

Reporting Summary

Nature Research wishes to improve the reproducibility of the work that we publish. This form provides structure for consistency and transparency in reporting. For further information on Nature Research policies, see [Authors & Referees](#) and the [Editorial Policy Checklist](#).

Statistics

For all statistical analyses, confirm that the following items are present in the figure legend, table legend, main text, or Methods section.

n/a Confirmed

- ☐ ☒ The exact sample size (n) for each experimental group/condition, given as a discrete number and unit of measurement
- ☒ ☐ A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
- ☐ ☒ The statistical test(s) used AND whether they are one- or two-sided
Only common tests should be described solely by name; describe more complex techniques in the Methods section.
- ☐ ☒ A description of all covariates tested
- ☒ ☐ A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons
- ☐ ☒ A full description of the statistical parameters including central tendency (e.g. means) or other basic estimates (e.g. regression coefficient) AND variation (e.g. standard deviation) or associated estimates of uncertainty (e.g. confidence intervals)
- ☒ ☐ For null hypothesis testing, the test statistic (e.g. F , t , r) with confidence intervals, effect sizes, degrees of freedom and P value noted
Give P values as exact values whenever suitable.
- ☒ ☐ For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings
- ☒ ☐ For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes
- ☐ ☒ Estimates of effect sizes (e.g. Cohen's d , Pearson's r), indicating how they were calculated

Our web collection on [statistics for biologists](#) contains articles on many of the points above.

Software and code

Policy information about [availability of computer code](#)

Data collection No software was used in the data collection process

Data analysis Data analysis was performed in R v 3.6.1. Computer code used in the analysis is available on request from the authors. Code and results data to make figures 2-4 is available at figshare (10.6084/m9.figshare.11814633).

For manuscripts utilizing custom algorithms or software that are central to the research but not yet described in published literature, software must be made available to editors/reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Research [guidelines for submitting code & software](#) for further information.

Data

Policy information about [availability of data](#)

All manuscripts must include a [data availability statement](#). This statement should provide the following information, where applicable:

- Accession codes, unique identifiers, or web links for publicly available datasets
- A list of figures that have associated raw data
- A description of any restrictions on data availability

All datasets used are publicly available. We used expert verified range maps for 30,652 species from the International Union for Conservation of Nature (<https://www.iucnredlist.org/resources/spatial-data-download>) and BirdLife International (<http://datazone.birdlife.org/species/requestdis>) including: birds, mammals, reptiles, amphibians, marine fish, benthic marine invertebrates, and habitat forming corals and seagrasses. Climate change projections for RCPs 8.5, 4.5, and 2.6 for the Coupled Model Intercomparison Project 5 (CMIP5) are available from <https://esgf-node.llnl.gov/search/cmip5/>. Results data to make Figures 2-4 is available at figshare (10.6084/m9.figshare.11814633).

Field-specific reporting

Please select the one below that is the best fit for your research. If you are not sure, read the appropriate sections before making your selection.

☐ Life sciences ☐ Behavioural & social sciences ☒ Ecological, evolutionary & environmental sciences

For a reference copy of the document with all sections, see [nature.com/documents/nr-reporting-summary-flat.pdf](https://www.nature.com/documents/nr-reporting-summary-flat.pdf)

Ecological, evolutionary & environmental sciences study design

All studies must disclose on these points even when the disclosure is negative.

Study description	Future climate projections from earth system models are combined with information on species geographic distributions (n=30,652 species) to estimate species realised thermal niche limits and project the timing of future exposure to conditions beyond their niche.
Research sample	We used expert verified range maps for 30,652 species from the International Union for Conservation of Nature (https://www.iucnredlist.org/resources/spatial-data-download) and BirdLife International (http://datazone.birdlife.org/species/requestdis), including; birds, mammals, reptiles, amphibians, marine fish, benthic marine invertebrates, and habitat forming corals and seagrasses. This sample reflects availability of geographic range data for each organisms group globally.
Sampling strategy	The sample size reflects availability of geographic range data for each organisms group. These sample sizes make up the majority of species in each major taxonomic group included in the study.
Data collection	All data used here is already published and was downloaded from public data portals
Timing and spatial scale	The data on species distributions we use represents more than a century of collecting efforts and observations by scientists, naturalists and the public. The climate data we use is generated by simulations from computer models of the earth system. Both kinds of data are accurate to ~100km resolution and are available globally.
Data exclusions	We excluded marine species restricted to depths >200m to focus on the effects of sea surface temperatures on shallow water species. To prevent estimates of maximum temperature being inflated by either extreme outliers in the temperature time series or from the overestimation of species ranges we excluded outlier temperature values within each grid cell, defined as those more than three standard deviations from the mean. Once we had selected the maximum temperature for each cell, we excluded outlier temperature values across each species range, defined as those more than three standard deviations above the mean range value.
Reproducibility	This is not an experimental study so experimental replication was not attempted. All data used in our analysis is publicly available. The results can be reproduced using the publicly available data and the analysis code is available on request from the authors. Code and results data to reproduce Figures 2-4 is available at figshare (10.6084/m9.figshare.11814633).
Randomization	No randomization was required. Our study was not experimental, but based on observed biodiversity and climate patterns.
Blinding	Our study was not experimental and so blinding is not relevant
Did the study involve field work?	☐ Yes ☒ No

Reporting for specific materials, systems and methods

We require information from authors about some types of materials, experimental systems and methods used in many studies. Here, indicate whether each material, system or method listed is relevant to your study. If you are not sure if a list item applies to your research, read the appropriate section before selecting a response.

Materials & experimental systems

n/a	Involved in the study
☒	☐ Antibodies
☒	☐ Eukaryotic cell lines
☒	☐ Palaeontology
☒	☐ Animals and other organisms
☒	☐ Human research participants
☒	☐ Clinical data

Methods

n/a	Involved in the study
☒	☐ ChIP-seq
☒	☐ Flow cytometry
☒	☐ MRI-based neuroimaging