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	No new data were collected for this study. Analyses used the RivFishTIME database and associated source datasets listed in Supplementary Tables 1-2.
Data analysis	All analyses were conducted in R version 4.4.3. Hill diversity metrics were calculated using iNEXT.3D, principal component analyses were performed using FactoMineR, and generalized additive models were fitted using mgcv. Data processing and visualization followed standard R workflows. Custom R scripts are provided in the accompanying data and code package for editors and reviewers and will be made publicly available through Springer Nature figshare upon 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

The data supporting this study will be made available to editors and reviewers through the accompanying data and code package and/or Springer Nature figshare private reviewer access. Upon publication, the data will be made publicly available through Springer Nature figshare.

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

Life sciences study design

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

Sample size	
Data exclusions	
Replication	
Randomization	
Blinding	

Behavioural & social sciences study design

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

Study description	
Research sample	
Sampling strategy	
Data collection	

Timing	
Data exclusions	
Non-participation	
Randomization	

Ecological, evolutionary & environmental sciences study design

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

Study description	This is a retrospective observational analysis of global riverine freshwater fish community time series. The study tests whether biological invasions alter biodiversity-temporal stability relationships by comparing invaded and non-invaded communities and by modelling invasion intensity as a continuous gradient across global, biogeographic realm and ecoregion scales.
Research sample	The research sample consisted of riverine freshwater fish assemblage time series from RivFishTIME. After filtering, the dataset included 3,695 community time series from 281 drainage basins across 15 countries, 60,962 sampling events, 350,414 species-abundance records and 658 freshwater fish species. The most represented realms were the Palearctic, Nearctic and Australasia.
Sampling strategy	All available RivFishTIME assemblages satisfying predefined criteria were retained: minimum temporal length of 10 years, consistent sampling protocol through time, and consistent abundance unit within each time series. Sampling events were restricted to within +/-45 days of the most frequently sampled date at each site; when multiple events were available in the same year, the event closest to that focal date was retained. No prospective sample-size calculation was performed because the study reanalysed existing time-series data.
Data collection	No new field data were collected by the authors. Fish community records were obtained from RivFishTIME and the original monitoring sources listed in Supplementary Table 1. Native and non-native status was assigned using a drainage-basin-scale freshwater fish framework and a global database of established non-native fish species.
Timing and spatial scale	Median time-series duration was 23 years (25th and 75th percentiles: 17, 29), median completeness was 78.26% (59.09%, 92.31%), and the median first sampling year was 1994 (1988, 2000). Sampling sites spanned 281 drainage basins across 15 countries.
Data exclusions	Exclusions were based on predefined comparability and robustness criteria. Assemblages were excluded if they had fewer than 10 years of data, inconsistent sampling protocol or inconsistent abundance units. Seasonal variation was minimized by excluding events outside +/-45 days of the site-specific focal sampling date. Species occurring in only a single year within a time series were removed before stability estimation, and time series retaining only one species after this step were excluded. Temporal stability was quantified for 3,524 time series retained in subsequent analyses.
Reproducibility	The analysis is reproducible from the filtered analysis-ready data and custom R scripts provided in the accompanying data and code package. Full model comparisons and outputs are reported in Extended Data Tables 1-4 and Supplementary Tables 3-30. The hypothesis-testing workflow was repeated across global, biogeographic realm and ecoregion scales.
Randomization	Not applicable. This was an observational analysis of existing monitoring time series; communities were not allocated to experimental treatments.
Blinding	Not applicable. The study used existing ecological time-series data and predefined classifications/metrics; there was no experimental group allocation or subjective outcome assessment requiring blinding.

Did the study involve field work? ☒ Yes ☐ No

Field work, collection and transport

Field conditions	The source datasets represent riverine freshwater fish community monitoring under the original survey protocols. Electrofishing accounted for 97.81% of time series; other methods included seining/netting, trapping and trawling.
Location	Sampling sites were located in 281 drainage basins across 15 countries, primarily in the Palearctic, Nearctic and Australasia. The largest contributions were Sweden (37.51%), the United Kingdom (27.66%), France (17.67%) and the United States (5.90%).
Access & import/export	No field access or biological material import/export was conducted by the authors for this study. Analyses used existing monitoring datasets compiled in RivFishTIME and listed in Supplementary Table 1.
Disturbance	No experimental disturbance or additional sampling disturbance was introduced by this study. Original monitoring disturbance, where relevant, followed the protocols of the source datasets.

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

Antibodies

Antibodies used	
Validation	

Eukaryotic cell lines

Policy information about cell lines and Sex and Gender in Research

Cell line source(s)	
Authentication	
Mycoplasma contamination	
Commonly misidentified lines (See ICLAC register)	

Palaeontology and Archaeology

Specimen provenance	
Specimen deposition	
Dating methods	

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

Ethics oversight	

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

Animals and other research organisms

Policy information about studies involving animals; ARRIVE guidelines recommended for reporting animal research, and Sex and Gender in Research

Laboratory animals	Not applicable. No laboratory animals were used.
Wild animals	The study analysed existing monitoring records of wild freshwater fish communities, covering 658 freshwater fish species. No animals were newly captured, handled or sampled by the authors for this study.
Reporting on sex	Sex was not recorded or analysed. The unit of analysis was species-level community abundance through time, not individual-level sex-specific responses.
Field-collected samples	No new field-collected samples were collected by the authors. The analyses used existing field-collected freshwater fish monitoring records from RivFishTIME and associated source datasets.
Ethics oversight	No new animal capture, handling or experimental procedures were performed by the authors; therefore, additional institutional

Ethics oversight	animal ethics approval was not required for this secondary analysis of existing ecological monitoring data. Original data providers were responsible for permits and approvals associated with their monitoring programmes.

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

Clinical data

Policy information about clinical studies

All manuscripts should comply with the ICMJE guidelines for publication of clinical research and a completed CONSORT checklist must be included with all submissions.

Clinical trial registration	
Study protocol	
Data collection	
Outcomes	

Dual use research of concern

Policy information about dual use research of concern

Hazards

Could the accidental, deliberate or reckless misuse of agents or technologies generated in the work, or the application of information presented in the manuscript, pose a threat to:

No	Yes	
☐	☐	Public health
☐	☐	National security
☐	☐	Crops and/or livestock
☐	☐	Ecosystems
☐	☐	Any other significant area

Experiments of concern

Does the work involve any of these experiments of concern:

No	Yes	
☐	☐	Demonstrate how to render a vaccine ineffective
☐	☐	Confer resistance to therapeutically useful antibiotics or antiviral agents
☐	☐	Enhance the virulence of a pathogen or render a nonpathogen virulent
☐	☐	Increase transmissibility of a pathogen
☐	☐	Alter the host range of a pathogen
☐	☐	Enable evasion of diagnostic/detection modalities
☐	☐	Enable the weaponization of a biological agent or toxin
☐	☐	Any other potentially harmful combination of experiments and agents

Plants

Seed stocks	
Novel plant genotypes	
Authentication	

ChIP-seq

Data deposition

☐ Confirm that both raw and final processed data have been deposited in a public database such as GEO.

☐ Confirm that you have deposited or provided access to graph files (e.g. BED files) for the called peaks.

Data access links *May remain private before publication.*	
Files in database submission	
Genome browser session (e.g. UCSC)	

Methodology

Replicates	
Sequencing depth	
Antibodies	
Peak calling parameters	
Data quality	
Software	

Flow Cytometry

Plots

Confirm that:

☐ The axis labels state the marker and fluorochrome used (e.g. CD4-FITC).

☐ The axis scales are clearly visible. Include numbers along axes only for bottom left plot of group (a 'group' is an analysis of identical markers).

☐ All plots are contour plots with outliers or pseudocolor plots.

☐ A numerical value for number of cells or percentage (with statistics) is provided.

Methodology

Sample preparation	
Instrument	
Software	
Cell population abundance	
Gating strategy	

☐ Tick this box to confirm that a figure exemplifying the gating strategy is provided in the Supplementary Information.

Magnetic resonance imaging

Experimental design

Design type	
Design specifications	
Behavioral performance measures	

Acquisition

Imaging type(s)

Field strength

Sequence & imaging parameters

Area of acquisition

Diffusion MRI ☐ Used ☐ Not used

Preprocessing

Preprocessing software

Normalization

Normalization template

Noise and artifact removal

Volume censoring

Statistical modeling & inference

Model type and settings

Effect(s) tested

Specify type of analysis: ☐ Whole brain ☐ ROI-based ☐ Both

Statistic type for inference

(See Eklund et al. 2016)

Correction

Models & analysis

n/a	Involved in the study
☐	☐ Functional and/or effective connectivity
☐	☐ Graph analysis
☐	☐ Multivariate modeling or predictive analysis

Functional and/or effective connectivity

Graph analysis

Multivariate modeling and predictive analysis