

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 The Triton dataset using R software (version 4.1.2). This code is available at <https://doi.org/10.6084/m9.figshare.c.5242154>

Data analysis All analyses were performed using R Studio 2022.07.1 Build 554 and R v4.2.1. All R packages used in the study are cited in the manuscript and in the code at <https://github.com/anshuman21111/foram-networks>

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 was sourced from the Triton dataset: <https://doi.org/10.1038/s41597-021-00942-7>

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 work with planktonic foraminiferal species occurrences within samples, and use a network-based method to explore the spatio-temporal patterns in the data, with a focus on ecology and morphology.
Research sample	The research sample is sourced from the Triton dataset (Fenton & Woodhouse et al. 2021). This dataset contains planktonic foraminiferal occurrences through the last 66 million years, and due to the high preservation potential and taxonomic completeness of this organism record, they are the best fossil group available to perform global analyses of the scale presented.
Sampling strategy	The data is originally from Fenton & Woodhouse et al. (2021). The data was sub-sampled at 250 ka after assessing sampling at different resolutions from 1 Ma-100 ka. All resolutions showed similar patterns, and 250 ka time-bins gave us a middle ground where the data presence was neither too noisy nor too aggregated.
Data collection	Data was extracted from from the Triton dataset (Fenton & Woodhouse et al. 2021).
Timing and spatial scale	Start date: 15 Ma; end date: 0 Ma; sampling resolution: 250 ka. We assessed sampling resolutions from 1 Ma-100 Ka, all resolutions showed the same patterns explored in the manuscript, and opted for 250 ka.
Data exclusions	We used the Triton dataset from 15-0 Ma, excluding all 38,046 planktonic foraminiferal occurrences for species exhibiting microperforate and medioperforate wall textures as these species have a less well-refined phylogeny compared to macroperforate species (Pearson, 2018). All macroperforate planktonic foraminiferal species were assigned speciation and extinction datums in accordance with Aze et al. (2011) and Fenton & Woodhouse et al. (2021), and all species occurrences located outside of the assigned stratigraphic ranges were removed to eliminate much of the occurrence data likely attributable to misidentification and/or reworking.
Reproducibility	All code and data is available in public domain. Data is from Fenton & Woodhouse et al. (2021) and code is on https://github.com/anshuman21111/foram-networks
Randomization	Planktonic foraminifera were grouped into the ecogroups and morphogroups of Aze et al. (2011), to test the primary hypotheses.
Blinding	Blinding is not applicable as we were working with aggregate data and occurrences of species.
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 and archaeology
☒	☐ Animals and other organisms
☒	☐ Human research participants
☒	☐ 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	The Triton dataset (Fenton & Woodhouse et al. 2021)
Specimen deposition	The Triton dataset (Fenton & Woodhouse et al. 2021)

Dating methods

No new dates provided.

☒ Tick this box to confirm that the raw and calibrated dates are available in the paper or in Supplementary Information.

Ethics oversight

No ethical approval or guidance was required, as the data was already collected/collated in Fenton & Woodhouse et al. (2021)

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