

Reporting Summary

Nature Portfolio 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 Portfolio policies, see our [Editorial Policies](#) 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 code was needed for data collection.

Data analysis All code was written in the R programming language. This code is provided at the following DOI: <https://doi.org/10.6084/m9.figshare.21355467>. The following R packages were included in the custom code provided in the above DOI link:
HH R package v. 3.1-47
spatialreg R package v.1.2-3
geosphere R package
vegan R package v.2.5-7
mapast R package v.0.1

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 and reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Portfolio [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 description of any restrictions on data availability
- For clinical datasets or third party data, please ensure that the statement adheres to our [policy](#)

All data to replicate these analyses are publicly available at the following DOI: <https://doi.org/10.6084/m9.figshare.21355467>. The specimen occurrence records derive from the Triton Database, which is freely available (Fenton et al. 2021. Scientific Data): <https://www.nature.com/articles/s41597-021-00942-7>. Climate data derive from the Bridge Model Group: <https://www.paleo.bristol.ac.uk/resources/simulations/>. Climatic values across space and through time needed to replicate our analyses are included in data package in the DOI link above.

Human research participants

Policy information about [studies involving human research participants and Sex and Gender in Research](#).

Reporting on sex and gender

N/A

Population characteristics

N/A

Recruitment

N/A

Ethics oversight

N/A

Note that full information on the approval of the study protocol must also be provided 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)

Life sciences study design

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

Sample size

We quantified temporal patterns in LDGs using 434,113 unique species-by-locality-by-age records from the Triton database. All data from Triton were used, unless deemed to have been subject to dissolution. Patterns were quantified both with and without sub-sampling. Details of our sub-sampling procedure are provided in section 1.3.1 of the methods.

Data exclusions

No data were excluded from our study, unless samples were deemed to have been subject to dissolution, which could distort understanding of species richness.

Replication

We analysed latitudinal diversity gradient patterns using five different approaches, in order to assess the sensitivity of our pattern to methodological choice. All replication methods were successful, and details are provided in the methods.

Randomization

We employed subsampling to estimate diversity using bootstrap replicates, detailed in the methods.

Blinding

Blinding was not relevant to this study, since no human subjects were involved.

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 and archaeology
- ☒ ☐ Animals and other organisms
- ☒ ☐ Clinical data
- ☒ ☐ Dual use research of concern

Methods

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

Palaeontology and Archaeology

Specimen provenance	We quantified temporal patterns in LDGs using 434,113 unique species-by-locality-by-age records from the Triton database. Specimen locality information in Triton was derived primarily from ocean drilling projects over the last two decades. Planktonic foraminifera are single-celled protists that live in the open ocean.
Specimen deposition	All data can be accessed through the code and materials provided with this paper (https://doi.org/10.6084/m9.figshare.21355467), and through the open access database, Triton (Fenton et al. 2021 Scientific Data): https://www.nature.com/articles/s41597-021-00942-7
Dating methods	No new dates were obtained in this study. Ages of samples were taken from the Triton database (Fenton et al. 2021 Scientific Data): https://www.nature.com/articles/s41597-021-00942-7 .
☒ Tick this box to confirm that the raw and calibrated dates are available in the paper or in Supplementary Information.	
Ethics oversight	None.

Note that full information on the approval of the study protocol must also be provided in the manuscript.