

Reporting Summary

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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

R software version 3.4.

Data analysis

R software version 3.4.

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

A full data availability statement is included 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](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

Here we have achieved the unprecedented feat of high-resolution mapping of the global diversity of all known marine fish species and their ecological interactions. Using this map, we compute for the first time the complex network of feeding interactions among all fish species around the world in order to better understand the consequences of extinctions and the propagation of perturbations. Among the key focal points of our manuscript, we find the particularly surprising result that this global food web is highly connected geographically, indicating that marine food webs have an elevated robustness to extinctions, yet their spatial connectivity may also propagate perturbations rapidly across oceans. Maps of local food webs also reveal that coastal ecosystems are more robust to extinction than those from the open water, an observation that generalizes previous findings based on punctual studies.

Research sample

Species data were obtained from the Ocean Biogeographic Information System (OBIS, <http://www.iobis.org>) on 08/27/2014 that represents the best available data set for a global study of marine fish food webs. We inventoried 16,238,200 occurrence records from 34,883 entries. We cleaned the data by identifying the synonyms, misspellings and rare species (only one occurrence) and by restricting it to species present in the marine environment according to FishBase (13). Synonyms were converted to accepted names. This resulted in a set of 11,503,257 occurrences for 11,345 fish species around the world. We considered the entire occurrences available in the OBIS database spanning from 1826 to 2013 as the occurrences inferior to 1950 represent solely 0.28% of the entire data set. To counteract some known biases in OBIS data (e.g., not all species/regions are equally represented), we reconstructed distribution maps for each species, defined as the convex polygon surrounding the area where each species was observed (see for details Fig. S3). The resulting polygon was divided into four parts across the world to integrate possible discontinuity between the two hemispheres and the Atlantic and Pacific Oceans. Then we refined each species distribution map by removing areas where maximal depths fell outside the minimum or maximum known depth range of the species (13). Final distribution maps of well-known species were checked visually and reviewed by the authors according to their expertise. We also compared the distribution of ~3500 tropical species present in this database to the Gaspar database frequently use in reef fish analyses (32). Finally, we aggregated fish distributions on a 1° resolution grid covering all oceans. All the data are freely available at this address <https://figshare.com/s/c9ca229cc1f3548f8b5c>. This scale allows computational feasibility and reproducibility of all analysis conducted here. We compiled the following environmental descriptors: distance to land, sea surface temperature (SST), sea surface salinity (SSS) and chlorophyll-a. Environmental descriptors were compiled from different sources and resolutions, and were fit to our grid system (Table S2).

Sampling strategy

NA

Data collection

NA

Timing and spatial scale

NA

Data exclusions

NA

Reproducibility

NA

Randomization

NA

Blinding

NA

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 | Involvement in the study |
|-------------------------------------|--|
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Antibodies |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Eukaryotic cell lines |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Palaeontology |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Animals and other organisms |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Human research participants |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Clinical data |

Methods

- | n/a | Involvement in the study |
|-------------------------------------|---|
| <input checked="" type="checkbox"/> | <input type="checkbox"/> ChIP-seq |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> Flow cytometry |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> MRI-based neuroimaging |