



Short communication

Citizen science monitoring demonstrates dramatic declines of monarch butterflies in western North America



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ABSTRACT

Count-based PVA allows researchers to assess patterns of population change through time and to evaluate future persistence. We combined state-space models and citizen science data to evaluate viability of the western population of monarch butterflies over 36 years. A key feature of our analysis was combining irregular sampling from multiple sites to obtain a single estimate of total abundance using state-space models. The average population growth rate was negative, $u = -0.0762$ ($\lambda = 0.927$), average abundance in the 2000s was < 5% of average abundance in the 1980s, and current quasi-extinction risk is 72% within 20 years. Despite wide confidence intervals in some parameter estimates, western monarch monitoring data provide unambiguous evidence for dramatic population declines. To obtain viable populations, managers could target historic abundance and high enough growth rates to avoid near-term extinction.

1. Introduction

From time to time, widespread species decline in abundance so much that they appear to be at risk of extinction. Assessing such declines in the context of historic observations and yearly fluctuations, however, presents a challenge: Are observed declines sufficient to substantially increase extinction risk? Abundance data from long-term monitoring allow us to quantitatively evaluate this question. Count-based population viability analysis (PVA; Dennis et al., 1991; Morris and Doak, 2002; Fieberg and Ellner, 2000) estimates two parameters from monitoring data: a density-independent annual rate of population growth or decline, and year-to-year variation in this population growth rate, i.e., environmental stochasticity. These parameters, combined with current population size, can be used to predict extinction risk (Morris and Doak, 2002) and evaluate the magnitude of changes needed to ensure persistence (e.g., Molano-Flores and Bell, 2012).

Here, we used count-based PVA to evaluate the current status and future prospects of monarch butterflies (*Danaus plexippus plexippus*) in western North America. Like many at-risk species, systematic monitoring of this population began after dramatic declines had already been noticed. Therefore, it has been difficult to assess the status of the western monarch population with respect to historic abundance. We addressed this concern by finding appropriate statistical models to

integrate irregular sampling during the 1980s and 1990s with more systematic monitoring during the past 20 years. Our case study highlights how modern statistical tools can help us make use of long-term monitoring data collected by citizen scientists for status assessment of at-risk species.

Monarchs, well-known for their distinctive migration from their breeding range to overwintering sites in Mexico and coastal California, were once common throughout most of North America. Recently, the viability of eastern monarchs, which overwinter in Mexico, has received considerable attention (Inamine et al., 2016; Pleasants et al., 2016; Semmens et al., 2016). Western monarchs, which breed west of the Rocky Mountains and are considered a distinct population from eastern monarchs, have been largely ignored in the literature and popular press. Most western monarchs overwinter in wooded groves along coastal California, with limited numbers overwintering in Mexico (Morris et al., 2015; Yang et al., 2016). As with eastern monarch declines in Mexico, changes in California overwintering populations may indicate threats occurring in breeding states, or coastal overwintering habitat loss and degradation, and beg the question of population viability.

For several decades, volunteers have been counting overwintering monarchs in coastal California. The data consist of overwintering butterfly counts in individual groves, each of which represents a subset of

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the entire breeding population. The vagaries of the data, e.g., year-to-year fluctuations in population size, added or missing sites across years, and count errors, require sophisticated methods of analysis only recently available to ecologists. State-space models account for noisy data by separating observation error from processes of population growth and environmental stochasticity (DeValpine and Hastings, 2002; Holmes et al., 2012). Here, we used state-space models to estimate the western monarch population growth rate from spatially and temporally erratic sampling data, and show how short-term population fluctuations can have long-term consequences in a species of conservation concern.

2. Materials and methods

2.1. Western monarch wintering sites database

We used overwintering monarch count data from the Xerces Society's Western Monarch Overwintering Sites Database (Xerces Society for Invertebrate Conservation, 2017). This database includes monitoring data from the Western Monarch Thanksgiving Count (WMTC, 1997–present), information from numerous reports, and personal communications (Pelton et al., 2016; see westernmonarchcount.org). For our study, we included records from this database collected using a similar protocol during comparable time periods to the WMTC (November–December). We filtered the full dataset to include only sites monitored at least five years (see Supplement 6). Our analysis includes 186 sites, with counts from 1981–2016 (Fig. 1).

2.2. State-space models

We analyzed count data using multivariate autoregressive state-space (MARSS) models implemented in the MARSS package in R (Holmes et al., 2012; R Core Team, 2016; commented R code in Supplement 1). Similar to published PVA for eastern monarchs (Semmens et al., 2016), we assumed that western monarchs comprise a single population with a single rate of overall change in abundance and a single parameter for among-year variation in the population growth

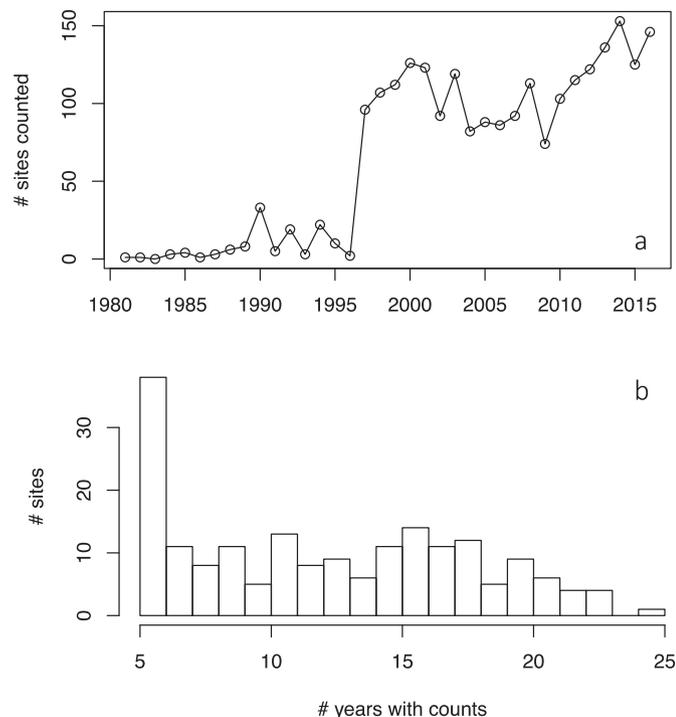


Fig. 1. Number of (a) sites counted per year and (b) frequency of years of data per site for sites used in analyses. All data are from the Western Monarch Overwintering Sites Database.

rate. We also assumed that each site at which monitoring took place in a given year was an independent index of the total abundance in that year (see supporting analyses in Supplements). For each site, the MARSS procedure estimates a parameter for proportionality between the site count and the total population, and an observation error variance parameter unique to each site but stationary through time. These assumptions are expressed using two sets of equations. The first set describes stochastic, density independent, population dynamics:

$$\ln(N_t) = \ln(N_{t-1}) + u + \varepsilon_t$$

$$\varepsilon_t \sim \text{Normal}[0, \sigma_u]$$

where N_t is the regional abundance (total number of western monarchs) in year t , u is the log-scale annual population growth rate, and ε_t is environmental stochasticity (year-to-year variation in population growth rate). Back-transforming this model yields a simple stochastic population growth model, $N_t = \lambda_t N_{t-1}$, where $\lambda_t = \exp(u + \varepsilon_t)$.

The second set of equations describes the relationship between counts at each site and the regional abundance:

$$\begin{bmatrix} \ln(y_{1,t}) \\ \vdots \\ \ln(y_{186,t}) \end{bmatrix} = \ln(N_t) + \begin{bmatrix} a_1 \\ \vdots \\ a_{186} \end{bmatrix} + \begin{bmatrix} v_{1,t} \\ \vdots \\ v_{186,t} \end{bmatrix}$$

$$v_{i,t} \sim \text{Normal}[0, \sigma_{a,i}]$$

where $y_{i,t}$ is the count of butterflies at site i , a_i describes the relationship between the average count at site i and regional abundance (i.e., N_t), and $v_{i,t}$ is the normally-distributed among-year “observation error” with mean 0 and standard deviation $\sigma_{a,i}$. Back-transforming the log-scale relationship makes the count versus abundance strictly proportional: $y_{i,t} = N_t \exp(a_i + v_{i,t})$. In addition, there are different constants of proportionality and observation error parameters for each site, but all sites contribute to inference about the total population.

MARSS models assume that each site contributes to the total abundance, and fit models of y_t to each site based on years when counts were made at that site. In other words, in a year when four sites are counted, we expect the total count to be $\exp(a_1 + a_2 + a_3 + a_4)N_t$. If ten sites are counted, the expected total is $\exp(a_1 + a_2 + a_3 + a_4 + a_5 + a_6 + a_7 + a_8 + a_9 + a_{10})N_t$, etc. Therefore, this model implicitly adjusts for missing data (Holmes et al., 2012; Tolimieri et al., 2017). Because of the scaling factor, the MARSS model gives an index of abundance proportional to total abundance.

2.3. Model checks and evaluation

Visually, annual estimates of monarch abundance did not meet our expectations for stereotypical stochastic exponential decline (see Results and Fig. 2a); specifically, there seemed to be a change in the growth rate over time. To evaluate whether growth rates were stationary over time, we converted log-scale annual abundance estimates to log-scale annual population growth rates, i.e.,

$$\hat{u}_t = \ln(\hat{N}_t) - \ln(\hat{N}_{t-1})$$

where \hat{u}_t and \hat{N}_t are the estimated annual growth rate and regional abundance in year t . We used the MARSSparamCIs function to estimate the standard error associated with \hat{N}_t and converted this to standard error of \hat{u}_t using the delta method implemented via the msm package in R (Jackson, 2011).

We used Generalized Additive Models (GAMs, Zuur, 2012), estimated with generalized cross-validation as implemented in the mgcv package in R (Wood, 2011), to evaluate trends in annual population growth rate, and squared deviations of \hat{u}_t from the average \hat{u}_t (i.e., variance of \hat{u}_t ; cf. Fagan and Holmes, 2006). If population growth were consistent with the simple exponential model, we would expect non-significant smoothed terms for the mean and variance of \hat{u}_t in relation to time. We also evaluated stationarity of the mean and variance in

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