

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

- | | | |
|-------------------------------------|-------------------------------------|--|
| ☐ | ☒ | 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
<i>Only common tests should be described solely by name; describe more complex techniques in the Methods section.</i> |
| ☐ | ☒ | 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
<i>Give P values as exact values whenever suitable.</i> |
| ☐ | ☒ | 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 software was used to collect the data.

Data analysis We developed code to run models in R (version 4.0.1) and JAGS executed from R using the package jagsUI (version 1.5.1). R scripts to run the analyses associated with this study using example data (for which data sharing permissions were obtained) is provided in Audubon's GitHub repository (https://github.com/audubongit/multispecies_connectivity_risk) and will be permanently archived on Zenodo upon acceptance.

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](#)

The tracking data shared with Audubon's Migratory Bird Initiative are proprietary and were contributed through data sharing agreements that limit the ability to re-share. Requests for data should be directed to the contributing data holder or organization, according to the data owner's terms set on Movebank; a list of

participating data contributors is available at <https://movebank.org/cms/movebank-content/audubon-mbi-collection>. Band re-encounter data are available through the USGS Bird Banding Laboratory at <https://usgs.gov/labs/bird-banding-laboratory/data>. Land cover vulnerability to change by 2050 spatial data are available on the ArcGIS Living Atlas (<https://livingatlas.arcgis.com/landcover-2050>), and the temperature change by mid-century spatial data are available from the IPCC WGI Interactive Atlas (<https://interactive-atlas.ipcc.ch>). Conservation assessment scores are available through the Partners in Flight Avian Conservation Assessment Database at <https://pif.birdconservancy.org/avian-conservation-assessment-database>.

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

To characterize multispecies migratory connectivity and risk to migratory birds across space, we developed a methodological framework that leveraged observations from five movement data types collected across the Western Hemisphere: band re-encounters, light-level geolocators, automated radio telemetry, GPS tags, and satellite PTT tags. We applied a hierarchical Bayesian analytical approach to account for uncertainty and propagate it throughout the analyses. We estimated species-specific migratory connectivity by fitting integrated models to a database of re-encounter and tracking observations consolidated for 112 migratory bird species. Although the original database contained observations for 458 bird species (those considered migratory and that breed in North America), we filtered species based on data availability, namely a sufficient number of individuals with both breeding season and nonbreeding season observations (see below). In total, movement data from 329,179 individual birds was included in analyses. We combined estimates from species to quantify multispecies migratory connectivity by calculating weighted means and variances to derive average connectivity proportions along with bootstrapped estimates of uncertainty. Once we generated multispecies connectivity between regions of the Western Hemisphere, we then used these estimates in combination with species' biological vulnerabilities and spatial summaries of projected global changes (temperature change and land-cover conversion) to estimate how risk to migratory birds varies over space as a function of the interdependencies between regional populations.

Research sample

We used all available connectivity information for 112 North American-breeding migratory bird species as representative of Western Hemisphere migratory birds in our study. From Audubon's database of year-round observations of 458 migratory birds, we filtered species based on sufficient sample sizes of individuals with both breeding season and nonbreeding season observations given that we were estimating connectivity between breeding and nonbreeding regions per species (see below). Movement data from a total of 329,179 individual birds was ultimately used in analyses.

Sampling strategy

A species was included in analyses if the following criteria were met: either the total sample size (that is, the number of individuals with known breeding-nonbreeding connections) was (i) at least five times greater than the number of pre-defined spatial units in the species' nonbreeding range ($n = 97$ species) or (ii) at least 2.5 times greater than the number of spatial units if the species had ≤ 15 spatial units in their nonbreeding range ($n = 15$ species). The latter criterion allowed us to include additional species from orders of smaller-bodied birds (Passeriformes, Piciformes, Charadriiformes) that had relatively less tracking data due to technological limitations.

Data collection

Data were collected by individual researchers and consolidated by Audubon's Migratory Bird Initiative. Band re-encounter data were obtained from the USGS Bird Banding Laboratory (<https://www.usgs.gov/labs/bird-banding-laboratory>); observations from light-level geolocators, GPS tags, and satellite tags were obtained from Movebank (<https://www.movebank.org/cms/movebank-main>) and individual researchers who shared data with Audubon; and observations from automated radio telemetry were obtained from BirdsCanada via the Motus Wildlife Tracking System (<https://motus.org/>). We combined all available data from these sources for individual species to estimate migratory connectivity, and then combined data across species to estimate multispecies migratory

connectivity. Data holders and individuals (and their respective organizations) who assisted with curating datasets are properly acknowledged in the Acknowledgments.

Timing and spatial scale	We used band re-encounter data from 1930 - 2022 and tracking data (the four remaining data types) made available to Audubon through December 2022. These data were available across the Western Hemisphere, including Canada, the United States, Mexico and the Caribbean, Central America, and South America. The spatial units of analysis were terrestrial polygons that closely resembled Bird Conservation Regions and Level II ecoregions, which we called "migratory connectivity regions" or MCRs.
Data exclusions	We excluded data for species that did not meet sample size requirements (see above) or species for which no connectivity data were available (i.e. no individuals with both breeding and nonbreeding season observations). Thus, 346 migratory bird species that breed in North America were not included in our analyses either because of limited or no data availability. We briefly indicate guilds for which more data are needed in the "research needs" section of the Discussion.
Reproducibility	No experiments were conducted.
Randomization	Randomization is not relevant. This was not an experimental study and no treatments were applied.
Blinding	Blinding is not relevant. This was not an experimental study and no treatments were applied.
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
☒	☐ Clinical data
☒	☐ Dual use research of concern
☒	☐ Plants

Methods

n/a	Involved in the study
☒	☐ ChIP-seq
☒	☐ Flow cytometry
☒	☐ MRI-based neuroimaging

Animals and other research organisms

Policy information about [studies involving animals](#); [ARRIVE guidelines](#) recommended for reporting animal research, and [Sex and Gender in Research](#)

Laboratory animals	<i>For laboratory animals, report species, strain and age OR state that the study did not involve laboratory animals.</i>
Wild animals	We used data collected previously by individual researchers who captured and tagged birds under their independent permits and protocols. The data were then shared with Audubon's Migratory Bird Initiative or made publicly available on the aforementioned platforms (Motus, BBL, Movebank), which we then analyzed for this study. Thus, no wild animals were captured and no field work was conducted specifically for this study.
Reporting on sex	<i>Indicate if findings apply to only one sex; describe whether sex was considered in study design, methods used for assigning sex. Provide data disaggregated for sex where this information has been collected in the source data as appropriate; provide overall numbers in this Reporting Summary. Please state if this information has not been collected. Report sex-based analyses where performed, justify reasons for lack of sex-based analysis.</i>
Field-collected samples	<i>For laboratory work with field-collected samples, describe all relevant parameters such as housing, maintenance, temperature, photoperiod and end-of-experiment protocol OR state that the study did not involve samples collected from the field.</i>
Ethics oversight	<i>Identify the organization(s) that approved or provided guidance on the study protocol, OR state that no ethical approval or guidance was required and explain why not.</i>

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

Seed stocks

Report on the source of all seed stocks or other plant material used. If applicable, state the seed stock centre and catalogue number. If plant specimens were collected from the field, describe the collection location, date and sampling procedures.

Novel plant genotypes

Describe the methods by which all novel plant genotypes were produced. This includes those generated by transgenic approaches, gene editing, chemical/radiation-based mutagenesis and hybridization. For transgenic lines, describe the transformation method, the number of independent lines analyzed and the generation upon which experiments were performed. For gene-edited lines, describe the editor used, the endogenous sequence targeted for editing, the targeting guide RNA sequence (if applicable) and how the editor was applied.

Authentication

Describe any authentication procedures for each seed stock used or novel genotype generated. Describe any experiments used to assess the effect of a mutation and, where applicable, how potential secondary effects (e.g. second site T-DNA insertions, mosaicism, off-target gene editing) were examined.