

Reporting Summary

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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

Range shift measures were obtained from a literature search as described in the Methods section. Climatic data were obtained from WorldClim v. 1.4, the Climate Research Unit (CRU) TS v. 3.23, BIO-ORACLE and the Met office Hadley Centre observations datasets. We used global terrestrial human footprint maps for the year 2009 (Venter et al. 2016) as well as a global map of human impact on marine ecosystems (Halpern et al. 2008).

Data analysis

R code used to perform the analyses are available together with the underlying data at <https://figshare.com/s/ebd19485a00757ababb0>.

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

WorldClim, CRU, BIO-ORACLE, Met office Hadley Centre and human footprint datasets (Halpern et al. 2008; Venter et al. 2016) are freely available. Links to datasets are included in the Methods and References sections in the manuscript.

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	In this study, we introduce BioShifts, a global geo-database which includes 30,534 range shift measures. We provide robust estimates of the velocity of latitudinal and elevational range shifts for the 20 most studied taxonomic classes. We also assess the coupling between the velocity of isotherm shifts and the velocity of range shifts and evaluate the influence of life-form categories, historical mean annual temperature regime and the standardized human footprint index on range shifts.
Research sample	The BioShifts dataset contains 30,534 range shifts obtained from 258 published and peer-reviewed papers. The dataset includes 12,415 species following taxonomic harmonization.
Sampling strategy	For statistical reasons, we focused on the set of species belonging to the taxonomic classes with more than 30 observations. For our analyses to assess the velocity of species range shift at the taxonomic class level (see section entitled 'Detection: estimating the velocity of range shifts per taxonomic class' of the Methods for more information), this criteria resulted in 16,399 and 13,341 observations for latitudinal and elevational range shifts, respectively. Regarding our analyses of the coupling between the velocity of range shifts at the species level vs. the velocity of isotherm shifts, this criteria of more than 30 observations per taxonomic class resulted in 16,521 and 13,459 observations for latitudinal and elevational range shifts, respectively (see section entitled 'Attribution: coupling between species' range shifts and isotherms' shifts' of the Methods for more information).
Data collection	The BioShifts database was built from a literature review as described in the Methods section of the manuscript. Other freely available datasets were obtained from the sources mentioned above and in the Methods and References sections in the manuscript.
Timing and spatial scale	The literature search was performed between 2014 and 2018. The spatial scale is global.
Data exclusions	No data were excluded from the dataset provided at https://figshare.com/s/ebd19485a00757ababb0 .
Reproducibility	R code used to perform the analyses are available at https://figshare.com/s/ebd19485a00757ababb0 .
Randomization	Data on species range shifts were allocated to groups depending on methodological attributes used as covariates in the analyses (see Methods section of the manuscript for more information on the factor variables we used as covariates in the analyses). Randomization procedures were carried out to assess the statistical significance of the velocity of range shifts per taxonomic class as well as when analysing the coupling between the velocity of species range shifts and the velocity of isotherm shifts (see Methods section of the manuscript for more details on the randomization procedure we used).
Blinding	Blinding was used during data analysis by simply allocating a unique running ID to each of the study from which we extracted data on species range shifts (see Methods section of the manuscript for more information).
Did the study involve field work? <input type="checkbox"/> Yes <input checked="" type="checkbox"/> 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
<input checked="" type="checkbox"/>	<input type="checkbox"/> Antibodies
<input checked="" type="checkbox"/>	<input type="checkbox"/> Eukaryotic cell lines
<input checked="" type="checkbox"/>	<input type="checkbox"/> Palaeontology
<input checked="" type="checkbox"/>	<input type="checkbox"/> Animals and other organisms
<input checked="" type="checkbox"/>	<input type="checkbox"/> Human research participants
<input checked="" type="checkbox"/>	<input type="checkbox"/> Clinical data

Methods

n/a	Involved in the study
<input checked="" type="checkbox"/>	<input type="checkbox"/> ChIP-seq
<input checked="" type="checkbox"/>	<input type="checkbox"/> Flow cytometry
<input checked="" type="checkbox"/>	<input type="checkbox"/> MRI-based neuroimaging