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Reporting Summary

Nature Research 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 Research 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	All data are from publicly available sources identified in the manuscript.
Data analysis	All data analysis was performed by the authors using our own code.

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 Research 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 list of figures that have associated raw data
- A description of any restrictions on data availability

All datasets analyzed during the current study are available in a Dryad repository: https://datadryad.org/stash/share/1hAjS-Q3nwsUAgrShYfVm6yNZSTF9oJpGWrT1_J0NyU [Note: this is currently a private repo but we will provide a public link prior to publication]. All code used to conduct the study are available in a GitHub repository: https://github.com/emlab-ucsb/future_food_from_sea.

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	Analysis of existing data to derive supply of seafood.
Research sample	Publicly available data sources used: FAO Fishery and Aquaculture Statistics (FishstatJ); FAOSTAT; Costello, C., Ovando, D., Clavelle, T., Strauss, C.K., Hilborn, R., Melnychuk, M.C., Branch, T.A., Gaines, S.D., Szuwalski, C.S., Cabral, R.B. and Rader, D.N., 2016. Global fishery prospects under contrasting management regimes. Proceedings of the National Academy of Sciences, 113(18), pp.5125-5129; Mangin, T., Costello, C., Anderson, J., Arnason, R., Elliott, M., Gaines, S.D., Hilborn, R., Peterson, E. and Sumaila, R., 2018. Are fishery management upgrades worth the cost?. PLOS One, 13(9).; Cai, J. & Leung, P. Short-term projection of global fish demand and supply gaps. Food and Agriculture Organization of the United Nations, 2017; Gentry, R.R., Froehlich, H.E., Grimm, D., Kareiva, P., Parke, M., Rust, M., Gaines, S.D., Halpern, B.S. (2017) Mapping the global potential for marine aquaculture. Nature Ecology & Evolution 1(9) 1317-1324.
Sampling strategy	Sample is a census of all available fisheries data.
Data collection	Only pre-existing data was used in the analysis.
Timing and spatial scale	FAO Fishstat-J: 1950-2017; global scale Costello et al. 2016: historical 1950-2012; projections 2013-2050; global scale Mangin et al. 2018: 2012; global scale Cai et al. 2017: mean values based on mid-2010s to early 2020s; global scale Gentry et al. 2017: no temporal aspect; global scale
Data exclusions	No data were excluded from the analysis.
Reproducibility	Experimental replication was not attempted, as no experiment was performed.
Randomization	The study did not involve group allocation.
Blinding	Experiment was not performed, so blinding is not relevant to the study.

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
☒	☐ Human research participants
☒	☐ Clinical data
☒	☐ Dual use research of concern

Methods

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