



Long-term trends of local bird populations based on monitoring schemes: are they suitable for justifying management measures?

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Abstract

Local biodiversity monitoring is important to assess the effects of global change, but also to evaluate the performance of landscape and wildlife protection, since large-scale assessments may buffer local fluctuations, rare species tend to be under-represented, and management actions are usually implemented on local scales. We estimated population trends of 58 bird species using open-population N-mixture models based on count data in two localities in southeastern Spain, which have been collected according to a citizen science monitoring program (SACRE, Monitoring Common Breeding Birds in Spain) over 21 and 15 years, respectively. We performed different abundance models for each species and study area, accounting for imperfect detection of individuals in replicated counts. After selecting the best models for each species and study area, empirical Bayes methods were used for estimating abundances, which allowed us to calculate population growth rates (λ) and finally population trends. We also compared the two local population trends and related them with national and European trends, and species functional traits (phenological status, dietary, and habitat specialization characteristics). Our results showed increasing trends for most species, but a weak correlation between populations of the same species from both study areas. In general, local population trends were consistent with the trends observed at national and continental scales, although contrasting patterns exist for several species, mainly with increasing local trends and decreasing Spanish and European trends. Moreover, we found no evidence of a relationship between population trends and species traits. We conclude that using open-population N-mixture models is an appropriate method to estimate population trends, and that citizen science-based monitoring schemes can be a source of data for such analyses. This modeling approach can help managers to assess the effectiveness of their actions at the local level in the context of global change.

Keywords Imperfect detection · Global change · Local scale · Population growth rate · Population trend · Species specialization index

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Zusammenfassung

Langfristige Trends lokaler Vogelpopulationen auf der Grundlage von Monitoringprogramm: Sind sie geeignet, um Managementmaßnahmen zu rechtfertigen?

Die Überwachung der biologischen Vielfalt auf lokaler Ebene ist wichtig, um die Auswirkungen des globalen Wandels zu bewerten, aber auch, um die Leistung des Landschafts- und Artenschutzes zu beurteilen, da groß angelegte Bewertungen lokale Schwankungen puffern können, seltene Arten tendenziell unterrepräsentiert sind und Managementmaßnahmen in der Regel auf lokaler Ebene durchgeführt werden. Wir schätzten die Populationstrends von 58 Vogelarten mit Hilfe von N-Mischungsmodellen mit offener Population auf der Grundlage von Zählungen an zwei Orten im Südosten Spaniens, die in einem Citizen Science Monitoringvorhaben (SACRE, Monitoring häufiger Brutvögel in Spanien) über 21 bzw. 15 Jahre gesammelt wurden. Wir haben für jede Art und jedes Untersuchungsgebiet verschiedene Abundanzmodelle angewandt und dabei die unvollständige Erfassung von Individuen bei wiederholten Zählungen berücksichtigt. Nach der Auswahl der besten Modelle für jede Art und jedes Untersuchungsgebiet wurden empirische Bayes-Methoden zur Schätzung der Abundanzen verwendet, die es uns ermöglichten, Populationswachstumsraten (λ) und schließlich Populationstrends zu berechnen. Außerdem verglichen wir die beiden lokalen Populationstrends und setzten sie in Beziehung zu den nationalen und europäischen Trends sowie zu den funktionalen Merkmalen der Arten (phänologischer Status, Nahrungs- und Habitatspezialisierungsmerkmale). Unsere Ergebnisse zeigten für die meisten Arten zunehmende Trends, aber eine schwache Korrelation zwischen den Populationen derselben Arten aus beiden Untersuchungsgebieten. Im Allgemeinen stimmten die lokalen Populationstrends mit den auf nationaler und kontinentaler Ebene beobachteten Trends überein, obwohl es für mehrere Arten gegensätzliche Muster gibt, vor allem mit steigenden lokalen Trends und sinkenden spanischen und europäischen Trends. Darüber hinaus fanden wir keine Hinweise auf einen Zusammenhang zwischen Populationstrends und Artenmerkmalen. Wir kommen zu dem Schluss, dass die Verwendung von N-Mischungsmodellen für offene Populationen eine geeignete Methode zur Abschätzung von Populationstrends ist und dass bürgerwissenschaftliche Überwachungsprogramme eine Datenquelle für solche Analysen darstellen können. Dieser Modellierungsansatz kann Managern helfen, die Wirksamkeit ihrer Maßnahmen auf lokaler Ebene im Kontext des globalen Wandels zu bewerten.

Introduction

The increasing amount and availability of biodiversity information provides the opportunity not only to monitor and assess the effects of environmental changes on species distributions and population trends (Wetzel et al. 2018), but also to facilitate research on global biodiversity issues (Bisby 2000; König et al. 2019). Given the need of resource managers and policy makers for data on biodiversity changes (Geizendorffer et al. 2016), the development of effective, long-term monitoring programs is critical to assess management and improve conservation practices (Moussy et al. 2021).

Under a global change scenario, long-term ecological studies are essential for informing the management of the effects of habitat loss, land-use transformation, and climatic change (Wells et al. 2019). The assessment of long-term population changes is frequently used to evaluate global extinction risk for species, as for example with the Red List Index (RLI) of species survival for taxonomic groups (<https://www.iucnredlist.org/>), which can be disaggregated by functional group, geographical area or country (Rodrigues et al. 2014). Also, comparisons between historical and modern populations sampled at the same locations (Verheyen et al. 2017), as well as the analyses of repeated atlas data (Peach et al. 2017), provide important insights into the effects of environmental change on biodiversity. In this context, continuous monitoring surveys conducted on a yearly

(or breeding season) basis provide improved information for understanding population dynamics (White 2018) and other ecological processes (Jiménez-Franco et al. 2020). The recent development of hierarchical models accounting for imperfect detection, provides an appropriate modeling framework for these analyses (Kéry et al. 2009; Jiménez-Franco et al. 2019; Kéry and Royle 2020).

Long-term biodiversity monitoring benefits from the development of citizen science projects (Magurran et al. 2010), which usually provide large-scale data on species distribution and abundance (Chandler et al. 2016) and allow the assessment of global population trends over time (Gouraguine et al. 2019; Taylor et al. 2019). Most of the early and well-established volunteer-based monitoring schemes were developed for bird species (Bonney et al. 2009; Kamp et al. 2021), which are generally considered as excellent indicators of environmental changes (Gregory and van Strien 2010). Pioneer initiatives at continental scales such as the Christmas Bird Count in North America (Bonney et al. 2009) are now complemented by other continental- or global-scale citizen science projects. Remarkable examples include eBird (Sullivan et al. 2017), the North American Breeding Bird Survey (BBS; Pardieck et al. 2020) and the Pan-European Common Bird Monitoring Scheme (PECBMS; Gregory and van Strien 2010). Many important bird monitoring projects are conducted at a national level compiling this information for studying bird populations, such as the Integrated Population

Monitoring program of the British Trust for Ornithology (Robinson et al. 2014), the Spanish SACRE program (Monitoring Common Breeding Birds in Spain; Seoane and Carrascal 2008; Díaz et al. 2022), and the French Breeding Bird Survey (FBBS; Princé et al. 2021).

Despite the obvious interest in assessing population trends across broad-scale areas, monitoring programs cannot effectively detect trends in all species at all spatial scales (Nielsen et al. 2009), and some studies have pointed out contrasting results between different countries or regions (Gregory et al. 2005; Riou et al. 2011). Therefore, regional and local biodiversity monitoring remains important to assess both the influence of global change and local threats on biodiversity decline, because conservation policies and management actions are usually implemented on regional scales (Kamp et al. 2021), large-scale assessments may buffer local fluctuations (Keith et al. 2015), and rare species tend to be underrepresented in continental-scale surveys (Ralston et al. 2015). In addition, in local monitoring programs, sampling designs are often adapted to locally important habitat gradients. The value of this local information in the data is easily overlooked in large-scale analyses (e.g., patchy habitat in a gradient of urban forest environments) (Pino et al. 2000; Pagaldai et al. 2021). Nevertheless, small and locally focused monitoring programs should be put into a broader-scale perspective to determine if changes are due to local or external factors (Schmeller et al. 2012).

The combined effects of global change drivers (i.e., climate change, land-use transformation, invasive alien species) are expected to vary largely across different geographical areas, ecosystems, and species (Oliver and Morecroft 2014). Different trends have been reported for European birds of different habitat types (Gregory et al. 2019; Keller et al. 2020). Globally, while common forest species are relatively stable or even increasing, a sharp decline is observed in farmland species' populations, because of agricultural intensification. However, contrasting trends can be observed in farmland bird specialists between Eastern and Western European countries (Gregory et al. 2005). Also, in Europe, the bird species richness of the Mediterranean region has decreased over the last 30 years, while the coldest Arctic and Alpine regions (coldest areas from north of Europe) have shown a positive net change in the number of species (Keller et al. 2020). This pattern indicates that the overall distribution of native European bird species has moved northwards, driven by climate change (Brommer et al. 2012; Keller et al. 2020). Global change is also expected to cause contrasting effects on species with different functional traits, i.e., belonging to different functional groups (de Groot and Vrezec 2019; Fogarty et al. 2020) or with different phenological status (i.e., migratory versus resident species, Both et al. 2009; Rushing et al. 2020). Despite regional differences and contrasting trends depending on habitat type or

species group (Díaz et al. 2022), a long-term consequence of global change is biotic homogenization, a generalized process consisting of a systematic replacement of specialist by generalist species (McKinney and Lockwood 1999; Clavel et al. 2011). A relevant study of Le Viol et al. (2012) analyzing changes in breeding bird communities across several European countries showed a significant decrease of habitat specialists over two decades, which may be attributed to land-use changes as well as to climatic change (Kerbiriou et al. 2009; Davey et al. 2011; Le Viol et al. 2012).

Within this framework, we have analyzed long-term monitoring data collected on the bird communities of two representative localities from a Mediterranean region of southeastern Spain, included in the citizen science-based SACRE monitoring program (<https://seo.org/sacre/>). We fitted open-population N-mixture models (Dail and Madsen 2011) to count data obtained in the two study areas (10 × 10 km each) during 21 and 15 years of monitoring, respectively, and estimated abundances which were used to calculate population growth rates (λ). Our objectives were (1) to assess long-term population trends of bird species, (2) compare trends between the two local populations, (3) relate local trends to national and European trends, (4) examine possible differences in local trends among species grouped by functional traits, and the generalist/specialist character of the species, and (5) interpret the observed trends in the context of local management of the study sites, as examples of areas with little change in landscape composition and structure. This study emphasizes the importance of citizen science monitoring schemes as a source of data in local areas relevant to the conservation of declining bird species, as well as the importance of open-population N-mixture models to obtain population trends.

Materials and methods

Study area and sampling design

The two study areas are La Muela (mainly scrubland habitat) and Carrascoy (mainly forest habitat), located in two localities in southeastern (SE) Spain (Supporting Information Fig. S1). Both 10 × 10 km study areas belong to areas protected under Murcia Region and European Union nature conservation regulations. La Muela is a littoral mountain massif belonging to the Natura 2000 Bird Special Protected Area (SPA) ES0000264 and Site of Community Importance (SCI) ES6200015 “La Muela-Cabo Tiñoso” (10,938.36 ha). Carrascoy is a pre-littoral mountain range (near coastal areas) belonging to the SCI ES6200002 “Carrascoy y el Valle” (11,833.25 ha.). Descriptions of both areas can be found in their Natura 2000 Standard Data Forms (<https://natura2000.eea.europa.eu/>). Both localities are separated by about 30 km

of predominantly agricultural lowlands. During the period of study, both areas have experienced great stability in landscape composition and structure (i.e., no change in the initial habitat characterization of census points). Although dominated respectively by Mediterranean shrubland and woodland, both areas experienced historical transformations creating agroforestry landscapes with sparse rural settlements and even small residential resorts. In the case of Carrascoy, urbanization and irrigation had a greater role in this historical transformation, the latter being largely abandoned and naturalized. But there have been no major changes in land use or management status since the study began (both areas have been protected by regional law since 1992 and designated as Sites of Community Importance since 2000 under European Union EU's Habitat Directive). Superimposed on this, the study region is currently experiencing the effects of climate change at an accelerated rate (e.g., species range shifts; Esteve et al. 2012).

Point count sampling was conducted at twenty sites in each study area of 10×10 km Universal Transverse Mercator (UTM) squares, with two surveys every year (first survey April 15–May 15; second survey May 15–June 15). The distance between sampling points was variable but never less than 500 m. These surveys form part of the Spanish national monitoring program for common breeding bird species (SACRE) coordinated by SEO/BirdLife (Seoane and Carrascal 2008). Following the guidelines of SACRE, each survey initially consisted of 20 sampling points, distributed along a route that could be completed during the first four hours of sunlight, through a vehicle tour with stops at the observation points. Since SACRE is based on a selection of Spanish 10×10 km UTM squares (Seoane and Carrascal 2008), the surveys typically extended from the mountain areas to their piedmonts to sample all the different habitats represented. In practice, this allowed observers to survey the entire landscape gradient from core forest areas to agricultural piedmonts.

The point counts had a duration of 5 min during which all visual or auditory contacts were recorded, ruling out possible double counts and differentiating between the birds visually or acoustically detected within and outside a radius of 25 m from the observer's position. For model analyses, we used the pooled data (counts within and outside the 25 m radius). As per the protocol of the SACRE Monitoring Program, a single observer consistently covers the same route. Therefore, all the surveys were carried out by the same observer for each study area during the study period (experienced ornithologists and authors of this study; A. J. Hernández-Navarro and F. Robledano for La Muela and Carrascoy, respectively). La Muela was sampled every year from 1999 to 2019 (21 years), and Carrascoy from 2005 to 2019 (15 years). The dataset is available in the Figshare repository (Hernández-Navarro et al. 2023).

Data analyses

We performed trend population analyses for each species in both study areas using the models of Dail and Madsen (2011) and Hostetler and Chandler (2015), which generalize the Royle (2004) N-mixture model by relaxing the closure assumption. The models require count data collected at R sites surveyed on T primary sampling periods and, optionally, J replicate observations at each site (secondary sampling periods). In our case, we collected count data at 20 sites surveyed during 21 years in La Muela, and 20 sites surveyed during 15 years in Carrascoy, with two secondary sampling periods ($J = 2$) each year in both study areas.

The models include component models that describe the initial population abundance, and dynamics of the population in the form of recruitment and survival and, finally, an observation model that allows for imperfect detection of individuals.

The initial abundance distribution describes spatial variation in abundance at site i during the first sample occasion (i.e. year 1):

$$N_{i,1} \sim \text{Poisson}(\Lambda_{i,1}),$$

where spatial covariates can be modeled on the log-transform of the expected abundance $\Lambda_{i,1}$. In addition to Poisson, abundance models can also be considered such as negative binomial, or zero-inflated Poisson (ZIP), with the Poisson and ZIP ones being used for our analyses for their better convergence.

The Dail–Madsen model assumes that population size is a Markovian process in which population size at $t + 1$ is related to population size at time t through recruitment and survival processes. Various alternative models can be used to describe the dynamics of the population, in terms of survival and recruitment or population growth rate. For example, a basic model is that in which the number of survivors follow a binomial distribution: $S_{i,t} \sim \text{Binomial}(N_{i,t-1}, \omega_{i,t})$, where S is the number of individuals surviving from $t - 1$ and not emigrating, ω is the apparent survival probability, and the number of recruits follow a Poisson distribution: $G_{i,t} \sim \text{Poisson}(\gamma_{i,t})$, where G is recruitment (number of new individuals entering the population).

There are several possible ways to parametrize population growth in the Dail–Madsen model which involve specific assumptions about survival and recruitment (Dail and Madsen 2011), and also allow us to evaluate classical density-independent and density-dependent models (Hostetler and Chandler 2015). Specifically, we fitted the six population dynamics models implemented in a publicly available software package (the function *pcountOpen* from the R package *unmarked*; Fiske and Chandler 2011). We

describe these six population dynamic models (Hostetler and Chandler 2015) below:

Constant. This model implies that the expected number of recruits is a constant that does not depend on the previous population size:

$$E(N_{i,t+1}) = \omega_{i,t}N_{i,t} + G_{i,t},$$

where $N_{i,t}$ denotes the estimated abundance at site i and primary period t , ω is the apparent survival probability, and G is recruitment $G_{i,t} \sim \text{Poisson}(\gamma_i)$. $G_{i,t}$ may vary by site (i) and primary occasion t .

Auto-regressive. Auto-regressive model:

$$E(N_{i,t+1}) = \omega_{i,t}N_{i,t} + \gamma_{i,t}N_{i,t},$$

where γ is the recruitment rate.

No-trend. Model of no temporal trend:

$$E(N_{i,t+1}) = E(N_{i,t}).$$

This arises by setting the recruitment rate $\gamma = E(N_{i,t}) * (1 - \omega)$.

Trend. Classical model of exponential growth:

$$E(N_{i,t+1}) = \lambda_{i,t}N_{i,t},$$

where λ is the population growth rate.

Ricker. Classical Ricker model for density-dependent growth:

$$E(N_{i,t+1}) = N_{i,t}e^{r(1-N_{i,t}/K_c)},$$

where r is the maximum instantaneous rate of population increase and K_c is the equilibrium abundance (carrying capacity).

Gompertz. A modified version of the Gompertz logistic model:

$$E(N_{i,t+1}) = N_{i,t}e^{r(1-\log(N_{i,t+1})/\log(K_c+1))}.$$

For simplicity, we did not use additional immigration terms in the population dynamics model, which are also implemented in the publicly available software (function *pcountOpen* from the *unmarked* package in R), and

modeled all population dynamic parameters (ω , γ , λ , r and K_c) as time-independent (i.e., not varying across years).

In addition to these six dynamic type models, the detection process was modeled as binomial:

$$y_{i,j,t} \sim \text{Binomial}(N_{i,t}, p_{i,j,t}).$$

We considered two variants for the detection part of the model, modelling the detectability probability either as constant or varying with the survey period (i.e., two values of detectability for all the year from the survey period).

The resulting 12 models (combinations of the survival/recruitment state models and detection models) considered both Poisson and zero-inflated Poisson (ZIP) mixtures, giving a total of 24 models fitted for each species in both study areas, which were ranked according to their Akaike Information Criterion (AIC) values. We did not use the negative binomial mixture because preliminary analyses showed important identifiability problems on parameters (Kéry 2018). These problems arise when parameter estimates vary depending on the chosen value of K (an integer defining the upper bound of summation in computing the marginal likelihood, Fiske and Chandler 2011). We initially set the value of K as the maximum count plus 100 and systematically checked the parameter stability of the best models (see below) using a similar approach to that used by Kéry (2018), increasing the value of K (by an amount of 100 in each step) for assessing the stability of model estimates. Specifically, we considered that estimated parameters were identifiable when the difference in the (Δ AIC) between models differing by 100 in their K values was < 0.01 . When the stabilization checking failed, the unstable model was excluded from the AIC comparison.

The model with the lowest AIC value for each species was used to estimate posterior distributions of the latent abundance for all sites and years, using empirical Bayes methods (with the *ranef* function in the *unmarked* R package). Yearly abundance estimates were summed across sites to obtain total population sizes for each species, each year at both study areas. These population sizes were used to obtain estimates of annual population growth rates ($\lambda_t = N_{t+1}/N_t$). Finally, population trends for each species were assessed by calculating the geometric mean of the population growth rates across years (Morris and Doak 2002):

$$\lambda_G = \left(\prod_{t=1}^T \lambda_t \right)^{(1/T)},$$

where T is the number of years surveyed minus 1 (20 in La Muela and 14 in Carrascoy).

Additionally, for those species for which the *Trend* model was the best estimated model, we assessed population trend

using the population growth rate (λ) which is estimated directly by that model.

Local population trends of species were compared with their Spanish and European trends obtained from Carrascal and del Moral (2020) and the PanEuropean Common Bird Monitoring Scheme (EBCC/BirdLife/RSPB/CSO 2019), respectively. Spanish trends were available for all species except one (*Tachymarptis melba*) and European trends were available for 49 species (Supporting Information Table S1).

Box plots were used to explore patterns of species population trends among functional traits, i.e., dietary groups and phenological status (migrant vs resident) in the study area (Supporting Information Table S1). Population trends were also correlated with the values of the species specialization index (SSI; Supporting Information Table S1), obtained from Le Viol et al. (2012). This index provides the variation in species preference for different habitat types, obtained from the Bird EUNIS database (Le Viol et al. 2012).

The correlation between variables was assessed using nonparametric statistics (Kendall's τ). (All analyses were run in R version 3.6.3 (R Core Team 2020)).

Results

During the study period, a total of 72 species were observed in La Muela and 76 in Carrascoy. Species with a very low number of individuals recorded during the study (<5), migrants, species out of their habitat (e.g., gulls and aquatic birds), or with identification problems (e.g., swifts, *Apus apus* and *Apus pallidus*) were excluded from population trend analyses. A total of 49 species were modeled from La

Muela, and 50 species were modeled from Carrascoy, 40 of which were shared by both localities.

Of the populations analyzed, our procedure for assessing parameter stabilization required the integer K to be selected as the maximum observed count plus 200 in 27 cases, and the maximum observed count plus 300 in 6 cases. The increase of K in the models produces a general increase in the abundance estimates (Fig. S2), which in some cases may appear to be unreliable. However, for these cases, we verified that the over-increase in abundance did not affect the estimation of population trends (i.e., the estimated λ was substantially unaffected by K). In such cases, estimates from the Dail-Madsen model might best be regarded as indices of relative abundance, suitable for trend estimation and describing relative patterns in species abundance (Kéry and Royle 2020).

Our checking procedure also detected that the best models for 14 of the species had parameter identifiability problems, mainly those with Ricker and Gompertz logistic dynamics (six cases). In these cases, we removed these models from the AIC selection table and selected alternative best models, which were checked for parameter identifiability. For three species in La Muela (*Falco tinnunculus*, *Myiopsitta monachus*, and *Turdus viscivorus*) and one in Carrascoy (*Emberiza cirrus*), we could not find identifiable models and, therefore, we excluded them from further analyses. Finally, a total of 46 and 49 species were modeled for La Muela and Carrascoy, respectively. These species had a low number of recorded individuals during the study period: 19, 13, 7, and 7, respectively.

Most of the best models (23 out of 46 and 26 out of 49 for La Muela and Carrascoy, respectively) were those considering the classical exponential growth (*Trend* model; Fig. 1

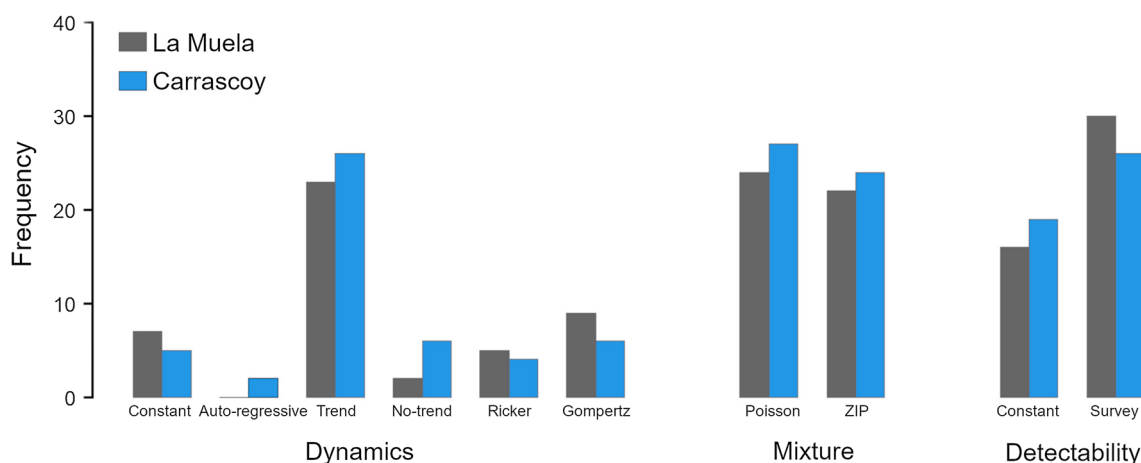


Fig. 1 Frequency of best model types (dynamics, mixture, and detectability) for population trends of bird species in the two study areas La Muela and Carrascoy (southeastern Spain) surveyed during 21 and 15 years, respectively as part of the Spanish national monitoring pro-

gram for common breeding bird species (SACRE). The models with the lowest Akaike Information Criterion (AIC) values are considered the “best models” (for more information see data analyses section)

and Supporting Information Table S2). Poisson models were somewhat more selected as best than ZIP models (24 out of 46 and 25 out of 49 for La Muela and Carrascoy, respectively), as well as models with survey-dependent detection probabilities (30 out of 46 and 26 out of 49 for La Muela and Carrascoy, respectively; Fig. 1 and Supporting Information Table S2).

The estimated population growth rates (λ) were > 1 for most species in both study areas (71.58%; Table S3). *Fringilla coelebs* and *T. viscivorus* had the highest mean population growth rate for the study area La Muela, and *Delichon urbicum* for Carrascoy, whereas *Oenanthe hispanica* and *Oenanthe leucura* had the lowest population growth rate for La Muela and Carrascoy, respectively (Table S3). For 12 species (26.09%) in La Muela, and 18 species (36.73%) in Carrascoy the 95% confidence interval did not overlap 1, which indicates an increasing or decreasing population trends. Only five species showed confidence intervals that did not include 1 in both areas, three with the positive sign (*Burhinus oedicnemus*, *F. coelebs* and *Galerida cristata*), one with negative sign (*Cuculus canorus*), and one with the opposite (*Upupa epops*).

The correlation between estimated λ 's for populations in La Muela and Carrascoy was weak ($\tau=0.29$ [CI 0.09, 0.49], $n=37$). Twenty-six out of the 37 species modeled in both study areas (70.27%) showed the same trend (19 increasing and 7 decreasing), while 11 (29.73%) showed opposite population trends in both study areas (Table S3).

For those species for which the *Trend* model was their best model, a similar trend pattern was observed when

considering the population growth rate (λ) estimated directly by this model (Supporting Information Fig. S3). Consequently, the correlation between the λ 's estimated by *Trend* models and those obtained with the yearly population sizes were very high ($\tau=0.89$ [CI 0.83, 0.95], $n=49$).

Estimated detection probabilities of individuals varied considerably across species and study areas (Supporting Information Table S4). For constant detectability models the probabilities of individuals' detection ranged from 0.001 to 0.262. For survey-dependent detectability models, the probabilities of detection tended to be slightly higher in the first survey in Carrascoy's populations (survey 1 average [range]=0.088 [0.001, 0.393]; survey 2 average [range]=0.079 [<0.001 , 0.213]), but not in La Muela's populations (survey 1 average [range]=0.043 [0.002, 0.179]; survey 2 average [range]=0.048 [<0.001 , 0.194]).

In general, local population trends were unrelated with trends observed at national and continental scales (Fig. 2). Correlation tests showed weak associations between trends for populations from both study areas (La Muela–Spanish trends: $\tau=0.19$ [CI -0.02 , 0.41], $n=45$; La Muela–European trends: $\tau=0.17$ [CI -0.06 , 0.41], $n=39$; Carrascoy–Spanish trends: $\tau=0.29$ [CI 0.13, 0.45], $n=49$; Carrascoy–European trends: $\tau=0.08$ [CI -0.12 , 0.28], $n=43$). However, clear contrasting patterns exist for several species, mainly those with increasing local trends and decreasing Spanish and European trends (e.g., *Alectoris rufa*, *Passer domesticus*, *Streptopelia turtur*, and *Sylvia undata*; Supporting Information Table S1 and Table S3, respectively).

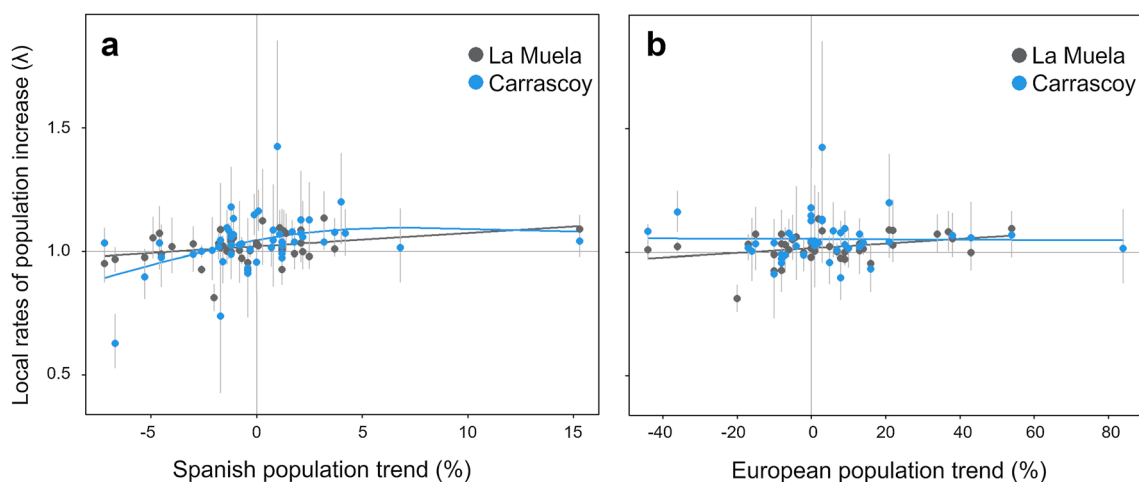


Fig. 2 Relationship between the estimated bird population λ 's from both study areas (La Muela and Carrascoy, southeastern Spain, surveyed during 21 and 15 years, respectively as part of the Spanish national monitoring program for common breeding bird species SACRE) with the Spanish (a) and European (b) population trends (segments represent 95% Confidence Intervals). Spanish trend values are average yearly changes in %, from 1998 to 2011 (Carrascal

and del Moral 2020). European trend values are percent population changes for a 10-years period 2008–2017 (EBCC/BirdLife/RSPB/CSO 2019). The curves represent a cubic smoothing spline fitted to the data to better illustrate the trends. List of species considered in this study are included in Table S3. One species with no information on its Spanish trend, and 9 species with no information on their European trend are not represented

The comparison of the estimated population growth rates among species grouped by phenological status and dietary group showed no clear patterns of variation (Fig. 3). Correlation tests also showed a weak relationship between the species specialization index and the population trends from both study areas (La Muela: $\tau = 0.12$ [CI $-0.05, 0.30$], $n = 46$; Carrascoy: $\tau = -0.02$ [CI $-0.20, 0.16$], $n = 49$; Fig. 4).

Discussion

Birds are good environmental indicators, and the long-term monitoring of their populations is well established in numerous programs (Gregory and van Strien 2010). As populations trends and abundance estimation are affected by species detection probabilities (Sanz-Pérez et al. 2020), dynamic N-mixture modelling provides an appropriate framework to estimate population size and to analyze trends and demographic characteristics while accounting for imperfect detection (Kidwai et al. 2019; Kéry and Royle 2020). Our trend analysis of local populations of 58 species and the comparison with national and continental analyses show an inherent variability of population trends at different spatial scales.

The Spanish common bird census scheme (SACRE) offers an excellent opportunity to assess population changes at these different scales, be it the whole state or large geographical or administrative subunits. With two replicated surveys per spring season in 20 circular plots (with a radius of 25 m) per site, it has been shown to provide highly reliable indications of population trends (Carrascal and del Moral 2020), as well as comparing different trends according to

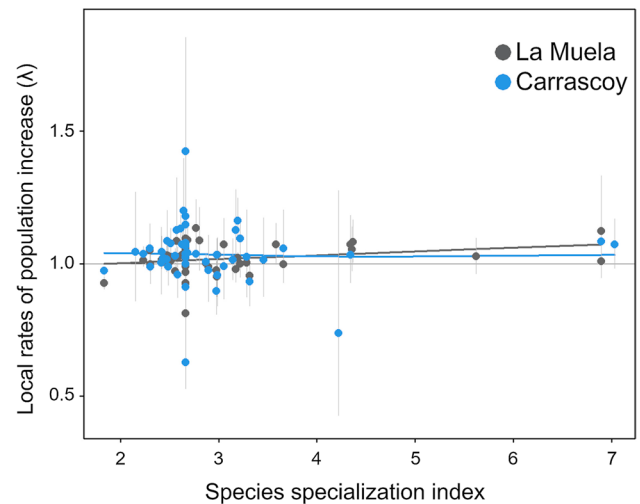


Fig. 4 Relationship between the estimated bird population λ 's from both study areas La Muela and Carrascoy, southeastern Spain, surveyed during 21 and 15 years, respectively as part of the Spanish national monitoring program for common breeding bird species SACRE. Segments represent 95% Confidence Intervals with the species specialization index (SSI)

agricultural habitat types and locations inside or outside Natura 2000 sites (Díaz et al. 2022), but the value of this census method for local management and conservation of bird habitats has not yet been assessed.

We highlight the importance of analyzing local population trends and its usefulness for conservation management for different reasons. First, even when consistent long-term trends are observed at broad scales (i.e., country or continental scales), trajectories of local populations can be highly

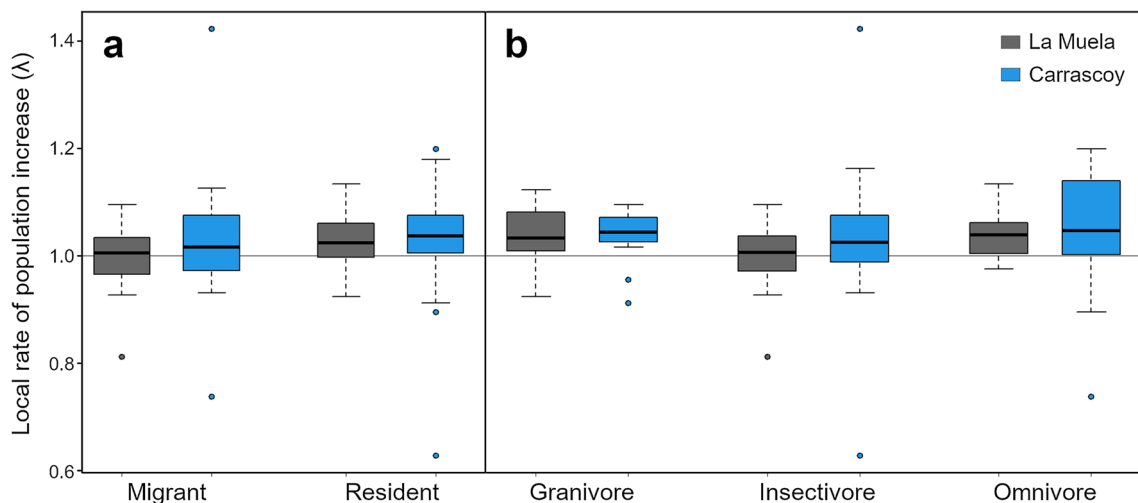


Fig. 3 Boxplots comparing the estimated population λ 's among species grouped by (a) phenological status and (b) functional group dietary, for both study areas (La Muela and Carrascoy, southeastern Spain, surveyed during 21 and 15 years, respectively as part of the

Spanish national monitoring program for common breeding bird species SACRE). Note that boxes show the first and third quartiles and whiskers show the last observation within 1.5 times the interquartile range from the edge of the box for values of λ

variable (Vercelloni et al. 2017). In this sense, it is important to identify local factors influencing trends, as well as to identify those areas with increasing local population trends of species with declining global populations. These local areas may be identified for special conservation of relevant species (e.g., endangered species that have increasing trends in local areas, but decreasing trends in broad scales). Second, some species are better monitored on a local scale than on broad ones with some studies indicating that not all species (from different taxonomic groups) can be effectively monitored in broad-scale programs (Manley et al. 2004; Nielsen et al. 2009). Comparisons may generate trends in opposite direction, with wide inter-site and inter-annual fluctuations (Greenberg et al. 2018). Third, estimates of local trends may be affected by site-selection bias, defined by Mentges et al. (2020) as a preference for sites that are either densely populated or species rich (and specifically ranked by these authors as occurring with decreasing likelihood across four major sources of biodiversity data: citizen science, museums, national park monitoring, and academic research), which may even reverse the direction of trends. These possible differences in population trends between scales allow us to redefine sample sites as well as objectives from the former population monitoring framework. For instance, a biased selection of non-impacted locations, may be used as control sites and are required to appropriately assess population changes (Fedy et al. 2015) and to set target reference sites. However, when the aim is to monitor local indicators of biodiversity and environmental quality, a single or a few sampling units can provide a useful and cost-effective assessment tool. Nevertheless, in our case, these low number of sampling routes and annual surveys does not allow to test for observer effects, being the observer experience also a common aspect to be considered in the monitoring frameworks (Zuberogoitia et al. 2020).

Our results showed weak correlation between the local populations of the same species from both study areas and only five species showed similar trends in both areas (one species showed trends from the two study areas with opposite directions). Moreover, contrasting patterns exist between local and national and continental scales for several species. This is the case for several species around which there is much debate about the evaluation of their threatened status or their response to certain management models (e.g., Red List Team 2020). For example, *A. rufa* has a positive trend in both localities (significant in Carrascoy) and is considered in decline in both Spain and Europe (Supporting Information Table S1, and references cited there). This species could be responding locally to agroforestry systems with moderate hunting pressure combined with low intensity agricultural systems and protected areas that can act as a refuge (Vargas et al. 2006). The same could apply to *S. turtur*, for which the agroforestry mosaics of both areas, including orchards

in the case of Carrascoy, could explain a non-declining status (Moreno-Zarate et al. 2020; contrary to that of the Spanish and especially European populations, Supporting Information Table S1). Such mosaics and the persistence within them of patches of shrubland large enough to host fragmentation-sensitive species could also explain the favorable (and opposite to Spanish and European) trend for *S. undata* (Zapata and Robledano 2014). Overall, it seems to be confirmed (for Carrascoy), the importance of agroforestry mosaics with irrigated crops in semi-arid areas of the Iberian Peninsula, as long as patches with low human disturbance are maintained within them (Lara-Romero et al. 2012). Similarly, some degree of sparse urban development could provide additional resources favoring species that also decline at larger scales (e.g., *P. domesticus*, Supporting Information Table S1).

Despite some disagreement among European, Spanish, and local trends of some species populations, our results showed increasing trends for most species, which contrast with the overall decline of common passerine species observed worldwide (Inger et al. 2015; Rosenberg et al. 2019). Similarly, there are species with strong expansive dynamics, related to natural processes of range expansion (e.g., *Streptopelia decaocto*), or even exotic invasive species whose regional trends are reflected in one or both study areas (Calvo et al. 2017). The latter is the case with *M. monachus* in La Muela which could not be modeled but is known to be expanding from its initial urban settlements in the nearby city of Cartagena, Spain, and could create conflicts with agricultural activity in these suburban rural areas (Calvo et al. 2017). On the contrary, there are species (*O. leucura*, *Merops apiaster*) whose local dynamics are concordant with their decreasing population trend as in Spain (Table S3), but opposite to the increasing population trend expected from their predicted response to climatic change (Huntley et al. 2008). For these species, local management issues can be relevant, particularly for perturbation-dependent species like *O. leucura*. Given the ecology of the species of this genus, it is not surprising that *O. hispanica* decreases markedly in La Muela, while *O. leucura* does so in Carrascoy. Both species are negatively affected by afforestation or encroachment of formerly low-cover dry pastures and shrublands (Birdlife International 2015), and *O. leucura* is affected specifically by degradation of human-made nest sites like abandoned quarries, uninhabited shelters and buildings (Moreno 2016).

Our results showed no clear relationships between population trends and species phenological status, dietary or habitat specialization characteristics. However, it has been suggested that climate change can alter competitive relationships between resident and migratory birds (Ahola et al. 2007) and may benefit insectivores by increasing food availability (Vafidis et al. 2021). Moreover, there exists strong evidence of a biotic homogenization process affecting

breeding bird species across Europe, driven by population declines in specialized species (e.g., farmland birds; Díaz et al. 2022) and population increases of habitat generalists (Le Viol et al. 2012; Gregory et al. 2019). Systematic monitoring of populations like those studied here could help to detect the occurrence of such processes locally. Furthermore, depending on the characteristics of the bird species at local scale, other indices can be applied, such as multi-species indices to compare between two specific habitats, e.g., farmlands and forest birds (Gregory et al. 2019).

These results may be useful for local managers when validating actions taken to preserve current land uses and landscape environments, as a means of detecting management gaps and identifying lines of improvement, although further research is needed to provide evidence of causal relationships and to disentangle different management practices and other confounding factors. The main steps to follow when taking advantage of local censuses in conservation management could include incorporation of main protected areas of a regional network as monitoring sites similar to those included in this study (including their peripheral areas), cooperation with academic entities and scientific-conservation-oriented Non-Governmental Organizations (NGOs; e.g., Birdlife International), and the incorporation of local management variables and other potential influencing factors for optimal interpretation of results. Environmental managers could encourage the monitoring of many strategically distributed sampling units (in our case 10×10 UTM squares, e.g., one per protected area), either through their own technical staff, citizen science schemes, or both. We consider that the 10×10 km units are suitable for sampling average protected areas (mountain massifs) and its buffer zones, which in Murcia region are around 100 km^2 (10,000 ha). Where such units are not covered regularly by volunteers, 2 days of field work per year may be sufficient to provide annual coverage (Carrascal and del Moral 2020) and allow for comparison of local and regional trends. Although our study focuses on protected landscapes, similar monitoring units could be deployed in areas experiencing extensive anthropogenic pressure.

The interest in long-term monitoring programs stems from the potential of using them to evaluate extinction risks (e.g., IUCN Red List assessments; Rodrigues et al. 2006) and from the use of populations trends as indicators of environmental health (e.g., European wild bird indicators; Gregory and van Strien 2010). The assessment of biodiversity change is a challenge under scenarios involving climate change, land-use transformation, pollution threat and invasive species spread (de Chazal and Rounsevell 2009), for which assistance through citizen science can contribute locally across extensive regions (Pereira et al. 2013). Monitoring of local species richness is crucial to track global biodiversity changes, and representative sites can provide useful

information about what is happening locally to bird species under well-defined management conditions (Valdez et al. 2023). For those species exhibiting trends different from those established at larger spatial scales, local monitoring and data modelling can provide the first step to investigating potential causes and to assessing the effectiveness of land use and nature management decisions affecting biodiversity and ecosystem services (Requena-Mullor et al. 2018). A further step is to consider control zones at a local scale that do not change over time (e.g., our study areas), where increasing population trends of bird species adapted to these habitats may be observed in comparison with country or European trends representing a general situation (e.g., *S. turtur* in our study areas). In this sense, some study areas could be indicators of local conservation/management and others could simply reflect general status. A recent study has evaluated sites inside and outside Natura 2000 to validate this pattern (Díaz et al. 2022). Comparisons of local and national trends might not be the most informative ones, due to different land-use patterns. However, national trends are an obligate reference framework, and regional data on trends in areas with similar ecological land-use patterns are unfortunately not available.

In a wider context, variation in local trends and random local fluctuations, or even imperfect monitoring, could be buffered by large-scale assessments (e.g., through a portfolio effect; Keith et al. 2015), but systematic local assessments remain important because management actions may be implemented on regional or local scales (Kamp et al. 2021). Therefore, it can be beneficial to link conservation and management actions for local populations with regional/global efforts (Warnock et al. 2021), and the monitoring of local populations can help in the implementation of management plans for the European Union's Natura 2000 sites (Wätzold et al. 2010), as well as for other complementary areas contributing to green infrastructure: buffer zones, green corridors, and municipality parks (Zapata and Robledano 2014).

Conclusions

In this study, we evaluate long-term trends of local bird populations based on the Spanish common bird census scheme (SACRE), which offers an opportunity to assess population changes as well as to compare the estimated local trends with other spatial scales (at country or European level). Our results show that local population trends may differ from global trends, informing conservation and management in two ways: increasing local population trends of species with declining global populations indicate the importance of conserving local habitat, while declining local trends inform managers on threats or local changes in conditions for these species. Our study also shows how the use of citizen science

data and hierarchical modelling allow us to cost-effectively assess population trends, mainly to validate local management actions aimed at habitat and landscape preservation. We also conclude that N-mixture models provide useful detectability-corrected values of population estimates and trends.

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Declarations

Conflict of interest The authors have no competing interests to declare that are relevant to the content of this article.

Ethical approval This research did not require ethics approval or field work permissions.

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