

Reporting Summary

Nature Portfolio 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 Portfolio 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 checked="" type="checkbox"/>	<input checked="" type="checkbox"/> The exact sample size (<i>n</i>) 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 checked="" type="checkbox"/>	<input 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 checked="" type="checkbox"/>	<input type="checkbox"/> A description of all covariates tested
<input checked="" type="checkbox"/>	<input type="checkbox"/> A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons
<input checked="" type="checkbox"/>	<input 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 checked="" type="checkbox"/>	<input type="checkbox"/> For null hypothesis testing, the test statistic (e.g. <i>F</i> , <i>t</i> , <i>r</i>) with confidence intervals, effect sizes, degrees of freedom and <i>P</i> 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 <i>d</i> , Pearson's <i>r</i>), 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 were collected from the scientific literature using human readers, not software code.
Data analysis	All papers reviewed, and data extracted from them, are accessible via online repositories. The full underlying literature review data (109 species) can be uploaded at request: a sample species demonstrating the full workflow is available in the GitHub repository named in the manuscript draft. Code utilised in the back end of the mico.eco system is available to replicate analyses and produce figures, also in the GitHub repository named in the manuscript draft.

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 Portfolio [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 description of any restrictions on data availability
- For clinical datasets or third party data, please ensure that the statement adheres to our [policy](#)

All network models are available on the open source system, MiCO.eco, and filegeodatabases for all species data can be downloaded publicly. Raw literature review datasheets can be made available to reviewers.

Research involving human participants, their data, or biological material

Policy information about studies with [human participants or human data](#). See also policy information about [sex, gender \(identity/presentation\), and sexual orientation](#) and [race, ethnicity and racism](#).

Reporting on sex and gender	NA
Reporting on race, ethnicity, or other socially relevant groupings	NA
Population characteristics	NA
Recruitment	NA
Ethics oversight	NA

Note that full information on the approval of the study protocol must also be provided in the manuscript.

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	The study reviewed literature from 1990 to 2017 - the data collected are not experimental but are representative of the literature collected.
Research sample	The sample is unlikely to be representative of the true extent of global migratory species movements, however we aim to provide a baseline of all known connectivity for migratory marine species. This requires an inclusion of all information available, and is accompanied by discussion regarding the likely unrepresentative nature of the dataset.
Sampling strategy	NA
Data collection	<p>We used Clarivate's Web of Science and Elsevier's Scopus citation databases to search for literature on ecological connectivity data collected by the movements of 173 marine species within 4 taxa (Appendices A and B in Kot et al 2023). Sources for marine connectivity data were determined as having geospatial information on sites and routes; sites were defined as areas used by animals that were described in the literature (usually associated with a specific animal behavior activity) and routes were defined as connections among sites.</p> <p>Four reviewers compiled references to be included for review following methods by Moher et al. (2009), after identifying, screening, and selecting references with eligible telemetry data by using information from the title, abstract, or full text. After the four reviewers agreed upon a standardized method to extract information from the references we should include for review, these references were divided among a team of nine additional reviewers that were trained to collect details from the full text. Information was recorded within organized spreadsheets for each reviewed reference, including the: 1) publication year, 2) study's ocean region where data were collected, 3) type of results presented, whether it was "raw" telemetry data (i.e., trackline, points) or "processed" telemetry data (i.e., methods used for processing or modeling tracks), and 4) the repository if data were archived (Appendix B). In addition, we noted the journals that were most frequently found with relevant telemetry data and included in our review to compare the current data sharing policies of the top journals. (Text from Kot et al 2023, which is cited in manuscript).</p>
Timing and spatial scale	The search was conducted in February to June 2017 for references published beginning in 1990 on 61 marine fish, 42 marine mammal, 7 sea turtle, and 63 seabird species. The list of species was identified by Dunn et al. (2019) as migratory megavertebrates,

based on input from multiple expert sources.

Data exclusions Data were excluded if they did not contain relevant information as determined by the criteria for inclusion in the systematic literature review.

Reproducibility The dataset could be reproduced by a similar massive systematic literature review. Our literature review included training of readers on previously read papers to ensure reproducibility across readers. All code to reproduce the aggregation of sites has been made available through GitHub.

Randomization Samples were not randomized, as we aimed to collate as close to possible an exhaustive literature review.

Blinding Because participants were collecting specific information on migratory movements from the literature, it was not possible to blind readers to this information, as they were intentionally looking for data on migratory connectivity.

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"/>	<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"/> Clinical data
<input checked="" type="checkbox"/>	<input type="checkbox"/> Dual use research of concern
<input checked="" type="checkbox"/>	<input type="checkbox"/> Plants

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

Plants

Seed stocks NA

Novel plant genotypes NA

Authentication NA