

Reporting Summary

Nature Research 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 Research policies, see [Authors & Referees](#) 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

All data in this study is from previous studies and is available online for researchers to reproduce our results. All data are also available on the Github repository for the project, at github.com/cjcarlson/brevity.

Data analysis

All code is available on a Github repository found at github.com/cjcarlson/brevity. The codependent R package is available at github.com/cjcarlson/codependent.

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

All data in this study is from previous studies and is available online for researchers to reproduce our results. Original sources can be found as follows: global diversity of viruses in mammal hosts can be found in Carroll et al. (2018); plant-pollinator interactions can be found in Robertson (1929) and reproduced in Marlin (2001); mycorrhizal networks are described in Toju et al. (2018); and the host-helminth network can be obtained from the Natural History Museum London's Helminth Database, through the helminthR API. All data are also available on the Github repository for the project, at github.com/cjcarlson/brevity.

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	We generated curves from the size of iteratively subsampled bipartite networks to extrapolate global viral diversity.
Research sample	We reused several large, open data sources that describe ecological networks in the process, including the largest available database of host-virus associations for mammals. We generated no original primary data in the study.
Sampling strategy	We subsampled bipartite networks iteratively, selecting sample sizes based on a number far past the sample size at which the models converged. Sample size was standardized and reported for all analyses.
Data collection	Data were collected by previous studies, and can be found in the Github repository for the study.
Timing and spatial scale	N/A (ecological association data drawn from the literature)
Data exclusions	No data were excluded from analyses except for human-viral associations, which were disproportionately represented in the data and prevented curve fitting.
Reproducibility	All code is made available to ensure reproducibility.
Randomization	Not applicable to computational study.
Blinding	Not applicable to computational 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

Methods

n/a	Involved in the study
☒	☐ Antibodies
☒	☐ Eukaryotic cell lines
☒	☐ Palaeontology
☒	☐ Animals and other organisms
☒	☐ Human research participants
☒	☐ Clinical data

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