

RESEARCH ARTICLE

Aggregating three sources of long-term trends of swallows and martins to identify priority conservation areas in the Great Lakes region

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Abstract

1. Long-term monitoring of bird populations across scales is important in evaluating conservation targets and creating effective conservation strategies. For nearly six decades, the Breeding Bird Survey (BBS) has served as the primary broad-scaled source of relative abundance trends of swallows and martins in North America. Recently, however, it has become possible to obtain breeding population trends using semi-structured eBird community science data. Moreover, weather surveillance radar data of swallow and martin roosting populations yield a third complementary source of trend information.
2. Using results from these three approaches, we propose a novel method of spatially combining estimates of percent change per year into a probability of directional agreement and/or disagreement that describes (1) the direction of the trend within a given region, (2) the amount of evidence associated with the estimate and (3) how much uncertainty surrounds it. We focus our efforts on an area of high Hirundinidae concentration in the North American Great Lakes region and predict trends from 2012 to 2022.
3. We found a high probability of agreement between all three sources about observed declines in swallow and martin trends in the region surrounding Lake Ontario and to the west of Lake Michigan. Focusing future research on these regions could improve our understanding of these declines and help build more targeted conservation initiatives.
4. *Synthesis and applications.* Our data integration methodology allows managers to identify regions that accumulate evidence of concerning trends across multiple wildlife monitoring schemes. These regions can thus be prioritized in conservation and management efforts. This approach can be generalized to other sources of long-term monitoring data of different species, at different stages of their annual cycle, in any geographic location.

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avian conservation, Bayesian analysis, citizen science, hierarchical modelling, North American Breeding Bird Survey, radar ornithology, species monitoring

1 | INTRODUCTION

Relative abundance estimates and trends are a crucial source of information for conservation decision-making, determining land use policies and allocation of conservation funds (Hudson et al., 2017). Long-term monitoring programmes that yield such trends are even more important in the face of a changing climate, when there is an urgent need to understand if and how animals are changing their use of space and time to adapt to new environmental conditions (Magurran et al., 2010; Parmesan et al., 2005; Wolkovich et al., 2014). Additionally, due to their straightforward interpretation, relative abundance trends act as headline indicators, packing what can be a complex biological process into a metric that is easily understood by the public and by policy-makers, gathering support for conservation and promoting discussion about the biodiversity crisis (Gregory et al., 2008; Loh et al., 2005; van Strien et al., 2012).

In recent years, there has been growing concern about observed declines of avian aerial insectivores in North America, with some authors estimating a decrease of 31.8% (95% confidence intervals: 26% and 36.4%) in breeding population abundance of 26 species of this guild between 1970 and 2017 (Nebel et al., 2010; Rosenberg et al., 2019; Smith et al., 2015). Causes for these declines are complex and hard to disentangle, particularly for migratory species, but include habitat loss, impacts from environmental contaminants and phenological mismatches due to climate change (Cox et al., 2019; Hallmann et al., 2014; Kardynal et al., 2020; Spiller & Dettmers, 2019). In Canada and the United States, two sources of large-scale relative abundance trends of songbirds are available: the North American Breeding Bird Survey (hereon, BBS) and, more recently, the data products from eBird Status and Trends (hereon, eBird).

The BBS has been conducted annually since 1966 (with an exception in 2020 due to the COVID pandemic) across 2500–3000 roadside routes where expert volunteers conduct 50 3-min point counts (Droege, 1990). The surveys are coordinated by the United States Geological Survey, the Canadian Wildlife Service and the Mexican National Commission for the Knowledge and Use of Biodiversity (the latter since 2008). Multiple organizations and decision makers use data from the BBS to inform avian conservation decisions in Canada and the United States. In their Avian Conservation Assessments Database, for example, Partners in Flight and Bird Conservancy of the Rockies used BBS data to support status assessments of more than 260 species with regard to relative abundance trends and population size scores (Hudson et al., 2017). Furthermore, BBS data have been used to inform status assessments for species at risk both in the context of the Endangered Species Act in the United States and of the Canadian Species at Risk Act (Hudson et al., 2017). The main challenge

faced when modelling and analysing BBS data, however, is that it does not take probability of detection into account, which makes results less comparable between species if their breeding behaviour results in variation in detectability (Somershoe et al., 2006). Additionally, due to challenges with counting the number of birds in breeding colonies, there is more inter-year variation in counts of social breeders such as Cliff Swallows (*Petrochelidon pyrrhonota*), Purple Martins (*Progne subis*), Bank Swallows (*Riparia riparia*) and Barn Swallows (*Hirundo rustica*) (Droege, 1990; Johnson et al., 2017).

While BBS has served as the keystone data for assessing relative abundance trends of bird populations throughout North America for many years, it is not the only data source that allows this type of inference. Recently, the Cornell Lab of Ornithology published a dataset of breeding population trends of hundreds of avian species from 2012 to 2022 that can be downloaded and manipulated with the R package *ebirdst* (Fink, Auer, et al., 2023; Strimas-Mackey et al., 2023). One of the main challenges of obtaining trends with eBird data is the pervasive confounding between real relative abundance changes and year-to-year variation in the observation process, particularly due to the growing number of checklists received by eBird every year (Johnston et al., 2021). To address this and other sources of temporal confounding, Fink, Johnston, et al. (2023) and Johnston et al. (2025) developed a double machine learning model that yields trend estimates while explicitly accounting for spatial dependency between trends.

In addition to these two approaches, we propose a complementary source of trends in the overall seasonal impact of swallow and martin communal roosts. These large aggregations of Hirundinidae occur in North America after these aerial insectivores finish breeding, before starting their southward migration (Russell & Gauthreaux, 1998). Due to the high density and flight altitudes reached during the early morning roost dispersal, roosts are systematically detected by weather surveillance radars, which can be used to estimate roost size, timing and location (see Belotti et al., 2023; Bridge et al., 2015; Deng et al., 2023; Kelly et al., 2012; Kelly & Pletschet, 2017; Russell, 1996). We focus our study on the Great Lakes region, where swallow and martin roosting occurs mainly from late July to early September, gathering adults and juveniles of five species of Hirundinidae: Purple Martins, Tree Swallows (*Tachycineta bicolor*), Barn Swallows, Bank Swallows and Cliff Swallows. The roost size estimates obtained from the radars reflect daily relative abundances of Hirundinidae, but because the roost turnover rate is unknown, we cannot compose them into a regional relative abundance across the roosting season (e.g. individuals could be double counted). Instead, we define a metric of overall seasonal impact of swallow and martin roosts, which is the sum of the daily number of birds found between 1st of June and 31st of October for each season, balancing changes in population size and season duration.

Having three different sources of trends gives rise to the challenge of comparing different estimates and correctly interpreting them in light of their strengths and weaknesses. A commonly used approach treats the BBS estimates as a benchmark against which to test other sources of data, as done by Walker and Taylor (2017), Horns et al. (2018) and Saracco et al. (2008). This approach is justified by the fact that the BBS is the longest running structured survey of breeding species in North America, and both the survey design and statistical models used to analyse these data have been widely discussed within the scientific community following the publication of foundational works, such as Link and Sauer (2002) and Link et al. (2020). Studies with this methodology have found some agreement between trends derived from models using eBird checklists and BBS trends; however, because of the different sampling biases and process-specific characteristics of each source, it is unlikely that trend estimates will be pointwise similar or highly correlated, particularly when examining a wide range of species with varying detection characteristics Horns et al. (2018) and Walker and Taylor (2017). Understanding the methodological reasons for disagreements between sources is a fundamental problem; however, the reality could be that a single source of data may not be able to describe the full complexity of all species' temporal dynamics. Additionally, a pointwise match with BBS trends is even less likely in estimates from data collected at different moments of the annual cycle, like radar data, yet each of these metrics can offer valuable information about the state of bird populations.

Rather than prioritizing one data source to the detriment of the others, we aim to maximize the use of available information across sources by spatially combining trend estimates to identify regions of conservation concern, using the Great Lakes region of the United States as a testbed for our analyses. We present a method that accomplishes this by leveraging the fact that the three models used to analyse the three data sources output realizations of the distribution of estimated trends: that is, posterior distributions, in the case of the Bayesian models employed for both radar and BBS data, and resampling folds, in the case of eBird. We employ this technique to identify regions that accumulate evidence of important declines across our three data sources and could, thus, be considered priority conservation areas. We use species-specific estimates from eBird and BBS to complement the results from the radar data, which lack the same taxonomic resolution. Finally, we discuss the significance of these findings for aerial insectivores and comment on the applicability of this technique to other species, highlighting its advantages in structured conservation decision-making frameworks.

2 | MATERIALS AND METHODS

2.1 | Spatial sampling

In order to spatially combine and compare the three different sources of trends, we needed to establish a spatial partitioning of the Great Lakes region that matched the sampling limitations of all three

sources. Inference on the BBS data is possible in any spatial partition if at least one route per cell exists. The original survey design includes sampling routes in a grid with cells of 1° in longitude and 1° in latitude, equivalent in area to a square with a width of 100km (Droege, 1990). The eBird trends are released as model predictions within a grid of square cells with a width of 27km. Lastly, the radar data can be partitioned into cells with any radius larger than approximately 10km, to account for possible error in the estimation of roost location (Kelly & Pletschet, 2017). We accommodated these different prediction frames by aggregating eBird cells until each larger cell had the same average area as the original BBS cell in the Great Lakes region (see Figures S1 and S2 in the supplements for maps of eBird and BBS sampling schemes). This procedure resulted in a square grid with cells of approximately 100km by 100km. While the area covered by BBS and eBird spans the entire Great Lakes region, radar coverage is limited by the radar range of 150km (roosts farther away are likely missed due to higher beam heights, see Figure S3 in the supplements for radar coverage map). Our analyses focus on 65 cells that were sampled by all three sources.

2.2 | Radar data filtering and processing

In what follows, we describe specific aspects of the data filtering and processing relevant to this study, but refer the reader to Belotti et al. (2023) for additional details. The machine learning pipeline is thoroughly described and evaluated in Cheng et al. (2020).

Swallow and martin roosts typically occur in the summer, after these species have finished breeding and before they start their southwards migration (Kelly & Pletschet, 2017; Russell, 1996). We captured the roosting period by downloading all radar scans available between 1st of June and 31st of October for the Great Lakes region (12 radar stations) from 2000 to 2022. We restricted our sample to scans made between 30min before local sunrise and 90min afterwards (an average of 16.2 scans per day), when we typically observe roost departures. Radial velocity and reflectivity in these scans were used as input to a machine learning pipeline that leverages the capabilities of a Faster R-CNN model coupled with a Kalman Filter to detect and track roost dispersals in radar data (Cheng et al., 2020). The pipeline outputs collections of bounding boxes (so-called tracks), each collection representing a single dispersal event.

The machine learning pipeline can identify roosts with reasonable accuracy; however, the differentiation between roost dispersals and precipitation still requires quality control (for details about model performance, please see Cheng et al., 2020). Because of this, we designed a manual screening protocol used by three independent screeners to examine all the scans overlaid with bounding boxes to evaluate the predicted positive tracks, classifying them according to the predominant type of noise, if there was any, or labeling them as clear roosts if they were not contaminated. The screeners also labelled days when precipitation, anomalous propagation or other sources of radar noise were so intense that we could not see roosts in the scan if they were present; we considered those days unsampled.

After the manual screening, we used the coordinates of the bounding box centroid and the radius of the bounding box to extract radar reflectivity measurements for each detection. Under conditions specified in Chilson et al. (2012), radar reflectivity can be interpreted as the density of scatterers of a given radar cross section within each radar sampling volume. We make the assumption that all scatterers within the roosts are Purple Martins—which yields conservative estimates of the number of birds, since they are the largest Hirundinidae in the Americas—and use the relationship established by Horton et al. (2019) to infer their radar cross section of 15.62 cm^2 from their average mass of 51 g (Dunning, 2008). By dividing radar reflectivity (measured in linear scale) within each pixel by the target radar cross section and multiplying it by the radar sampling volume, we obtain estimates of the number of birds within each volume of the airspace sample by the radar.

We summarized counts across radar sweeps to obtain estimates of the numbers of birds across the entire vertical structure of each dispersal. To do this, we grouped the sweeps in each detection in bins of 1° , according to their elevation angle. We then took the mean bird count of each bin and summed counts across altitudinal bins. Doing so helps minimize the double counting of birds in airspace regions sampled twice by two consecutive sweeps with less than a 1° angle change between them. The last post-processing step was to handle roost departures found in regions sampled by more than one radar. We accounted for that by grouping overlapping tracks so that each group of tracks corresponds to a single dispersal event.

At this stage in the data processing workflow, we generated estimates of the number of birds per clear dispersal, and we could then aggregate those to get daily estimates of the number of birds within any geographical subregion of our study area. We did so by summing dispersal size estimates per day for each grid cell. This yielded counts per day within a season. We further summarized those by summing the counts across each season, which gave us an estimate of what we called 'population impact' (in units of number of birds \times day) of swallow and martin roosts on each cell for each year. This metric is proportional to the amount of faecal matter deposited during one season, for example, or to the consumption of biomass by roosting swallows and martins. It thus describes that the potential influence roosts could have on the landscapes that support them and has been used in studies of water quality to calculate nutrient deposition rates of waterfowl flocks (Gremillion & Malone, 1986; Manny et al., 1994).

We extracted two metrics of the quality of our sampling effort per year. The first was the percentage of unobserved days within each season for each cell. This reflected the fact that some scans were missing from the Amazon Web Services archive, which stores all the radar data collected in the United States, or that weather and/or noise were so intense on a given day that we would not have been able to see the roosts if they were present. The second metric was the percentage of groups of tracks that were classified as noise by the screeners. We used this metric to account for the fact that some dispersals had to be removed from our daily count summaries because they were contaminated with noise. We emphasize that low values of both metrics reflect

poor observation quality of a given cell-year, whereas high values reflect better observation quality.

2.3 | Population impact trends

We obtained trends of population impacts by adapting the hierarchical generalized additive model with cell-year random effects established by Knappe (2016) for the Swedish Breeding Bird Survey and employed in Smith and Edwards (2020) to analyse BBS data. Our model accounts for spatial autocorrelation in the residuals by using an intrinsic conditional autoregressive (iCAR) structure detailed in Morris et al. (2019) and implemented in Smith et al. (2023) and Bled et al. (2013) for the BBS data.

Our estimates of population impact were either zero or a very large number, with a mean of 93,415 and a standard deviation of 179,646. In order to model such large variation, we divided the impacts for each cell and year by the maximum impact observed on that cell across all years. This rescaling mapped our large numbers to the interval between 0 and 1 with a cell-specific scaling factor, where 1 corresponds to the maximum value observed within a cell across all years of our study. However, our model should be capable of estimating values that exceed the maximum value of each cell, so our response should not be constrained to the unit interval. Because of this, we used a gamma likelihood with an exponential link to connect the nonlinear model expression to our adjusted response $Y_{i,t}$, where $i = 1 \dots I$ indexes cells and $t = 1 \dots T$ indexes years (scaled so that 2000 is year 1, 2001 is year 2, etc.). The model can then be written as:

$$Y_{i,t} \sim \text{gamma}\left(a, \frac{a}{\mu_{i,t}}\right) \quad (1)$$

$$\log(\mu_{i,t}) = \psi_i + S_i(t) + \eta \times \text{unobserved}_{i,t} + \delta \times \text{noise}_{i,t}$$

where the rate parameter of the gamma distribution can be written as a function of the distribution's mean ($\mu_{i,t}$) and shape (a).

The parameter ψ_i is random intercept representing initial population size in the baseline year. The smooth function $S_i(t)$ describes the nonlinear relationship between impact and year within each cell. We attempted to add cell-year effects to describe fluctuations around the mean smooth function for each cell, as was done in Link et al. (2020) and Smith and Edwards (2020); however, our data did not allow estimation of both the smooth function and the fluctuations. We accounted for incomplete observation of a given season and for the presence of noise-contaminated tracks not included in the measured total impact by adding the percentage of unobserved days and the percentage of noise-contaminated tracks as covariates in the model. The coefficients for these covariates are η and δ , respectively.

The influence of both effort correction covariates on the scaled total impact is mediated by the exponential function. We designed these covariates so that when they are equal to zero, a season was completely observed and their effect on the total impact will be

equal to 1 ($\exp(0) = 1$). As the covariates move towards 1, our observation of the season becomes increasingly incomplete, requiring increasingly larger corrections, that is, we need to multiply the total impact by a number greater than 1. Because of this, we restrict η and δ to be positive values to reflect the fact that lower observation of a season requires a greater correction factor (recalling that $\exp(x) > 1 \Leftrightarrow x > 0$).

We used thin plate regression splines to build a basis of K knots $B_i = \{b_{i,1}(t), \dots, b_{i,K}(t)\}$ for each cell of our grid (Wood, 2017). We can then write the smooth function for each cell as a linear combination of the elements of the basis and a series of cell-specific coefficients $\beta_{k,i}$:

$$S_i(t) = \sum_{k=1}^K \beta_{k,i} b_{k,i}(t) \quad (2)$$

where each $\beta_{k,i}$ is drawn from a normal distribution with standard deviation σ_β and a cell-specific mean α_i . We accounted for spatial autocorrelation by adding an iCAR structure to the α_i parameters describing the mean smooth coefficient per cell. This model structure makes it so that each α_i inherits information from the set N_i of its neighbours, here defined as all the adjacent cells to cell i (using the queen neighbourhood rule, where each cell has at most eight neighbours). This is formalized by drawing α_i from the following distribution:

$$\alpha_i \sim \text{normal}\left(\frac{\sum_{n \in N_i} \alpha_n}{N_i}, \frac{\sigma_\alpha}{N_i}\right) \quad (3)$$

We fit our model in Stan (Stan Development Team, 2023) via the R programming language (R Core Team, 2018) using the package `rstan` (Stan Development Team, 2023). We estimated l parameters ψ_i , two parameters η and δ , $l \times K$ coefficients $\beta_{i,k}$ and l coefficients α_i

for the smooth terms, one parameter a determining the shape of the gamma likelihood and standard deviations σ_β , σ_α and σ_ψ . We used a truncated Student- t prior on all the standard deviations and on the parameters η and δ and specified it with three degrees of freedom, location equal to zero and a scale parameter of 2.5. This choice of prior provides minimal information about possible parameter range to improve convergence, but does not make strong assumptions about its real value (Gelman et al., 2008). The prior for the shape of the gamma distribution, a , is a flat gamma distribution with rate and scale equal to 0.01, which did not cause issues in our case because the variance was not close to zero (Gelman, 2006). In Table 1, we provide a list of model parameters, their interpretation and the priors assigned to them.

We fit our model using 6500 Markov chain Monte Carlo (MCMC) iterations and 1000 warm-up iterations, evaluating convergence and parameter estimates in a thinned subset of 2400 samples. We thinned the samples of the posterior distribution of all parameters to reduce within-chain autocorrelation. Even though we fitted the model with data from 2000 to 2022, we estimated the posterior distributions of population impact predictions from 2012 to 2022. With this, we leverage all the information contained in the data for the years before our study period but match the fixed timeframe of the eBird Status and Trends product (the same was done with the BBS model, see below). We used the population impact estimates to obtain the posterior distribution of the geometric mean trend from 2012 to 2022, which are samples of the geometric mean trend and describe the variation of estimates around the mean.

2.4 | BBS and eBird trends

We downloaded ensembles of eBird estimates of percent per year change from 2012 to 2022 for our target species—Purple Martin,

TABLE 1 Parameters used to assess population trends of swallows and martins in the Great Lakes region listed with their verbal interpretation and the prior we assigned to them. Cells are indexed by $i = 1 \dots l$, years are represented by $t = 1 \dots T$ and knots are indexed by $k = 1 \dots K$. We fit a model with intrinsic conditional autoregressive structure (iCAR) to describe spatial relationships between cells.

Symbol	Prior	Interpretation
η	Zero-truncated Student- $t(3,0,2.5)$	Coefficient of the correction for unobserved days within a season
δ	Zero-truncated Student- $t(3,0,2.5)$	Coefficient of the correction for tracks lost to noise contamination within a season
α_i	$\text{normal}\left(\frac{\sum_{n \in N_i} \alpha_n}{N_i}, \frac{\sigma_\alpha}{N_i}\right)$	Cell-specific mean smooth coefficient (with iCAR structure)
ψ_i	Zero-truncated Student- $t(3,0,2.5)$	Cell-level intercepts
$\beta_{i,k}$	$\text{normal}(\alpha_i, \sigma_\alpha)$	Smooth coefficient per cell per knot
σ_α	Zero-truncated Student- $t(3,0,2.5)$	Standard deviation of cell-specific smooth coefficients
σ_β	Zero-truncated Student- $t(3,0,2.5)$	Standard deviation from mean smooth across cells
σ_ψ	Zero-truncated Student- $t(3,0,2.5)$	Standard deviation of the cell-level intercepts
a	$\text{gamma}(0.01,0.01)$	Shape parameter of the gamma likelihood

Tree Swallow, Barn Swallow, Bank Swallow and Cliff Swallow—using the package *ebirdst* (Strimas-Mackey et al., 2023). These ensembles are samples of trend estimates ($n=100$ in this case) obtained from using different subsets of the data to make predictions with a fitted double machine learning model and are used to describe the mean estimate and the confidence intervals for each species and cell (Fink, Johnston, et al., 2023). To make these estimates comparable to the radar and BBS estimates, we aggregated the estimates within each ensemble across species and between groups of 27-km cells to obtain a single ensemble of estimates for all our target species within each 100-km cell of our sampling grid. We do so as follows: we start with one ensemble of estimates of percent per year change per species per grid cell of 27 km size. These are aggregated in space using an average weighted by the relative abundance of that species (average from 2012 to 2022 provided in the data) to obtain one ensemble per species per cell within our grid of 100km. Finally, using summed relative abundances across species as weights, we grouped the ensembles of the five species into a single ensemble of percent per year change per cell.

We obtained relative abundance estimates from BBS data using the generalized additive mixed model with iCAR structure described in Smith et al. (2023). Instead of adopting the standard grid of 1 degree cells typically used for analysis of BBS data, we fitted the model with data partitioned within our grid of cells of the same size, but in slightly different locations. We accomplished this using the *bbsBayes2* package, which fits the model in Stan (Edwards et al., 2023; Sauer et al., 2021). Similar to what we did with the population impact trends, we fitted the model for the five target species with data from 2000 to 2022, to ensure we leverage all the information contained within the data, summing the relative abundances across species to get a posterior estimate of the total relative abundance. Lastly, we subset estimates for 2012 and 2022 to calculate the posterior distribution of the geometric mean trend between those years.

2.5 | Comparison strategy

Using the estimates of percent per year change in relative abundance and population impact from 2012 to 2022 for each data source, we estimated the distribution of the correlation coefficients between trends of all possible pairs of sources (BBS–eBird, BBS–radar, radar–eBird) across cells. To examine whether breeding population trends of a single species were driving observed population impact trends, we calculated distributions of estimated correlation coefficients between radar-derived trends and trends from BBS and eBird for each species. We then used the percent overlap between the empirical distributions of correlations to describe how similar/distinct the estimated coefficients were. This metric, called the similarity index, is proposed in Pastore & Calcagni, 2019 to describe sample differences without making assumptions about the underlying distributions (Pastore & Calcagni, 2019).

Additionally, we estimated the empirical cumulative distribution of the geometric mean estimates of change of each data source and obtained the probability of the trend within a given cell being positive or negative. We then used these probabilities to calculate the joint probabilities of every combination of trend direction between the sources, which provide estimates of the probabilities of directional agreements and disagreements between them. When examining directional probabilities for a single data source, we created four tiers corresponding to confidence levels that the trend has a given direction. If the observed probability is lower than 0.5 (the flip of a fair coin), we consider that trend direction to be unlikely ('Very Low' probability tier). We then divide the remaining values from 0.5 to 1 into three equally spaced tiers from 'Low' to 'High' probabilities of a given trend direction. We follow a similar rationale when examining the probabilities of the three-way comparison. If the observed probability of a combination of directions is lower than the probability of flipping three fair coins and getting that same outcome ($1/8$), we consider that combination improbable. The remaining values between $1/8$ and 1 are divided into three equally spaced tiers from 'Low' to 'High', representing how much certainty we have that combination is occurring. With the exception of the maps per species for BBS and eBird, the figures in this paper represent the tiered probabilities, but the reader will find the maps with probabilities in a continuous scale for each source in Figure S4 in the supplements.

3 | RESULTS

The BBS estimates per species generally suggest relatively high probabilities of declines in the northern part of the Great Lakes region, particularly for Tree Swallows, Purple Martins and Cliff Swallows (see Figure 1). These three species also face relatively high probabilities of a positive trend to the south of the Great Lakes region. The predicted probabilities for Bank and Barn swallows are less extreme (values closer to 0.5 than to 0 or 1) in both directions, indicating more uncertainty in the estimates for these two species. The eBird data, on the other hand, point to relatively high probabilities of widespread declines across the entire study region for all species but Purple Martins, for which it predicts relatively high probabilities of increases (see Figure 2). The aggregated estimates from BBS and eBird across all species are driven by these species-specific patterns. The aggregated estimates from BBS predict a diagonal line crossing southern Lake Michigan and separating a southern region of widespread positive trends from an area of spatially consistent negative trends in the northern Great Lakes region (see Figure 3). The aggregated eBird estimates, however, predict a smooth range-wide decline (see Figure 3). Our results from the radar data showed more spatial heterogeneity in population impact trends when compared to the breeding population trends (see Figure 3). In general, we observed medium to high probabilities of declines in roosting activity in the eastern Great Lakes, particularly in the region to the east of Lake Ontario and to the west of Lake Erie. Conversely, we found medium to high probabilities

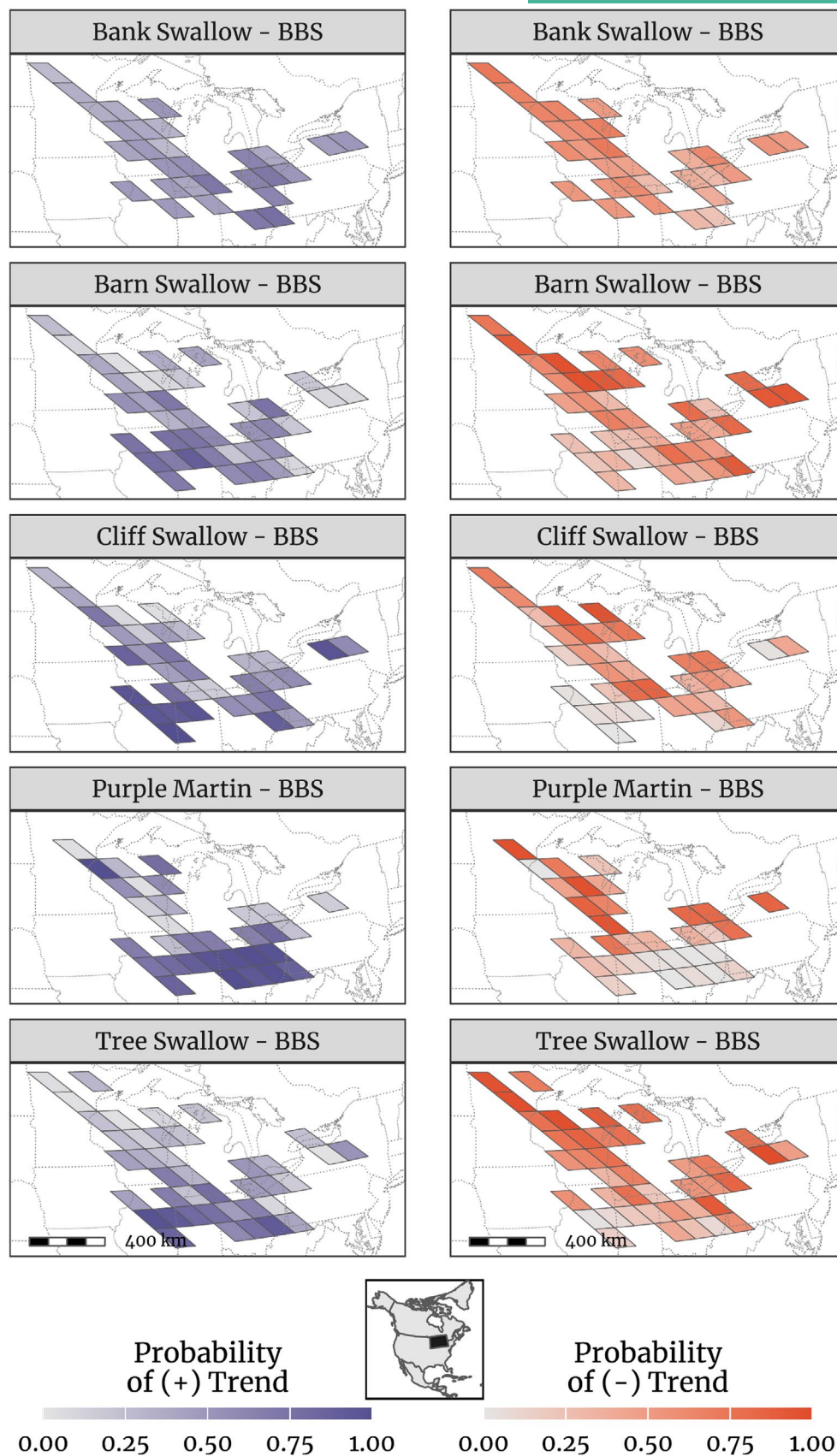


FIGURE 1 Probabilities of positive and negative trends for each species, obtained using BBS data. We interpret the posterior probabilities as follows: If the probability of a trend direction is lower than the probability of the flip of a fair coin, we consider that trend direction to be very unlikely. Shades of red from light to dark reflect increasing certainty on the direction of the trend in a cell.

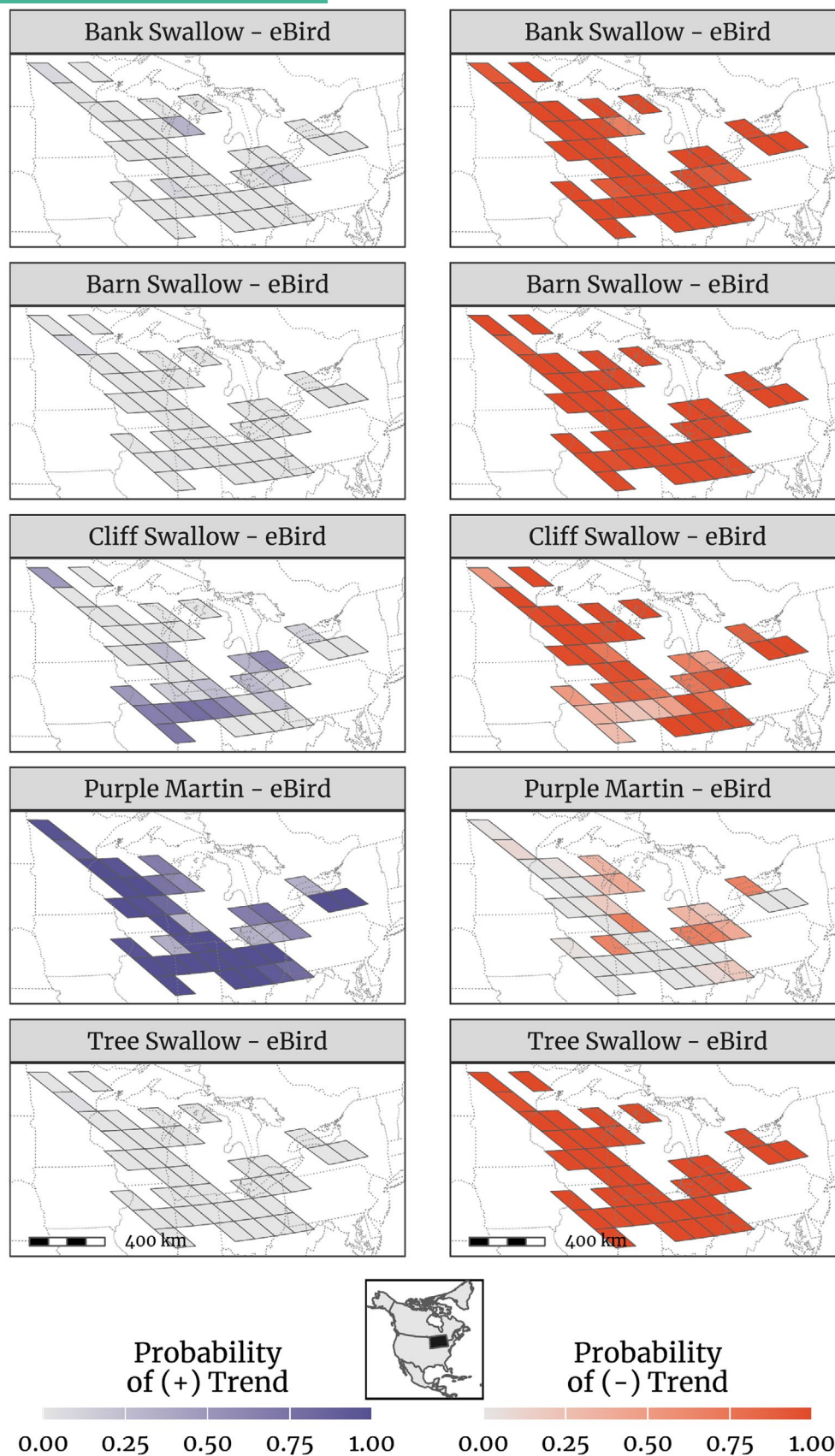
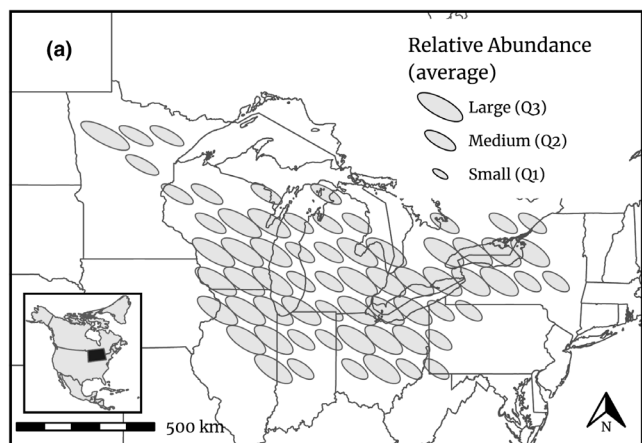
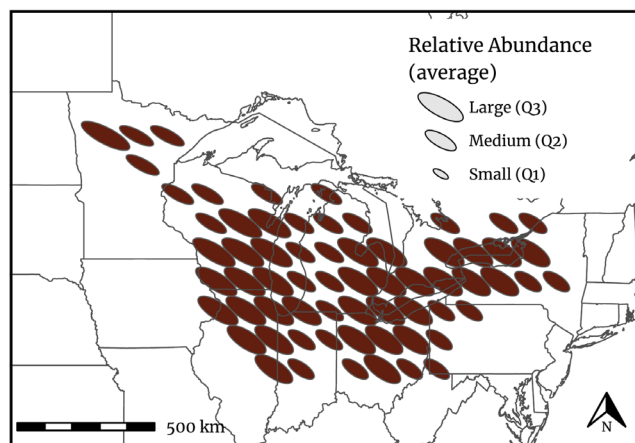


FIGURE 2 Probabilities of positive and negative trends for each species, obtained using eBird data. We interpret the posterior probabilities as follows: If the probability of a trend direction is lower than the probability of the flip of a fair coin, we consider that trend direction to be very unlikely. Shades of red from light to dark reflect increasing certainty on the direction of the trend in a cell.



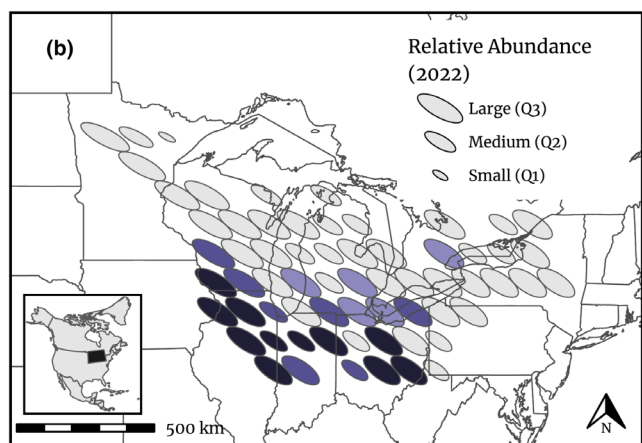
Probability of (+) Trend

Very Low (<0.5)	Medium (>0.67, <0.83)
Low (>0.5, <0.67)	High (>0.83)



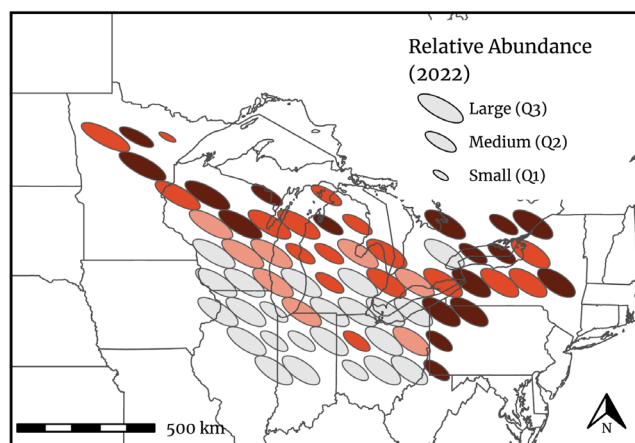
Probability of (-) Trend

Very Low (<0.5)	Medium (>0.67, <0.83)
Low (>0.5, <0.67)	High (>0.83)



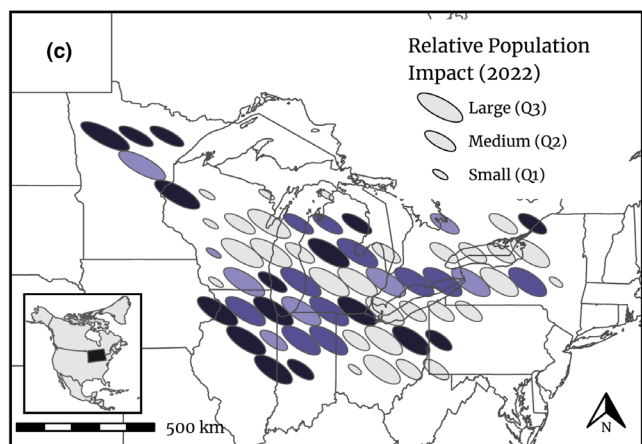
Probability of (+) Trend

Very Low (<0.5)	Medium (>0.67, <0.83)
Low (>0.5, <0.67)	High (>0.83)



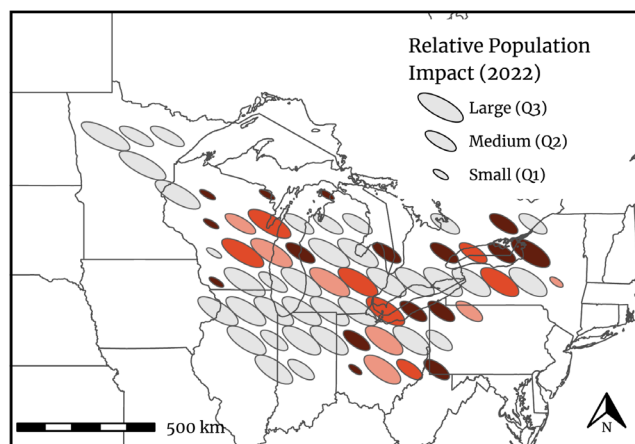
Probability of (-) Trend

Very Low (<0.5)	Medium (>0.67, <0.83)
Low (>0.5, <0.67)	High (>0.83)



Probability of (+) Trend

Very Low (<0.5)	Medium (>0.67, <0.83)
Low (>0.5, <0.67)	High (>0.83)



Probability of (-) Trend

Very Low (<0.5)	Medium (>0.67, <0.83)
Low (>0.5, <0.67)	High (>0.83)

FIGURE 3 Maps representing the modelled probability of a negative or a positive trend for each of our data sources (BBS, a; eBird, b; radar, c). If the probability of a trend direction is lower than the probability of the flip of a fair coin, we consider that trend direction to be very unlikely. Shades of red from light to dark reflect increasing certainty on the direction of the trend in a cell.

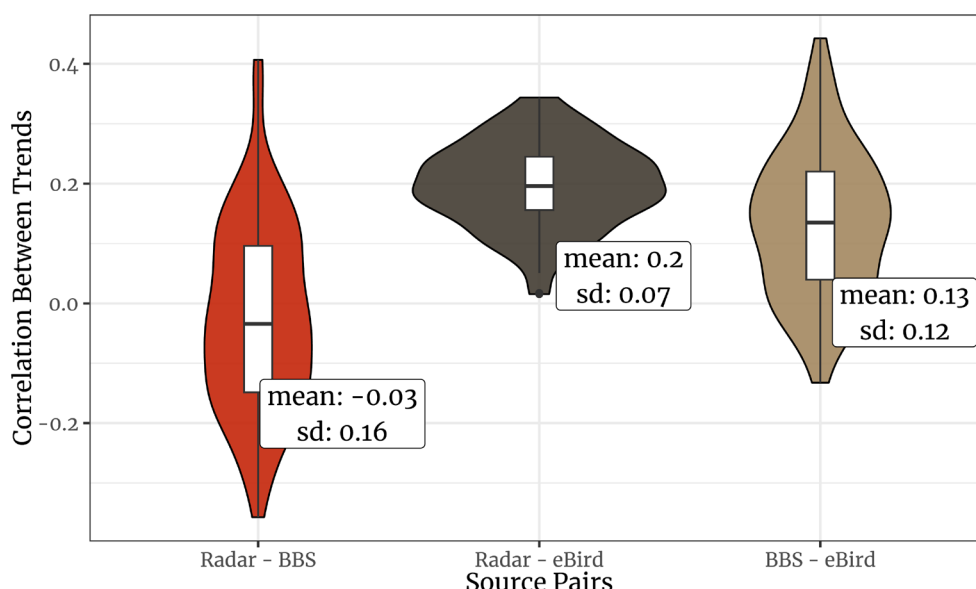


FIGURE 4 Density distribution of correlation coefficient estimates between geometric mean trends of each pair of sources, with respective means and standard deviations of each distribution. We consider these estimates to be statistically significant if their 95% credible interval (represented above as a black vertical line) overlaps 0. In this case, only the correlation between radar and eBird is significantly different from 0.

of increases in roosting activity in the west/southwestern Great Lakes region.

We estimated the correlations between the geometric mean trends of each pair of sources across cells. Our results show little evidence of correlation (see Figure 4), even though our estimates are biased towards predicting positive or negative associations due to the significant spatial autocorrelation present within each variable. The average correlation between BBS and radar estimates was -0.01 (SD: 0.12), and between eBird and radar estimates was 0.2 (SD: 0.06). The average correlation between eBird and BBS was slightly higher, with an average of 0.25 (SD: 0.11). We further explored these results by calculating correlations between radar trends and trends for each species across cells, for both BBS and eBird (see Figure 5). On both sources, no correlation estimate per species was significantly different from zero (all credible intervals overlap 0). Additionally, within each source, the posterior distributions of correlations had high overlapping areas between species (average similarity index greater than 0.6, see Figure 5), indicating that there is not a significant difference between species in their estimated correlation distributions. The same is generally true when comparing BBS trends per species with radar-derived trends. We found, however, that BBS trends for Purple Martins were slightly more correlated to radar-derived trends (average correlation coefficient 0.14 , SD: 0.11, vs. average coefficients between -0.08 and 0.02 for the other four species) and that their distribution is less similar to other species (average similarity index: 0.5); however, results are inconclusive since the correlation estimates are not significant.

Because eBird estimates within the Great Lakes region were consistently negative across the entire study region, any three-way comparison that incorporated the probability of a positive eBird trend resulted in a very low joint probability. We found that all sources likely agree on a negative trend in the eight cells surrounding Lake Ontario and in seven cells to the west of Lake Michigan, where the joint probability of a negative trend in all sources was greater than 0.42 and classified as medium or high (see Figure 6). We found mostly very low or low probabilities of BBS predicting a positive trend when radar predicts a negative trend (Figure 6), whereas there are 21 cells in which it is likely that BBS predicts a negative trend in disagreement with the trend predicted by the radar data, particularly in the four cells to the east of Lake Michigan and in the four northernmost cells to the east (Figure 6). Lastly, even though BBS and radar disagree with eBird, they both agree on a positive trend in the southwest of our study region (south of Lake Michigan, see Figure 6).

4 | DISCUSSION

4.1 | Trend comparisons

We developed a workflow to combine multiple lines of evidence to provide robust inference on changes in population-level state variables. This technique can be generalized to other species or even include sources of trend estimates of other variables of interest, such

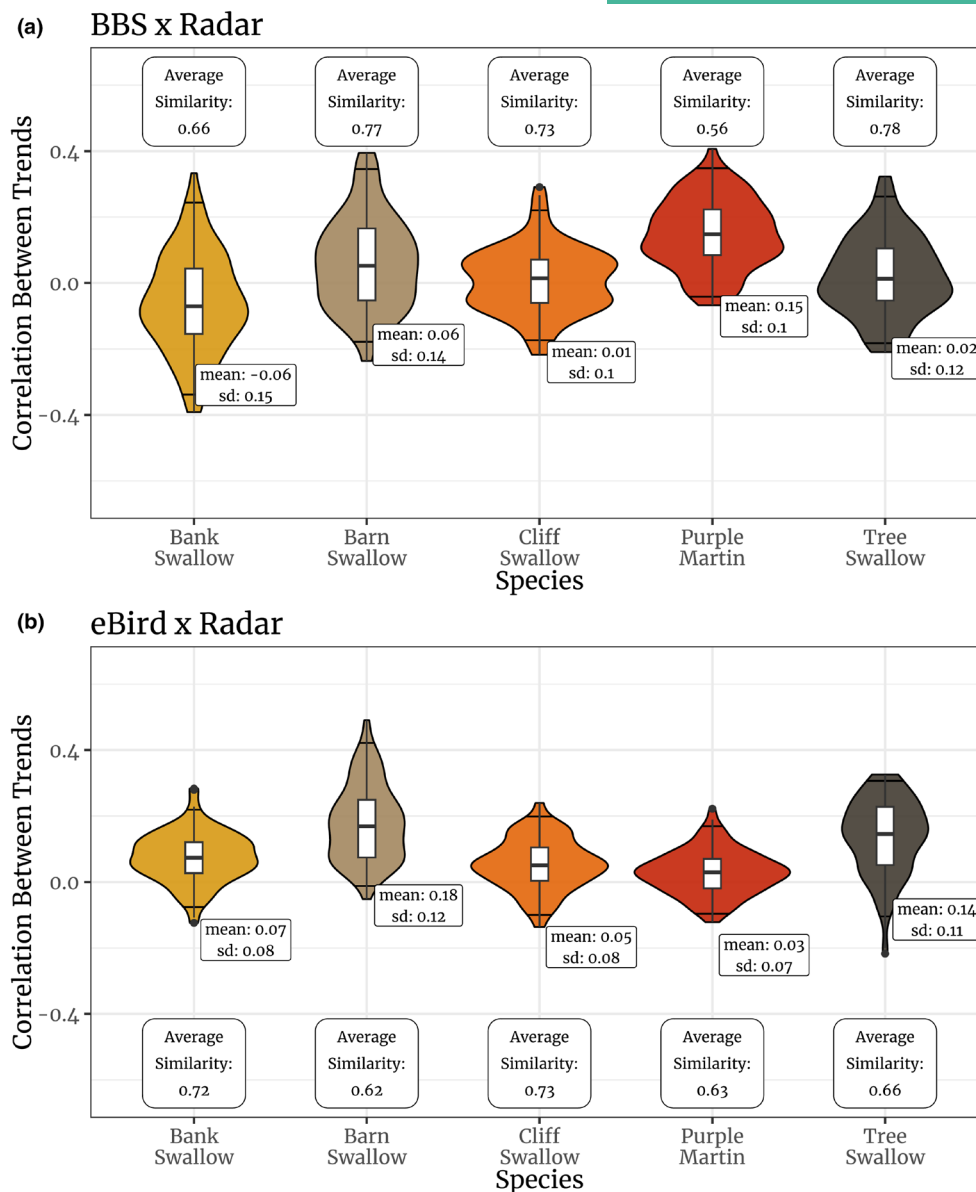


FIGURE 5 Density distributions of correlation coefficient estimates between radar-derived population impact trends and breeding population trends for each species, for each source (BBS, a or eBird, b). A correlation estimate is significant if its 95% credible interval (represented as black vertical lines) does not overlap zero. All the correlation estimates were not significant, suggesting that radar-derived trends do not match any one species individually. We calculated the percentage of overlapping area between empirical distributions of correlations of each pair of species to establish if correlation estimates were different between species. The mean similarity between a single species and all others is the average similarity described in the labels. All our similarity estimates were high, indicating that no species was more or less correlated to radar-derived trends than all the others.

as demographic rates obtained by the Monitoring Avian Productivity and Survivorship (MAPS) program (Saracco et al., 2008). This approach can be used with modelling frameworks that output realizations of the estimated trend, such as Bayesian hierarchical models or resampling methods. By transforming realizations into directional probabilities of agreement within a region of a grid, we can multiply probabilities of different sources in the same cell to obtain regional joint probabilities of agreement and disagreement on trend direction scenarios. In the particular case of swallows and martins, because we can estimate roosting activity trends from weather radar data,

we can compare and combine trends from the latter with other well-known sources of relative abundance trends of breeding populations, such as eBird and the BBS.

Our comparison between BBS, eBird and radar data suggests that Lake Ontario is observing both a decrease in breeding populations and a decrease in roosting activity, indicating that this region should be prioritized in future conservation efforts. This region could also be the focus of studies aimed at understanding if declines in local breeding populations are directly causing declines in roosting activity in the same region. Data from light-level geolocators suggest that Tree Swallows are

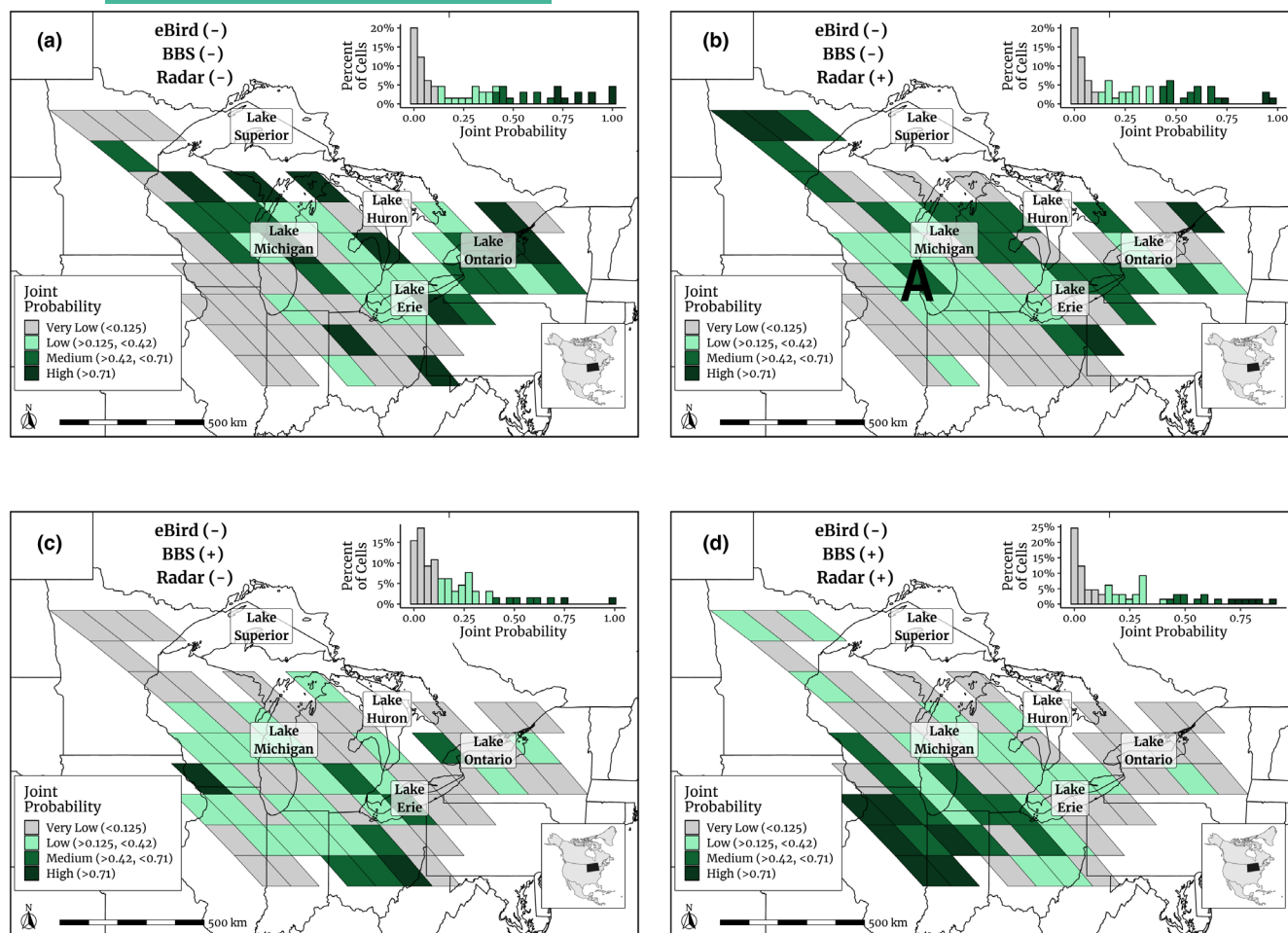


FIGURE 6 Maps representing joint directional probabilities, that is, probabilities of scenarios of negative or positive trends across all sources, except for eBird (+), since that is approximately equal to zero regardless of the estimates for the other two trends. Panel (a) represents probabilities of negative trends across all sources; panel (b) represents a scenario in which eBird and BBS predict negative trends, but radar predicts a positive trend; panel (c) shows probabilities that eBird and radar predict negative trends while BBS predicts positive trends; and panel (d) presents the probability that BBS and radar agree on a positive trend, while eBird predicts a negative trend. Grey cells represent regions where the probability of a given combination is lower than the probability of obtaining that trend combination by flipping three fair coins. The different shades of green, from light to dark, reflect an increase in certainty about a given trend combination scenario (dark green colours in plot (d), for example, reflect high probabilities of positive BBS and radar trends and negative eBird trends). Histograms are a representation of the same joint probabilities, but better highlight the frequency of each value without the spatial information.

using the Great Lakes region both as a breeding site and a stopover location (see Knight et al., 2018). It is possible, nonetheless, that individuals of other species breeding in Canada, for example, might use roosts in the Great Lakes region as stopover or staging sites, which would cause trends in seasonal impact in this region to reflect changes in northern breeding populations.

Regions that observe increases in roosting activity without a corresponding increase in breeding populations—that is, regions with a high probability of eBird (-), BBS (-) and radar (+)—give rise to many questions and hypotheses that can be tested in studies at smaller scales. This pattern could be caused, for example, by increases in relative abundance in northern breeding populations, or it could be a result of local birds staying in their pre-migratory roosts for much longer. The latter hypothesis is a cause of concern since it could suggest that birds might be facing challenges to refuel in time for their fall migration. This

type of delay has been observed in Barn Swallows that needed to stay for a longer period in their nonbreeding grounds in order to prepare for spring migration (Saino et al., 2003). Conversely, regions in which we observe decreases in roosting activity paired with increases in breeding populations prompt us to wonder where and why breeding birds are moving to roost. These regions would show a high probability of a negative trend in population impact, combined with a high probability of a positive trend in BBS data, even though the latter does not agree with the negative eBird estimate.

4.2 | Trends in roosting activity

Our study suggests that roosting activity is increasing towards the west/southwest Great Lakes region and is decreasing towards the

east/southeast. Increases in population impact could be a result of two biological processes: an increase in roosting season duration and/or increases in daily relative abundances. Conversely, decreases in population impact could be caused by corresponding decreases in relative abundance and/or a shortening of the roosting season. Disentangling these two processes can be challenging. We have some evidence of breeding season advancements for all our study species except for Bank Swallows (for Cliff Swallows in Nebraska, US, see Brown & Brown, 2014; for Tree Swallows across the United States, see Dunn & Winkler, 1999; for Purple Martins across the United States, see Shave et al., 2019; lastly, Imlay et al., 2018, found no evidence of Bank Swallow breeding initiation advancements in Nova Scotia and New Brunswick, Canada). Additionally, previous studies of roosting phenology in the Great Lakes region found that the second half of the roosting season (50%, 75% and 95% passage dates) has advanced on average between 2.23 and 4.09 days over two decades (from 2001 to 2020, Deng et al., 2023). It is unclear, however, if those advancements are different enough to cause changes in roosting season length.

Regardless of the processes causing the observed changes in population impact, trends in this metric could reflect changes in the impact these large aggregations have on the landscape that supports them and/or changes in the ecosystem services they provide. Studies indicate that seabird colonies concentrate nutrients around the locations that support them and increase the biomass and species composition of seagrasses (Powell et al., 1991). The same effects on local food webs could occur in areas around swallow and martin roosts, and our population impact metric could be used as a proxy for the intensity of these effects. In addition, because the presence of waterfowl has been associated with changes in water quality (Manny et al., 1994), and Cliff Swallow colonies have caused seasonal surges of higher concentrations of *Escherichia coli* in the underlying creek (Sejkora et al., 2011), the population impact of roosts, which is proportional to how much faecal matter is deposited in an ecosystem, could be a state variable of interest for water quality monitoring schemes.

4.3 | Application to conservation and management

Our proposed metrics for decision-making—the probabilities of agreement and disagreement—maximize the use of available information while describing both the uncertainty associated with each estimate and the uncertainty associated with our lack of knowledge about the system (epistemic uncertainty, Van Der Bles et al., 2019). Thus, for example, when implementing the structured decision-making framework proposed in Fournier et al. (2023) and other conservation priority-setting strategies such as the one discussed in Wilson et al. (2007), in addition to relying on expert opinion and working group consensus to establish the degree of uncertainty associated with the estimated trend, one could define thresholds on the probabilities of agreement dividing regions on a low to high scale of overall uncertainty levels across sources. This allows a distribution of

conservation efforts and funds proportional to how certain we are, what types of errors we are willing to make and how much evidence we have that those resources are needed in a given region.

Probabilities of agreements and disagreements can also be used during Stage 2 of the Species Status Assessment (SSA) Framework used by the US Fish and Wildlife Service to determine if a species should be protected under the Endangered Species Act (U.S.F.W.S., 2016). At this stage of the SSA report, practitioners assess current species conditions, looking for changes in its abundance and distribution and trying to explain how those changes arose, based on perceived threats and knowledge about the species' life history. Examining spatial patterns of agreement and disagreement in trends of multiple species health indicators can inform on the species' ability to respond to habitat improvements, for example, in regions where there are islands of high degree of agreement on concerning trends, surrounded by regions where the species is faring better. Lastly, pairing probabilities of indicators from multiple moments of a species' annual cycle can provide information on the time of the year when intervention is most needed, which could be used to minimize the impact of conservation action on local economic cycles in a way similar to what is described in Horton et al. (2021) for the management of artificial light at night.

Trend estimates from all three of our data sources have some degree of confounding between local changes in abundance and changes in annual cycle timing, though the radar data do so more explicitly. As we gather further evidence of advances in the breeding season in North America and across the globe (Horton et al., 2020; Parmesan & Yohe, 2003; Youngflesh et al., 2021), it becomes clearer that the fixed sampling dates of BBS and eBird could gradually be observing a different moment of the breeding period, which could lead to changes in species detectability (e.g. availability). These changes would produce trends that might not correspond to actual population declines or increases as shown in Massimino et al. (2020). However, because the seasonal impact metric used for the radar data incorporates both daily relative abundances and season duration, it is expected that changes in timing alone will produce trends in population impact. This concern, however, should not diminish the relevance of trend estimates of breeding populations, but it can help us improve our ability to interpret them.

In this study, we proposed a novel technique that can be used to spatially combine a wide range of data sources that monitor the state of a given population into a single metric describing the probability of agreement or disagreement across sources on the direction of the trend. This maximizes the use of available information while also describing the uncertainty associated with our incomplete knowledge of the limitations associated with the observation process and of the drivers and constraints of the real population dynamics. It also allows decisions to be made based on the amount of evidence that supports the conclusions about trend direction. We demonstrate the use of this method by combining eBird, BBS and radar data to conclude that consensus around the declines observed in Lake Ontario requires further investigation.

AUTHOR CONTRIBUTIONS

Maria C.T.D. Belotti: Conceptualization, investigation, methodology, software, data curation and writing. Brian D. Gerber: Conceptualization, methodology, writing and supervision. Wenlong Zhao: Methodology, software and data curation. Victoria F. Simons: Investigation. Yuting Deng: Methodology and investigation. Gustavo Perez: Methodology and investigation. Subhransu Maji: Conceptualization, methodology and supervision. Daniel Sheldon: Conceptualization, methodology and supervision. Jeffrey F. Kelly: Conceptualization, methodology and supervision. Kyle G. Horton: Conceptualization, methodology, supervision and writing.

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CONFLICT OF INTEREST STATEMENT

The authors have no conflict of interest to report.

DATA AVAILABILITY STATEMENT

The data that support the findings of this study are openly available in Zenodo under the following link: www.doi.org/10.5281/zenodo.16764321 (Belotti, 2025). The radar data from the Great Lakes region are available in www.doi.org/10.6084/m9.figshare.20137961 (Belotti et al., 2024).

ETHICS STATEMENT

This study did not involve the capture or handling of animals. No ethical concerns are to report.

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SUPPORTING INFORMATION

Additional supporting information can be found online in the Supporting Information section at the end of this article.

Figure S1. Map of the sampling grid used by the Breeding Bird Survey. Each cell has 1° of width and height, which corresponds to approximately 100km within our study region.

Figure S2. Map of the sampling grid used by eBird. Each cell has 27 km of width and height.

Figure S3. Map of the sampled regions around each of the twelve radar stations in the Great Lakes region.

Figure S4. Maps representing the modeled probability of a negative or a positive trend for each of our data sources (eBird, A; BBS, B; radar, C). Darker colors reflect increasing certainty on the direction of the trend in a cell.

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