

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 No data collection software was used.

Data analysis All analyses described were undertaken in R.

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

Data and source code used for preparing figure maps (shark relative spatial density, longline-fishing effort and shark–longline-fishing overlap and FEI) are available on GitHub (<https://github.com/GlobalSharkMovement/GlobalSpatialRisk>).

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

This study is a Reply to a Matters Arising comment on our original paper. To answer the points raised we re-plotted some of the original shark movements and fishing effort data in our paper which are fully described in figure and table legends and in the original paper. We also carried out new analyses using newer data releases of global longline fishing effort data that were freely available from Global Fishing Watch (www.globalfishingwatch.org).

Research sample

In this Reply, the additional data used were the Global fishing Watch updated data release for AIS-monitored longline fishing effort in 2012–2018.

Sampling strategy

Global longline fishing effort data were obtained for automatic identification system (AIS) monitored vessels >300 gross tons.

Data collection

Global longline fishing effort data for automatic identification system (AIS) monitored vessels >300 gross tons were made available by the Global Fishing Watch.

Timing and spatial scale

Global for 2012–2018.

Data exclusions

No relevant data were excluded.

Reproducibility

No experiments as such were conducted, rather our data are based on satellite tracked movements of individual pelagic sharks and fishing vessels.

Randomization

Randomization procedures were used when removing 1, 5, 25, 50 and 75% of the AIS data for breakpoint sensitivity analysis. Methods are fully described in the Reply and Supplementary Information files.

Blinding

Blinding is not relevant to this type of study because our original data were based on movements of wild animals and fishing vessels.

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 |
| <input checked="" type="checkbox"/> | Antibodies |
| <input checked="" type="checkbox"/> | Eukaryotic cell lines |
| <input checked="" type="checkbox"/> | Palaeontology and archaeology |
| <input checked="" type="checkbox"/> | Animals and other organisms |
| <input checked="" type="checkbox"/> | Human research participants |
| <input checked="" type="checkbox"/> | Clinical data |
| <input checked="" type="checkbox"/> | Dual use research of concern |

Methods

- | | |
|-------------------------------------|------------------------|
| n/a | Involved in the study |
| <input checked="" type="checkbox"/> | ChIP-seq |
| <input checked="" type="checkbox"/> | Flow cytometry |
| <input checked="" type="checkbox"/> | MRI-based neuroimaging |