

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

- | | | |
|-------------------------------------|-------------------------------------|--|
| <input type="checkbox"/> | <input checked="" type="checkbox"/> | The exact sample size (n) for each experimental group/condition, given as a discrete number and unit of measurement |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> | A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> | 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> |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> | A description of all covariates tested |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> | A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> | 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) |
| <input type="checkbox"/> | <input checked="" type="checkbox"/> | 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> |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> | For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> | For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes |
| <input checked="" type="checkbox"/> | <input type="checkbox"/> | 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 analysis

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 used in linear regression modelling are available on GitHub (https://github.com/GlobalSharkMovement/GlobalSpatialRisk/derived_data/). 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](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 is a Reply to a Matters Arising comment on our original paper. To answer the points raised we re-plotted some of the original data from our paper which are fully described in figure and table legends and in our original paper. We carried out new analyses using general linear regression modelling to examine relationships between shark catch per unit effort and fishing exposure risk (FEI), number of longline sets and fishing effort.
Research sample	In this Reply, pelagic shark catch in biomass (kg) retained (recorded in skipper's logbooks) by the Spanish pelagic longline fleet in the North Atlantic was used. Catch data were available and were included for the following tracked sharks: blue shark (<i>Prionace glauca</i>), shortfin mako (<i>Isurus oxyrinchus</i>), longfin mako (<i>I. paucus</i>), tiger shark (<i>Galeocerdo cuvier</i>), white shark (<i>Carcharodon carcharias</i>), porbeagle shark (<i>Lamna nasus</i>), silky shark (<i>Carcharhinus falciformis</i>), smooth hammerhead shark (<i>Sphyrna zygaena</i>), bigeye thresher shark (<i>Alopias superciliosus</i>), copper shark (<i>Carcharhinus brachyurus</i>) and the sandbar shark (<i>C. plumbeus</i>).
Sampling strategy	Shark catch data recorded by the Spanish longline fleet in the North Atlantic were made available by the Spanish authorities after data collection so we had no control over the sampling strategy.
Data collection	Shark catch data recorded by the Spanish longline fishing fleet in the North Atlantic were made available by the Spanish authorities.
Timing and spatial scale	Shark catch data were available from the Spanish longline fishing fleet in the North Atlantic between January 2013 and November 2017.
Data exclusions	In this Reply, no data were excluded except when running sensitivity analysis for linear regression modelling. Here, models were compared using the Akaike and Bayesian information criterion (AIC) and the models strength of evidence assessed using the AIC weights (wAIC). We then used r^2 to quantify the models goodness of fit, and repeated the same procedure when randomly removing 1, 5, 10 and 25 % of the data.
Reproducibility	No experiments as such were conducted, rather our data are based on satellite tracked movements of individual pelagic sharks and fishing vessels, and shark catch data from fisheries.
Randomization	Randomization procedures were used when removing 1, 5, 10 and 25 % of the data for sensitivity analysis using linear regression modelling. 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?	<input type="checkbox"/> Yes <input checked="" type="checkbox"/> 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"/>	<input type="checkbox"/> Antibodies
<input checked="" type="checkbox"/>	<input type="checkbox"/> Eukaryotic cell lines
<input checked="" type="checkbox"/>	<input type="checkbox"/> Palaeontology and archaeology
<input checked="" type="checkbox"/>	<input type="checkbox"/> Animals and other organisms
<input checked="" type="checkbox"/>	<input type="checkbox"/> Human research participants
<input checked="" type="checkbox"/>	<input type="checkbox"/> Clinical data
<input checked="" type="checkbox"/>	<input type="checkbox"/> Dual use research of concern

Methods

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