

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 WebPlotDigitizer v4.2 (data visualizations to extract the underlying numerical data)

Data analysis www.github.com/henning-winker/JARA; Analyses were performed using R Statistical Software v3.5.2 and via the interface from R ('R2jags' package v0.5-7) to JAGS ('Just Another Gibbs Sampler' v4.3.0).

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 are available on www.sharkipedia.org and at <https://zenodo.org/badge/latestdoi/307472870>.

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	First, we used a Bayesian state-space framework (Winker et al. 2018, Sherley et al. 2020) to estimate trends in relative abundance of 18 species from 57 time-series compiled and reviewed at an expert workshop convened by the IUCN Species Survival Commission's Shark Specialist Group (IUCN SSC SSG). Using these trends, we calculated the global LPI for oceanic sharks from the reference year 1970 (which was set at 1) to 2018 — and then extrapolated each time-series to 2020 to encompass the Aichi Target assessment year — by hierarchically aggregating the annual rates of change from each time-series for a species by region, then globally (see Text box 1 and Extended Data Figure 1a). Second, we combined a retrospective Red List assessment (1980) with two recent assessments (~2005 and 2018) from the IUCN Red List of Threatened Species for all 31 species of oceanic sharks to build the RLI (see Text box 1). Finally, we develop three lines of evidence to attribute decreasing abundance (shown by the LPI) and rising extinction risk (shown by the RLI) for oceanic sharks to overfishing: (i) increasing Relative Fishing Pressure over time (measured as changes in catch relative to the changes in the LPI), (ii) increasing proportion, over time, of oceanic sharks that are overfished below biomass or abundance levels that could produce Maximum Sustainable Yield (MSY, which is the equilibrium state of the exploited population that can sustain the greatest yield [catch] over long time periods Punt and Smith 2001), and (iii) the near-absence of significant threats other than fishing reported in each species' IUCN Red List assessment.
Research sample	Time-series data on relative abundance (n=57) for 18 species (see Supplementary Table S1) were gathered from peer-reviewed publications and the grey literature, including government reports. Relative abundance indices, and associated uncertainty estimates when available, included formal stock assessment outputs (trends in biomass), as well as standardized or nominal catch per unit effort (CPUE) or sightings per unit effort (SPUE) from scientific surveys, fisheries data, or bather protection nets (see Supplementary Table S1 and EDF 4 to 8).
Sampling strategy	Time-series data gathered from peer-reviewed publications and the grey literature, including government reports.
Data collection	Data collection of oceanic shark and ray time-series and expert selection: Time-series data on relative abundance (n=57) for 18 species (see Supplementary Table S1) were gathered from peer-reviewed publications and the grey literature, including government reports. Relative abundance indices, and associated uncertainty estimates when available, included formal stock assessment outputs (trends in biomass), as well as standardized or nominal catch per unit effort (CPUE) or sightings per unit effort (SPUE) from scientific surveys, fisheries data, or bather protection nets (see Supplementary Table S1 and EDF 3 to 7). Entry of original time-series (in the database available at www.sharkipedia.org) was conducted by J.S.Y. and N.K.D. and subsequently independently checked by C.L.R. and N.P. All datasets underwent extensive checks prior to analyses, their reliability was reviewed and assigned to ocean regions (North, South Atlantic Ocean; Indian Ocean; North, South Pacific Ocean) by experts during an IUCN SSC SSG workshop (Dallas, Texas, USA, 5–9 November 2018). Stock assessment outputs were preferred over standardized, then nominal CPUE or SPUE time-series when multiple data sets were available for the same species and region. Stock assessment models integrate the catch history, abundance trends and life-history information to infer population dynamics, whereas CPUE or SPUE represents the trend in relative abundance of the sampled fraction of the population. The details and rationale for the selection of datasets, where pertinent, are presented in the Population section of the relevant Red List assessment (www.iucnredlist.org). Two stock assessments were updated (International Commission for the Conservation of Atlantic Tunas (ICCAT) 2019, Tremblay-Boyer et al. 2019) after the workshop and are thus included in our analysis. Data collation and calculation of ecological and life history traits: Estimates of shark age and maximum size can vary regionally, as well as between studies and across regions. Where possible, estimates of generation time (GT) were based on observed rather than theoretical maximum age. Within regions, preference was given to studies that used: validated ages; the widest size range; and, age estimates that included repeat readers, measuring precision, and bias. The validated age estimates from the closest region were used in cases where there was not a published age and growth study for a region, or validated ages from a region (Cailliet and Goldman 2004, Cailliet 2015, Harry 2018). The details of GT were presented to the workshop for review and the final choices were used in the published IUCN Red List assessments and associated supplementary material for each species (see Supplementary Red List assessments, Supplementary Methods 2).
Timing and spatial scale	Entry of original time-series (in the database available at www.sharkipedia.org) was conducted by J.S.Y. and N.K.D. and subsequently independently checked by C.L.R. and N.P.
Data exclusions	No data were excluded from the analyses.
Reproducibility	Code and data are available
Randomization	Not relevant. No randomization needed.
Blinding	Entry of original time-series (in the database available at www.sharkipedia.org) was conducted by J.S.Y. and N.K.D. and subsequently independently checked by C.L.R. and N.P.
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