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Source: Folia Zoologica, 64(4) : 330-336

Published By: Institute of Vertebrate Biology, Czech Academy of Sciences

URL: https://doi.org/10.25225/fozo.v64.i4.a7.2015

Folia Zool. – 64 (4): 330–336 (2015)

Using integrated population modelling in conservation monitoring: a case study in the common dormouse (*Muscardinus avellanarius*)

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Received 20 March 2015; Accepted 10 May 2015

Abstract. Integrated Population Modelling (IPMs) is a computational method for estimating population and demographic parameters that can improve precision relative to traditional methods. Here we compare the precision of IPM to traditional mark-recapture analysis to estimate population parameters in the common dormouse (*Muscardinus avellanarius*). This species is relatively rare across its European range and field estimation of demographic parameters can be challenging, as several parts of the life history are difficult to observe in the field. We develop an IPM model incorporating dormouse nest counts and offspring counts, which is data often recorded as a standard part of dormouse nest box monitoring. We found a significant improvement in precision in the estimation of demographic parameters using IPM compared to standard mark-recapture estimation. We discuss our results in the context of common dormouse conservation monitoring.

Key words: Bayesian population modelling, IPM, population biology, population growth rate

Introduction

One of the primary tools employed to measure anthropogenic impacts and environmental change on natural populations can be referred to as conservation monitoring. Conservation monitoring programmes often focus on individual species that are prominent in the habitat, ecologically important or otherwise of interest. A fundamental goal of such monitoring is to estimate the abundance of particular species and how it changes through time. Concerns for the decline or loss of species have motived the widespread implementation of conservation programmes worldwide (Nichols & Williams 2006). There are several challenges to successfully measuring animal abundance. First, the empirical observation that most species are rare creates a practical constraint when resources to devote to monitoring are limited (Prendergast et al. 1993). This effect is exacerbated when populations of a rare species becomes fragmented across a fragmented landscape, or when density declines due to factors impacting habitat quality or, more generally, fitness of individuals. Also, the effect of "elusive" behaviour or habitat complexity may impact the effectiveness of monitoring unless specific tactics are used to overcome them (Thompson 2013). Second, sustained effort at a large spatial scale is often required to detect population changes independent of inherent demographic stochasticity. The meta-population view of species, where "populations of populations" interact dynamically, has been widely adopted in conservation science, creating the need to simultaneously monitor populations at the landscape level to understand population changes (and cause and effect thereof). Finally, because the goal of many conservation programmes is to monitor species persistence through time, continuous surveillance of these populations for the duration of possible change (negative in the case of impacts, positive in the case of mitigation efforts) is required. This temporal requirement is perhaps most important when focal species have high longevity combined with low fecundity, when a species is acutely sensitive to environmental change, and when the global population or geographical distribution is small. While the practice of monitoring populations is central to many conservation programmes, it has been observed that success in detecting population change may be relatively rare partly due to the difficulties mentioned here, but often due to a mismatch between

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monitoring goals and design (Caro 1999, Legg & Nagy 2006, Nichols & Williams 2006).

Several related approaches are typically employed to estimate population changes through time. Perhaps the most basic is that of the census count method, sometimes conducted at different locations and repeated through time (Elzinga et al. 2009). The aim here may be to monitor broad trends in population change, however the assumption must be made that there is no interaction between habitat differences and any pressures influencing population change between locations. Another approach is that of mark-recapture or presence-absence surveys. Here the goal is often to explicitly estimate population trends by estimating, e.g. demographic parameters such as the intrinsic rate of increase of the population (Lebreton et al. 1992). While mark-recapture studies are powerful, they tend to be labour intensive to conduct and making explicit inferences about mortality and fecundity is difficult in some situations. A relatively new analysis approach called Integrated Population Modelling (IPM), aims to improve the efficiency of mark-recapture studies. Here, data that has traditionally been ancillary to mark-recapture, but which has a low cost to collect and is typical of conservation monitoring, such as census data, offspring counts and occupancy data, are incorporated into a single modelling framework (Besbeas et al. 2002, Abadi et al. 2010a, Tempel et al. 2014). This approach is potentially superior to mark-recapture alone or to modelling monitoring data from different sources separately, because it tends to reduce error in the estimation of demographic parameters (Abadi et al. 2010a). Another advantage is that some population parameters important to understanding population trends, such as immigration and emigration, which are notoriously difficult to measure directly, can be inferentially modelled using IPMs (Schaub & Abadi 2011). Thus, in a metapopulation conservation monitoring context, understanding immigration is essential to identify potential source or sink populations and IPM has been proposed as a way to do this efficiently using similar effort to traditional mark-recapture methods (Abadi et al. 2010a, Tempel et al. 2014). While there has been recent advancement of a unified and robust framework for this type of modelling (e.g. Kéry & Schaub 2012, Newman et al. 2014), there have been relatively few empirical applications to date to aid conservation monitoring (Gauthier et al. 2007). Here, we aim to evaluate the use of IPM models to improve the precision of estimating demographic parameters in a small mammal for the first time to our knowledge, the common dormouse (*Muscardinus avellanarius*: Linnaeus).

The common dormouse has a wide geographical range across Europe, inhabiting areas of deciduous woodland, especially where scrubby understory is present (Bright et al. 2006). While the species has an overall categorisation of "Least Concern" by the IUCN (IUCN 2014), there is evidence that in some parts of its broad range, notably in northern Europe (including the U.K., Denmark, Germany, Sweden and the Netherlands), the species is declining and there is cause for conservation concern. The cause for this decline is thought to be anthropogenic disturbance in the form of habitat reduction and fragmentation, leading to an estimated decline of 64 % across the U.K. (Bright et al. 2006). As a consequence of this decline, the species is protected in many areas, and in the U.K. there is a biodiversity action plan in place to stabilise the decline by improving habitat quality locally and to increase the number of populations (through captive reintroduction in its historical range where it has gone locally extinct). There is sustained monitoring effort across many parts of range, including a sustained effort in the U.K., the National Dormouse Monitoring Project (NDMP) (Williams et al. 2013), where dormouse numbers in nest boxes are recorded at least twice per year in participating areas. The NDMP is primarily a conservation monitoring programme with the goal of estimating common dormouse population trends, both with the aim of estimating chronic population decline but also to document stable populations and populations increasing in size, e.g. due to habitat restoration efforts (Bright et al. 2006). Amongst challenges in the monitoring of the common dormouse are that the species is small, nocturnal, arboreal and naturally occurs at very low density in ideal habitat (~ 10 individuals/ha in the U.K., Bright & Morris 1990, Juškaitis 2008). While the U.K. national trend in dormouse numbers is monitored by the People's Trust for Endangered Species using this long term dataset, which began in 1988 (Williams et al. 2013), quantitative estimates of specific populations are difficult to achieve.

Here, we will focus on a local conservation monitoring project for the common dormouse in North Wales, U.K., which has been conducted by members of the Northwest Dormouse Monitoring Project. This project has been conducted using passive integrated transmitters (PIT tags) inserted into each captured individual during the course of monitoring since 2005. Using this method, individual capture histories

have been recorded, and thus mark-recapture analysis is possible (Bird 2011). The data made available to use for this study were collected between 2005 and 2010. Our aim for this study was to evaluate the utility of IPM modelling for use as a conservation tool in the monitoring of a marked, small mammal population for the purpose of estimating demographic parameters. Specifically, we 1) develop an IPM model of the population growth rate, based on the available data to estimate demographic parameters in the common dormouse, 2) compare population growth rate estimates for IPM versus a non-IPM model, and 3) evaluate the utility of IPM as a standard conservation monitoring tool to use for the common dormouse.

Material and Methods

Mark recapture

The study population is in north Wales, U.K., Bontuchel Wood (53.109364 N-3.370318 W). This area is characterised as a mixed broadleaf and conifer woodland. The population contains approximately 250 nest boxes placed at 20-40m intervals. Most boxes are monitored in the NDMP programme up to four times per year. As a baseline model of populations growth (here we focus on the population growth parameter, λ, see below), we used standard Cormack-Jolly-Seber (CJS) mark-recapture analysis (Cormack 1989). Because the population has been monitored for a relatively long period of time, we assume that mortality may occur during the monitoring period. Also because the common dormouse is relatively long-lived, and because we cannot exclude the possibility of immigration and emigration in our population, we assume that the population is open to unobserved movement of individuals to and from the monitored population. To accommodate these assumptions, we fit a standard log-linear CJS mark-recapture model as implemented in the R 3.2.1 (R Core Team 2013) package Rcapture using the open p function with default settings, following the guidelines described by Baillargeon & Rivest (2007).

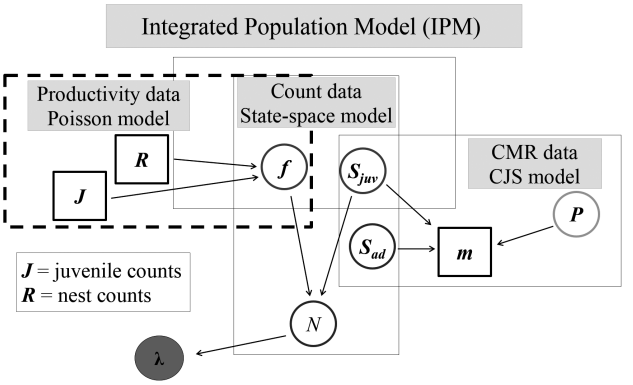

Fig. 1. Graphical representation of an integrated population model for the hazel dormouse (*Muscardinus avellanarius*), a population found in North Wales, U.K. The model framework is adapted from Abadi et al. 2010a and Tempel et al. 2014. R = number of nest counts, J = juvenile counts for each nest box during each capture occasion, f = number of young produced per adult, S_{juv} = juvenile survival probability, S_{ad} = adult survival probability, m = capture-recapture data, P = population count data, N = population size.

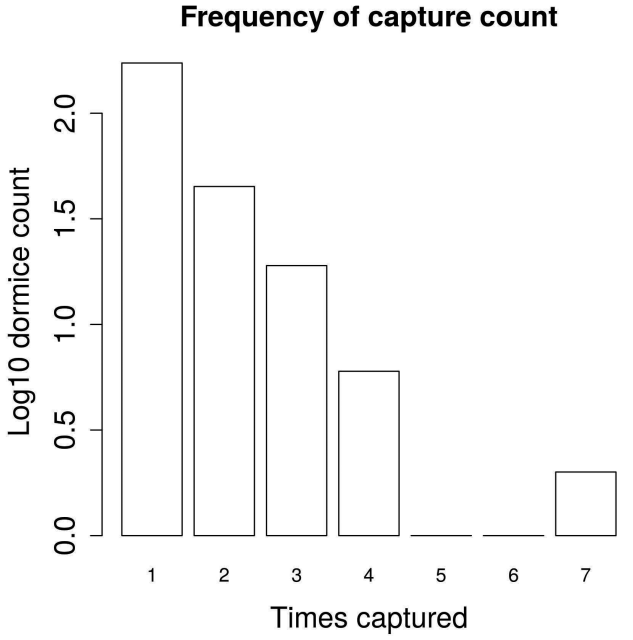

Fig. 2. Distribution of frequency counts of captured dormice at Bontuchel Wood, Wales over a six year period (2005-2010). Some individuals have been captured up to seven times in survey periods however number of captures decrease.

IPM model

To develop our IPM model of population growth for the common dormouse, we followed the framework described by Kéry & Shaub (2012) which has been adopted in conservation monitoring studies in bird species (e.g. Abadi et al. 2010a, Tempel et al. 2014). We adopted a model framework (Fig. 1) similar to that described in Abadi et al. (2010b). The data we used came from two sources. The first dataset was annual counts of adults (y) and juveniles (j), and these second dataset consisted of a set of mark recapture histories of individuals recorded for the duration of the study. The population parameter we focus on estimating is the fundamental rate of increase, λ, based on time specific estimates of population size for juveniles and adults. In order to estimate the true population sizes from the observed population count data we relate adult and juvenile population sizes between years using the following distributions, which also take into account demographic stochasticity. This is a state-space model

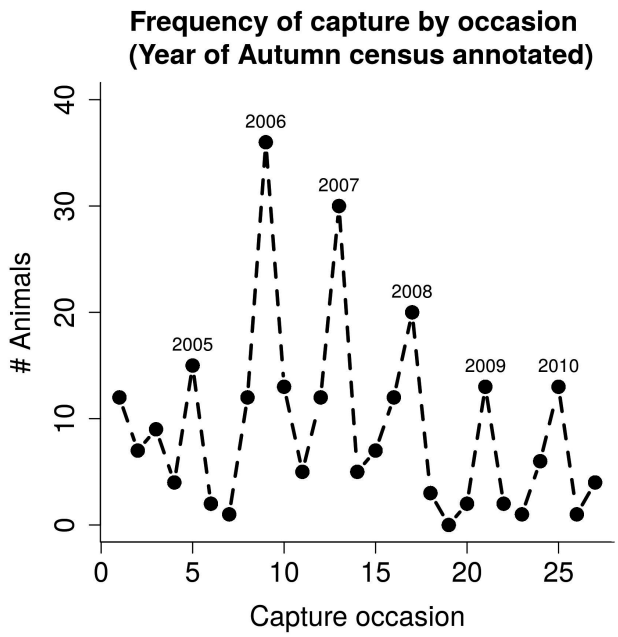

Fig. 3. Trends in number of dormice captured at each occasion and year of census annotated at each yearly peak. Greatest frequencies in autumn nest box checks due to young of the year maturing to PIT tagging age.

approach similar to Abadi et al. (2010b) and Tempel et al. (2014):

$$N_{1,\,t+1} \text{ Poisson } (N_{1,\,t} S_{juv,\,t} \frac{f_t}{2} + N_{ad,\,t} S_{ad,\,t} \frac{f_t}{2})$$

$$N_{ad,\,t+1} \text{ Binomial } (N_{1,\,t} + N_{ad,\,t,}\, S_{ad,\,t})$$

We assume that the violation of independence exhibited between the juvenile and nest counts we use has a negligible effect on our model results, as has been demonstrated previously (Abadi et al. 2010b). IPM analysis was conducted using R2WinBUGS (Sturtz et al. 2005) package available in R 3.2.1 (R Core Team 2013) that calls the program WinBUGS (Lunn et al. 2000). The model ran in a Bayesian framework using Markov Chain Monte Carlo (MCMC) to estimate model parameters, three chains of 50000 iterations with a burn-in of the initial 10000 iterations of each chain.

Results

There were 247 individual capture histories recorded during the period of study, with 369 total captures recorded. The number of times individuals were captured ranged from 1 to 7 times, with the vast majority being caught 1-3 times (237/247) and the remainder being caught 4-7 times (see Fig. 2). The dataset consisted of 27 observation occasions over a six year period, with four or five observation occasions for each year. The number of dormice captured during individual occasions varied greatly (range between 1 and 36 individuals, see Fig. 3) according the time during the season, with expected peaks occurring during autumn each year, coinciding with the capture of young of the year in nest boxes.

Our CJS model estimated mean capture probability for the duration of the study at 0.70 (SD = 0.25) and a mean population size of 62.1 individuals (SD = 21.6). Mean survivorship was estimated to be 0.34 during the study period (SD = 0.21), with an estimate of the finite rate of population growth, lambda, ranging from 0.42 to 1.24 (mean = 0.84, SD = 0.30, see Fig. 4a).

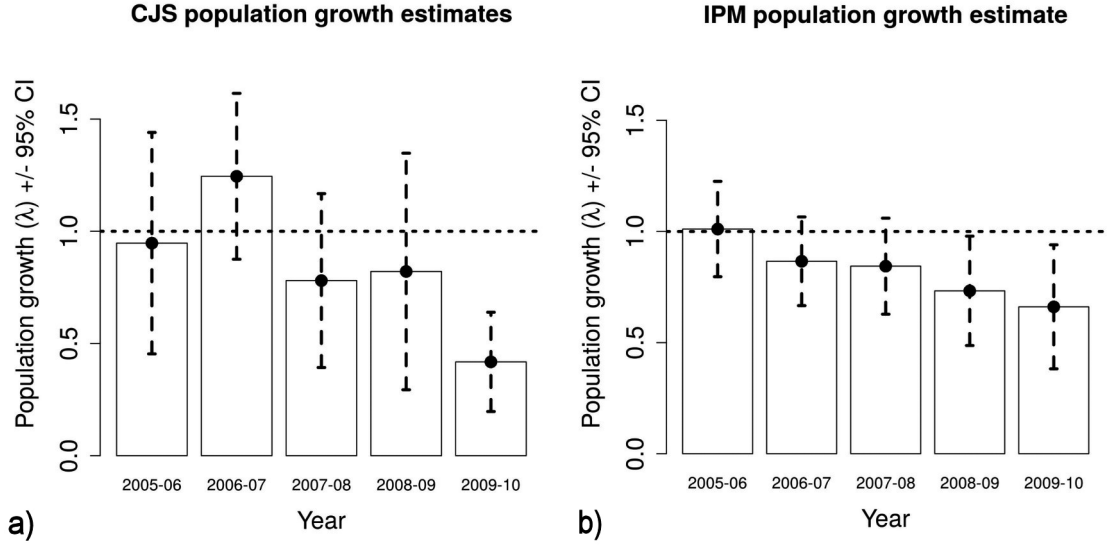

Fig. 4. Estimated population growth estimates, Lambda (λ) and 95 % confidence intervals for the common dormouse *Muscardinus avellanarius* using a) Cormack-Jolly-Seber (CJS) and b) Integrated Population Modelling (IPM) approach, dashed line is lambda (λ) at constant growth rate (1.0). CJS estimates (a) indicate growth rates are constant in the first four years and negative (< 1.0) in the last year (2009-10). IPM shows an overall decline over the six years (< 1.0), however not significant in the first three years.

Our IPM estimate of the finite rate of population growth had a smaller range to that estimated by our CJS model, ranging from 0.66 to 1.01, however the estimated mean was similar (mean = 0.82). The variation of the IPM estimate were smaller than those estimated from CJS (SD = 0.13, see Fig. 4b). The mean population growth estimate seen in the IPM model shows a monotonically decreasing pattern during the period of the study, with the 95 % confidence interval estimates overlapping 1.0 (zero net population growth) for the first three time periods and with the upper 95 % estimate falling below one for the last two time periods of the study (Fig. 4). The pattern we see in our CJS estimates of population growth is that the mean lambda estimates fluctuate around 1.0 and the 95 % confidence interval overlaps 1.0 for the first four time periods, and the upper 95 % confidence interval is below 1.0 for the last time interval. Thus, while the demographic pattern we estimate is similar for the two approaches, the resolution of the pattern is more precise for the IPM model compared to CJS estimates.

Discussion

Our main result is that mark-recapture modelling of population growth is much more accurate for dormice in an IPM framework compared to a non-integrated approach. For the duration of the study here, the population growth parameter, λ, generally tended to become smaller over time decreasing below one (Fig. 4). With the non-integrated model, the estimate of the mean population growth parameter fluctuated around one and was lower than one in the 2009-10 time period, while IPM estimates showed a monotonic decrease in the mean estimate, which was lower than one in both the 2008-09 and 2009-10 time periods. When the population growth parameter is less than one, it may indicate negative population growth, which, if the pattern persists over a long period of time or is caused to some extrinsic factor beyond the scope of natural variation, is critical to understand in the context of conservation monitoring. Another reason to focus on the population growth parameter is its importance in understanding the function relationship between metapopulation subunits. This is of critical importance to understand trends in monitoring data, but also to inform management decisions. For example, we may use such analyses as we present here to identify so-called source populations, which produce an excess of offspring that disperse to adjacent patches. Complementing this is the ability to identify sinks where growth is negative and the population persists by immigration. While this kind of information is valuable to understand the ecology or conservation of populations, it is costly to collect the required data. Mark-recapture data for both IPM and non-integrated models are time and labour intensive. The extra data required for IPM models is relatively more common and less costly to collect, often being incidental to recording individual capture histories (nest counts, offspring counts, etc.). Another consideration is that of statistical power required to detect a difference in population growth from one, if it exists. Because the precision of estimating population parameters is improved in the IPM framework, the statistical power to resolve model parameters should be higher compared to mark-recapture alone. Thus, a lower sample will be required for a given study, which should offset the cost of performing mark recapture in the first place, and will be an important consideration in any situation when research or monitoring resources are limited. Here, we highlight the improvement in incorporating mark recapture data into an IPM framework that can be made to the assessment of population status.

Our results compare well with a recent evaluation of the precision of IPM in estimating population vital rates. Abadi et al. (2010) used IPM to model data in several scenarios varying sample size and model configuration. Their study concluded that combining data sets in the IPM framework in any way with mark recapture data alone had a dramatic effect in increasing precision in the estimation of population vital rates. Although the parameterization of our model is different, the structure of the model is similar in that we combined offspring counts with mark recapture survey data, and it did markedly reduce error in our estimation of the population growth parameter. Another finding in Abadi et al. (2010) is that there is a sample size effect in the degree to which IPM improves the precision of parameter estimation. They found that the largest impact on improving precision was in simulated studies with very small samples sizes. We suggest that this has an important implication for the use of IPM in conservation monitoring for several reasons. First, the statistical power required to resolve model parameters will in principle be achievable with less monitoring effort, when resources to devote to monitoring are limited as they often are in a conservation context. Second, sample sizes are often small in studies targeting species inhabiting a fragmented landscape, where target sample size is not under the control of researchers. These points are particularly relevant for species that occur at naturally low density, like the common dormouse (Bright & Morris 1990, Bright et al. 2006).

Although there have been significant developments of IPM in the literature, there have been relatively few examples applied to wild populations (Tempel et al. 2014). IPM analysis of avian model organisms have proven to be powerful in predicting population trends, relative to traditional mark recapture modelling (Abadi et al. 2010a). There have been very few application of IPM to monitoring and conservation in mammals (e.g. Fieberg et al. 2010), and to our knowledge here we present the first IPM case study for conservation and monitoring using IPM in a small mammal species, the common dormouse. Because the research investment in mark recapture studies is high, we strongly recommend the use of an IPM framework in order to fully capitalize on the investment and to increase the statistical power to resolve important patterns in monitored populations. Model validation in IPM is a very important step for the useful application of this technique, but several recent publications have introduced this tool to workers in ecology and conservation (Abadi et al. 2010a, Kéry & Schaub 2012), making it accessible in these fields. Thus, we strongly recommend the IPM framework for monitoring the common dormouse where mark recapture is feasible, especially when the modelling framework can improve estimation of population growth, survivorship, recruitment and migration.

Acknowledgements

We wish to thank Nida Al-Fulaij, Ian White and others at the People's Trust for Endangered Species for funding this research. We thank Chester Zoo, Natural Resources Wales, Cheshire Wildlife Trust and the Northwest Dormouse Monitoring Project for supporting this research and making data available. We thank Simone Bullion and the Suffolk Wildlife Trust for discussion of count data. This project was funded by the Peoples Trust for Endangered Species, Small Mammal Grant.

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