

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

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|-------------------------------------|-------------------------------------|--|
| ☐ | ☒ | 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

No software was used.

Data analysis

To analyze the data, we used several open source code as follows

<https://skccm.readthedocs.io/en/latest/>

<https://github.com/Partial-Cross-Mapping>

Also, we used MATLAB package 'Granger Causality Test' as follow (version 1.3.0.0)

<https://www.mathworks.com/matlabcentral/fileexchange/25467-granger-causality-test>

Lastly, computational package including the codes for the manuscript are provided in github (<https://github.com/Mathbiomed/GOBI>).

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 data sets generated in this study are publicly available on Github (<https://github.com/Mathbiomed/GOBI>). The references for the public data sets used and analyzed during this study can be found in the Results section. Specifically, we used public datasets from several references as follows.

- 1) DOI: 10.1126/science.1227079
- 2) DOI: 10.1038/s41467-022-30478-2
- 3) DOI: 10.1038/nature19841
- 4) DOI: 10.1016/s0092-8674(03)00934-6
- 5) DOI: 10.1038/s41467-020-16238-0

Human research participants

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

Reporting on sex and gender	This information has not been collected
Population characteristics	This information has not been collected
Recruitment	This information has not been collected
Ethics oversight	This information has not been collected

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)

Life sciences study design

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

Sample size	We used 5 different time series datasets as follows. 1) Prey predator system (DOI: 10.1126/science.1227079) - Time-series data for two species - Each time series contain 71 time points 2) Genetic oscillator (DOI: 10.1038/s41467-022-30478-2) - Time-series data for two proteins. Data are obtained in eight different conditions. - Each time series contain 84 or 96 time points 3) Repressilator (DOI: 10.1038/nature19841) - Time-series data for three proteins. - Each time series contain 85 time points 4) Estradiol dataset (DOI: 10.1016/s0092-8674(03)00934-6) - Time-series data for four proteins. - Each time series contain 212 time points 5) Air pollutants and cardiovascular disease dataset (DOI: 10.1038/s41467-020-16238-0) - Time series data for 4 air pollutants and hospital admission time-series data for cardiovascular disease. - each time series contain 1032 time points (about 3 years)
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Data exclusions	As we only generated in silico simulation data, we do not need to provide regarding data exclusions.
Replication	As we only generated in silico simulation data, we do not need to provide regarding replication.
Randomization	As we only generated in silico simulation data, we do not need to provide regarding randomization.
Blinding	As we only generated in silico simulation data, we do not need to provide regarding blinding.

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

Methods

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