

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

Optical-density (600 nm) time-series were acquired on a BioTek Synergy H1 microplate reader controlled by Gen5 software v3.12.08 (read interval = 6 min, temperature = 37 °C, orbital shaking = 800 rpm). At least two blank wells were included on every plate. This instrument was calibrated against the ThermoFisher Genesys spectrophotometer (600nm wavelength).

Data analysis

All analyses were performed with the open-source Julia package Kinbiont (Julia 1.11.0 and 1.11.4; Kinbiont v1.1.8). Kinbiont is freely available at <https://github.com/pinheiroGroup/Kinbiont.jl>, which includes comprehensive documentation and examples for code usage. All scripts and data necessary to reproduce the analyses from the paper are available at https://github.com/pinheiroGroup/Kinbiont_utilities. All scripts, raw data, and exact software versions used in this study are permanently archived in the Zenodo record DOI 10.5281/zenodo.15488336.

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](#)

All raw plate-reader time-series, preprocessing files, fitted-parameter tables and downstream-analysis outputs generated in this study are openly available at https://github.com/pinheiroGroup/Kinbiont_utilities. All scripts, raw data, and exact software versions used in this study are permanently archived in the Zenodo record "Kinbiont utilities" (DOI 10.5281/zenodo.15488336).

Research involving human participants, their data, or biological material

Policy information about studies with [human participants or human data](#). See also policy information about [sex, gender \(identity/presentation\), and sexual orientation](#) and [race, ethnicity and racism](#).

Reporting on sex and gender	N/A
Reporting on race, ethnicity, or other socially relevant groupings	N/A
Population characteristics	N/A
Recruitment	N/A
Ethics oversight	N/A

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

To demonstrate and validate the Kinbiont pipeline we analyzed six independent datasets that span key ecological and evolutionary questions:

* Resource utilisation: public diauxic-growth curves of *Acinetobacter* grown on alanine + glutamate (Bloxham et al., 2022).

* Bacteria-phage interaction: optical-density (OD) time series from *E. coli* (DSMZ 613) cultures infected with T4 phage (Rajnovic et al., 2019).

* Bioproduction efficiency: multichannel batch-fermentation data—biomass, substrate and ethanol—for *Kluyveromyces marxianus* (Salazar et al., 2023; raw files supplied by authors).

* Nutrient limitation (new data): high-resolution growth curves of a methionine-auxotroph *E. coli* Δ metA strain (gift of Prof. Martin Ackermann) across a methionine gradient, recorded in 48-well plates (37 °C, OD600 every 6 min).

* Antibiotic stress (new data): chloramphenicol dose–response time series for *E. coli* BW25113 (DSM 27469) taken under the same plate conditions.

* Ecotoxicological pressure: high-throughput screen of 12 freshwater isolates (15 120 OD curves) exposed to 255 single and combined pollutant treatments (Smith et al., 2024).

Plate assays used independent overnight cultures, ≥ 2 blank wells per plate, continuous shaking at 37 °C, and multiple-scattering correction via external calibration. Published data were analysed exactly as provided by the original authors.

Kinbiont executes three steps—(i) preprocessing, (ii) model-based parameter inference (with automatic segmentation when needed), and (iii) interpretable machine-learning analyses—to link experimental conditions to inferred growth parameters. Applying the same

workflow across all six data sets allowed us to benchmark fitting accuracy, rediscover classical empirical laws (Monod kinetics, Langmuir-type antibiotic inhibition) and identify growth-phase-specific sensitivities to chemical stressors.

All primary data, raw plate files, scripts and fitted outputs are openly archived (Zenodo DOI 10.5281/zenodo.15488336; GitHub: pinheiroGroup/Kinbiont_utilities).

Study design

Treatment factors:

- Methionine concentration (8 values)
- Chloramphenicol concentration (6 values)
- Alanine:glutamate ratio (25 combinations)
- Phage infection (2: $\pm$ T4)
- Yeast strain (we use data of one strain for the main text analysis)
- Pollutant/stressors (255 combinations)

Interactions:

- The chemical stressors screen is a full factorial of 8 chemicals (single & combined effects).

Other assays manipulate one factor at a time (no interactions tested).

Design structure:

- New assays: factor $\times$ replicate.
- Published datasets keep their original design (see cited papers).

Research sample

Pure cultures of *Escherichia coli* (K-12 BW25113 and Δ metA auxotroph; data generated for this study), *Acinetobacter* sp., T4 bacteriophage, and *Kluyveromyces marxianus* laboratory strains; 12 freshwater bacterial isolates used in Smith et al. 2024 high-throughput screen; 10-strain community used in the same study. These samples represent widely used laboratory models and environmentally relevant taxa.

Sampling strategy

Sampling procedure

- New laboratory assays (methionine-auxotroph and chloramphenicol experiments): For every condition we inoculated fresh overnight cultures on two independent days (biological replicates). Each assay was run in 48-well plates with 2–3 parallel wells per condition (technical replicates) and ≥ 2 blank wells to monitor instrument drift. No wells were removed from the analysis.
- Published datasets (diauxic, phage-bacteria, ethanol, ecotoxicology): All time-series files were used exactly as released by the original authors; the full set of conditions and replicates was retained.

Sample-size rationale

No formal power calculation was performed. Instead, replicate numbers were set on the basis of common practice in growth-kinetics work:

- 1) In-house experiments: Low well-to-well variance within technical replicates and use of biological replicates.
- 2) Large public screens: The ecotoxicology dataset contains 15 120 growth curves, providing sufficient resolution for the decision-tree analyses.

These replicate numbers match common practice in microbial growth-kinetics studies and proved sufficient for all statistical and machine-learning procedures reported in the manuscript.

Data collection

New laboratory assays (auxotroph growth, chloramphenicol; both performed by A.P.): Cultures were grown in 48-well plates (1 mL well⁻¹) containing M9 + 0.36 g L⁻¹ glucose at 37 °C with double-orbital shaking (800 rpm) in a BioTek Synergy H1 plate reader (firmware v3.12.08). Optical density at 600 nm (OD₆₀₀) was recorded every 6 min for 24 h. Each plate contained ≥ 2 blank wells; OD values were baseline-subtracted and corrected for multiple scattering using an external calibration against a ThermoFisher Genesys spectrophotometer. Instrument settings, calibration curves, and raw CSV files are deposited in the “Kinbiont_utilities” repository and Zenodo record.

Published datasets (phage-bacteria, diauxic, ethanol, ecotoxicology): Time-series files were obtained from the authors’ public repositories or provided directly by the authors, as cited in the manuscript. Aside from the background or scattering corrections described in Methods, no additional transformations were applied before analysis.

Timing and spatial scale

New laboratory assays were carried out by A.P. at Human Technopole: the methionine-auxotroph nutrient-limitation screen in May 2023 and the chloramphenicol dose-response in February 2024. Each plate-reader run tracked 48 wells simultaneously for 24 h with 6-min temporal resolution (240 time points per well). The spatial scale is a well-mixed 1 mL (48-well plates); no broader spatial gradients were imposed.

Published datasets (phage–bacteria interaction, diauxic growth, ethanol bioproduction, ecotoxicology screen) retain the timing and spatial scale reported in the original studies: laboratory microcosms (1–100 mL) sampled at 1–10 min intervals over 12–48 h (details and citations in Methods). No field or landscape-scale measurements were involved.

Data exclusions

Laboratory plate-reader assays (auxotroph and chloramphenicol experiments): No wells were removed.

Ecotoxicology screen (Smith et al. 2024): 1 367 of 15 120 growth curves ($\approx 9\%$) were excluded from subsequent analysis because the Richards-model fit returned an average relative error $> 5\%$, indicating instrument or inoculation failures (criteria pre-registered in the analysis script).

Other published datasets (diauxic shift, phage–bacteria, ethanol bioproduction).

All time-series supplied by the original authors were retained; no exclusions were necessary.

The exclusion rules were fixed prior to analysis and applied uniformly; all decisions are documented in the associated Jupyter notebooks in the “Kinbiont_utilities” repository.

Reproducibility

Laboratory assays

Each growth-kinetics experiment (methionine-auxotroph nutrient limitation and chloramphenicol dose–response) was performed on two independent days, each starting from a separate overnight culture.

Within every run, two to three technical replicates per condition were recorded in parallel wells.

At least two blank wells per plate were included to monitor instrument drift; no systematic drift was detected.

Raw plate-reader CSV files, calibration data, and unmodified analysis notebooks are archived in the GitHub repository Kinbiont_utilities, and every figure can be regenerated with a single julia command (see the README).

Published datasets

Public data were analysed exactly as provided by the original authors.

All parameter-inference and downstream machine-learning steps are executed by version-controlled scripts in Kinbiont_utilities/notebooks.

Because all primary data, preprocessing steps, model-fitting routines, and figure scripts are openly available and automated, every numerical result and panel in the manuscript can be reproduced end to end without manual intervention.

Randomization

Laboratory assays – Biological replicates were performed on different days, providing temporal randomization.

Published datasets – No additional randomization was possible; data were analysed exactly as distributed by the original authors.

Blinding

No blinding was applied.

The experiments measured objective read-outs (optical density time-series) that were recorded automatically by the plate reader and analysed with fully scripted, deterministic pipelines.

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

Methods

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

Seed stocks

Report on the source of all seed stocks or other plant material used. If applicable, state the seed stock centre and catalogue number. If plant specimens were collected from the field, describe the collection location, date and sampling procedures.

Novel plant genotypes

Describe the methods by which all novel plant genotypes were produced. This includes those generated by transgenic approaches, gene editing, chemical/radiation-based mutagenesis and hybridization. For transgenic lines, describe the transformation method, the number of independent lines analyzed and the generation upon which experiments were performed. For gene-edited lines, describe the editor used, the endogenous sequence targeted for editing, the targeting guide RNA sequence (if applicable) and how the editor was applied.

Authentication

Describe any authentication procedures for each seed stock used or novel genotype generated. Describe any experiments used to assess the effect of a mutation and, where applicable, how potential secondary effects (e.g. second site T-DNA insertions, mosaicism, off-target gene editing) were examined.