

a more smoothed curve). The cell-specific year effect $\beta_{j(i),t}$ is drawn from a normal distribution with mean β_t as follows:

$$\beta_{j(i),t} \sim \text{normal}(\beta_t, \sigma_\beta^2)$$

Including the variance in the year effect σ_β^2 enables the model to account for variations in trends of population counts among grid cells. The variable $j(i)$ indicates that grid cell j includes site i . Assuming the same population trend across all sites within each grid cell, the mean count $\mu_{i,t}$ at site i in grid cell j and year t is modelled with the cell-specific year effect $\beta_{j(i),t}$, the site effect α_i , the spatially correlated random effect $\gamma_{j(i)}$ and the overdispersion effect $\delta_{i,t}$:

$$\log(\mu_{i,t}) = \alpha_i + \beta_{j(i),t} + \gamma_{j(i)} + \delta_{i,t} \quad (1)$$

Here, α_i and $\delta_{i,t}$ are drawn from a mean-zero normal distribution with variance σ_α^2 and σ_δ^2 , respectively. The variable $\gamma_{j(i)}$ is drawn from an intrinsic Gaussian conditional autoregressive (CAR) prior distribution:

$$\gamma_{j(i)} | \gamma_k \sim \text{normal} \left(\frac{\sum_{j \neq k} w_{j,k} \gamma_k}{n_j}, \frac{\sigma_\gamma^2}{n_j} \right) \quad (2)$$

where $w_{j,k} = 1$ if grid cells j and k are neighbours, and 0 otherwise. The variable n_j is the total number of neighbours of grid cell j ; neighbours are grid cells directly adjacent to grid cell j , and include cells that are diagonally adjacent. The amount of variation between the random effects is controlled by σ_γ^2 . The observed count $y_{i,t}$ in site i and year t is assumed to derive from a Poisson distribution with mean $\mu_{i,t}$.

We assumed constant survey efforts over time for the IWC, because regular and standardized surveys with constant methods, efforts and timing are strongly encouraged in this scheme³¹ (see Supplementary Discussion). However, survey efforts in the CBC are known to vary through time. By using the total number of survey hours per count as the measure of survey efforts, we explicitly accounted for the effort effect for the CBC data following a previously published analysis⁴¹:

$$\log(\mu_{i,t}) = \alpha_i + \beta_{j(i),t} + \gamma_{j(i)} + \delta_{i,t} + \frac{B \left(\left(\frac{\zeta_{i,t}}{\bar{\zeta}} \right)^p - 1 \right)}{p} \quad (3)$$

Here $\zeta_{i,t}$ is the total number of survey hours per count and $\bar{\zeta}$ is the mean value of $\zeta_{i,t}$. The parameters B and p determine a range of relationships between effort and the number of birds counted⁴¹. To test whether accounting for survey efforts changes the conclusions of this paper, we also applied the model without the effort effect to the CBC data, and compared the two models in terms of their estimated rate of abundance change within each grid cell for each of the 159 species with more than two grid cells. The estimated spatial patterns in abundance changes in each of the two models were highly correlated (median Pearson's $r = 0.99$, minimum $r = 0.88$), which indicates that the model without the effort effect that was used for the IWC data is valid. Further discussions on the potential effects of temporal changes in survey efforts are provided in the Supplementary Discussion.

We applied the models to count data for each species at a regional population level. For example, count data for the Eurasian wigeon *Mareca penelope* are separately compiled as five populations: three (northwest European, Black Sea–Mediterranean and southwest Asian–northeast African) in the AEWC, one in the AWC and one in the CBC. In this case, we applied the models separately to each of the five populations. As the result, we analysed 775 regional populations of 461 species (see Supplementary Data 2 for the full list of species). For 38 regional populations in which no grid cells with count records were adjacent to one other, we dropped the spatially correlated random effect $\gamma_{j(i)}$ from equations (1) and (3). For 32 regional populations with only one grid cell that included more than one survey site, we dropped $\gamma_{j(i)}$ and also replaced the cell-specific year effect $\beta_{j(i),t}$ with the overall year effect β_t . For 22 regional populations with only one survey site, we applied a generalized linear model with a Poisson distribution, using observed counts as the response variable and years as the explanatory variable, and used the estimated slope as the rate of abundance change.

Using only grid cells that had on average four or more non-zero records per site, we fitted the models to the data with the Markov chain Monte Carlo (MCMC) method in WinBUGS v.1.4.3⁴² and the R2WinBUGS package⁴³ in R v.3.3.2⁴⁴. Prior distributions of parameters were set as non-informatively as possible, to produce estimates similar to those generated by a maximum likelihood method. We used gamma distributions with a mean of 1 and variance of 100 for the inverses of σ_α^2 , σ_β^2 , σ_δ^2 and σ_γ^2 , normal distributions with a mean of 0 and variance of 100 for β_1 , β_2 and B , a beta distribution with a mean of 0.5 and variance of 0.083 ($\alpha = \beta = 1$), which is a uniform distribution, for r , and a uniform distribution on the interval $[-4, 4]$ for p following a previous study⁴⁵. Each MCMC algorithm was

initially run with three chains with different initial values for 300,000 iterations with the first 200,000 discarded as burn-in and the remainder thinned to one in every twenty iterations to save storage space. Model convergence was checked with R hat values⁴⁶. If the models did not converge with the initial conditions, we increased iterations up to 5,000,000 (with the first 1,000,000 discarded and the remainder thinned to one in every 800). We decided to remove grid cells in which parameter estimates did not converge even with the increased iterations, although the number of removed cells was very small (median of 2.5 grid cells in 20 out of the 775 (2.6%) regional populations).

To estimate the population-level change in abundance since 1990 for each species in a particular grid cell, we first regressed the estimates of the cell-specific year effect $\beta_{j(i),t}$ in every posterior sample against years. To account for uncertainty in slope estimates in this regression, we derived for every posterior sample a slope estimate from a normal distribution with the mean of the estimated mean slope and s.d. of the standard error of the slope. We then calculated the mean, median, variance and 2.5th and 97.5th percentiles of the estimated slopes from all posterior samples. We aggregated all estimates by species on the basis of definitions from BirdLife International³⁶. We used the mean and 2.5th and 97.5th percentiles of the estimated slopes for creating species-level maps (Fig. 1a–c and Supplementary Data 1). To calculate community-level changes in abundance (Fig. 2a) and community-level changes for species with different migratory statuses (Extended Data Fig. 2), we used the mean slopes across all species or all species in a particular group observed in each grid cell, weighted by the inverse of slope variance in each species to account for uncertainties. To further calculate mean community-level changes in each region (Fig. 2b), we used the mean of the community-level changes across all grid cells in each region, weighted by the inverse of associated variance.

Driver analysis. We first tested correlations among the nine spatial explanatory variables in 2,079 $1^\circ \times 1^\circ$ grid cells that had abundance change estimates (Extended Data Table 2). GDP per capita and governance were relatively strongly correlated ($r = 0.76$) with one another. Thus, considering that GDP growth rates are another measure of economic growth, we decided to exclude GDP per capita from the main analyses; instead, we tested its effect in a separate set of analyses in which governance was replaced with GDP per capita. In these analyses, considering the hypothesized nonlinear relationship between GDP per capita and species abundance changes (Extended Data Table 1), we used linear and quadratic terms of GDP per capita. We present the results of these analyses that use GDP per capita in Extended Data Fig. 5 and Supplementary Discussion.

To identify factors associated with waterbird abundance changes at the community, species and population levels, we conducted two types of analyses, both of which were implemented with WinBUGS v.1.4.3 and the R2WinBUGS package in R v.3.3.2.

In the first analysis, in which the response variable was community-level changes in abundance within each grid cell (Fig. 2a), we used a CAR model:

$$\mu_i = \alpha + \beta \mathbf{X}_i + \gamma_i$$

where the community-level change r_i in cell i was assumed to derive from a normal distribution with mean μ_i and variance σ_μ^2 ; β represents the vector of regression coefficients and \mathbf{X}_i the vector of explanatory variables. On the basis of the hypotheses shown in Extended Data Table 1, we used eight explanatory variables in each grid cell: surface water change, GDP growth rates, changes in human population density, crop area, temperature, and precipitation, protected area coverage and governance. We tested interaction terms between latitude and temperature change, and latitude and precipitation change, as population responses to temperature and precipitation can vary by latitude⁴⁷. We also tested a third interaction term between governance and protected area coverage, because governance can affect the effectiveness of conservation efforts⁴⁸. All explanatory variables were standardized before model fitting. The spatially-correlated random effect γ_i used an intrinsic Gaussian CAR prior distribution with variance σ_γ^2 , as described in equation (2). Prior distributions of parameters were set as non-informatively as possible; we used gamma distributions with a mean of 1 and variance of 1,000 for the inverse of σ_μ^2 and σ_γ^2 , normal distributions with a mean of 0 and variance of 1,000 for β_j , and an improper uniform distribution (a uniform distribution on an infinite interval) for the intercept α , as recommended by a previous study⁴⁹. Each MCMC algorithm was run with three chains with different initial values for 1,000,000 iterations, with the first 500,000 discarded as burn-in and the remainder thinned to one in every 100 iterations to save storage space. Model convergence was checked with R hat values.

Next, for 293 species observed in ten or more grid cells, we adopted the within-subject centring approach⁵⁰ under a hierarchical modelling framework to explicitly distinguish species-level effects (explaining variations in species-level abundance changes between species) and population-level effects (explaining variations in population-level abundance changes within species) of explanatory variables. In this model, the species effect μ_s , representing the species-level change