

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 (<i>n</i>) 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. <i>F</i> , <i>t</i> , <i>r</i>) with confidence intervals, effect sizes, degrees of freedom and <i>P</i> 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 <i>d</i> , Pearson's <i>r</i>), 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 for data collection.
Data analysis	Models were fit in R (v4.2.2) using the package brms (v2.21.0, Burkner 2017, DOI: doi:10.18637/jss.v080.i01). Posterior distributions were generated in rstan(v2.26.22, https://mc-stan.org/). Relative importance was calculated using the relaimpo package (v2.2.7, Groemping and Matthias 2021). All custom code is available at https://zenodo.org/records/12810136 .

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](#)

Annual estimates of Pacific salmon weights, return abundances, and return biomasses are available at <https://zenodo.org/records/12810136>. Modeled estimates of Pacific salmon escapement biomass and subsidy concentrations are available at <https://doi.org/10.5066/P97457VD>. Literature-sourced tissue concentrations of

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

Ecological, evolutionary & environmental sciences study design

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

Study description	We modeled escapement biomass of salmon from 1976 to 2015 using a generalized additive model with year as a predictor and species as a factor. We separately modeled contaminant and nutrient concentrations using literature derived data. Each nutrient or contaminant was modeled using concentration as a response variable, species as a fixed factor, and author and study region as varying intercepts. All models were fit using Bayesian modeling with priors determined using prior predictive simulation to generate weakly informative priors. After fitting the models for salmon escapement and nutrient and contaminant concentrations, we used Monte Carlo with the posteriors of each model to multiply modeled escapement estimates with concentration estimates, generating a distribution of salmon nutrient and contaminant export.
Research sample	Salmon escapement and individual mass estimates came from Dr. Greg Ruggerone (co-author). Contaminant and nutrient tissue concentrations came from primary and gray literature searches performed by Dr. Brandt, Dr. Wesner, and Dr. Jardine. A full list of citations is available in the data release and these data are provided in the Supporting Data File accompanying the manuscript.
Sampling strategy	We used all data available. There is no sample size calculation as we did not use statistical decision cutoffs (e.g., significance values).
Data collection	Salmon escapement and individual mass estimates came from Dr. Greg Ruggerone (co-author). Contaminant and nutrient tissue concentrations came from primary and gray literature searches performed by Dr. Brandt, Dr. Wesner, and Dr. Jardine. A full list of citations is available in the data release and these input data are provided in the Supporting Data File accompanying the manuscript.
Timing and spatial scale	Salmon data were analyzed from 1976 through 2015, with data collected annually therein. The spatial scale ranges from the West Coast of the United States to Bering Sea, Alaska, all in the Pacific Ocean. Data for contaminants and nutrients ranged from the 1970's through 2019.
Data exclusions	We excluded fish returns data prior to 1976 because data were only available then from a subset of species and regions. Instead, we fit the data prior to 1976 and used the posteriors as informative priors for the subsequent model.
Reproducibility	The procedures are reproducible as the data sources are given and all code is publicly available. We did not conduct any experiments.
Randomization	This does not apply to our study as we did not conduct any experiments. We used all the data that was available to us.
Blinding	This is not applicable to our study as we did not use blinding given that the purpose of this analysis is descriptive (i.e., to quantify annual nutrient and contaminant fluxes rather than to assess statistical differences in fluxes among years).
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