

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 (<i>n</i>) 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. <i>F</i> , <i>t</i> , <i>r</i>) with confidence intervals, effect sizes, degrees of freedom and <i>P</i> 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 <i>d</i> , Pearson's <i>r</i>), 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 software was used to generate or collect data, all data used is noted in the data availability. Data processing code is available as supplementary material and will be deposited in a public GitHub repository before publication.
Data analysis	Data analyses were conducted in R (v. 4.2.2). Spatial analysis was carried out using the packages sf and terra. Visualisations were created using ggplot2 with auxiliary functions from ggtern and ggridges. Colour palettes used were taken from Crameri et al and accessed through the R package scico. To ensure author anonymity during the review process, R code is available as supplementary material and will be deposited in a public GitHub repository before publication.

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 used in the study are from publicly available sources. Climate and palaeoclimate data are both available from <https://chelsa-climate.org/>, ice sheet data is available from <https://www.atmosp.physics.utoronto.ca/~peltier/data.php>. Layers used for building the defaunation data are available from https://megapast2future.github.io/PHYLACINE_1.2/. The exact GBIF data used for generating the nonnative occurrence data are available from <https://doi.org/10.15468/dl.6aebcd>, the country-level checklists from GRIIS are available from <https://zenodo.org/records/6348164>. The Biodiversity Intactness Index from Newbold et al was accessed from <https://doi.org/10.5519/0009936>. The World Database of Protected Areas can be accessed from <https://www.protectedplanet.net>, Key Biodiversity Areas can be requested from keybiodiversityareas.org.

Research involving human participants, their data, or biological material

Policy information about studies with [human participants or human data](#). See also policy information about [sex, gender \(identity/presentation\), and sexual orientation](#) and [race, ethnicity and racism](#).

Reporting on sex and gender

Reporting on race, ethnicity, or other socially relevant groupings

Population characteristics

Recruitment

Ethics oversight

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

Ecological, evolutionary & environmental sciences study design

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

Study description

We conducted an analysis to test the degree to which the terrestrial biosphere is experiencing conditions that are distinct from historical baselines, here called “novel conditions”. We conceptualized and analysed six metrics which describe this novelty, divided into three categories of “climate”, “defaunation” and “floristic disruption”. Specifically, the six metrics were temperature novelty, precipitation novelty, mammalian richness loss, mammalian body size loss, intactness, and proportion of nonnative alien species. Both temperature and precipitation were calculated as the most recent 300-year climate window which was fully outside the modern (1980-2018) climate range, using data from the CHELSA-TrACE21k dataset (Karger et al 2020). Defaunation metrics were calculated using PHYLACINE (Faurby et al 2018), comparing predictions of “present-natural” mammal distributions to current mammal distributions. Intactness was calculated as the change in the plant community abundance (Biodiversity Intactness Index or BII) relative to 1 (ie the absolute value of 1-BII). We used BII from Newbold et al 2016. Finally, for the nonnative alien species we used country level checklists of known nonnative species (GRIIS – Pagad et al 2018, 2022) and matched them to GBIF records for all species in the Kingdom Plantae. The final layers were produced at a 10x10km resolution and then combined in an equal-weight map to show overall novelty exposure. Analysis was then done comparing the novelty exposure to different regions and land management categories. We used tests of effect size to test the differences between broad climatic regions (n = 5 – polar, cold, temperate, arid, tropical), protected areas (n = 265289), and key biodiversity areas (n = 16012), using an extraction of all cells within each category. For the purposes of our analysis we grouped all protected areas into one group, and repeated this for key biodiversity areas, before splitting them into climate regions.

Research sample

The final data layers consisted of 10x10km pixels, with a total of 7,050,211 cells containing data.

Sampling strategy	No sample size calculations were done - all available terrestrial data were used. 10x10km resolution was chosen as the resolution of data in order to ensure small scale variations in climate simulations were not biasing the regional results.
Data collection	GBIF data was provided by a large number of individual data contributors, which will be provided as supplemental material.
Timing and spatial scale	Modern climate data was taken for the years 1980-2018, palaeoclimate data was taken from simulations run to 21k Before Present. GBIF data was downloaded on the 24th October 2023. All data used was taken for 10x10km cells.
Data exclusions	We excluded the following mammals from PHYLACINE dataset due to inaccuracies in the range estimates or for not being relevant to the terrestrial nature of the study: humans, marine mammals (whales, seals and marine otters), bats and the polar bear. We excluded key biodiversity areas which are inside protected areas, as well as marine protected areas. No other data were excluded.
Reproducibility	We include access links to each data source, along with processing code and analytical code as supplemental material. Post-processing data layers generated in the study can be deposited in a public repository.
Randomization	For comparing protected areas/key biodiversity areas to areas not in either category, novelty was calculated using a random sample of equal area within the same climate region. This was done for each protected area, and resampling was done 1,000 times for each.
Blinding	Blinding not relevant to the 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

n/a	Involved in the study
☒	☐ Antibodies
☒	☐ Eukaryotic cell lines
☒	☐ Palaeontology and archaeology
☒	☐ Animals and other organisms
☒	☐ Clinical data
☒	☐ Dual use research of concern
☒	☐ Plants

Methods

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

Plants

Seed stocks	Report on the source of all seed stocks or other plant material used. If applicable, state the seed stock centre and catalogue number. If plant specimens were collected from the field, describe the collection location, date and sampling procedures.
Novel plant genotypes	Describe the methods by which all novel plant genotypes were produced. This includes those generated by transgenic approaches, gene editing, chemical/radiation-based mutagenesis and hybridization. For transgenic lines, describe the transformation method, the number of independent lines analyzed and the generation upon which experiments were performed. For gene-edited lines, describe the editor used, the endogenous sequence targeted for editing, the targeting guide RNA sequence (if applicable) and how the editor was applied.
Authentication	Describe any authentication procedures for each seed stock used or novel genotype generated. Describe any experiments used to assess the effect of a mutation and, where applicable, how potential secondary effects (e.g. second site T-DNA insertions, mosaicism, off-target gene editing) were examined.