

## 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 analysis

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 GPDD data are available on KNB with identifier <https://doi.org/10.5063/F1BZ63Z8>. Zooplankton data were obtained for Oneida Lake from KNB (identifier kgordon.17.67), for Lake Zurich from Wasserversorgung Zürich, and for Lake Geneva from the Observatory on LAkes (© OLA-IS, AnaEE-France, INRA of Thonon-les-Bains, CIPEL; <https://doi.org/10.4081/jlimnol.2020.1944>). The simulated datasets and generating code are available in the code repository. The specific GPDD time series used and associated metadata (including compiled generation time and mass data) are available in the code repository.

## 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 evaluated the prevalence of chaos in a large sample of ecological time series using several independent chaos detection methods. Prior to this, we conducted an extensive simulation study to evaluate each method and found that 3 of 6 methods produced credible classification accuracy.
Research sample	We selected 172 time series from the Global Population Dynamics Database (GPDD) representing 138 taxa from 57 locations. These included phytoplankton, zooplankton, insects, fishes, mammals, and birds. To evaluate the generality of our results beyond the GPDD, we classified an additional 34 time series of zooplankton from 3 lakes.
Sampling strategy	We selected the time series from the GPDD that had at least 30 non-missing time points, at least 5 unique abundance values, less than 60% zeros, and less than 22% missing time points (these criteria were also applied to the lake zooplankton time series). We used only field-collected survey data (we excluded laboratory and harvest data), excluded human diseases, and excluded the shorter and lower-quality of duplicate time series in the GPDD that passed our filtering. GPDD time series were also required to have a reliability score of at least 2.
Data collection	All data were downloaded from public online repositories. The GPDD data were accessed via the R package 'rgpdd'.
Timing and spatial scale	The data in the GPDD span a wide range of time periods and come from many locations. Of the 175 GPDD time series, there were 112 sampled annually, 53 monthly, 8 semiannually, and 2 bimonthly. The lake zooplankton data were sampled monthly.
Data exclusions	The ability to detect chaos when it is present depends critically on time series length and quality. Consequently, we excluded time series that were unlikely to be classified with any confidence (see 'Sampling strategy'). No data were excluded from the selected time series.
Reproducibility	Our study is a meta-analysis. All code used for data processing and analysis is provided in the GitHub repository, and can be used to reproduce the results.
Randomization	We analyzed all time series that met the selection criteria.
Blinding	We analyzed all time series that met the selection criteria, regardless of any other characteristics (e.g. sampling method, organism identity, whether or not the time series was likely to be chaotic).

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"/>	<input type="checkbox"/> Antibodies
<input checked="" type="checkbox"/>	<input type="checkbox"/> Eukaryotic cell lines
<input checked="" type="checkbox"/>	<input type="checkbox"/> Palaeontology and archaeology
<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
<input checked="" type="checkbox"/>	<input type="checkbox"/> Dual use research of concern

### Methods

n/a	Involved 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