

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 collection was performed prior to this manuscript. For specifics we refer readers to Ribelet et al., 2020, doi: 10.5281/zenodo.3994953 for *Prochlorococcus* cell abundance; Mruwat et al., 2021, doi: 10.1038/s41396-020-00752-6 for virus abundance and infection; and Connell et al. 2020, doi: 10.3354/ame01950 for measurements of heterotrophic nanoflagellates.

Data analysis

All code used for data analysis and figure plotting is publicly archived in Zenodo (<https://zenodo.org/doi/10.5281/zenodo.4917226>). Software used in our analyses and plotting are: MATLAB 9.12.0.1927505 (R2022a) Update 1, and the Econometrics ToolBox; Julia v 1.6.3 and packages CSV v0.10.3, DataFrames v1.3.2, Distributions v0.25.49, Measures v0.3.1, LaTeXStrings v1.3.0, CairoMakie v0.7.4., MCMCChains v5.1.0, Plots v1.27.0, StatsPlots v0.14.33, DifferentialEquations v7.1.0, Turing v0.20.4, MCMCChains v5.1.0; R version 4.2.1 (2022-06-23) and packages *rnatureearth* 0.1.0, *vroom* 1.5.7, *sf* 1.0-8, *lubridate* 1.8.0, *lomb* 2.1.0, *RAIN* 1.34.0 (from Bioconductor).

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 sources that we use in our analysis have been published. Prochlorococcus cell abundances are from Ribelet et al. 2020, doi: 10.5281/zenodo.3994953, free virus and percentage of infected Prochlorococcus cells are from Mruwat et al. 2021, doi: 10.1038/s41396-020-00752-6, and heterotrophic nanoflagellate abundances are from Connell et al. 2020, doi: 10.3354/ame01950. All data from analyses, including for ECLIP and Bayesian parameter inference are archived on Zenodo, doi: 10.5281/zenodo.10127185.

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	This study aimed to monitor microbial ecological activity over the diel cycle via repeated sampling of surface waters (15m) on a Lagrangian cruise track over the course of several days in the North Pacific Subtropical Gyre.
Research sample	This study aimed to monitor microbial ecological activity over the diel cycle via repeated sampling of surface waters (15m) on a Lagrangian cruise track over the course of several days in the North Pacific Subtropical Gyre.
Sampling strategy	For specifics on data collection please refer to Ribelet et al., 2020, doi: 10.5281/zenodo.3994953 for Prochlorococcus cell abundance; Mruwat et al., 2021, doi: 10.1038/s41396-020-00752-6 for virus abundance and infection; and Connell et al. 2020, doi: 10.3354/ame01950 for measurements of heterotrophic nanoflagellates.
Data collection	For specifics on data collection please refer to Ribelet et al., 2020, doi: 10.5281/zenodo.3994953 for Prochlorococcus cell abundance; Mruwat et al., 2021, doi: 10.1038/s41396-020-00752-6 for virus abundance and infection; and Connell et al. 2020, doi: 10.3354/ame01950 for measurements of heterotrophic nanoflagellates.
Timing and spatial scale	Data were collected between 24 July 2015 and 4 August 2015 across an anticyclonic eddy in the North Pacific. Flow cytometry data were collected roughly every 3 minutes, with samples for cyanophage, infected cells and heterotrophic nanoflagellate grazers being made every 4 hours over two periods as highlighted in Fig1c. For specifics on data collection please refer to Ribelet et al., 2020, doi: 10.5281/zenodo.3994953 for Prochlorococcus cell abundance; Mruwat et al., 2021, doi: 10.1038/s41396-020-00752-6 for virus abundance and infection; and Connell et al. 2020, doi: 10.3354/ame01950 for measurements of heterotrophic nanoflagellates.
Data exclusions	No data were excluded from model-data fitting.

Reproducibility

Randomization

Blinding

Did the study involve field work? Yes No

Field work, collection and transport

Field conditions

Location

Access & import/export

Disturbance

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

Plants

Seed stocks

Novel plant genotypes

Authentication