in abundance of species s, is drawn from a normal distribution with a mean of ν_s and variance of σ_ν^2. The variable ν_s is further modelled with species-level explanatory variables:

$$\nu_s = \alpha + \sum_{k=1}^{9} \beta_{Bk} \bar{x}_{k,s} + \sum_{k=10}^{12} \beta_{Bk} z_{k,s} + \eta_s$$

where α is the global intercept and β_{Bk} represents the species-level effect. The mean of spatial explanatory variable k across all grid cells where species s was recorded is represented by $\bar{x}_{k,s}$. Even if the estimated species-level abundance changes are biased owing to geographical biases in available grid cells, they match up with $\bar{x}_{k,s}$ because the calculation of both variables is performed on the same set of grid cells. The spatial explanatory variables used were derived from the hypotheses in Extended Data Table 1; we dropped changes in human population density and crop area, as these were least influential in the analysis of community-level population changes and also in a preliminary analysis of this species-level model. We therefore used the remaining six explanatory variables (surface water change, GDP growth rates, changes in temperature, changes in precipitation, protected area coverage and governance) and the same three interaction terms as used in the community-level analysis. The term $z_{k,s}$ represents three explanatory variables in species characteristics, described in Extended Data Table 1. The random term η_s accounts for phylogenetic dependence among species and is drawn from a multivariate normal distribution (MVN)[51,52]:

$$\eta_s \sim \text{MVN}(0, \ \delta^2 \Sigma_\lambda)$$
$$\Sigma_\lambda = \lambda \Sigma + (1-\lambda) I \qquad (4)$$

where Σ is a scaled variance–covariance matrix calculated from an ultrametric phylogenetic tree. By scaling Σ to a height of one, we can interpret δ^2 as the residual variance[51]. To enable the strength of phylogenetic signal to vary, we also incorporated Pagel's λ[53,54] into the matrix in equation (4) with the identity matrix I. Here λ is a coefficient that multiplies the off-diagonal elements of Σ; a λ close to zero implies that the phylogenetic signal in the data is low, which suggests independence in the error structure of the data points, whereas a λ that is close to one suggests a good agreement with the Brownian motion evolution model and thus suggests correlation in the error structure[51,54]. To incorporate uncertainties[55] in phylogenetic trees in the calculation of Σ, we used a sample of 100 trees from a comprehensive avian phylogeny[56] as the prior distribution for our analysis[51]. More specifically, one of the 100 trees was randomly drawn in each iteration and used for the calculation of Σ.

The population-level change in abundance $r_{s,i}$ of species s in grid cell i was then assumed to derive from a normal distribution with mean $\mu_{s,i}$ and variance σ_μ^2, where $\mu_{s,i}$ is modelled using the species effect μ_s:

$$\mu_{s,i} = \mu_s + \sum_{j=1}^{6} \beta_{Ws,j} (x_{j,i} - \bar{x}_{j,s}) + \gamma_{s,i}$$

Here $\beta_{Ws,j}$ represents the population-level effect for species s, explaining within-species variations in population-level abundance changes ($\mu_{s,i} - \mu_s$) by within-species variations in explanatory variables ($x_{j,i} - \bar{x}_{j,s}$); here, $x_{j,i}$ is the explanatory variable j in grid cell i and $\bar{x}_{j,s}$ is the mean of x_j for species s. The species-specific $\beta_{Ws,j}$ is the random effect governed by hyper-parameters as:

$$\beta_{Ws,j} \sim \text{normal}(h\beta_{Wj}, \sigma_{\beta_{Wj}}^2)$$

For population-level effects, we used the six explanatory variables (surface water change, GDP growth rates, changes in temperature, changes in precipitation, protected area coverage and governance). Spatial autocorrelation within each species is accounted for by $\gamma_{s,i}$, which is drawn from an intrinsic Gaussian CAR prior distribution with variance $\sigma_{\gamma_s}^2$ as in equation (2).

As non-informative prior distributions, we used a gamma distribution with a mean of 1 and variance of 100 for σ_ν^2, δ^2, σ_μ^2, $\sigma_{\beta_{Wj}}^2$ and $\sigma_{\gamma_s}^2$, uniform distribution on the interval [0, 1] for λ, normal distributions with a mean of 0 and variance of 100 for α, β_{Bk}, and $h\beta_{Wj}$. Each MCMC algorithm was run with three chains with different initial values for 10,000 iterations with the first 5,000 discarded as burn-in and the remainder thinned to one in every two iterations to save storage space. Model convergence was checked with R hat values. Owing to differences in the definition of species between the two sources used[36,56], in four cases we combined two separate species defined in the BirdLife Checklist[36] into one for the species-level analysis. These were the Kentish plover *Charadrius alexandrinus* and snowy plover *C. nivosus*, common snipe *Gallinago gallinago* and Wilson's snipe *G. delicata*, European herring gull *Larus argentatus* and Arctic herring gull

L. smithsonianus, and common moorhen *Gallinula chloropus* and common gallinule *G. galeata*.

Code availability. All the R and WinBUGS codes used for the analyses are available from the corresponding author upon request.

Data availability. The waterbird count data used in this study are collated and managed by Wetlands International and the National Audubon Society, and are available on request. All maps in figures are derived from the Natural Earth dataset (v.1.4.0) at 1:110 m scale (http://www.naturalearthdata.com/downloads/110m-cultural-vectors/110m-admin-0-countries/). All the data that pertain to explanatory variables are freely available, as specified in Extended Data Table 1. Supplementary Data 1 is available at https://doi.org/10.6084/m9.figshare.5669827. Supplementary Data 2 is available in the online version of the paper.

29. Delany, S. *Guidance on Waterbird Monitoring Methodology: Field Protocol for Waterbird Counting* (Wetlands International, 2010).
30. Dunn, E. H. *et al.* Enhancing the scientific value of the Christmas Bird Count. *Auk* **122,** 338–346 (2005).
31. van Roomen, M. *et al. Waterbird and Site Monitoring along the Atlantic Coast of Africa: Strategy and Manual* (BirdLife International, Common Wadden Sea Secretariat and Wetlands International, 2014).
32. LeBaron, G. S. *The 115th Christmas Bird Count* (National Audubon Society, 2015).
33. van Roomen, M., van Winden, E & van Turnhout, C. *Analyzing Population Trends at the Flyway Level for Bird Populations Covered by the African Eurasian Waterbird Agreement: Details of a Methodology* (SOVON Dutch Centre for Field Ornithology, 2011).
34. Kaufmann, D., Kraay, A & Mastruzzi, M. *The Worldwide Governance Indicators: Methodology and Analytical Issues (September 2010)* https://ssrn.com/abstract=1682130 (2010).
35. Hsu, A. *et al. 2016 Environmental Performance Index* http://epi.yale.edu/reports/2016-report (2016).
36. BirdLife International. *The BirdLife Checklist of the Birds of the World: Version 7* http://www.birdlife.org/datazone/userfiles/file/Species/Taxonomy/BirdLife_Checklist_Version_70.zip (2014).
37. BirdLife International and NatureServe. *Bird Species Distribution Maps of the World* (BirdLife International and NatureServe, 2014).
38. Gill, F. & Donsker, D. (eds) *IOC World Bird List (v 5.1)* http://www.worldbirdnames.org/DOI-5/master_ioc_list_v5.1.xls (2015).
39. Amano, T., Okamura, H., Carrizo, S. F. & Sutherland, W. J. Hierarchical models for smoothed population indices: the importance of considering variations in trends of count data among sites. *Ecol. Indic.* **13,** 243–252 (2012).
40. Amano, T., Székely, T., Koyama, K., Amano, H. & Sutherland, W. J. A framework for monitoring the status of populations: an example from wader populations in the East Asian–Australasian flyway. *Biol. Conserv.* **143,** 2238–2247 (2010).
41. Link, W. A. & Sauer, J. R. Seasonal components of avian population change: joint analysis of two large-scale monitoring programs. *Ecology* **88,** 49–55 (2007).
42. Lunn, D. J., Thomas, A., Best, N. & Spiegelhalter, D. WinBUGS – a Bayesian modelling framework: concepts, structure, and extensibility. *Stat. Comput.* **10,** 325–337 (2000).
43. Sturtz, S., Ligges, U. & Gelman, A. R2WinBUGS: a package for running WinBUGS from R. *J. Stat. Softw.* **12,** 1–16 (2005).
44. R Core Team. *R: a Language and Environment for Statistical Computing* http://www.R-project.org/ (R Foundation for Statistical Computing, 2016).
45. Link, W. A., Sauer, J. R. & Niven, D. K. A hierarchical model for regional analysis of population change using Christmas Bird Count data, with application to the American Black Duck. *Condor* **108,** 13–24 (2006).
46. Gelman, A., Carlin, J., Stern, H. & Rubin, D. *Bayesian Data Analysis* 2nd edn (Chapman & Hall and CRC, 2003).
47. Pearce-Higgins, J. W. *et al.* Geographical variation in species' population responses to changes in temperature and precipitation. *Proc. R. Soc. Lond. Ser. B* **282,** 20151561 (2015).
48. Bare, M., Kauffman, C. & Miller, D. C. Assessing the impact of international conservation aid on deforestation in sub-Saharan Africa. *Environ. Res. Lett.* **10,** 125010 (2015).
49. Thomas, A., Best, N., Lunn, D., Arnold, R. & Spiegelhalter, D. *GeoBUGS User Manual* http://www.mrc-bsu.cam.ac.uk/software/bugs/ (2004).
50. van de Pol, M. & Wright, J. A simple method for distinguishing within- versus between-subject effects using mixed models. *Anim. Behav.* **77,** 753–758 (2009).
51. de Villemereuil, P., Wells, J. A., Edwards, R. D. & Blomberg, S. P. Bayesian models for comparative analysis integrating phylogenetic uncertainty. *BMC Evol. Biol.* **12,** 102 (2012).
52. Abadi, F. *et al.* Importance of accounting for phylogenetic dependence in multi-species mark–recapture studies. *Ecol. Modell.* **273,** 236–241 (2014).
53. Pagel, M. Inferring the historical patterns of biological evolution. *Nature* **401,** 877–884 (1999).
54. Freckleton, R. P., Harvey, P. H. & Pagel, M. Phylogenetic analysis and comparative data: a test and review of evidence. *Am. Nat.* **160,** 712–726 (2002).
55. Donoghue, M. J. & Ackerly, D. D. Phylogenetic uncertainties and sensitivity analyses in comparative biology. *Philos. Trans. R. Soc. Lond. B* **351,** 1241–1249 (1996).
56. Jetz, W., Thomas, G. H., Joy, J. B., Hartmann, K. & Mooers, A. O. The global diversity of birds in space and time. *Nature* **491,** 444–448 (2012).
57. Grossman, G. M. & Krueger, A. B. Economic growth and the environment. *Q. J. Econ.* **110,** 353–377 (1995).