

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 We provide a thorough description of the code and software in the MS methods, and we provide an appendix with links to all soft code, which is freely-available and open source.

Data analysis We provide a thorough description of the code and analyses in the MS methods.

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 data are available in the main text, supplementary materials or via Dryad.

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

Ecological, evolutionary & environmental sciences study design

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

Study description	The study used simulated species in a cellular automaton framework to examine expected patterns of diversity that resulted from the spatio-temporal dynamics of climate over the last 120 Kyr. We used 2000 initial seed points for the simulated species, but we tested each seed point under different niche and dispersal parameters. Global climate models drove speciation and extinction dynamics in the study, and were derived from the HadCM3 model, which was originally developed at the UK Met Office. In all, the 2000 initial seeds (i.e., incipient 'species') were tested under all combinations of niche breadth (narrow and broad), dispersal ability (poor and good), and climate scenario from HadCM3 (no ice, ice, and probability of ice), resulting in 24,000 total simulations.
Research sample	Patterns of biodiversity were quantified for each of the 24,000 simulations. For most analyses in the manuscript (see text for details), we drew randomly one simulation from each 1 degree latitudinal band for a series of 100 bootstrap replicates. These random draws were then used to quantify latitudinal diversity curves and to examine map-based diversity patterns.
Sampling strategy	As noted, we used 2000 initial seeds, randomly distributed over the surface of the Earth.
Data collection	All dispersal, extinction, and speciation dynamics were recorded for each simulation.
Timing and spatial scale	Simulations were conducted using global climate model data for the last 120 Kyr at a spatial resolution of 1 degree.
Data exclusions	No data were excluded.
Reproducibility	We repeated each simulation 2000 times, and we examined patterns under different niche and dispersal traits. We did so in order to assess how the starting location of a simulation may affect resulting diversity patterns, and how the traits assigned to species may affect resulting diversity patterns.
Randomization	The initial starting location of each simulation was randomized. Moreover, we selected randomly one simulation per latitudinal band to analyze resulting diversity patterns: this process was repeated over a series of 100 bootstrap replicates.
Blinding	Not relevant to our study.
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	Methods
n/a	n/a
Involvement in the study	Involvement in the study
☒ ☐ Antibodies	☒ ☐ ChIP-seq
☒ ☐ Eukaryotic cell lines	☒ ☐ Flow cytometry
☒ ☐ Palaeontology	☒ ☐ MRI-based neuroimaging
☒ ☐ Animals and other organisms	
☒ ☐ Human research participants	
☒ ☐ Clinical data	