

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

The food webs data was collected from the existing dataset in pdf format and converted to csv format (no software used). The data was organized and filtered (see Research sample section and Data exclusions section below) using Matlab (version: 9.8.0.1417392 (R2020a) Update 4).

Data analysis

Built-in linear regression, histogram, mean, and variance function in Matlab (version: 9.8.0.1417392 (R2020a) Update 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 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](#)

We confirm that, should the manuscript be accepted, the data and code supporting the results will be archived and available in the Figshare Repository (or any other appropriate open access repository) and the data DOI will be included at the end of the article.

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

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Ecological, evolutionary & environmental sciences study design

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

Study description

In this study, in order to test and confirm the validity of the model and model output, i.e. food web stability and connectance. We utilize two well-curated datasets. For food web stability, we are comparing the frequency of stability produced by the model for different consumer-resource size-ratios with the empirical consumer-resource size-ratio distribution. Because empirical food webs represent the consumer-resource interactions that exist in nature, we expect more stable consumer-resource mass-ratios to be present at a higher frequency than less stable ones. Furthermore, we compare the empirical food web connectance (the number of observed links divided by the number of all possible links in a food web) and the connectance produced by the food web models.

Research sample

For both food web stability and connectance analysis, we use the 3082 consumer-resource interaction data with masses of species from eight food webs across different habitats [Pawar et al. 2012, Pawar et al. 2019]. And for food web connectance analysis, we use the previous eight food webs plus 181 binary food web data from the Ecologists' co-operative web bank [Cohen 1989]. The eight food webs used for stability analysis are Eastern Weddell Sea (305 trophic interactions), Grand Caricaie Marsh (459 trophic interactions), Scotch Broom (347 trophic interactions), Skipwith Pond (264 trophic interactions), Broadstone Stream (138 trophic interactions), UK Grassland (113 trophic interactions), GearaghWoodland (370 trophic interactions), and Estero de Punta Banda (1086 trophic interactions). Each trophic interaction contains (1) Community name, (2) Consumer-Resource names and relations, (3) Consumer mass (kg), (4) Resource mass (kg), and (5) Trophic interaction dimensionality (the space in which trophic interaction occur). Dividing resource mass by consumer mass, we get the consumer-resource mass-ratio for each trophic interaction. Since we are only using the consumer mass, the resource mass, and the trophic interaction dimensionality, we use Matlab to filter out the other information.

Sampling strategy

No sample-size calculation was performed. For model validation, we use the 3082 consumer-resource interaction data from eight food webs across different habitats. In addition, we also utilize 181 binary food web data from the Ecologists' co-operative web bank.

Data collection

The food webs data was collected from the existing datasets in pdf format and converted to csv format (no software used). The data was organized and filtered using Matlab (version: 9.8.0.1417392 (R2020a) Update 4). The data collection is completed by Tianyun Lin.

Timing and spatial scale

The data used were from existing datasets [Cohen 1989, Pawar et al. 2012, Pawar et al. 2019]. Spatial scale and timing are reported in the studies and publications in which the data were originally collected.

Data exclusions

The original dataset contains two types of trophic interaction dimensionality, i.e. 2D and 3D. The dimensionality is based on the space through which the resource moves and thus the consumer must catch it (Pawar et al. 2012). Because different dimensionalities have distinct scaling relationships with mass, and for model development purposes, we only use 2D interactions.

Reproducibility

Since we did not conduct any experiment for this study, the reproducibility of experimental findings is not relevant to this study. To reproduce model outputs, please use the provided code.

Randomization

We are only using the mass and mass-ratio distributions of the consumers and resources to compare with model output. Thus, randomization is not relevant to this study.

Blinding

We are only using the mass and mass-ratio distributions of the consumers and resources to compare with model output. Thus, blinding is not relevant to this 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
<input checked="" type="checkbox"/>	Antibodies
<input checked="" type="checkbox"/>	Eukaryotic cell lines
<input checked="" type="checkbox"/>	Palaeontology and archaeology
<input checked="" type="checkbox"/>	Animals and other organisms
<input checked="" type="checkbox"/>	Human research participants
<input checked="" type="checkbox"/>	Clinical data
<input checked="" type="checkbox"/>	Dual use research of concern

Methods

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