nature portfolio

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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	Data was collected from open source online repositories as described in the Methods section. Data processing was done in R version 4.1.0 and the code used is available on zenodo at: https://doi.org/10.5281/zenodo.15482434. Extraction of satellite remote sensing data was done in Google Earth Engine, code available at: https://code.earthengine.google.com/b0d68ff3faa1b0e04d9b7f5f4e6133ba.
Data analysis	Alla analyses were done in R version 4.1.0. Specific R packages are described in the Methods section and the code used is available on zenodo at: https://doi.org/10.5281/zenodo.15482434

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

The data necessary to reproduce the analyses is available on figshare at: https://doi.org/10.6084/m9.figshare.29235323

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	*Use the terms sex (biological attribute) and gender (shaped by social and cultural circumstances) carefully in order to avoid confusing both terms. Indicate if findings apply to only one sex or gender; describe whether sex and gender were considered in study design; whether sex and/or gender was determined based on self-reporting or assigned and methods used.* *Provide in the source data disaggregated sex and gender data, where this information has been collected, and if consent has been obtained for sharing of individual-level data; provide overall numbers in this Reporting Summary. Please state if this information has not been collected.* *Report sex- and gender-based analyses where performed, justify reasons for lack of sex- and gender-based analysis.*
Reporting on race, ethnicity, or other socially relevant groupings	*Please specify the socially constructed or socially relevant categorization variable(s) used in your manuscript and explain why they were used. Please note that such variables should not be used as proxies for other socially constructed/relevant variables (for example, race or ethnicity should not be used as a proxy for socioeconomic status).* *Provide clear definitions of the relevant terms used, how they were provided (by the participants/respondents, the researchers, or third parties), and the method(s) used to classify people into the different categories (e.g. self-report, census or administrative data, social media data, etc.)* *Please provide details about how you controlled for confounding variables in your analyses.*
Population characteristics	*Describe the covariate-relevant population characteristics of the human research participants (e.g. age, genotypic information, past and current diagnosis and treatment categories). If you filled out the behavioural & social sciences study design questions and have nothing to add here, write "See above."*
Recruitment	*Describe how participants were recruited. Outline any potential self-selection bias or other biases that may be present and how these are likely to impact results.*
Ethics oversight	*Identify the organization(s) that approved the study protocol.*

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 tested the biodiversity-ecosystem function and multifunctionality relationship at the ecosystem scale. We derive ecosystem functional properties, climatic covariates, and vegetation structure from a global dataset (147 sites) of surface gas exchange measurement stations. We also derive vegetation indexes from satellite remote sensing data from which we infer vegetation structure and biodiversity.
Research sample	The data used for the calculation of ecosystem functional properties belongs to the FLUXNET global network of CO2, water and energy flux measurements, including the La Thuile, FLUXNET2015, AmerifluxFLUXNET, and WarmWinter2020 data products. The sites used cover a wide variety of climate zones (from tropical to arctic) and vegetation types (wetlands, shrublands, savannahs, grasslands, evergreen and deciduous forests boreal, temperate and tropical forests). The FLUXNET LaThuile product is available at: https://fluxnet.fluxdata.org/data/la-thuile-dataset/, the FLUXNET2015 product at: https:// fluxnet.fluxdata.org/data/fluxnet2015-dataset/, the AmerifluxFLUXNET product at: https://ameriflux.lbl.gov/data/download-data/, and the WarmWinter2020 product at: https://doi.org/10.18160/2G60-ZHAK. Information on the sites used and related sources are included in the supplementary materials (Supplementary Table S2). Vegetation structure information for the sites were collected from databases, site websites, and literature as described in Supplementary Table S2. Satellite remote sensing data for Leaf Area Index is available at: https://doi.org/10.5067/MODIS/MCD15A3H.061. The land cover data used for filtering is available at: https://doi.org/10.5281/zenodo.5571935. The Sentinel-2 data used to derived proxies of biodiversity is available e.g. at: https://land.copernicus.eu/en/products/global-image-mosaic?tab=overview.
Sampling strategy	The available data were used with the exception of data coming from cropland sites to avoid effects derived by strong management practices. Measurements were also removed in case the data quality was not enough to fulfill the required criteria described in the Methods section.

Data collection	Data for the calculation of ecosystem functional properties were recorded using the eddy covariance technique, which is based on a combination of a gas analyzer and ultrasonic anemometer associated with a meteorological station. FLUXNET is global network of site principle investigators and collaborators and processed with standardized procedures.
Timing and spatial scale	We used eddy covariance flux measurements from the available time-series that depend on each site, with a minimum of five years of data acquisition. Flux data acquisition is based on high-frequency measurements that are generally provided at half-hour resolution. Flux spatial footprints can vary from a few dozen to several hundred meters in scale. We extracted Sentinel-2 satellite remote sensing data for the calculation of biodiversity proxies between 2016-01-01 and 2024-03-31 at a spatial resolution of 20 m.
Data exclusions	From the original flux datasets we excluded cropland sites to avoid the inclusion of sites heavily managed in the analysis (e.g. fertilization, irrigation, etc). Sites were additionally excluded if they did not fulfill the filtering criteria described in the Methods section (e.g. based on quality, precipitation, day/night), or if the measurement period was shorter than five years. We excluded plant traits measurements conducted under experimental setups that would not represent natural ambient conditions (e.g. elevated CO2).
Reproducibility	We did not collect measurements directly but used widely documented global datasets and literature data. The code used for the processing of the data is available on zenodo at: https://doi.org/10.5281/zenodo.15482434.
Randomization	We did not perform randomization.
Blinding	We did not perform blinding.

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, mosiacism, off-target gene editing) were examined.*