

Multispecies migratory connectivity indicates hemispheric-scale risk to bird populations from global change

Corresponding Author: Dr Sarah Saunders

Version 0:

Decision Letter:

18th March 2024

*Please ensure you delete the link to your author homepage in this e-mail if you wish to forward it to your co-authors.

Dear Dr Saunders,

Your manuscript entitled "Multispecies migratory connectivity reveals hemispheric risk to birds" has now been seen by 3 reviewers, whose comments are attached. The reviewers have raised a number of concerns which will need to be addressed before we can offer publication in Nature Ecology & Evolution. We will therefore need to see your responses to the criticisms raised and to some editorial concerns, along with a revised manuscript, before we can reach a final decision regarding publication.

We therefore invite you to revise your manuscript taking into account all reviewer and editor comments. Please highlight all changes in the manuscript text file. Please note that our methods sections are unlimited, which may help you to focus on the narrative in the main section. We also think it would be useful to give a clear and precise definition of your usage of the term risk.

We are committed to providing a fair and constructive peer-review process. Do not hesitate to contact us if there are specific requests from the reviewers that you believe are technically impossible or unlikely to yield a meaningful outcome.

When revising your manuscript:

* Include a "Response to reviewers" document detailing, point-by-point, how you addressed each reviewer comment. If no action was taken to address a point, you must provide a compelling argument. This response will be sent back to the reviewers along with the revised manuscript.

* If you have not done so already please begin to revise your manuscript so that it conforms to our Article format instructions at <http://www.nature.com/natecolevol/info/final-submission>. Refer also to any guidelines provided in this letter.

* Include a revised version of any required reporting checklist. It will be available to referees (and, potentially, statisticians) to aid in their evaluation if the manuscript goes back for peer review. A revised checklist is essential for re-review of the paper.

Please use the link below to submit your revised manuscript and related files:

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Note: This URL links to your confidential home page and associated information about manuscripts you may have submitted, or that you are reviewing for us. If you wish to forward this email to co-authors, please delete the link to your homepage.

We hope to receive your revised manuscript within four to eight weeks. If you cannot send it within this time, please let us know. We will be happy to consider your revision so long as nothing similar has been accepted for publication at Nature Ecology & Evolution or published elsewhere.

Nature Ecology & Evolution is committed to improving transparency in authorship. As part of our efforts in this direction, we are now requesting that all authors identified as 'corresponding author' on published papers create and link their Open Researcher and Contributor Identifier (ORCID) with their account on the Manuscript Tracking System (MTS), prior to acceptance. ORCID helps the scientific community achieve unambiguous attribution of all scholarly contributions. You can create and link your ORCID from the home page of the MTS by clicking on 'Modify my Springer Nature account'. For more information please visit www.springernature.com/orcid.

Please do not hesitate to contact me if you have any questions or would like to discuss these revisions further.

We look forward to seeing the revised manuscript and thank you for the opportunity to review your work.

[redacted]

Reviewers' comments:

Reviewer #1 (Remarks to the Author):

Thank you very much for the opportunity to review manuscript NATECOLEVOL-24020481 "Multispecies migratory connectivity reveals hemispheric risk to birds". I enjoyed reading this work and think its well done. The approach presented does make sense to me, but throughout reading the manuscript I felt like this is out of place for Nature Ecology & Evolution. This started reading the abstract, but I thought maybe its just that the abstract would need some work to match the rest of the manuscript.

As I kept reading that feeling never went away. Again, I think this is a great manuscript, but I just wonder whether you have considered a more specialized journal such as Conservation Biology or even a more methods heavy journal such as Methods in Ecology and Evolution?

Conservation Biology makes a lot of sense to me given the subject matter and recent papers in there. One of our recent papers of protected area planning incorporating risks (climate, land use, and governance) for example (Schuster et al. 2023). The proposed framework could also be used as a great addition to another of our previous papers on optimizing the conservation of migratory species over their annual cycle (Schuster et al. 2019).

Schuster, R., Buxton, R., Hanson, J. O., Binley, A. D., Pittman, J., Tulloch, V., La Sorte, F. A., Roehrdanz, P. R., Verburg, P. H., Rodewald, A. D., Wilson, S., Possingham, H. P., & Bennett, J. R. (2023). Protected area planning to conserve biodiversity in an uncertain future. *Conservation Biology*, 37, e14048. <https://doi.org/10.1111/cobi.14048>

Schuster, R., Wilson, S., Rodewald, A. D., Arcese, P., Fink, D., Auer, T., & Bennett, J. R. (2019). Optimizing the conservation of migratory species over their full annual cycle. *Nature communications*, 10(1), 1754.

Mentioning this last paper does lead me to a question that I have: why not expand on the work you have done and apply this framework to conservation planning as well? It could be useful to incorporate your findings with previous work (like the one I referenced above) and more explicitly tie this into the Kunming-Montreal Global Biodiversity Framework.

As for my earlier mention of a 'more methods heavy' journal. I see glimpses of quite sophisticated methodological details in the Methods section but given the current journal you never go into much detail. The 'methods person' in me is sad about this, but I do understand the why related to submitting to Nature Ecology and Evolution. As a reviewer, regardless of the journal I am reviewing for, I would like to see more information on the methods used. In particular (and this will be the last point of my review below as well), I want to be able to properly validate the methods used by re-running analyses. At this point this is not possible for the work reviewed here. I know that we have been generally very lenient about not being able to replicate work that's under review but I feel strongly that we collectively need to make sure others can replicate what we do (and review our methods).

Finally, I would like to include a request to the authors to make their data and code as available as possible. I'm a big believer in the FAIR (Findable, Accessible, Interoperable and Reusable) principle for scientific data management and stewardship (e.g. <https://www.nature.com/articles/sdata201618>), which is why I include a request like this in all my reviews. Both at the review process and once the paper is published this would help a lot for replicating a study and validating findings.

Best regards,
Richard Schuster, PhD

Director of Spatial Planning and Innovation, Nature Conservancy of Canada
Email: richard.schuster@natureconservancy.ca

Reviewer #2 (Remarks to the Author):

Review for: Multispecies migratory connectivity reveals hemispheric risk to birds

This paper proposes a framework to assess migratory bird risk for North American breeding migrants across the Western Hemisphere and the annual cycle. The framework combines multispecies migratory connectivity, environmental change variables and conservation assessment scores to produce a risk map for migrants. The study finds that exposure was the strongest driver of risk, that Arctic breeding birds had the most at-risk pathways, and that the Eastern USA was included in the majority of high-risk connections.

Multispecies migratory connectivity is a topical and interesting subject that has proven hard to conceptualize in the literature, and the idea of coupling breeding and nonbreeding areas into a single risk framework is a useful step forward. I think that the method has tremendous promise and that the authors have produced a very interesting dataset with this analysis. However, I found that the paper focuses heavily on methods, with comparatively little emphasis on the importance and consequences of their findings

that I'd expect in a Nature paper. The emphasis on exhaustive methods and highly detailed figures makes the paper overwhelmingly detailed, which I think detracts from the neat analysis that has been conducted. The authors have produced an exceptional dataset but not finished the very last step of synthesizing it into a strong narrative. My review is focused on recommending ways to pare back the detail in the figures and methods to focus on one or two clear messages. The authors can use the supporting information to ensure that sufficient detail is still described.

Some of the potential narratives that could be used to drive the paper might include (suggestions only):

- Which are the specific highest-risk connections, and what does that mean for conservation (I really liked the specific information provided at lines 231-238)? Should new partnerships be set up to protect particular groups of species based on these analyses?
- Where should conservation action occur (and what should it do)? Should conservation focus on protecting/restoring the Eastern USA? Would there be any value in protecting the Arctic, given that temperature change is a diffuse threat that doesn't occur at the Arctic?

Minor comments:

Lines 87-107: It would be useful to cite Figure 1 somewhere here. Also, there is a lot of detail in this section that would best be included in the methods where it can be more fully explained. Would you lose anything if you removed all the text from lines 87-107? The description here should preferably focus on conveying roughly how the study was conducted, to only the level of detail required to understand the results. Ideally, the results would be sufficiently interesting that the methods could be left until the end of the manuscript, so perhaps moving some emphasis off the methods and onto the findings would make restructuring easier?

Line 89: what is the 'average proportion of individuals'? Is this the average proportion of the estimated population size (might be best explained later in the methods section)? What are 'stationary' breeding regions? Does this just mean geographically fixed areas?

Line 134-6: I'd delete this sentence as it doesn't add anything and there's no suggestion in the previous sentence that the high-risk should be prioritized for conservation (that would be best in the discussion rather than the results anyway).

Lines 231-238: These are neat examples—great way to illustrate the potential of this work.

Methods: Almost half this paper is dedicated to methods, which is unusual for a Nature journal paper. This focus on detail is also reflected in the figures, which are largely focused on presenting large amounts of technical information rather than conveying a key finding. Unless this is a methods paper, much of the methods detail could be moved to supporting information (e.g. much of the details of the species included and the section on data cleaning could be described in the supporting info) I'd like to see greater emphasis on the findings—what do these results mean and how can they lead to improved conservation of migratory species?

Line 448: It would be good to clarify in the introduction that 'migratory connectivity' here refers only to the strength of the affiliation between the breeding and non-breeding destinations of sampled birds (and not the migratory pathways that they follow en route). Other work (e.g. see work by Richard Fuller and coauthors) considers stopovers as a critical element of migratory connectivity. Making this clear early in the paper would be helpful (I note it is mentioned in the discussion, lines 253).

Lines 503-517: I didn't understand this section. Are these sentences describing the process for estimating the uncertainty or the weighted mean of the combined exposure score?

Lines 531- Hazard section and Figure 4: Did the authors create a figure showing the hazard maps for temperature and land-use change? It would be interesting to compare the hazard maps against the proportion of at-risk connections in figure 4. Eyeballing these maps, it looks like the areas of highest temperature change (Arctic) and the areas of high landuse change (eastern USA and eastern Brazil) might match well with the at-risk connections? Is there any relationship between the temperature change and the breeding area risk, or the landuse change and the nonbreeding area risk?

Line 566: What are the implications of summing the rescaled climate and land-use hazard scores? Does the rescaling of the climate scores to a 0-1 scale have any influence on the finding that the Arctic MCRs were overwhelmingly the most at risk locations? For example, if the range of predicted temperature changes is small but the range of the land use change values is large, then, when summed, a relatively small change in temperature will have a larger relative effect on the sum than a similarly sized change in land use, regardless of their actual impact on the species. It seems conceivable that this is happening, as I'd expect a lot more variability in land use change predictions than in temperature change? Is there a way to test the sensitivity of the findings to the assumption of equally weighted hazard components?

How do the number of species vs risk factors combine in the risk scores? I note that at line 156-7, the highest-risk connections have very few (only one or two) species. From lines 503-, it looks like a weighted average of sorts was used (I apologize that I did not understand the method used to create the average). If a kind of average is created, then does this create a higher risk weighting for MCRs with relatively few species (because each species then contributes more to the average)? Naively, I would have thought a sum would be useful as a measure of exposure, i.e. each additional species should contribute to a higher exposure score? I may have misunderstood the method here, so I'm happy to be corrected, but if an assumption has been made here, it'd be good to make it explicit in the text.

Figures: One figure that seems to be missing is a simple figure that shows the most at-risk connections. These would presumably be the top priorities for conservation investment and would give the paper a clear key result to discuss. Figures 4b and c do this well, but it'd be good to see this for more than just an unspecified selection of routes.

Figure 2: This figure is overwhelming due to the amount of information that is being communicated. Are there one or two key

messages (e.g. perhaps panels a and b only?) that the reader needs to get from the figure that could be presented instead? If so, the rest of the figure could be moved to supporting information.

Figure 2d: Change the title from “Migratory Connectivity Regions (MCRs)” to “highest risk MCRs” (or similar)

Figure 3a, b: Plots in (a) are very difficult to interpret. Is the intention to illustrate how risk components vary by region? If so, adding an ellipse for each to represent the clustered density would help readers better interpret the plots. In plot (b), adding “Exp.” or similar (to represent exposure, which is constant in both figures) to the color caption would make readability much easier (so the reader doesn’t have to flick to the caption to remember which components “High and Low” refers to)

Figure 4b is very neat—would the authors consider producing that figure on a Shiny/web app or similar? That would make the findings very accessible and increase the impact of the work (I realize this suggestion is beyond the scope of this paper, but it may be something to consider after publication if the authors would like to see this work achieve wider uptake).

Figure 6: also a very nice figure—it’s interesting to see how migratory connectivity varies by these key breeding regions

Data availability: Is there a good reason why the authors didn’t publish their connectivity data? “Available on reasonable request” is not conducive to reproducible science (it is notoriously unavailable on request in most cases). It’d be useful to add the data for the outcomes of this study, i.e. the migratory connectivity risk scores and their three component parts, to a publicly available data repository. Is this what is implied by the phrase “data products will be provided” in the code availability section? A working example dataset should also be provided so that readers can run the provided code (this could be a subset of the full source dataset if necessary).

Reviewer #3 (Remarks to the Author):

This is an interesting manuscript which aims to estimate future vulnerability of species in various migratory connectivity groups. The results are based on large amount of data and high level of statistics. Although I have some comments to the methods, I feel that most of the analyses have been conducted appropriately. My main concerns are that how reliable the overall estimates are, does the used set of species represent the overall composition of migratory species and how the vulnerability is estimated in the non-breeding grounds. First, it would be important to convince the reader that this a large-scale modelling work, which can really have conservation implications. Because of this, some kind of reliability analyses could be important. Second, the analyses concern only c. one fourth of migratory species from N America. Third, there are several uncertainties how the risks have been estimated starting from are the migratory data presenting the breeding and non-breeding grounds, what is meant in non-breeding grounds (wintering site or the whole migration route). I have listed my comments more detailed below.

L36-37 Although you have been analysing the future risk of migratory species, the work would strongly be improved, if you could present how the population of species are doing in each migratory connectivity group or BCR in relation to calculated risks. Are species already declining more in areas which are predicted to face higher vulnerability in the future.

L273 Is the asynchrony really a problem for the species? Phenological mismatches rarely have strong population consequences.

L341-349 Many species were excluded due to the lack of data. Could the results be biased because only certain type of species can be analysed. How the selected species reflect the overall composition of migratory species in the study and their ecological traits. I would imagine that given the numbers, waterbirds are overrepresented and landbirds underrepresented?

L359 Banding data has also plenty of limitations (biases) as there are large spatial differences in the detection probability reflecting both human and bird enthusiastic densities. How did you take this into account? Did you test the consistency in the measured connectivity values based on re-counters and tracking data in species where you had data collected using both methods (L359).

L395 How did you defined that the banding data were from the breeding area and not from stop over site of the migration route? Or encounters of the banding data were from the wintering areas destination. Surely the EDTable 5 values help in definition here but how accurate they are? How could this influence the connectivity values?

L447-449 In cases where you only had the tracking migration route to one direction (not the whole migration cycle), how can you be sure that that the final signal was from the wintering location and not somewhere along the migration route? Or did you use multiple records from the non-breeding areas?

That been said, the current approach is investigating the drivers at the breeding and non-breeding (wintering) sites, but species can be equally affected along the migration. It is not clear to me when reading the methods are you targeting the migratory connectivity between the breeding areas and destination or in general the migration route of the non-breeding area. This should be clarified. The new review (Newton 2024; <https://onlinelibrary.wiley.com/doi/full/10.1111/ibi.13316>) suggest that migration period is actually highly vulnerable time in life cycle of species and thus any changes in the conditions along the migration route could affect the demography of species even more than at breeding and wintering sites.

L531 Most of the climate change driven impacts will likely be gradual along thermal gradient of species range. Some species may benefit and some not from increased temperature, but rate of change in temperature does not necessarily increase the risks only. It would be good to discuss what do you really mean with the temperature increase and clarify that it does not necessarily mean only risks for populations.

L549 Precipitation can be much more important in the non-breeding grounds as these can affect the productivity of the plants and thus the overall food chain (e.g. Studds & Marra 2011 Proc R). This should be considered too in the analyses despite the uncertainties.

Species has also show to be able to do large shifts especially in their non-breeding ranges. It would be at least good to discuss, the shifts could also change the migratory connectivity of populations.

*****END*****

Version 1:

Decision Letter:

6th June 2024

*Please ensure you delete the link to your author homepage in this e-mail if you wish to forward it to your co-authors.

Dear Dr Saunders,

Your manuscript entitled "Multispecies migratory connectivity reveals hemispheric risk to birds" has now been seen again by our 3 reviewers, whose comments are attached. The reviewers have raised a number of further concerns which will need to be addressed before we can offer publication in Nature Ecology & Evolution. We will therefore need to see your responses to the criticisms raised before we can reach a final decision regarding publication.

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* If you have not done so already please begin to revise your manuscript so that it conforms to our Article format instructions at <http://www.nature.com/natecolevol/info/final-submission>. Refer also to any guidelines provided in this letter.

* Include a revised version of any required reporting checklist. It will be available to referees (and, potentially, statisticians) to aid in their evaluation if the manuscript goes back for peer review. A revised checklist is essential for re-review of the paper.

Please use the link below to submit your revised manuscript and related files:

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Note: This URL links to your confidential home page and associated information about manuscripts you may have submitted, or that you are reviewing for us. If you wish to forward this email to co-authors, please delete the link to your homepage.

We hope to receive your revised manuscript within four to eight weeks. If you cannot send it within this time, please let us know. We will be happy to consider your revision so long as nothing similar has been accepted for publication at Nature Ecology & Evolution or published elsewhere.

Nature Ecology & Evolution is committed to improving transparency in authorship. As part of our efforts in this direction, we are now requesting that all authors identified as 'corresponding author' on published papers create and link their Open Researcher and Contributor Identifier (ORCID) with their account on the Manuscript Tracking System (MTS), prior to acceptance. ORCID helps the scientific community achieve unambiguous attribution of all scholarly contributions. You can create and link your ORCID from the home page of the MTS by clicking on 'Modify my Springer Nature account'. For more information please visit <http://www.springernature.com/orcid>.

Please do not hesitate to contact me if you have any questions or would like to discuss these revisions further.

We look forward to seeing the revised manuscript and thank you for the opportunity to review your work.

[redacted]

Reviewers' comments:

Reviewer #1 (Remarks to the Author):

Thank you very much for the opportunity to review manuscript NATECOLEVOL-24020481A "Multispecies migratory connectivity reveals hemispheric risk to birds". I very much appreciate the effort you have put into responding to all reviewer comments from the first round of review of this manuscript. I think you have done a great job addressing comments where you could, even when reviewers had varying opinions (e.g., wanting more details on methods vs less).

The revised manuscript does a great job pointing out the relevance of this work and I think its much improved based on your edits related to reviewer comments. At this point I do not have any major comments on the manuscript itself anymore.

My main comment about the fit of this work in Nature Ecology and Evolution (NEE) remains however, as I still think this work would be more appropriate in a conservation (or methods) journal. As this is just my opinion I will not further belabor that point and if others agree that this work fits with NEE I am happy with that decision as well.

The second comment I have is related "Software and Code" requirements as stated in the Reporting Summary document and the "Guidelines for authors submitting code & software" (<https://www.nature.com/documents/GuidelinesCodePublication.pdf>). The requirements are not met at this point and there is no way for editors or reviewers assess the approach taken in for this work. The link provided in the rebuttal document only provides access to a specific subset of the analytical work undertaken and does not meet the software and code requirements that Nature journals have. I would like to request that you make your code and software available to us in a form that can be evaluated. This would include a minimal reproducible example of code and data to run through your analysis and documentation sufficient for a reviewer to be able to interpret your analyses.

Best regards,
Richard Schuster, PhD

Director of Spatial Planning and Innovation, Nature Conservancy of Canada
Email: richard.schuster@natureconservancy.ca

Reviewer #2 (Remarks to the Author):

Thanks to the authors for comprehensively addressing the items in my review. The re-arranged results and discussion have resolved my concerns about the manuscript, which I think now has a much clearer set of implications. I really like the approach that the authors have taken in separately addressing different groups of readers in the discussion. Similarly I think the authors have struck a good balance in reconciling my concerns about the methods with those of reviewer 1, and the extended methods section is a neat way to ensure that all the details are recorded in a single location (i.e. vs flicking to and from a SI section).

The revised figures are also welcome, and I think they are much clearer to read. I particularly like the new figures 3 and 4.

Thanks again to the authors for taking time to fully address my review. I have no further concerns with the manuscript and am happy to recommend it for publication.

Dr Sam Nicol

PS there is one minor typo in the ms: in the caption for figure 4a. The caption refers to top and bottom panels, but they are located side-by-side in the updated figure. I assume this can be corrected in production, but I am just bringing it to the authors' attention so it can be corrected at the right time.

Reviewer #3 (Remarks to the Author):

Although the authors have been able to improve the manuscript, I think there are still some weaknesses. Based on the replies by the authors there are several points that have not been considered in the analysis (biases in species groups, migration period and precipitation not considered). This is OK as one can not take everything into account in a single paper. However, I think it would be important try to estimate how reliable the estimated risks are for the populations and do they already reflect the observed population trends. A couple of papers have already shown that estimated future population trends are reflecting the observed trends – climate change is already affecting species, not only in the future. I would strongly encourage authors to compare their risk estimates to the species level population trends, e.g. BBS trends.

<https://doi.org/10.1080/00063657.2012.733337>
<https://link.springer.com/article/10.1007/s10584-017-2081-2>

If the risks and trends are connected it can support that your model is working, but if they do not, you should think why.

I also feel that the paper is in the current format pretty descriptive and lacks clear study questions and hypotheses. This makes the result section in to a listing of risks of various areas or species instead of giving an answer to a clear ecological question. I would encourage having clearer questions and hypotheses in the introduction. Here one should explain also what is the novelty in these questions and the new information.

*****END*****

Version 2:

Decision Letter:

16th August 2024

Dear Dr. Saunders,

Thank you for submitting your revised manuscript "Multispecies migratory connectivity reveals hemispheric risk to birds" (NATECOLEVOL-24020481B). It has now been seen again by the original reviewers and their comments are below. The reviewers find that the paper has improved in revision, and therefore we'll be happy in principle to publish it in Nature Ecology & Evolution, pending minor revisions to satisfy the reviewers' final requests and to comply with our editorial and formatting guidelines.

In regard to reviewer #3's comments, we are happy to move forward with the study without the suggested additional analyses. However, we would like to request toning down in the abstract, title and discussion to reflect that the analyses suggested by reviewer #3 are not part of the study. For example, in the title and abstract, we think 'reveals' and 'revealing' should be changed to 'suggests' and 'suggesting'. Also in the abstract and title, we think the use of 'hemispheric' should be reconsidered given the comments from reviewer #3 on data biases. Finally, in an earlier decision letter we mentioned that we think it would be useful to give a clear and precise definition of your usage of the term risk in your study. Please can you add this to your Introduction.

We are now performing detailed checks on your paper and will send you a checklist detailing our editorial and formatting requirements in about a week. Please do not upload the final materials and make any revisions until you receive this additional information from us.

Thank you again for your interest in Nature Ecology & Evolution. Please do not hesitate to contact me if you have any questions.

[redacted]

Reviewer #1 (Remarks to the Author):

Thank you very much for the opportunity to review manuscript NATECOLEVOL-24020481B "Multispecies migratory connectivity reveals hemispheric risk to birds". I very much appreciate your continued work to constructively respond to reviewer comments.

I have reviewed your work again and am happy with the changes you have made. I really appreciate the effort you have put into addressing my (probably nitpicky) comments. I am happy to see that you have added code and example datasets to the GitHub repository to allow for reproduction of your analyses. This will certainly help others build on the great work you are doing.

At this point I am happy to recommend acceptance of this manuscript. Thank you very much for sharing this fine contribution to the literature with us!

Best regards,
Richard Schuster, PhD

Director of Spatial Planning and Innovation, Nature Conservancy of Canada
Email: richard.schuster@natureconservancy.ca

Reviewer #1 (Remarks on code availability):

The code is well enough documented so interested individuals can reproduce a subset of the results of the manuscript (as data sharing permissions allow).

There is a README file that should be sufficient to get R coders started.

The structure of the code repository on GitHub is consistent with what I would expect to see from a person or group with a conservation background. It might not follow best practices from computer science but that can't be expected because most biologist or conservation biologists are not trained in that field. Given that fact I think this is a well developed repository that others can use to get started with the analysis or build on.

Reviewer #3 (Remarks to the Author):

I thank the authors for the improved version of the manuscript. However, I slightly surprised that the authors were reluctant to test are the predicted risks matching with the observed population trends of species. At least if I were co-author of the paper, I would be very interested in knowing are these two matching and thus partly validate the results. I understand that there are limitations for doing this and not all the species are suitable for the analyses given the reliability of the data, but there should be enough data to test this with a subset of the species.

In addition, given the biases in the data (not all species of North America considered), I think it should be mentioned how many species are included in the analyses in the abstract. Currently one gets an impression when reading the abstract that it covers all /most species of the Western Hemisphere.

I also wish to highlight that I highly appreciate all the work that the authors have done in the demanding modelling and writing so far.

Version 3:

Decision Letter:

1st October 2024

Dear Dr Saunders,

We are pleased to inform you that your Article entitled "Multispecies migratory connectivity indicates hemispheric-scale risk to bird populations from global change", has now been accepted for publication in *Nature Ecology & Evolution*.

Over the next few weeks, your paper will be copyedited to ensure that it conforms to *Nature Ecology and Evolution* style. Once your paper is typeset, you will receive an email with a link to choose the appropriate publishing options for your paper and our Author Services team will be in touch regarding any additional information that may be required

After the grant of rights is completed, you will receive a link to your electronic proof via email with a request to make any corrections within 48 hours. If, when you receive your proof, you cannot meet this deadline, please inform us at rjsproduction@springernature.com immediately.

Due to the importance of these deadlines, we ask you please us know now whether you will be difficult to contact over the next month. If this is the case, we ask you provide us with the contact information (email, phone and fax) of someone who will be able to check the proofs on your behalf, and who will be available to address any last-minute problems . Once your paper has been scheduled for online publication, the Nature press office will be in touch to confirm the details.

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Thank you for the review of our manuscript and for the opportunity to address reviewer concerns. Our responses to reviewer comments are in *italics*. In summary, major changes to the manuscript include:

- (1) re-writing the Abstract, Results, and Discussion sections to tighten the narrative and better emphasize the key findings
- (2) re-organizing the Discussion section to better describe the implications of this work for three primary audiences: global policymakers, migratory bird researchers, and conservation practitioners
- (3) replacing and reworking figures to tell a more streamlined, cohesive story along with figure captions that lead with a sentence describing the major finding(s) depicted
- (4) moving extraneous methodological details and nuanced results from the narrative to the Methods section and/or Extended Data
- (5) clearly defining what we mean by “risk” throughout the paper
- (6) clarifying the representativeness of the analysis for migratory birds as a whole

Together, we hope these changes have sufficiently addressed the thoughtful comments raised by the reviewers. Please contact me if you have any additional questions.

Sincerely,
Sarah Saunders, corresponding author

Reviewer #1 (Remarks to the Author):

Thank you very much for the opportunity to review manuscript NATECOLEVOL-24020481 “Multispecies migratory connectivity reveals hemispheric risk to birds”. I enjoyed reading this work and think its well done. The approach presented does make sense to me, but throughout reading the manuscript I felt like this is out of place for Nature Ecology & Evolution. This started reading the abstract, but I thought maybe its just that the abstract would need some work to match the rest of the manuscript.

As I kept reading that feeling never went away. Again, I think this is a great manuscript, but I just wonder whether you have considered a more specialized journal such as Conservation Biology or even a more methods heavy journal such as Methods in Ecology and Evolution? Conservation Biology makes a lot of sense to me given the subject matter and recent papers in there. One of our recent papers of protected area planning incorporating risks (climate, land use, and governance) for example (Schuster et al. 2023). The proposed framework could also be used as a great addition to another of our previous papers on optimizing the conservation of migratory species over their annual cycle (Schuster et al. 2019).

Schuster, R., Buxton, R., Hanson, J. O., Binley, A. D., Pittman, J., Tulloch, V., La Sorte, F. A., Roehrdanz, P. R., Verburg, P. H., Rodewald, A. D., Wilson, S., Possingham, H. P., & Bennett, J. R. (2023). Protected area planning to conserve biodiversity in an uncertain future. *Conservation Biology*, 37, e14048. <https://doi.org/10.1111/cobi.14048>

Schuster, R., Wilson, S., Rodewald, A. D., Arcese, P., Fink, D., Auer, T., & Bennett, J. R. (2019). Optimizing the conservation of migratory species over their full annual cycle. *Nature communications*, 10(1), 1754.

We thank the reviewer for the positive assessment of our work and agree that our framework would be a useful addition to the analysis presented in Schuster et al. 2019 aimed at comparing prioritization approaches for migratory bird land conservation. Indeed, we envision that the results of this hemispheric analysis could serve as valuable inputs for downstream analyses, such as spatial prioritizations with a more regional focus, to help guide on-the-ground interventions. We added this idea to the Discussion (lines 291-293) and included a reference to a recent paper that proposes such a conceptual framework (DeLuca et al. 2023; please see References below).

*While the reviewer raises a good point about the conservation relevance and methodological innovation of our study (hence the suggestion of journals specializing in those areas), we maintain that the combination of those attributes – in addition to the timely policy implications – make this paper ideally suited for *Nature Ecology & Evolution*, which seeks to “provide a place where all researchers and policymakers interested in all aspects of life’s diversity can come together to learn about the most accomplished and significant advances in the field and to discuss topical issues” (per *NEE Aims & Scope*). In particular, the integration of multiple movement data sources for >300k individual birds, spanning the Western Hemisphere, and the development of a novel metric for multispecies migratory connectivity represents a significant step forward in understanding population dynamics of migratory species, as such information dictates the consequences of localized events for the whole population network. To further fit within *NEE*’s scope as stated above, we expanded the discussion of policy implications in the revised manuscript (lines 195 – 231).*

Mentioning this last paper does lead me to a question that I have: why not expand on the work you have done and apply this framework to conservation planning as well? It could be useful to incorporate your findings with previous work (like the one I referenced above) and more explicitly tie this into the Kunming-Montreal Global Biodiversity Framework.

This is a great suggestion and again, one that we see as a possible future direction. As we mention above, results from the current analysis would be useful inputs for subsequent analyses, especially those related to subregional conservation planning for the GBF. Although such analyses are outside the scope of this paper (and would add additional complexity, further diluting the messaging), we agree that expanding on the conservation planning implications of this work is warranted. We provided additional examples in the two paragraphs starting on line 252 in the Discussion. We also added language to the concluding paragraph emphasizing the applicability of this framework for estimating and mapping risk to migratory species from other taxa to more explicitly tie this work to the GBF (lines 312-322).

As for my earlier mention of a ‘more methods heavy’ journal. I see glimpses of quite sophisticated methodological details in the Methods section but given the current journal you never go into much detail. The ‘methods person’ in me is sad about this, but I do understand the why related to submitting to *Nature Ecology and Evolution*. As a reviewer, regardless of the journal I am reviewing for, I would like to see more information on the methods used. In

particular (and this will be the last point of my review below as well), I want to be able to properly validate the methods used by re-running analyses. At this point this is not possible for the work reviewed here. I know that we have been generally very lenient about not being able to replicate work that's under review but I feel strongly that we collectively need to make sure others can replicate what we do (and review our methods).

We appreciate the reviewer's request for more methodological details in the main narrative, and attempted to reconcile this comment with those of other reviewers (and the Chief Editor) requesting less emphasis on methods. Ultimately, we opted to streamline the narrative per the editor's suggestion and because the Methods section is unlimited (revised Methods is now >14 pages with further details added).

To the reviewer's point about validating the methods used, scripts to run connectivity analyses are publicly available on Zenodo (<https://doi.org/10.5281/zenodo.5996798>) for an example species (Blackpoll Warbler) for which we have permission to make the data available. We have also published on the movement data integration method previously (please see Meehan et al. 2022), i.e. a foundational component to estimate exposure has already been validated/peer-reviewed. Scripts to run the full analyses associated with this study will be provided in Audubon's GitHub repository and permanently archived on Zenodo upon acceptance. Because the connectivity data for the 112 species used in this study are proprietary (please see our response to Reviewer 2's 'Data availability' comment below for more details on data availability), we are restricted in what can be made available in terms of reproducing the exact results. Thus, we are currently in conversations with certain data holders regarding example species for which data can be made public so that future researchers will be able to re-run analyses for a subset of the species analyzed here (in addition to being able to freely re-use the scripts for their own purposes and datasets).

Finally, I would like to include a request to the authors to make their data and code as available as possible. I'm a big believer in the FAIR (Findable, Accessible, Interoperable and Reusable) principle for scientific data management and stewardship (e.g. <https://www.nature.com/articles/sdata201618>), which is why I include a request like this in all my reviews. Both at the review process and once the paper is published this would help a lot for replicating a study and validating findings.

We wholeheartedly agree about the importance of making data and code as available as possible. In addition to the details we shared in the response above, we will be providing the full risk output (i.e. exposure, hazard [and its components], vulnerability, risk, and risk categorization), as well as the mean estimates of multispecies connectivity (exposure) and associated uncertainties for each of the 921 MCR pairs (i.e. data shown in Extended Data Fig. 2 [original ED Fig. 3]) on GitHub/Zenodo so that researchers interested in using these results in subsequent analyses (per this reviewer's comment above) will be able to do so. We clarified this in the Code Availability statement so that readers are aware; thank you for advocating for this!

Best regards,
 Richard Schuster, PhD
 Director of Spatial Planning and Innovation, Nature Conservancy of Canada
 Email: richard.schuster@natureconservancy.ca

Reviewer #2 (Remarks to the Author):

Review for: Multispecies migratory connectivity reveals hemispheric risk to birds

This paper proposes a framework to assess migratory bird risk for North American breeding migrants across the Western Hemisphere and the annual cycle. The framework combines multispecies migratory connectivity, environmental change variables and conservation assessment scores to produce a risk map for migrants. The study finds that exposure was the strongest driver of risk, that Arctic breeding birds had the most at-risk pathways, and that the Eastern USA was included in the majority of high-risk connections.

Multispecies migratory connectivity is a topical and interesting subject that has proven hard to conceptualize in the literature, and the idea of coupling breeding and nonbreeding areas into a single risk framework is a useful step forward. I think that the method has tremendous promise and that the authors have produced a very interesting dataset with this analysis. However, I found that the paper focuses heavily on methods, with comparatively little emphasis on the importance and consequences of their findings that I'd expect in a Nature paper. The emphasis on exhaustive methods and highly detailed figures makes the paper overwhelmingly detailed, which I think detracts from the neat analysis that has been conducted. The authors have produced an exceptional dataset but not finished the very last step of synthesizing it into a strong narrative. My review is focused on recommending ways to pare back the detail in the figures and methods to focus on one or two clear messages. The authors can use the supporting information to ensure that sufficient detail is still described.

Thank you for the time spent reviewing, the positive feedback, and thoughtful recommendations for paring back some of the details. We are glad the reviewer appreciated the rigor of the dataset and analyses, and are particularly grateful for the suggestions for potential narratives, which we have followed (please see below). Briefly, major changes in the revised manuscript that reflect the above comments include: (1) re-writing the Abstract, Results, and Discussion sections to tighten the narrative and better emphasize the key findings; (2) re-organizing the Discussion section to better describe the implications of this work for three primary audiences: global policymakers (starting on line 195), migratory bird researchers (starting on line 232), and conservation practitioners (starting on line 252; please note that per NEE formatting guidelines, subheadings are not allowed in the Discussion); (3) reworking the figures to tell a more streamlined, cohesive story along with figure captions that lead with a sentence describing the major finding(s) depicted; and (4) moving extraneous methodological details and results from the narrative to the Methods section (which is unlimited) and/or Extended Data.

Some of the potential narratives that could be used to drive the paper might include (suggestions only):

- Which are the specific highest-risk connections, and what does that mean for conservation (I really liked the specific information provided at lines 231-238)? Should new partnerships be set up to protect particular groups of species based on these analyses?
- Where should conservation action occur (and what should it do)? Should conservation focus on protecting/restoring the Eastern USA? Would there be any value in protecting the Arctic, given that temperature change is a diffuse threat that doesn't occur at the Arctic?

These are great suggestions that allowed us to re-examine the major findings we would like to emphasize in the paper. Following this reviewer's first suggestion, we have re-framed the majority of the Results (and subsequently Discussion) around the very-high risk connections. This includes the addition of one figure and modification of another to focus on those 59 connections found to be of the greatest risk, which in turn helped us streamline the ideas in our Discussion to three focus areas: conservation, research, and global policy and international collaborations. To that end, we also elaborated on conservation priorities given our findings, which addresses this reviewer's second suggestion. While much of the original content discussed remains the same, we have re-organized the ideas to improve flow and fleshed out certain lines of thought as they relate to the very-high risk connections and the associated study species. The latter change serves to address the reviewer's positive feedback regarding original lines 231-238; we now have additional examples describing where conservation actions can have the most benefit for species in other stages of the annual cycle (lines 252 – 270).

Minor comments:

Lines 87-107: It would be useful to cite Figure 1 somewhere here. Also, there is a lot of detail in this section that would best be included in the methods where it can be more fully explained. Would you lose anything if you removed all the text from lines 87-107? The description here should preferably focus on conveying roughly how the study was conducted, to only the level of detail required to understand the results. Ideally, the results would be sufficiently interesting that the methods could be left until the end of the manuscript, so perhaps moving some emphasis off the methods and onto the findings would make restructuring easier?

Agreed; we added two citations for Figure 1 in this section and moved several sentences of methodological details to the Methods where they are more fully explained. We did retain some information (i.e. the overall stages of the analysis shown in Fig. 1) that was necessary to introduce before the results for full understanding.

Line 89: what is the 'average proportion of individuals'? Is this the average proportion of the estimated population size (might be best explained later in the methods section)? What are 'stationary' breeding regions? Does this just mean geographically fixed areas?

'Average proportion of individuals' refers to the average of the species-specific proportions of individuals migrating between breeding and nonbreeding regions, in which those proportions sum to one within breeding regions. The full details are described in the Methods section. 'Stationary' refers to the periods of the annual cycle when birds are not migrating, which typically is in reference to stationary nonbreeding to differentiate from the nonstationary, nonbreeding periods of fall and spring migration. We clarified this throughout the revised manuscript by referring only to nonbreeding as 'stationary'.

Line 134-6: I'd delete this sentence as it doesn't add anything and there's no suggestion in the previous sentence that the high-risk should be prioritized for conservation (that would be best in the discussion rather than the results anyway).

Done.

Lines 231-238: These are neat examples—great way to illustrate the potential of this work.

Thank you! We added additional examples in the revised manuscript to further highlight the conservation and collaboration implications of the work.

Methods: Almost half this paper is dedicated to methods, which is unusual for a Nature journal paper. This focus on detail is also reflected in the figures, which are largely focused on presenting large amounts of technical information rather than conveying a key finding. Unless this is a methods paper, much of the methods detail could be moved to supporting information (e.g. much of the details of the species included and the section on data cleaning could be described in the supporting info) I'd like to see greater emphasis on the findings—what do these results mean and how can they lead to improved conservation of migratory species?

To reconcile this comment and those of Reviewer 1 who desired to see more methods details, we opted to (1) move any extraneous methodological details that are not needed for reader comprehension from the narrative sections (Intro through Discussion) to the Methods; and (2) provide all necessary technical information in the Methods rather than the supplementary material given that this section is unlimited (per the Chief Editor's suggestion). In that way, readers are not required to navigate to supplemental materials for full methodological details. We also simplified the figures to better convey key findings via clearer captions and graphical elements, i.e. less detailed plots and more infographic-style summaries of results. We re-wrote the Abstract to shorten the methodological content and instead emphasize the major findings and implications. Finally, we revised the Discussion section such that the key results (highlighted in the leading sentence of each figure) are clearly tied to relevant conservation, research, and/or policy recommendations.

Line 448: It would be good to clarify in the introduction that 'migratory connectivity' here refers only to the strength of the affiliation between the breeding and non-breeding destinations of sampled birds (and not the migratory pathways that they follow en route). Other work (e.g. see work by Richard Fuller and coauthors) considers stopovers as a critical element of migratory connectivity. Making this clear early in the paper would be helpful (I note it is mentioned in the discussion, lines 253).

Great point; done (line 92).

Lines 503-517: I didn't understand this section. Are these sentences describing the process for estimating the uncertainty or the weighted mean of the combined exposure score?

We added several additional phrases to improve the clarity of this section (lines 515-522 and 530-533).

Lines 531- Hazard section and Figure 4: Did the authors create a figure showing the hazard maps for temperature and land-use change? It would be interesting to compare the hazard maps against the proportion of at-risk connections in figure 4. Eyeballing these maps, it looks like the areas of highest temperature change (Arctic) and the areas of high landuse change (eastern USA and eastern Brazil) might match well with the at-risk connections? Is there any relationship between

the temperature change and the breeding area risk, or the landuse change and the nonbreeding area risk?

Yes, we provide a figure that maps the two components of hazard (temperature change and land-cover change) as Extended Data Figure 3 (originally was ED Fig. 2). The reviewer makes a keen observation – the areas of highest temperature change are indeed the Arctic and other high-latitude breeding MCRs, and the areas of high land-cover vulnerability to change are eastern U.S. and eastern Brazil. Because the MCRs in the Arctic/Canada/Alaska are only considered breeding, there is inherently a relationship with temperature change as the primary driver of hazard for breeding regions. Likewise, because South American MCRs are only considered nonbreeding, there is inherently a relationship with land-cover change as the primary driver of hazard for nonbreeding regions. However, we point out that the U.S. MCRs are both breeding and nonbreeding, which introduces considerable spatial variation in hazard across the hemispheric connections.

Line 566: What are the implications of summing the rescaled climate and land-use hazard scores? Does the rescaling of the climate scores to a 0-1 scale have any influence on the finding that the Arctic MCRs were overwhelmingly the most at risk locations? For example, if the range of predicted temperature changes is small but the range of the land use change values is large, then, when summed, a relatively small change in temperature will have a larger relative effect on the sum than a similarly sized change in land use, regardless of their actual impact on the species. It seems conceivable that this is happening, as I'd expect a lot more variability in land use change predictions than in temperature change? Is there a way to test the sensitivity of the findings to the assumption of equally weighted hazard components?

We used min-max scaling (normalization) to re-scale climate and land-cover change scores given that the two variables had substantially different ranges (0-1 for land-cover change and 1-4 for temperature change; see Extended Data Fig. 3) and we wanted to bring both to a common scale so that temperature change (the larger of the two variables) would not have an undue influence on the final hazard score, i.e. both hazard components were considered equally important and we had no a priori hypothesis regarding which was the greater threat. Importantly, min-max normalization preserves the relationships among the original data values; however, because the range is now bounded between zero and one, the weight of outliers is suppressed. Thus, the issue that the reviewer mentions here regarding the Arctic and temperature change scores is actually somewhat reduced given this feature of min-max scaling. Further, connections including breeding MCRs in Canada (including the Arctic) were at the greatest risk primarily due to high exposure and high vulnerability, not high hazard; we revised the Results to clarify this finding.

How do the number of species vs risk factors combine in the risk scores? I note that at line 156-7, the highest-risk connections have very few (only one or two) species. From lines 503-, it looks like a weighted average of sorts was used (I apologize that I did not understand the method used to create the average). If a kind of average is created, then does this create a higher risk weighting for MCRs with relatively few species (because each species then contributes more to the average)? Naively, I would have thought a sum would be useful as a measure of exposure, i.e. each additional species should contribute to a higher exposure score? I may have

misunderstood the method here, so I'm happy to be corrected, but if an assumption has been made here, it'd be good to make it explicit in the text.

This is a great question regarding the relationship between exposure and the number of species contributing to the exposure score. We calculated an average rather than a sum for exactly the reason the reviewer alludes to: a sum of species-specific connectivity estimates would reflect the connections that include more species as higher exposure (regardless of the strength of those species' connectivity estimates), which is what we sought to avoid. Instead, we wanted higher exposure to reflect higher average connectivity across species, i.e. the greatest mean proportion of individuals migrating from a given breeding region to a stationary nonbreeding region is the greatest exposure score. Thus, higher exposure reflects higher connectivity (i.e., more birds migrating between a given MCR pair), regardless of the number of species contributing to the estimate (ensuring that critical connections for regional populations of even just a few species are important). We added clarifications of this in lines 151 – 152 and 517 – 518.

Given that each species' estimate of connectivity between two MCRs had an associated uncertainty, we then used that to weight the multispecies average such that connectivity estimates with greater certainty contributed more to the multispecies average than those estimated with less certainty. In this way, the multispecies averages were more informed by species with more data (and hence more precise connectivity estimates), rather than the number of species per se. To further verify this, we calculated a correlation of 0.08 between the number of species/connection and the exposure score. We added this to the Results section (lines 176 – 178); thank you for the idea to include this! We also note that the new Figures 3 and 4 now better showcase the variation in number of species represented in very-high risk connections and we include additional details in the Results, such as the mean number of species/connection for very-high risk connections vs. all those included in analyses. That being said, we did find a moderate positive correlation ($r = 0.54$) between exposure and uncertainty, meaning that connections with larger multispecies connectivity estimates were somewhat less precise. We added this to the Results (line 172), as well as the low negative correlation between exposure uncertainty and the number of species/connection ($r = -0.31$), indicating that greater precision of multispecies connectivity estimates was not limited to connections with the most species.

Figures: One figure that seems to be missing is a simple figure that shows the most at-risk connections. These would presumably be the top priorities for conservation investment and would give the paper a clear key result to discuss. Figures 4b and c do this well, but it'd be good to see this for more than just an unspecified selection of routes.

This is a great suggestion; we added a figure (now Figure 3) that shows summaries of the very-high risk connections and modified the original Figure 4 (also still Figure 4 in revised manuscript) to include maps of only the very-high risk connections (not very-high and above-average risk) in order to better streamline the narrative and graphics of the Results section.

Figure 2: This figure is overwhelming due to the amount of information that is being communicated. Are there one or two key messages (e.g. perhaps panels a and b only?) that the reader needs to get from the figure that could be presented instead? If so, the rest of the figure could be moved to supporting information.

We omitted a panel in the revised version of this figure (still Figure 2 in revised manuscript) to improve interpretability. However, we opted to retain the information presented in the other panels as it is meant to convey the high-level summaries of risk across all 921 hemispheric connections. To further address the reviewer's point, we also revised the figure caption such that the first sentence summarizes the two main take-home messages of this figure: connections between Canada and South America are at the greatest risk (shown in panels a and b) and two breeding regions account for nearly half of the very-high risk connections (shown in panel c).

Figure 2d: Change the title from “Migratory Connectivity Regions (MCRs)” to “highest risk MCRs” (or similar)

This panel has been omitted from the revised figure so this suggestion is no longer relevant.

Figure 3a, b: Plots in (a) are very difficult to interpret. Is the intention to illustrate how risk components vary by region? If so, adding an ellipse for each to represent the clustered density would help readers better interpret the plots. In plot (b), adding “Exp.” or similar (to represent exposure, which is constant in both figures) to the color caption would make readability much easier (so the reader doesn't have to flick to the caption to remember which components “High and Low” refers to)

Thank you for bringing this up; we revised this figure to make it easier to interpret by making each breeding-nonbreeding group separate facets rather than six different colors in a single plot.

Figure 4b is very neat—would the authors consider producing that figure on a Shiny/web app or similar? That would make the findings very accessible and increase the impact of the work (I realize this suggestion is beyond the scope of this paper, but it may be something to consider after publication if the authors would like to see this work achieve wider uptake).

We love this idea and are already considering a results viewer for internal purposes; the reviewer makes an excellent point that making such a tool public would achieve wider uptake. At a minimum, a tabular version of these results will be publicly available (in spreadsheet form), but we agree that a web app version would be more engaging and intuitive for users. We will consider the feasibility of creating a public tool, which will be dependent upon available resources and necessary permissions in data sharing agreements.

Figure 6: also a very nice figure—it's interesting to see how migratory connectivity varies by these key breeding regions

Thank you! We note that in an attempt to simplify messaging across all figures (and due to the addition of the new Figure 3 and the journal's six figure/table limit), we have moved the original Figure 6 to Extended Data (now Extended Data Fig. 4).

Data availability: Is there a good reason why the authors didn't publish their connectivity data? “Available on reasonable request” is not conducive to reproducible science (it is notoriously unavailable on request in most cases). It'd be useful to add the data for the outcomes of this study, i.e. the migratory connectivity risk scores and their three component parts, to a publicly

available data repository. Is this what is implied by the phrase “data products will be provided” in the code availability section? A working example dataset should also be provided so that readers can run the provided code (this could be a subset of the full source dataset if necessary).

This is a great suggestion; thank you! Yes, this is what we meant by stating “data products will be provided”, but we have further clarified the statement in the revised manuscript. As the reviewer suggests, we plan to provide all the risk scores and its components, as well as mean estimates of multispecies connectivity (exposure) and uncertainty per connection (i.e. data shown in Extended Data Fig. 2) so that readers can use the results for their own purposes. Regarding the data availability, we have amended the statement to be more transparent about our ability to share tracking datasets which are proprietary; please see the revised Data Availability section for more details (regardless, band re-encounter data are publicly available through the USGS Bird Banding Laboratory, which we also clarified). Finally, thank you for the excellent recommendation for providing a subset of data so that readers can work through the provided code; we are currently working on securing permissions for a select group of study species (please see our response to Reviewer 1’s third comment above). We also have a working example dataset for running species-specific connectivity analyses (Blackpoll Warbler) available on Zenodo: <https://doi.org/10.5281/zenodo.5996798>.

Reviewer #3 (Remarks to the Author):

This is an interesting manuscript which aims to estimate future vulnerability of species in various migratory connectivity groups. The results are based on large amount of data and high level of statistics. Although I have some comments to the methods, I feel that most of the analyses have been conducted appropriately. My main concerns are that how reliable the overall estimates are, does the used set of species represent the overall composition of migratory species and how the vulnerability is estimated in the non-breeding grounds. First, it would be important to convince the reader that this a large-scale modelling work, which can really have conservation implications. Because of this, some kind of reliability analyses could be important. Second, the analyses concern only c. one fourth of migratory species from N America. Third, there are several uncertainties how the risks have been estimated starting from are the migratory data presenting the breeding and non-breeding grounds, what is meant in non-breeding grounds (wintering site or the whole migration route). I have listed my comments more detailed below.

We are grateful to the reviewer for the time spent reviewing and for the thoughtful comments; we respond in detail below but briefly address the comments above here. First, we strongly agree that elevating the conservation implications of this work is key. We have revised the Results and Discussion sections to better highlight the major findings and how those findings pertain to conservation, policy, and international collaboration (please see our response to Reviewer 2’s first comment for more details). Second, we have reiterated the importance of interpreting our uncertainty estimates along with multispecies connectivity estimates in the final paragraph of the Results (including new correlation calculations to report relationships between exposure uncertainty and several other metrics). One of the strengths of the exposure metric is that we were able to generate associated credible intervals based on the uncertainty of species-specific connectivity estimates, thus increasing the transparency of estimate reliability. We added language emphasizing this to the Discussion (lines 252 – 269). We also added a caveat to the Discussion that addresses the importance of further local-scale validation before implementation

(lines 291 – 293). Third, while the reviewer makes an excellent point that our analysis represents roughly 25% of North American-breeding migratory bird species, we point out that the 112 species included are a representative cross-section as they vary in their life histories, migratory strategies, population status, ranges, diets, and habitat requirements; 64 species (57%) are waterbirds and 48 (43%) are landbirds. Most importantly, the amount of movement data used in this study is remarkable, representing 329,179 individual birds. We added mention of this total sample size throughout the revised manuscript. Indeed, it is precisely because such data on individual animal movements is so challenging to obtain that we sought to design a method that leverages all available information across species to maximize the scope of inference. Finally, we clarified that we are only considering the stationary nonbreeding period (i.e., excluding migration routes) throughout the paper (e.g. line 92 in the Introduction).

L36-37 Although you have been analysing the future risk of migratory species, the work would strongly be improved, if you could present how the population of species are doing in each migratory connectivity group or BCR in relation to calculated risks. Are species already declining more in areas which are predicted to face higher vulnerability in the future.

This is a great suggestion. Although beyond the scope of the current study (which is hemispheric in scope and focuses on future risk as the reviewer states), it is an area of future research that we are already pursuing. We allude to this research need in lines 232-234 of the Discussion. Specifically, we are working to integrate multispecies connectivity results with breeding and nonbreeding trends estimated from the Breeding Bird Survey and Audubon's Christmas Bird Count, respectively, to understand differential consequences of connectivity on population trends for a subset of focal species within at-risk geographies. Stay tuned!

L273 Is the asynchrony really a problem for the species? Phenological mismatches rarely have strong population consequences.

While population-level consequences are challenging to attribute to phenological mismatch, several studies have provided such evidence for migratory bird species (e.g., Both et al. 2006; see References below). Most notably, a new study by Youngflesh et al. 2023 demonstrated a link between avian productivity and the timing of both bird breeding and arrival of spring across North America for 41 bird species. Given additional evidence that bird phenology is not keeping pace with climate change, negative population-level effects are likely to occur for many migratory birds. Nevertheless, we omitted this piece of the Discussion in our revised manuscript and replaced these ideas with specific conservation examples (lines 271 – 286).

L341-349 Many species were excluded due to the lack of data. Could the results be biased because only certain type of species can be analysed. How the selected species reflect the overall composition of migratory species in the study and their ecological traits. I would imagine that given the numbers, waterbirds are overrepresented and landbirds underrepresented?

We provide the full list of 112 species in the supplementary materials and note that the suite of species varies in life history, diet, range, population status, etc. in lines 287 – 289. As noted above, 64 species are waterbirds and 48 are landbirds so the reviewer is correct that there is a slight bias towards waterbirds, primarily because movement data are more easily collected on

these species (i.e., harvested species have more band re-encounters, larger-bodied waterbirds have been tracked for a longer period of time). Although we had included this information in the Methods, we have added a mention to the Introduction to be transparent (line 92). We also provide a caveat in the Discussion that our results are inherently a function of the species included (lines 289 – 291), so readers should consider this for appropriate implementation. Finally, we added a discussion of the importance of collecting more tracking data on a diversity of bird species in lines 241 – 247.

L359 Banding data has also plenty of limitations (biases) as there are large spatial differences in the detection probability reflecting both human and bird enthusiastic densities. How did you take this into account? Did you test the consistency in the measured connectivity values based on re-counters and tracking data in species where you had data collected using both methods (L359).

Our integrated model does account for potential spatial heterogeneity in re-encounter probabilities of banded birds (lines 438 – 442 and equation 1). In addition, the integration of band re-encounter data with tracking data helps alleviate spatial biases that may be present in banding data and increases precision of connectivity estimates. Although we did not compare estimates from integrated vs. independent models for the species in which both data types were available since this was not a goal of our work (rather, we sought to use all available data to inform species-specific connectivity estimates), we point the reviewer to other work with that objective, such as Korner-Nievergelt et al. 2017 and reviewed in Gregory et al. 2023 (please see References below).

L395 How did you defined that the banding data were from the breeding area and not from stop over site of the migration route? Or encounters of the banding data were from the wintering areas destination. Surely the EDTable 5 values help in definion here but how accure they are? How could this influence the connectivity values?

In addition to the temporal definitions for breeding and nonbreeding per species defined in Extended Data Table 5 (those used in eBird Status and Trends products: <https://ebird.org/science/status-and-trends>), we used each species' seasonal ranges (breeding and nonbreeding only, excluding pre-breeding and post-breeding ranges) to attribute observations spatially. Thus, we sorted observations temporally first (using breeding and stationary nonbreeding designations defined for each species in Extended Data Table 5, which does not include species' migratory periods) and then attributed each to the nearest seasonally-matching MCR (i.e. breeding season observation matched to breeding MCR) within a 250 km maximum distance. We described this process in more detail in lines 412 – 422. Regarding accuracy, the stationary periods used by eBird were defined by experts in the status and distribution of birds based on the eBird Status and Trends weekly abundance maps. The selected dates were then checked to make sure that they generally matched expected patterns of phenology for the species; please see <https://ebird.org/about/faq#seasons> for more details.

L447-449 In cases where you only had the tracking migration route to one direction (not the whole migration cycle), how can you be sure that that the final signal was from the wintering location and not somewhere along the migration route? Or did you use multiple records from the non-breeding areas?

In cases where we only had an observation of an individual in one season (either breeding or nonbreeding), we removed that individual from analysis. Thus, only individuals with both a breeding and nonbreeding observation were retained (as stated in line 420 – 422). As described above, we used temporal windows in which we assumed birds were in their stationary seasons (Extended Data Table 5). For an individual that had tracking data for one direction, we assumed that any locations within the stationary nonbreeding season window represented the wintering location, not migration. In cases where we had multiple individual records per a given season, we used either the deployment location (if known) or else the mode of the seasonal observations, assuming that represented the true origin/destination for that individual; we clarified that assumption in line 419. Note that observations were attributed to MCRs, which are fairly coarse in scale; thus, multiple within-season records during the breeding and stationary nonbreeding periods from the same individual were often attributed to the same seasonally-appropriate MCR regardless.

That been said, the current approach is investigating the drivers at the breeding and non-breeding (wintering) sites, but species can be equally affected along the migration. It is not clear to me when reading the methods are you targeting the migratory connectivity between the breeding areas and destination or in general the migration route of the non-breeding area. This should be clarified. The new review (Newton 2024; <https://onlinelibrary.wiley.com/doi/full/10.1111/ibi.13316>) suggest that migration period is actually highly vulnerable time in life cycle of species and thus any changes in the conditions along the migration route could affect the demography of species even more than at breeding and wintering sites.

Thank you for pointing this out for clarification, as did Reviewer 2. We have now specified ‘stationary nonbreeding’ as irrespective of migration routes in line 92 of the Introduction. We appreciate the reviewer’s point that the migration route itself can be a high-risk location/period for species, and we acknowledge this in lines 213 – 217 of the Discussion and state that future work could incorporate this concept of temporal migratory connectivity (i.e. connectivity between stopover locations) for a deeper understanding of risk for certain species in which such fine-scale data are available, e.g. those species which are tracked via GPS (lines 299 – 303).

L531 Most of the climate change driven impacts will likely be gradual along thermal gradient of species range. Some species may benefit and some not from increased temperature, but rate of change in temperature does not necessarily increase the risks only. It would be good to discuss what do you really mean with the temperature increase and clarify that it does not necessarily mean only risks for populations.

This is an important point; we added a clarifying sentence and citation to the Methods to address this: “Although not all bird species are similarly sensitive to the rate of global warming, we hypothesize that areas expected to warm faster are also more likely to experience other climate change-related threats (extreme heat events, fire weather, drought) that pose additional hazards for migratory birds (Bateman et al. 2020).”

L549 Precipitation can be much more important in the non-breeding grounds as these can affect the productivity of the plants and thus the overall food chain (e.g. Studds & Marra 2011 Proc R).

This should be considered too in the analyses despite the uncertainties. Species has also show to be able to do large shifts especially in their non-breeding ranges. It would be at least good to discuss, the shifts could also change the migratory connectivity of populations.

We agree that precipitation is also an important factor when considering potential climate change impacts. However, for the reasons outlined in the Methods (lines 563 – 572), we opted to use temperature change as the proxy for climate change hazard given that it is one of the most profound threats to the functional integrity of Earth’s ecosystems (García et al. 2018). For example, previous work has found that long-term bird population trends were more significantly correlated with species’ sensitivity to temperature than precipitation, suggesting that warming is likely to have a greater impact on populations than changes in precipitation (Pearce-Higgins et al. 2015); we added this justification and reference in line 567. In addition, our preliminary discussions to define a precipitation hazard were particularly problematic as the potential responses of bird species are more varied than that of temperature change. For example, some species in our analysis could benefit from increased rainfall (e.g. waterfowl due to increased habitat availability), while others would not (e.g. shorebirds due to increased nest flooding). Importantly, as mentioned in line 570, we sought to include an equal number of climate- and land cover-related variables in the definition of hazard so as to not unduly weight hazard by potential climate change impacts. Given that our assessment was designed to be broad (both in spatial scale and scope), we did not consider all potential hazards to migratory birds; further investigation is needed to directly inform on-the-ground application of this work. We added this caveat to line 291. We also suggest that future applications of this framework could be tailored to specific guilds, in which case hazard could be refined to include more nuanced and/or related threats, such as sea level rise and heavy rainfall/extreme storm events for coastal birds or drought and heatwaves for aridland birds; we added this future direction suggestion to line 297.

References

- Bateman, B. L. et al. Risk to North American birds from climate change-related threats. *Conservation Science and Practice* 2, e243 (2020).
- Both, C., et al. Climate change and population declines in a long-distance migratory bird. *Nature* 441, 81-83 (2006).
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- García, F. C., et al. Changes in temperature alter the relationship between biodiversity and ecosystem functioning. *PNAS* 115, 10989-10994 (2018).
- Gregory, K. A., et al. A synthesis of recent tools and perspectives in migratory connectivity studies. *Movement Ecology* 11, 69 (2023).
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- Pearce-Higgins, J., et al. Drivers of climate change impacts on bird communities. *Journal of Animal Ecology* 84, 943–954 (2015).
- Youngflesh, C., et al. Demographic consequences of phenological asynchrony for North American songbirds. *PNAS* 28, e2221961120 (2023).

Thank you for the review of our revised manuscript and for the opportunity to address further concerns raised by reviewers. Our responses to reviewer comments are in *italics*. In summary, revisions include:

- (1) providing code and example datasets on GitHub (as data permissions allow) to reproduce analyses and outputs for a subset of study species
- (2) providing download capabilities of outputs from the analysis of the full dataset (112 species) on GitHub; the shapefile of migratory connectivity regions (MCRs) is also available
- (3) clarifying the ecological knowledge gaps and study objectives in the Introduction
- (4) adding text to the Discussion, as well as a detailed explanation here, regarding the suggested use of population trends as validation

Together, we hope these changes have sufficiently addressed the reviewers' remaining comments. Please contact me if you have any additional questions.

Sincerely,
Sarah Saunders, corresponding author

Reviewer #1 (Remarks to the Author):

Thank you very much for the opportunity to review manuscript NATECOLEVOL-24020481A "Multispecies migratory connectivity reveals hemispheric risk to birds". I very much appreciate the effort you have put into responding to all reviewer comments from the first round of review of this manuscript. I think you have done a great job addressing comments where you could, even when reviewers had varying opinions (e.g., wanting more details on methods vs less).

The revised manuscript does a great job pointing out the relevance of this work and I think its much improved based on your edits related to reviewer comments. At this point I do not have any major comments on the manuscript itself anymore.

Thank you very much, Dr. Schuster, for taking the time to review our revision; we are glad that our changes have improved the manuscript and clarified the relevance of this work. We greatly appreciate your contributions to refining our paper!

My main comment about the fit of this work in Nature Ecology and Evolution (NEE) remains however, as I still think this work would be more appropriate in a conservation (or methods) journal. As this is just my opinion I will not further belabor that point and if others agree that this work fits with NEE I am happy with that decision as well.

We respect Dr. Schuster's opinion here as our study presents a complex modeling framework with important conservation implications, hence the suggestion of either a methods- or conservation-focused journal, respectively. However, we believe that the findings and methodologies presented in our study have broad implications and applications that are of significant interest to the readership of NEE. NEE's aims and scope states: "The most striking feature of Life on Earth is its diversity, and the fields of ecology and evolution are central to understanding how biodiversity arose, how it is maintained, what are its consequences, and how we should conserve it." We hope that Dr. Schuster would agree that this work advances our

understanding of the consequences of biodiversity (i.e. the scaling up of individual animal movements to species-level migratory patterns to multispecies connectivity, which in turn has consequences for how and why risk to migratory birds varies spatially and across the annual cycle) and how we should conserve it, in particular. We are grateful for your willingness to defer to the editorial team's judgment on the suitability of our manuscript for NEE.

The second comment I have is related “Software and Code” requirements as stated in the Reporting Summary document and the “Guidelines for authors submitting code & software” (<https://www.nature.com/documents/GuidelinesCodePublication.pdf>). The requirements are not met at this point and there is no way for editors or reviewers assess the approach taken in for this work. The link provided in the rebuttal document only provides access to a specific subset of the analytical work undertaken and does not meet the software and code requirements that Nature journals have. I would like to request that you make your code and software available to us in a form that can be evaluated. This would include a minimal reproducible example of code and data to run through your analysis and documentation sufficient for a reviewer to be able to interpret your analyses.

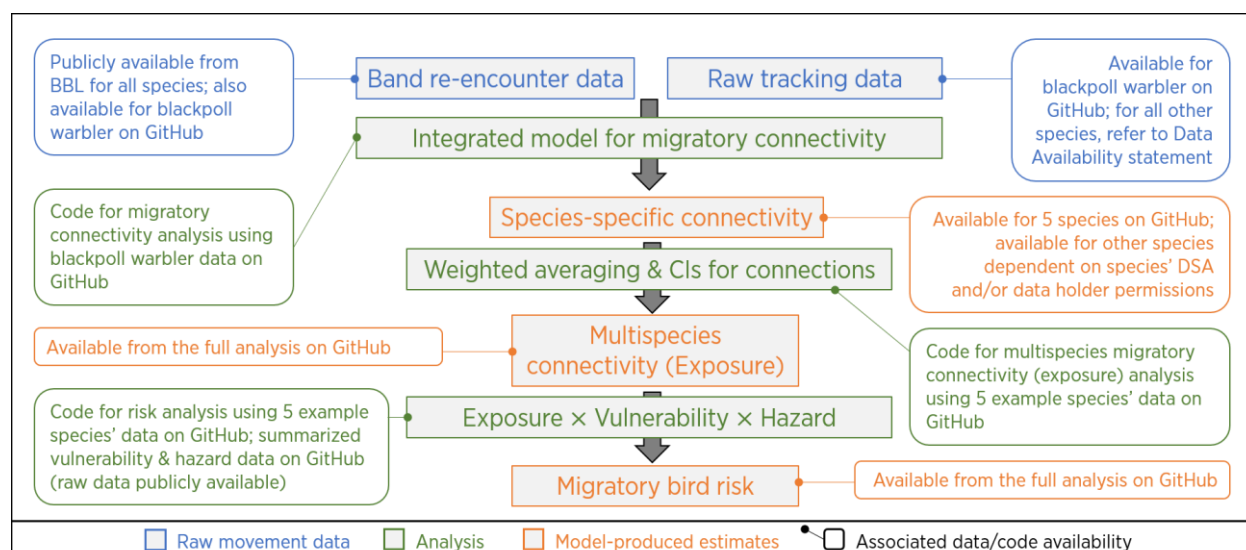
Best regards,

Richard Schuster, PhD

Director of Spatial Planning and Innovation, Nature Conservancy of Canada

Email: richard.schuster@natureconservancy.ca

Thank you for your patience as we secured permissions regarding sharing of species-specific movement data and results. We agree that a worked example would be helpful for readers. Please see below for a diagram of the phases of the analytical workflow and the associated data/code availability for each stage. We obtained permission to (1) make raw movement data available for Blackpoll warbler as an example of estimating species-specific connectivity; and (2) provide connectivity results for four additional species (five total) as an example group for estimating multispecies connectivity and risk. All code and example data to reproduce the analysis and major outputs is available in Audubon's GitHub repository: github.com/audubongit/multispecies_connectivity_risk. We have also provided the outputs from analysis of the full dataset in the repository, as well as a shapefile of the migratory connectivity regions (MCRs) so users can produce maps for their own purposes. We updated the Code Availability statement with the GitHub link and will archive the repository on Zenodo upon acceptance. Again, thank you for advocating for this and for understanding our data sharing limitations.



Reviewer #2 (Remarks to the Author):

Thanks to the authors for comprehensively addressing the items in my review. The re-arranged results and discussion have resolved my concerns about the manuscript, which I think now has a much clearer set of implications. I really like the approach that the authors have taken in separately addressing different groups of readers in the discussion. Similarly I think the authors have struck a good balance in reconciling my concerns about the methods with those of reviewer 1, and the extended methods section is a neat way to ensure that all the details are recorded in a single location (i.e. vs flicking to and from a SI section).

The revised figures are also welcome, and I think they are much clearer to read. I particularly like the new figures 3 and 4.

Thanks again to the authors for taking time to fully address my review. I have no further concerns with the manuscript and am happy to recommend it for publication.

Dr Sam Nicol

Thank you, Dr. Nicol, for your original suggestions for streamlining the take-home messages and clarifying the implications of our work – we agree that the manuscript has been strengthened as a result, and that the new visualizations based on your input tell a clearer story. We deeply appreciate your help in improving our manuscript and have been sure to recognize your contributions and those of the other reviewers in the Acknowledgements.

PS there is one minor typo in the ms: in the caption for figure 4a. The caption refers to top and bottom panels, but they are located side-by-side in the updated figure. I assume this can be corrected in production, but I am just bringing it to the authors' attention so it can be corrected at the right time.

Good catch! Fixed.

Reviewer #3 (Remarks to the Author):

Although the authors have been able to improve the manuscript, I think there are still some weaknesses. Based on the replies by the authors there are several points that have not been considered in the analysis (biases in species groups, migration period and precipitation not considered). This is OK as one can not take everything into account in a single paper. However, I think it would be important try to estimate how reliable the estimated risks are for the populations and do they already reflect the observed population trends. A couple of papers have already shown that estimated future population trends are reflecting the observed trends – climate change is already affecting species, not only in the future. I would strongly encourage authors to compare their risk estimates to the species level population trends, e.g. BBS trends.

<https://doi.org/10.1080/00063657.2012.733337>

<https://link.springer.com/article/10.1007/s10584-017-2081-2>

If the risks and trends are connected it can support that your model is working, but if they do not, you should think why.

Thank you for reviewing our revision and for your constructive feedback during the review process. We acknowledge the limitations of our study, including the ones the reviewer restates here, throughout the manuscript (e.g. lines 293 – 312, 565 – 574) and are grateful that the reviewer appreciates that we cannot address all of these within a single study. In particular, two of the ideas (bias in study species, migration period not considered) are inherently a function of data availability (please see lines 248 – 253 and 307 – 309 for more details). As such, we state in lines 295 – 296 that careful consideration be given to the species included here before implementation of results. Additionally, we provide the code to run the analysis on GitHub (please see our response to Reviewer 1 above) for those wishing to conduct their own customized risk assessments for their species of interest.

Thank you for the suggestion to compare estimated risk with observed population trends; we agree that validation of results is preferable when possible. However, after careful consideration, we concluded that such an analysis would not be feasible nor would it provide valuable insight in this case for several reasons. First and most relevant, BBS trends are not available or are unreliable for many of our species and regions. This is particularly true for many waterbird species (given the roadside nature of the BBS) and within the northernmost MCRs – some of the regions at highest risk – where there are very few BBS routes in the boreal and tundra regions. As a result of the latter, trend data are available for very few species and, where they do occur, are highly imprecise. Other potential trend datasets have similar spatial limitations, as well as offer too short of a time series (e.g., eBird) or do not occur at the continental scales needed for comparison (e.g., regional waterbird surveys), limiting our ability to rigorously conduct this validation step. Second, we are concerned about methodological confounding, given that population trend (drawn in large part from the BBS) is a substantial contributor to the Partners in Flight Avian Conservation Assessment Database score that we use as the vulnerability component of our analysis. Thus, post-hoc comparisons between risk and population trend would be substantially biased. Third, the link between current/historic and future population trends is inconsistent, as threats are not temporally stationary. Indeed, while the two studies the reviewer cites found a correlation, others (e.g., Betts et al. 2019; please see

References below) found that for many species, there were substantial discrepancies between modeled and observed trends. We also point out that we do not project future population trajectories specifically, nor do we make any speculations on the extent of future population changes. Finally, our paper is already methodologically complex, and this would add to the complexity and take space away from explaining the core methods and findings (please note that this revision is ~100 words over the text limit). In conclusion, while this is a thoughtful suggestion and perhaps could be explored in some fashion with a future paper focused on a subset of species and regions with reliable trend data, we believe that it is beyond the scope of the current manuscript. We added text highlighting this as a future direction along with a reference to one of the studies the reviewer mentions in lines 238 – 241. We also emphasize that the uncertainty measures provided for the exposure component, the incorporation of population trends into the vulnerability component, the focus on future (rather than current) hazards, as well as the careful interpretation of risk results (and transparency regarding study limitations) all serve to address the reviewer's request for validation. Once again, we appreciate your insights and hope that our rationale for not including this particular comparison in the present study is clear.

I also feel that the paper is in the current format pretty descriptive and lacks clear study questions and hypotheses. This makes the result section into a listing of risks of various areas or species instead of giving an answer to a clear ecological question. I would encourage having clearer questions and hypotheses in the introduction. Here one should explain also what is the novelty in these questions and the new information.

We agree with the reviewer that clearer articulation of our research aims in the Introduction is needed; thank you for pointing this out. We added text in lines 76 – 84 that delineates the study objectives and more explicitly outlines the ecological knowledge gaps addressed with this work. We mention the novelty and/or new information gained in several instances throughout the paper, including the Abstract, lines 71 – 73, 91 – 95, 194 – 197, 313 – 314, and 326 – 328. Given that the primary focus of our study is the development of an approach that unites migration science with ecological risk assessment, we do not test specific hypotheses but rather uncover patterns and insights to inform research, conservation, and policy for migratory birds. Thus, our overarching purpose is to provide an in-depth understanding of how and why risk to migratory birds varies across the Western Hemisphere and annual cycle. To do this, we address two gaps in ecological knowledge mentioned in lines 68 and 326: “much remains unknown regarding combined inference [of migratory connectivity] across species.”; and “...the explicit consideration of migratory animals in impact assessments and large-scale conservation planning is rare”. Again, thank you for your continued support in improving our manuscript.

References

Betts, M. G., Gutiérrez Illán, J., Yang, Z., Shirley, S. M., & Thomas, C. D. (2019). Synergistic effects of climate and land-cover change on long-term bird population trends of the western USA: a test of modeled predictions. *Frontiers in Ecology and Evolution*, 7, 186.

Thank you for the opportunity to address these final comments. Our responses to reviewer comments are in *italics*. In summary, revisions include:

- (1) tempering the language in the title and Abstract (e.g., changing “reveals” to “indicates”);
- (2) mentioning the number of species included in our analyses in the Abstract and Discussion;
- (3) revising the title to be more explanatory;
- (4) clarifying the definition of risk in the Introduction

Please contact me if you have any additional questions.

Sincerely,
Sarah Saunders, corresponding author

Reviewer #1 (Remarks to the Author):

Reviewer #1:

Remarks to the Author:

Thank you very much for the opportunity to review manuscript NATECOLEVOL-24020481B “Multispecies migratory connectivity reveals hemispheric risk to birds”. I very much appreciate your continued work to constructively respond to reviewer comments.

I have reviewed your work again and am happy with the changes you have made. I really appreciate the effort you have put into addressing my (probably nitpicky) comments. I am happy to see that you have added code and example datasets to the GitHub repository to allow for reproduction of your analyses. This will certainly help others build on the great work you are doing.

At this point I am happy to recommend acceptance of this manuscript. Thank you very much for sharing this fine contribution to the literature with us!

Best regards,
Richard Schuster, PhD

Director of Spatial Planning and Innovation, Nature Conservancy of Canada
Email: richard.schuster@natureconservancy.ca

We greatly appreciate the time and effort Dr. Schuster spent reviewing our work and are pleased that the code and data available on GitHub was useful.

Reviewer #3:

Remarks to the Author:

I thank the authors for the improved version of the manuscript. However, I slightly surprised that the authors were reluctant to test are the predicted risks matching with the observed population trends of species. At least if I were co-author of the paper, I would be very interested in knowing are these two matching and thus partly validate the results. I understand that there are limitations for doing this and not all the species are suitable for the analyses given the reliability of the data, but there should be enough data to test this with a subset of the species.

In addition, given the biases in the data (not all species of North America considered), I think it should be mentioned how many species are included in the analyses in the abstract. Currently one gets an impression when reading the abstract that it covers all /most species of the Western Hemisphere.

I also wish to highlight that I highly appreciate all the work that the authors have done in the demanding modelling and writing so far.

While we did not conduct the additional analysis the reviewer suggests for the reasons previously stated, we have made the following changes in the final version of the manuscript to address the reviewer's concerns regarding data biases:

1. *We now state the number of species (112) included in our analyses in both the Abstract and concluding paragraph of the Discussion, in addition to several other instances throughout the paper.*
2. *We changed all mentions of "hemispheric" to "hemispheric-scale" to emphasize that this refers to the spatial scale at which the study was conducted, and does not imply that all species of the Western Hemisphere were considered here.*
3. *Given the data limitations, we tempered the language throughout, including the title, Abstract, and Discussion, e.g. we changed "reveals" to "indicates" or "suggests" throughout the paper. Similarly, we rephrased all uses of the words "novel" and "new".*
4. *We revised the title to be more explanatory: "Multispecies migratory connectivity indicates hemispheric-scale risk to bird populations from global change".*
5. *We clarified our definition of risk in the Introduction: "Thus, we defined risk as the potential consequences of future global change to migratory species. More specifically, this analysis assesses the risk of migratory bird population declines from both anthropogenic climate change and land conversion, two processes widely considered to be the most important drivers of global biodiversity loss."*

Thank you again to the reviewer for the thoughtful comments throughout the review process.