

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
<i>Only common tests should be described solely by name; describe more complex techniques in the Methods section.</i> |
| ☐ | ☒ 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
<i>Give P values as exact values whenever suitable.</i> |
| ☒ | ☐ 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

All data used in this study are publicly available, and were collected as *.csv and *.txt files. Data sources are clearly defined in the manuscript methods and supplementary information files. Data curation was done in R 3.6.2. using custom code available in the supplementary information files.

Data analysis

All data analysis was done in R 3.6.2, using custom code (available in the supplementary information files) and R packages available in CRAN (as indicated in the manuscript)

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

Data supporting the findings of this study (curated arthropod abundances and estimated time trends) are available at Dryad Data Repository <https://doi.org/10.5061/dryad.cc2fqz645>.

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	We utilized a geographically and taxonomically broad suite of relatively long-term datasets available through the U.S. National Science Foundation network of Long-Term Ecological Research (LTER) sites established in 1980 to examine trends in arthropod abundance and diversity.
Research sample	Altogether, our LTER arthropod abundance meta-dataset compiled 82,777 arthropod observations from 68 datasets into 5,375 taxa time series that spans up to 36 years and is comprised of 48 arthropod orders made up of 1 to 658 taxa in a given dataset.
Sampling strategy	All data were gathered from public LTER data repositories. The only restriction was that LTER data must contain records of arthropod abundance.
Data collection	Data were downloaded from public LTER data repositories as *.csv or *.txt files.
Timing and spatial scale	Data span 1975-2019, the entire U.S. (from Alaska to Georgia, New Hampshire to Arizona).
Data exclusions	Non-arthropod LTER data were not included, except for birds and fish when available alongside arthropod data.
Reproducibility	R code used to curate and analyze data are available in the supplementary information files.
Randomization	Randomization is not relevant to this study, because we are observing trends among sites over time.
Blinding	Blinding is not relevant to this study, because human subjects were not involved.
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