992).

Results

For all data sets, DIC for the change point model was smaller than for the null model, suggesting that the change point model fit the data better (Fig. 1). Differences in DIC between the two models ranged from 14.7 to 380, which definitely support (differences of more than 10) the change point model (Spiegelhalter et al. 2003). There were greater reductions in DIC when change magnitudes were larger. For example, mean reduction in DIC was 19.8 for 20% decline scenarios and was 279.9 for 80% decline scenarios. The difference between the true change point (t) and the mean posterior change point $(\hat{t})$ was within 1 (-0.65 to 0.59) for all scenarios (Figs. 1 and 2). For large population change scenarios (60 and 80% declines), t equals $\hat{t}$ regardless of the number of observations. Overall, standard deviations of the posterior t were large with 20% decline scenarios (0.81–1.96) and become smaller with increased change magnitude (percentage decline) (0.13–1.49 for 40% decline, 0.01–0.05 for 60% decline, and <0.01 for 80% decline).

The true λ_1 and λ_2 were within 95% posterior intervals of $\hat{\lambda}_1$ and $\hat{\lambda}_2$ for all scenarios for our synthetic data (Fig. 1), but this was marginal for some cases. For example, λ_2 of the 20% decline scenario with 20 observations was close to the upper 95% boundary of $\hat{\lambda}_2$.

Overall posterior errors in change magnitude, which was derived as the difference between actual (Δ) and posterior $\left(\hat{\Delta}\right)$ change magnitude, tend to be centered on zero, and standard deviations become smaller with larger population decline scenarios (Fig. 2). Means of posterior errors in change magnitude for the 20% decline scenario range from 4.90 to 10.67 (SD 4.53–6.54) while those for the 80% decline scenario range from 0.42 to 1.97 (SD 1.91–2.48). These indicate that the accuracy and precision of posterior change magnitude increased with larger decline magnitudes.

Effects of the number of observations on parameter estimations were minor compared to the effects of change magnitude. For each decline scenarios (20, 40, 60, and 80), the accuracy of the estimated parameters $\left(t - \hat{t}, \Delta - \hat{\Delta}\right)$ does not necessarily improve with increased number of observations; however, the standard deviation of the estimated error in the change magnitude tends to decrease when the number of observations increases (Fig. 2).

Case study 1: Florida scrub-jay population in central Florida

Between 1979 and 1980 an apparent epidemic severely affected a population of Florida scrub-jays (*Aphelocoma coerulescens*), a threatened species, at Archbold Biological Station in Highlands County, Florida, USA (Woolfenden and Fitzpatrick 1984, 1990; Fitzpatrick et al. 1991; Woolfenden and Fitzpatrick 1991, 1996). From a local Florida scrub-jay banding project at the station, it was reported that this event caused 70% mortality of Florida scrub-jays on the site.

Unlike synthetic data, long-term monitoring data include various factors in addition to information on actual population change, such as variability in observers and years. Bayesian hierarchical models are flexible to include such effects (Link and Sauer 2002). We used two models with and without such effects in the model parameters to analyze Florida scrub-jay populations in central Florida.

Data

We used the BBS data from 1966 to 2005 at a survey route in Highland County, Florida, USA where epidemic mortality of this species was observed. The BBS surveys record counts of each bird species observed or heard during 3 min at locations with 0.8 km intervals on a 39.4-km-long route. BBS data for each year at each survey route are classified as either acceptable or unacceptable for use based on weather conditions. We excluded data classified as unacceptable. Observer information is provided as a unique identifier for each route. Data for 4 years, 1968 (indicated as unacceptable) and 1973, 1974, and 1999 (survey not conducted along this route), were treated as missing observations.
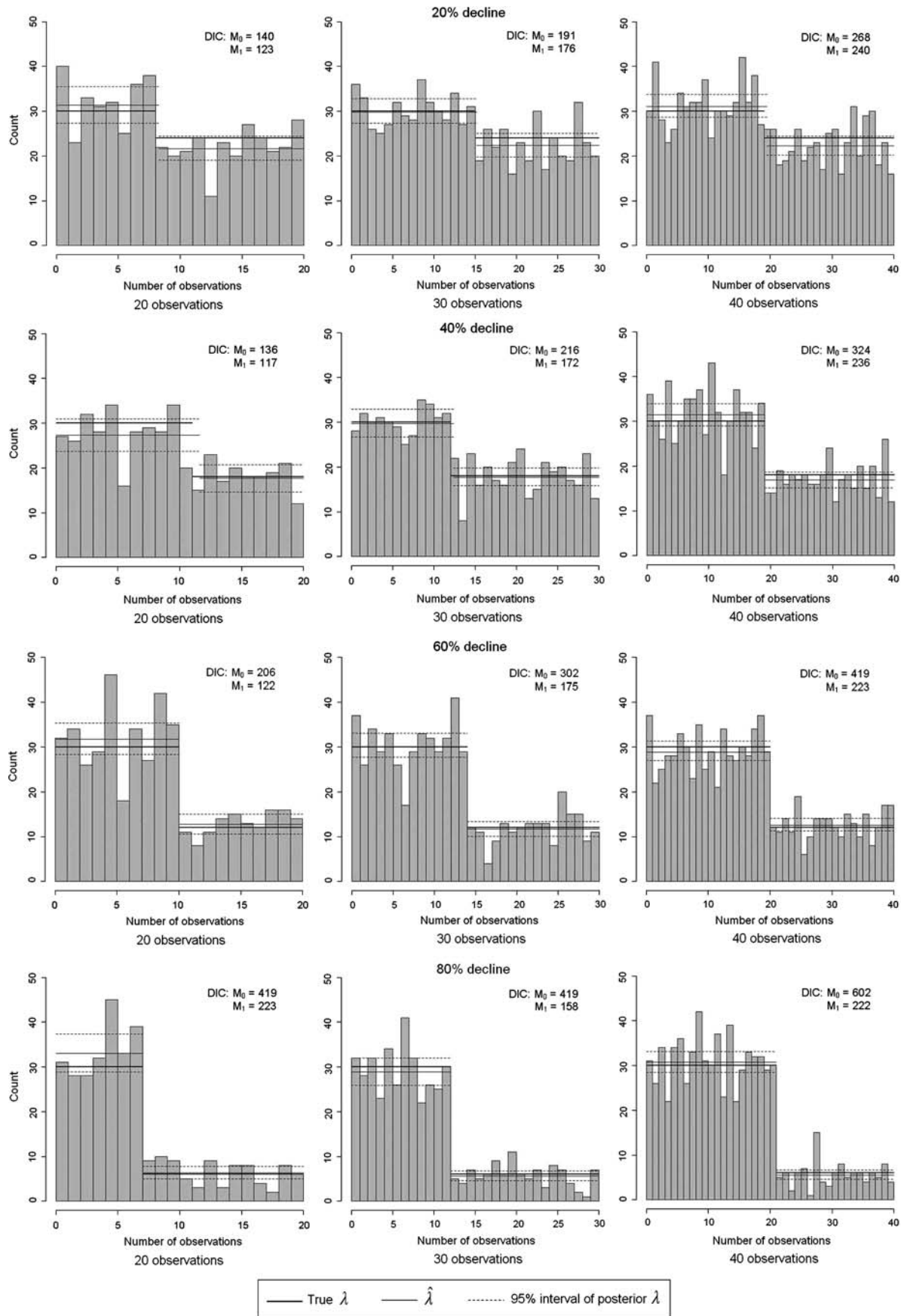
◄ **Fig. 1** Histograms of synthetic data with 20, 40, 60, and 80% population declines for each of 20, 30, and 40 observations. *Disconnected points of bold lines* (λ) are true change point (t) and *disconnected points of solid* ($\hat{\lambda}$) and *dashed* (*upper* and *lower* 95% intervals of $\hat{\lambda}$) *lines* are estimated change point ($\hat{t}$). DIC for null model (M_0) and change point model (M_1) is included in each plot. The parameters were estimated from 10,000 MCMC simulations

Table 1 Estimated model parameters (t, λ_1, and λ_2) and DIC of the null (M_0) and full (M_1) models for the Poisson (model 1) and Poisson-log (model 2) change point models with the Florida scrub-jay data from 10,000 MCMC simulations

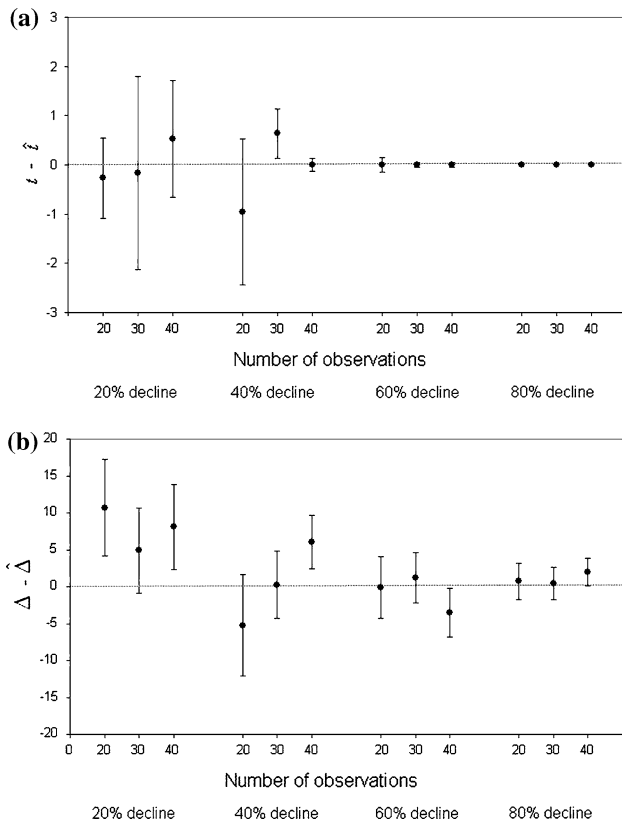|	Parameter	Mean	SD	2.5%	97.5%	DIC (M_0)	DIC (M_1)
Model 1	t	13.13	1.8	11.00	16.00	242.2	210.1
	λ_1	16.18	1.33	13.77	18.93		
	λ_2	8.69	1.65	7.62	9.95		
Model 2	t	13.28	2.16	10.0	17.0	186.4	187.7
	α_1	2.74	0.20	2.29	3.07		
	α_2	2.06	0.19	1.57	2.33		

(a)

(b)

Fig. 2 Posterior errors (true parameter value–predicted parameter value) of **a** change point, and **b** change magnitude (percentage change) (Δ) with 20, 30, and 40 observations for each of 20, 40, 60, and 80% decline scenarios from 10,000 MCMC simulations. The *vertical lines* indicate standard deviations

observer effect in a WinBUGS model. We also fit a null model of no change point to data for both the simple Poisson and Poisson-log models.

Results

The DIC of model 2 was smaller than the DIC of model 1 by 20.5; however, when compared to the null models, DIC was reduced only for model 1 (Table 1). A small difference in DIC (1.4) between the null and change point models for model 2 may indicate that the two models are not considerably different. The posterior mean of the change point ($\hat{t}$) of model 1 ($\hat{t} = 13.13$) and model 2 ($\hat{t} = 13.28$) differed only by 0.15 years. The 95% posterior interval of $\hat{t}$ for the both models included the year when local monitoring reported a large mortality of Florida scrub-jay (1980). Based on the posterior densities, $\hat{\lambda}_1$ and $\hat{\lambda}_2$ were distinctly different [$P(\lambda_1 < \lambda_2) < 0.05$] for both models, but model 2 resulted in a greater uncertainty of $\hat{\lambda}_1$ and $\hat{\lambda}_2$ (larger 95% posterior intervals) than model 1 (Fig. 3). Both models estimated over 45% decline in population counts (posterior means of $\hat{\Delta}$ by model 1 and model 2 are −46 and −49% respectively); however, model 2 again resulted in a greater uncertainty in posterior of change magnitude (95% posterior intervals of $\hat{\Delta}$ ranged from 34 to 56% decline by model 1 and from 30 to 65% decline by model 2) (Fig. 4).

Case study 2: West Nile virus infection on American crow

In our simulation studies and Florida scrub-jay case study, the population decline occurred around the middle of observations. In examining recent population incidences, change points likely occur towards the end of observations. Moreover, analysis of a large-scale population incidence may require analyzing population data at multiple

Model

We used two models for BBS's Florida scrub-jay data: the simple Poisson model that we used in the simulation study (model 1) and a model including effects associated with observers and years within log transformation (Poisson-log model) (model 2),

$$x_i \sim \text{Poisson}(\lambda_j)\, i = 1, \ldots, n, \quad \text{and}$$
$$\log(\lambda_j) = \alpha_i + \beta_k + \varepsilon_i$$

where $\lambda_j = \lambda_1$ and $\alpha_i = \alpha_1$ for $i = 1, ..., t - 1$, and $\lambda_j = \lambda_1$ and $\alpha_i = \alpha_2$ for $i = t, ..., n$ (β_k is the effect associated with the kth observer, and ε_i is an error term associated with year i). We referred to Link and Sauer (2007) to include an

Fig. 3 Histograms of annual BBS count of Florida scrub-jay in Highland County, Florida. *Solid lines* indicate posterior means of λ and *dashed lines* indicate upper and lower 95% intervals of posterior λ based on model 1 (*left*) and model 2 (*right*). *Disconnected points* of the lines indicate posterior means of the change point (*t*). The posterior interval of model 2 is skewed since we used log transformation to control over dispersion
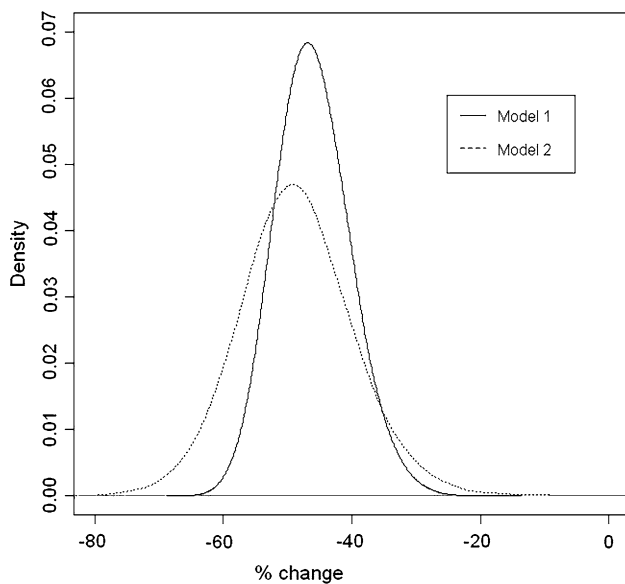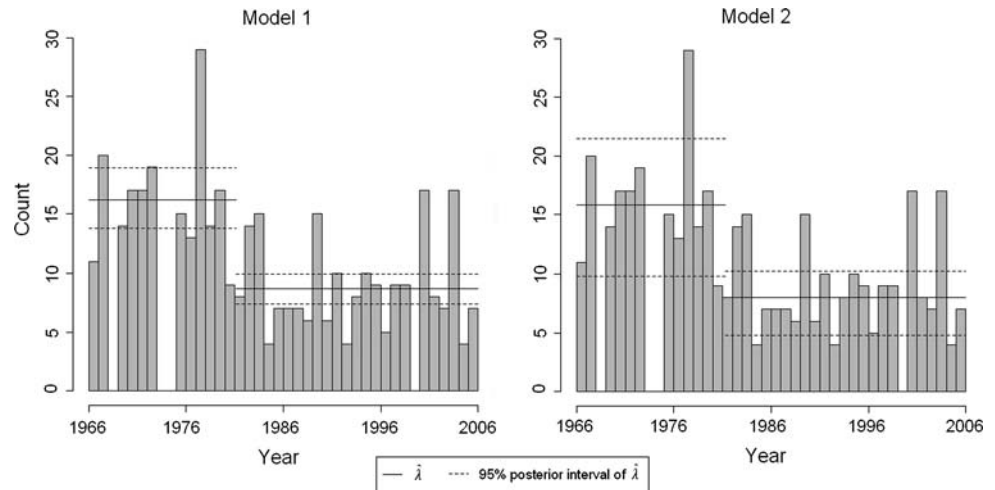
Fig. 4 Density plots of posterior change magnitude (percentage change) of Florida scrub-jay population estimated by two models using BBS data in Highlands County, Florida

locations. In this case study, we apply change point analysis to examine American crow population counts at multiple routes in Maryland and Virginia. West Nile virus was introduced in New York City in 1999 and affected all continental states (Steel et al. 2000). Among a number of affected species, American crow was the most susceptible (Yaremych et al. 2004; McLean 2006). LaDeau (2007) estimated a probability distribution of population abundance of birds based on the population count data prior to the West Nile virus emergence using a hierarchical model and considered that its effect is significant if observed abundances after virus emergence fell outside 95% credible intervals of posterior distributions. Their study indicated that the overall population of American crows in Maryland and Virginia was relatively stable prior to significant

population decline after the introduction of West Nile virus. This led us to believe that our model would be suitable for this case. Since LaDeau et al. (2007) conducted an extensive study of the effect of West Nile virus on the populations of North American birds, our analysis is only for methodological demonstration purposes.

Data

We used 26 years of BBS data between 1980 and 2005 as did LaDeau et al. (2007). We did not incorporate a method to adjust for missing data and excluded survey routes with missing observations. The number of survey routes with complete observations, which we used for our analysis, was 16 in Maryland and 10 in Virginia. These are 23 and 9% of all BBS survey routes in Maryland and Virginia, respectively.

Model

One approach is to fit a model with a common change point for all routes. This assumption may be unrealistic since occurrence of population decline can vary between locations. In fact, we did not find decreased population counts in some routes in preliminary exploration of data. Therefore, we used a model that assumes flexible model parameters for each route instead of introducing a new term for route effect, that is,

$$x_{i,j} \sim \text{Poisson}(\lambda_{i,k}) \; i = 1, \ldots, n, \; j = 1, \ldots, m, \; k = 1, 2, \text{ and}$$
$$\log(\lambda_{i,k}) = \alpha_{i,k} + \gamma_{i,j} + \varepsilon_{i,j}$$

where n denotes the number of routes and m denotes year; $\alpha_{i,k} = \alpha_{i,1}$ for $j = 1, \ldots, t_i - 1$, and $\alpha_{i,k} = \alpha_{i,2}$ for $j = t_i, \ldots, n$, $\gamma_{i,j}$ is an effect for variation in observers, and $\varepsilon_{i,j}$ is a normally distributed error term. This model is essentially similar to fitting the model to each survey route data, and may answer

questions such as where or in what proportion of survey routes population decline likely occurred. We implemented MCMC simulations with Maryland and Virginia data separately to compare the results.

Results

DIC was reduced for the change point model over the null model by 20 and 5 for Maryland and Virginia respectively, that is, a definite (differences from more than 10) and substantial (differences between 5 and 10) support of the change point models (Spiegelhalter et al. 2003). Reduction in DIC for Virginia appeared to be marginal in support of the change point model. The iterations resulted in mixture of converged and unconverged change point parameters (t_i). The parameters converged only for five routes in Maryland and one route in Virginia. Additional iterations did not change this convergence status. We suspected that this was because population decline might not have occurred or was too small to be detected for some routes, and thus a change point parameter might not be appropriate for those routes. All detected t_i values were points for

downward change. Figure 5 illustrates mean population counts of American crows for routes in which the change point parameters converged (a) and routes in which the parameters did not converge (b) in Maryland and Virginia. The plots indicate that, on average, the population decline was distinct for the routes where the t_i converged as compared to the routes in which t_i did not converge for both states. For those routes where t_i converged, average $\hat{t}$ was year 2003.4 $\left(\overline{SD} = 1.5\right)$ for five routes in Maryland and $\hat{t}$ was year 2003.9 (SD = 0.6) for one route in Virginia. This is about 3–4 years after the WNV positive test was first reported in 1999 in Maryland and 2000 in Virginia (McLean 2006). The average $\hat{\Delta}$ of the seven routes was -59.3% and ranged from -27.9 to -81.3%.

Discussion

There are various methods to analyze long-term trend of bird populations (Thomas 1996). Selection of an appropriate analysis method for a given application is critical to detect population declines and identify species for concern (Thomas and Martin 1996). We proposed to apply change
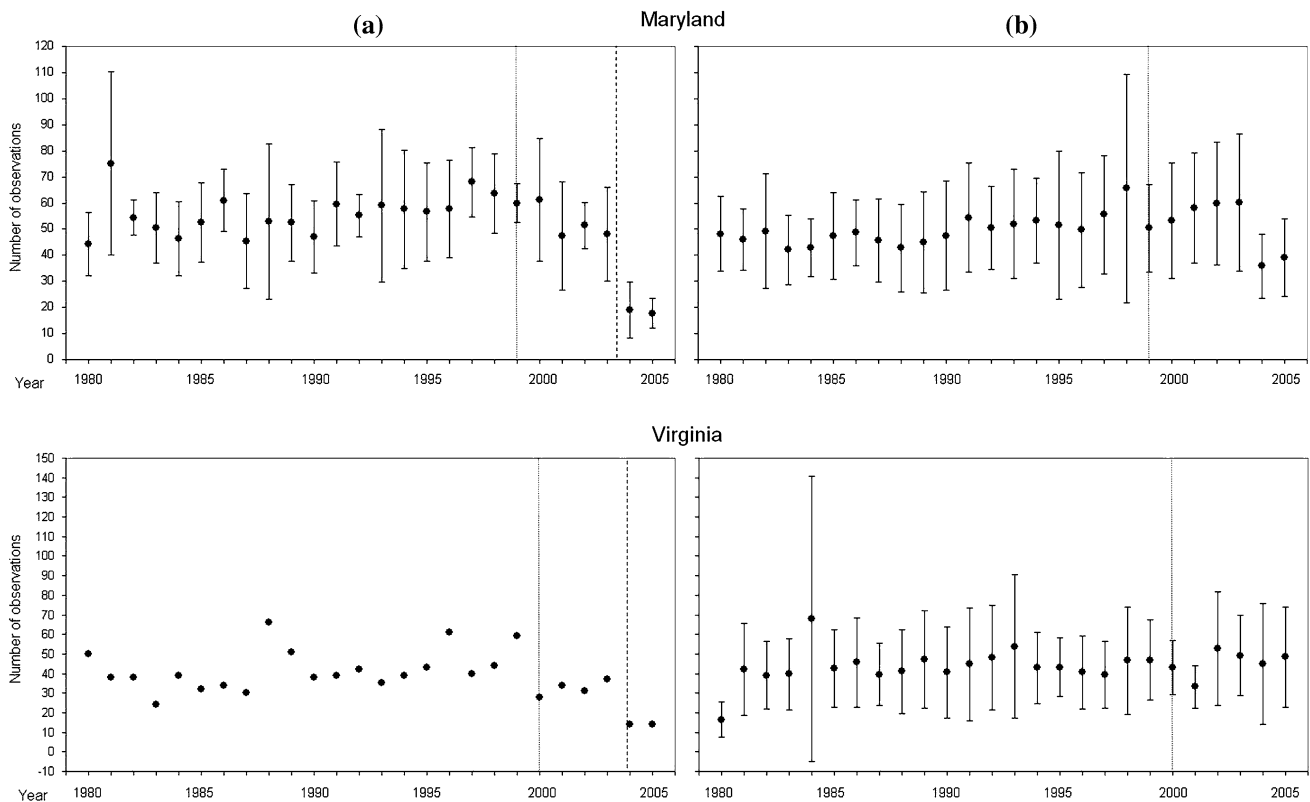

Fig. 5 Plots of mean population counts of American crows for survey routes in which the change point parameter (t_i) converged (six routes in Maryland and one route in Virginia) (**a**) and routes in which the parameter did not converge (ten routes in Maryland and six routes in

Virginia) with standard deviation for each year. The *fine vertical dashed line* indicates the year when the West Nile virus positive test was first reported in each state (McLean 2006). The *coarse vertical dashed line* in the plot (**b**) indicates the mean posterior change point

point analysis to model an abrupt population decline of birds using long-term monitoring data. Change point models are appropriate for abrupt change in model parameters instead of gradually varying change. This property makes the model useful to analyze the impact of a particular incident on population size. An analysis using synthetic data showed that the accuracy and precision of the estimated model parameters increased when the actual change magnitude (percentage decline) became larger. Most of the posterior change point $(\hat{t})$ was within 1 year of the actual change point (t) and the change magnitude $(\hat{\Delta})$ was within 10% of the actual change magnitude (Δ) in our synthetic data, with the exception of where the number of observations was small and there was a small population change (20% decline with 20 observations). These result suggested that the change point (time when decline in population counts occurred) and the change magnitude were estimated more accurately with larger decline scenarios. Also, there was a great reduction in uncertainty associated with estimated model parameters for large decline scenarios. The effect of the number of observations was minor compared to the effect of the magnitude of the change, but the precision of estimates appeared to increase with a larger number of observations. Based on these results, caution should be used when applying this method to detect minor population change with small numbers of observations. Such applications may result in inaccurate and broad posterior intervals.

In the case study of Florida scrub-jays, we analyzed the data at a single survey route on the site where the population incident was reported because it occurred locally. The BBS data for the Florida scrub-jay population count contained 37 observations and local monitoring reported large mortality of this species. Therefore, based on the results of the preliminary analysis with synthetic data, our method would result in reliable estimates for this case study. Unlike synthetic data, various uncontrolled factors exist in actual long-term monitoring data. The Poisson-log model which included variability in observers and years resulted in a better fit to data than the simple Poisson model which was used to analyze the synthetic data. The result suggested that both models accurately estimated the time when the population decline occurred since the estimated change point agreed with the year that local monitoring reported the population incidence of this species. This result was encouraging, although finding the change point may not be a primary objective for this method in the case of the Florida scrub-jay since the change point is known from the local monitoring. While both models estimated similarly large magnitude of population decline, over 45% decline, the Poisson-log model resulted in larger overall variability of the estimated parameters than the Poisson model. This is likely due to additional terms of observer

and year effects. A confounded result was that, despite accurately detecting the change point, DIC did not favor the Poisson-log change point model as compared to the null model while DIC was reduced considerably with the simple Poisson change point model over the null model. We cannot find a clear explanation for this, but suspect that it is related to increased uncertainty due to high variability by observer change and year in the Poisson-log model.

In the American crow case study, we did not have a means to verify the accuracy of the change point we detected since the actual time when a population decline occurred at each route is unknown. An unknown change point would more often be the case in actual population data analysis. The estimated change points appeared to be reasonable because all converged change point parameters point towards a downward change and occurred after the first WNV-positive case was reported in Maryland and Virginia. The magnitude of the decline varied largely between the survey routes. In a majority of the survey routes we analyzed, the change point parameter did not converge, which probably suggests either no or small population decline in these routes. The result of this case study indicates that relatively recent population decline, that is, when the change point does not occur in the middle of observations, is also detectable. Our case study examined bird populations in a limited range, but it would be possible to examine spatial variability in change point and magnitude of impact caused by population incidences using data from large-scale population monitoring.

There are several important issues that we did not address. First, our analysis did not include a case involving an increasing or decreasing population trend. Our model assumed relatively stable population counts before or after the change point. This assumption may not be appropriate for some occasions, for example, abrupt population decline may be followed by an increasing trend that eventually approaches the pre-decline level. Further sophistication of the model, such as including a linear trend after the change point, would be needed to address this issue. Second, our method solely depends on probability model to detect change point which most likely occurred and change gradient given historical population counts, and thus it does not aim to determine a causal factor. Caution is needed if other extreme external events are involved in the observation data. We only included variability associated with observers and year in hierarchical models, but other external variables, such as climate conditions, can also be included in a similar manner if data are available. Third, comparison of different methods was not within the scope of this paper. There are other methods that may also suit the cases we analyzed. Fitting a steeply decreasing nonlinear model to data (Dennis et al. 1995) is one possibility. Sequentially fitting separated models with all possible change points to

find the best one may be another possibility; however, creating large number of models for comparison is not generally recommended (Burnham and Anderson 2002). In either case, analyzing data in a Bayesian framework using hierarchical model or alternatively using a mixed model (McLean et al. 1991) appears to be essential to account for extra variability such as observer, route, and year-by-year effects. It is also noteworthy that change point analysis can be formed in other distribution models. Population count data, which is perhaps the most common parameter in population monitoring, are naturally modeled with Poisson distribution. Selection of a distribution depends on the modeled population parameter. For example, Fujisaki et al. (2007) analyzed nest failure proportion of alligators using a binomial change point model.

There are many agents that have historically caused large mortality of birds, including virus, bacteria, and fungus agent types. For example, exposure to mycotoxins was responsible for a large number of die-offs of sandhill cranes (*Grus canadensis*) in Texas from 1982 to 1987 (Roffe et al. 1989). Such large mortality may also affect the population size of the species. Further, anthropogenic factors such as accidental oil spills (Bailey and Davenport 1972; Clark 1984; Burger 1993; Wines et al. 1996) and rapid land use alteration (Boren et al. 1999; Mason and Macdonald 2000), and climatic factors such as hurricanes (Wunderle et al. 1992; Pierson et al. 1996; Jones et al. 2001) have also been reported to impact bird populations abruptly. The method of analysis presented here using long-term monitoring data would be useful to examine the impact of such incidences on bird populations.

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