

Reporting Summary

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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 used in this study were extracted from published literature. Full reference details for each study are provided in the dataset available at Figshare <https://doi.org/10.6084/m9.figshare.12768350>.

Data analysis We conducted our analyses in R v3.6.1 and fitted Bayesian mixed effect models using the brms package. The code used to conduct the analyses is available at Figshare <https://doi.org/10.6084/m9.figshare.12768350>

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 is available at Figshare <https://doi.org/10.6084/m9.figshare.12768350>

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 meta-analysis of the effects of human disturbance on animal movement. We compiled a database from the literature to assess how animals change their movement (home range size or movement distance) in response to disturbance (log response ratios) and if these responses vary according to disturbance type, taxonomic group, trophic level and body mass. We specified separate models for each predictor variable and analysed the movement distance and home range data separately. Samples sizes were: null model: 376 movement distance effect sizes, 343 home range effect sizes; taxonomic group: 376, 341; trophic level: 376, 343; mammal body mass: 182, 214; bird body mass: 36, 79; reptile body mass: 42, 32; fish body mass: 27, 16; amphibian body mass: 23, 0; arthropod body mass: 64, 0; broad disturbance type: 348, 296; and specific disturbance type: 224, 197.
Research sample	Our focus was on all animals and the final database comprised data on 167 species, spanning birds, mammals, reptiles, amphibians, fish and arthropods. The species included were determined by the data available in the published literature.
Sampling strategy	We compiled the database using systematic review methods, including searching Web of Science (Core Collection, BIOSIS, SciELO and Zoological Record) and Scopus using the following search string: ("home range" OR "home-range" OR "space use" OR "movement rate" OR "movement pattern" OR "movement ecology" OR "animal movement") AND (fragmented OR "habitat fragmentation" OR "habitat loss" OR "habitat modification" OR "habitat degradation" OR "land use change" OR agricultur* OR farmland OR urban* OR forestry OR logging OR plantation OR mining OR road* OR dams OR damming OR fishing OR hunting OR poaching OR dredg* OR pollut* OR aquaculture OR disturbance OR anthropogenic). We restricted the Scopus search to the subject areas of Environmental Science and Agricultural and Biological Sciences and the Web of Science search to the research areas of Environmental Sciences Ecology, Zoology, Biodiversity Conservation, Marine Freshwater Biology, Forestry, and Fisheries. This returned 10,267 results from Web of Science and 5,300 from Scopus, with 12,021 unique records remaining after removing duplicates. We first read paper titles and abstract to exclude papers that were clearly not relevant based on the inclusion criteria below. We then inspected 975 full texts to determine their suitability for the study. For a study to be included in the database, it had to be a peer reviewed journal article that met the following criteria: (1) study of animal home range size or movement distances in either: disturbed and undisturbed treatments (e.g. grazed vs. ungrazed), or before and during/after a disturbance (e.g. pre- vs. post-logging, before vs. during road crossing); (2) data were collected in a standardised way across treatments; (3) estimates were available for >1 individual animal in each treatment and recorded at the species level; and (4) sufficient information was available to calculate mean movement parameters, and, where possible, sample sizes and standard deviations. Our final database comprised data from 208 studies reporting 719 cases. Sample sizes were determined by the data available from the literature.
Data collection	T.S.D. extracted home range and movement distance data from the text, tables, figures and appendices of papers. We used WebPlotDigitiser to extract data from figures. We recorded separate estimates where data were recorded for discrete groups, such as age classes, sexes, years, seasons, or study regions. We only extracted one set of values where a study reported home range size based on multiple estimators (e.g. 95% minimum convex polygon and 95% fixed kernel home range). If a study reported data from multiple time points before and after disturbance, we only extracted one set of values that were closest in time to the disturbance. If standard deviations were not reported, we derived these from the sample size and standard error or confidence intervals, where possible. If this was not possible, we contacted authors to request missing values.
Timing and spatial scale	The database was compiled between May 2019 and January 2020. The geographic scale of the database is global, spanning six continents.
Data exclusions	As described in the Methods, we excluded one data point for the only non-arthropod invertebrate (<i>Paracentrotus lividus</i>) and another data point that was an extreme outlier (the effect size an order of magnitude larger than the next highest when back-transformed).
Reproducibility	All code and data are available online to reproduce the results. As this was a meta-analysis, we tested for potential publication bias using funnel plots, Egger's test and fail-safe numbers. There was no evidence of publication for the home range data. The funnel plot for the movement distance data was mildly asymmetrical and Egger's test was significant, but the fail-safe analysis indicated that 6,062 additional studies with null results would need to be added to the dataset to reduce the significance level to $P = 0.05$. As such, we do not consider publication bias to be an issue for interpretation of the results.
Randomization	Treatment allocations were determined by the original studies from which the data were sourced.
Blinding	It was not possible to incorporate blinding into our methods because it involved extracting data from published studies.
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