

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
<i>Only common tests should be described solely by name; describe more complex techniques in the Methods section.</i> |
| ☐ | ☒ | 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
<i>Give P values as exact values whenever suitable.</i> |
| ☒ | ☐ | 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	We run four previously published models. Each model was replicated and simulated within the system dynamics software STELLA Architect v.1.6.151. The models are available here: https://doi.org/10.5281/zenodo.7946433
Data analysis	Outputs were exported into CSV files as time series and analysed in the statistical software R v.4.1.0. The optimal breakpoint function of the R package 'strucchange' v.1.5-2 was used. Boxplots were graphed in R using the package 'ggplot' (v.3.3.5). The code supporting this is available here: https://doi.org/10.5281/zenodo.7946433

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 datasets generated during and/or analysed during the current study are available from <https://doi.org/10.5281/zenodo.7946433>

Human research participants

Policy information about [studies involving human research participants and Sex and Gender in Research](#).

Reporting on sex and gender

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](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 aim to generalise the dynamics of increasing the numbers of drivers, their rates and variability (as proxies for stronger interactions between systems and noise) on the speed at which tipping points are reached in four model social-ecological system dynamics models: Chilika fishery, Lake phosphorus, Easter Island, and a modified version of The Hadley Centre Dynamic Global Vegetation Model (TRIFFID) of forest dieback.

Research sample

The Chilika fishery model is a social-ecological model designed to simulate the future fish population and catch trajectories of the Chilika lagoon, Odisha, India. The Lake phosphorus model is a simplified version of the original 'lake response to P input and recycling' model, as modified by Wang et al. (48). The Easter Island model aims to explore alternative hypotheses behind the social-ecological collapse of the Easter Island civilisation. The TRIFFID model is a modified version of The Hadley Centre Dynamic Global Vegetation Model, originally developed by Cox et al. (50) to explore the effects of atmospheric CO₂ concentrations on the rate of Amazon dieback.

Sampling strategy

We performed four in silico experiments:

- Experiment #1: only the primary slow driver in each model changes over time, and all other drivers remain constant;
- Experiment #2: multiple slow rates, with up to two additional (i.e. 'secondary' and 'tertiary') slow trajectories on top of the primary driver changing over time;
- Experiment #3: the addition of noise to the primary trajectory, with all other drivers held constant. The magnitude of noise may be either coupled or uncoupled from the trajectory of the primary driver;
- Experiment #4: the addition of noise to the primary driver, with up to two additional slow drivers. The magnitude of noise may be either coupled or uncoupled from the trajectory of the primary driver.

Each of the models were ran for the following number of iterations (including both 'coupled' and 'uncoupled' settings):

- Chilika fishery: 70,000
- Easter Island: 70,000
- Lake Phosphorus: 120,000
- TRIFFID: 70,000

Data collection

All data are modelled from the above experiments.

Timing and spatial scale

All data are modelled from the above experiments. The time and spatial scale of the models vary

Data exclusions

This research focusses on tipping points, so only model runs that went through Type-1 or Type-2 boundaries defined by Dearing et al. (14) were included in the analysis

Reproducibility

Being modelled, the data are fully reproducible.

Randomization

Being modelled, we have full control of covariates and so randomisation is not necessary

Blinding

Blinding is not relevant to this study. Our data are identified using the optimal breakpoint function of the R package 'strucchange' v.1.5-2 and so observer bias is not possible

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
☒	☐ Antibodies
☒	☐ Eukaryotic cell lines
☒	☐ Palaeontology and archaeology
☒	☐ Animals and other organisms
☒	☐ Clinical data
☒	☐ Dual use research of concern

Methods

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