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FINAL REPORT

I. Project identification

Project title: Global redistribution of biodiversity: A macro- and eco-evolutionary approach to understand species vulnerability to global changes

[FR] Titre du projet : Redistribution de la biodiversité : une approche macro- et éco-évolutive de la vulnérabilité des espèces aux changements globaux

Acronym: BIOSHIFTS

Co-funding organization (if relevant):

Principal Investigator: Lise Comte, Jonathan Lenoir & Gael Grenouillet

Name of the person writing the report (if not the Principal Investigator):
E-mail of the person who wrote the report: lcgcomte@gmail.com

Starting date of the project: 7/03/2022
Finishing date of the project: 7/03/2025

Scientific summary of project (maximum of 300 characters, spaces included)
CESAB-FRB reserves the right to modify the text for publication on its platforms

***BIOSHIFTS** aimed to both synthesize and extend the conceptual and analytical tools in species redistribution research, thus advancing a predictive science seeking to improve our ability to forecast species responses to climate change and better inform management decision-making processes.*

[FR] Résumé du projet (maximum de 300 caractères, espaces inclus)
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BIOSHIFTS visait à la fois à synthétiser et à approfondir les outils conceptuels et analytiques utilisés dans la recherche sur les déplacements de répartition des espèces en réponse aux changements climatiques, contribuant ainsi à améliorer notre capacité à anticiper les redistributions futures de biodiversité et mieux orienter les processus décisionnels de gestion.

Key words (5): species redistribution; climate change; range limits; evolutionary potential; climate change vulnerability

Context and objectives (around 1,500 characters including spaces)

There is now compelling evidence that species from many different taxonomic groups and geographical areas are responding to climate change by shifting their geographical ranges, with important consequences for ecosystem functioning and human well-being. Despite considerable advances in our understanding of the mechanisms by which species redistribute, there is much left to explain the full range of variability observed in species range shifts, including the role of climate exposure, species characteristics, evolutionary mechanisms, and habitat constraints.

The overarching goal of BIOSHIFTS was to advance our understanding of the range shift processes, seeking to improve our ability to forecast and manage the implications of biodiversity redistribution in response to climate change. Building upon a comprehensive geo-database of range shift estimates from the scientific literature, enriched with a variety of climate velocities, habitat characteristics, study-level variables and species characteristics, our working group (1) explored the patterns and mechanisms of biodiversity redistribution on Earth, including biases in range shift research, (2) provided a set of recommendations to guide the study and management of species range shifts, (3) assessed the link between macroevolutionary processes and contemporary range shifts, and (4) investigated under which circumstances commonly used models were able to provide reliable forecasts of species redistributions.

[FR] Contexte et objectifs (environ 1 500 caractères espaces inclus)

Un nombre croissant d'études montre que des espèces issues de divers groupes taxonomiques et régions géographiques répondent aux changements climatiques en changeant leurs aires de répartition, avec des répercussions majeures pour le fonctionnement des écosystèmes et le bien-être des sociétés humaines. Malgré des avancées considérables dans la compréhension des mécanismes à l'origine de ces redistributions, de nombreuses incertitudes persistent quant aux facteurs sous-jascents.

L'objectif principal du projet BIOSHIFTS était de faire progresser notre compréhension des processus de déplacement des aires de répartition, afin d'améliorer notre capacité à prévoir et à gérer les conséquences de la redistribution du vivant en réponse aux changements climatiques. En s'appuyant sur une base de données compilant des estimations de déplacements d'aires de repartition issues de la littérature scientifique, enrichie par diverses vitesses climatiques, caractéristiques d'habitat, des variables méthodologiques propres aux études ainsi que des traits biologiques des espèces, notre groupe de travail a : (1) exploré l'ampleur et les mechanismes de la redistribution de la biodiversité à l'échelle mondiale, y compris les biais présents dans les recherches sur le sujet ; (2) formulé un ensemble de recommandations pour orienter l'étude et la gestion des changements d'aires de distribution ; (3) évalué le lien entre les processus macroévolutifs et les déplacements des aires de distribution ; et (3) analysé les conditions dans lesquelles les modèles communément utilisés par la communauté scientifique permettent de produire des projections fiables des redistributions d'espèces.

II. Project participants

List and attendance of project participants

Please indicate if any project participants were unable to attend a meeting, but were active remotely by using an asterisk (*).

	Name	Affiliation	Country	WS1	WS2	WS 3	WS 4	WS 5	WS 6
PI 1	Lise COMTE	Conservation Science Partners	USA	x	x	x	x	x	x
PI 2	Jonathan LENOIR	Université de Picardie Jules Verne	France	x	x	x	x	x	x
PI 3	Gaël Grenouillet	Université Toulouse 3 - Paul Sabatier	France	x	x	x	x	x	x
Post-doc	Brunno OLIVEIRA	Centre de Synthèse et d'Analyse sur la Biodiversité	France	*	x	x	x	x	x
1	Romain BERTRAND	Université Toulouse 3 - Paul Sabatier	France	x	x	*	x	x	x
2	I-Ching CHEN	National Cheng Kung University	Taiwan	*	x	x	*	x	x
3	Sarah DIAMOND	Case Western Reserve University	USA	x	x	x	x	x	x
4	Lesley LANCASTER	University of Aberdeen	UK	*	x	x	x	x	x
5	Jake LAWLOR	McGill University	Canada		x	x	x	x	x
6	Nikki MOORE	McGill University	Canada		x	x	x	x	x
7	Jerome MURIENNE	Université Toulouse 3 - Paul Sabatier	France	x	x	x	x		
8	Malin PINSKY	University of California Santa Cruz	USA	x	x	x	x		x
9	Jonathan ROLLAND	Université Toulouse 3 - Paul Sabatier	France	x	x	x	x	x	x
10	Brett SCHEFFERS	University of Florida	USA	x	x	x	*	*	x
11	Jennifer SUNDAY	McGill University	Canada	*	x	x	x	x	x
12	Fabricio VILLALOBOS	Instituto de Ecología A.C. - INECOL	Mexico	x	x	x			x
13	Gretta PECL	University of Tasmania	Australia					x	

Please list any additional invitees similarly, and identify their category: i.e. students, postdocs or visiting experts

1	Alex BAECHER	University of Florida	USA	Graduate student	WS2	
2	Jeewantha BANDARA	Rudgers University	USA	Graduate student	WS2/ WS3/ WS4/ WS5	
3	I-Wen CHEN (Ivory)	National Cheng Kung University	Taiwan	Graduate student	WS5/ WS6	
4	Aurore MAUREAUD	Rudgers University	USA/France	Postdoc	WS4/ WS5	
5	Madeleine RUBENSTEIN	U.S. Geological Survey National Climate Adaptation Science Center	USA	Visiting expert	WS2	
6	Laura THOMPSON	U.S. Geological Survey National Climate Adaptation Science Center	USA	Visiting expert	WS1*/ WS4	
	Marius VERDENNE	Université Toulouse 3 - Paul Sabatier	France	Graduate student	WS3 (1 day)	
7	Sarah WEISKOPF	U.S. Geological Survey National Climate Adaptation Science Center	USA	Visiting expert	WS1*/ WS2/ WS3/ WS5/ WS6	
8	Barrett WOLF	University of Tasmania	Australia	Postdoc	WS5/ WS6	

Comment: Thanks to the support of the CESAB, we were able to support the participation of six additional early career researchers to our working group meetings at CESAB in Montpellier. In addition, the CESAB gracefully welcomed Nikki Moore from September 2022 to February 2023 to complete a research project as part of her MS thesis and funded by a scholarship from the National Sciences and Engineering Research Council of Canada and the University of McGill. Sarah Weiskopf, Laura Thompson and Madeleine Rubenstein's participation was supported by the USGS Climate Adaptation Science Center. Due to COVID travel restrictions, WS1 was hybrid and half of the members participated remotely. Several members could not attend all the meetings in person but were given the opportunity to contribute to the different outputs of the group during and between the meetings.

III. Activity report

III.1 Description of the work conducted and scientific results obtained: for the scientific reader.

Shifts in species distributions are a common ecological response to climate change, as species move towards the poles or higher elevation to keep track of the shifting climates and dispear from areas that are no longer suitable. Global temperature rise is often hypothesized as the primary driver, but the directions and rates of distribution shifts are highly variable across species, systems, and studies, complicating efforts to anticipate and manage biodiversity responses to climate change (Rubenstein et al. 2023; Lenoir et al. 2021). Bodies of theory suggest that these idiosynchasies are the result both of the sensitivity of organisms to climate exposure and of their capacity to adapt to environmental changes, including by persisting in place through phenotypic and evolutionary adaptation or shifting in space through habitats that may have already been highly altered by human activities (Thurman et al. 2021). Yet, previous literature has suggested that species traits are weak predictors of species range shifts, thereby limiting the predictive utility of trait-based approaches for conservation and natural resource management (Beissinger & Ridell 2021). The extent to which the climate-induced redistribution of biodiversity on Earth is predictable thus remains an open question.

Scienthesis and conceptual developements

By assembling a team of scientists with extended expertise in the nascent field of species redistribution across lands, rivers and seas, covering temperate and tropical systems as well as plant and animal groups, BIOSHIFTS has been an incubator of new research ideas to advance the methodological and conceptual approaches needed to improve our ability to understand and manage species vulnerability to climate change across taxonomic groups and under a range of environmental and anthropogenic contexts.

Our working group first reviewed the history of the field of species redistribution and current knowledge on the mechanisms of climate-induced species redistribution (**Lawlor et al. 2024**). We reported that only less than one third of all documented range shifts (59%) are directionally consistent with what would be expected if species had follow the shifting isotherms along mountain slopes and latitudes. Instead, many species have not shifted or have shifted in directions opposite to temperature-based expectations. Our review offers some potential explanations for these lagging or expectation-contrary shifts, including the role of other climatic variables such as changes in precipitation patterns, the presence of microrefugia that may shelter species from climatic changes operating at larger spatial scales, the fragmentation of habitat that may impede movement, as well as the role of biotic interactions that may indirectly affect the sensitivity to changing climates and ability of species to persist locally or establish into new areas. We also highlighted the need to address current taxonomic and geographic unbalances in research (Figure 1). We suggested to increase the collection and connection among different biodiversity databases, test the generality of range shift patterns and mechanisms across systems, as well as develop predictive approaches at management-relevant scales.

Next, we synthetized previous research using traits-based approaches to understand the rates of species redistribution, and provided a road map to improve the inference gained from range shifts-traits relationships (Figure 2; **Comte et al. 2024**). In this perspective article, we argued that to fully grasp the role of intrinsic species characteristics, we need to (1) better conceptualize the role of species traits on species range shifts, including by considering interdependencies and interactions among traits, as well as potential non-linearities in the traits versus range shifts relationships, (2) identify opportunities for new trait integration, (3) better account for exposure to extrinsic drivers of change, habitat and biotic constraint variables, and (4) explore the influence of the estimation process and biases on our ability to detect meaningful relationships. As part of this work, we also synthetized bodies of theory and empirical evidence regarding the expectations between the range shift processes (range contraction and expansion) and species traits, and explored the consequences of functional biases on our understanding of these relationships.

Finally, we developed a set of best practices to inform the decision making in the context of species redistribution using the Resit-Accept-Direct framework (Figure 3; **Thompson et al. In Preparation**). This work emphasizes the importance of understanding the large scale impacts of local management actions on socio-ecological systems and the need for enhancing communication among managers. Such coordination is crucial for prioritizing actions that support species resistance and resilience to climate change. Indeed, because species' ranges often span multiple management jurisdictions, and because the effectiveness of specific management strategies varies across different parts of the range, it is crucial to consider both where focal populations fall within the range and how local management decisions affect the range as a whole.

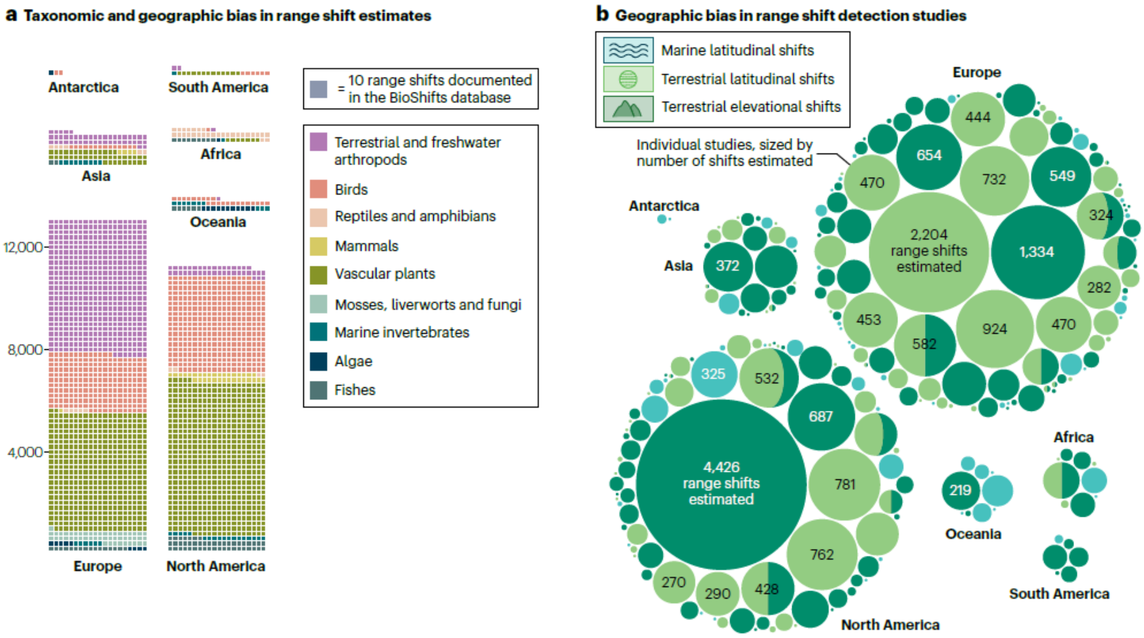
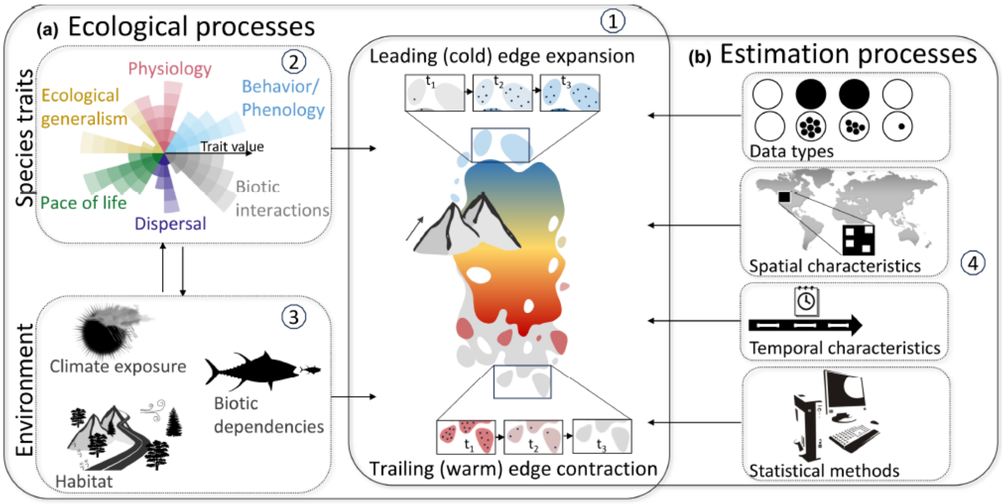


Figure 1. (a) Taxonomic and geographic breakdown of latitudinal and elevational range shift estimates in the BioShifts database where each tile represents ten empirically estimated range shifts of a given taxonomic group, always rounded up. (b) Geographic bias of range shift studies in the BioShifts database where each circle represents one range shift estimation study; circle sizes and inset numbers represent the number of species ranges assessed in each study and colour represents the type of shift estimated (marine latitudinal, terrestrial latitudinal, and terrestrial elevational shifts).



① Develop strong a priori hypotheses and account for trait (co)variations
→ *What are the expectations regarding the range shift-trait relationships (shape and direction)?*

② Identify new opportunities for trait integration
→ *Are the key mechanisms captured by the available traits?*

③ Account for abiotic and biotic context dependencies
→ *Is the influence of species traits likely to vary according to the local environmental context?*

④ Account for estimation processes & research biases
→ *How do the underlying datasets and statical methods influence the detected range shifts and ability to detect range shift-trait associations?*

Figure 2. Set of factors and interactions that may influence the documented patterns of range shifts and recommended steps to model range shifts-trait associations. Documented patterns of range shifts at the trailing (i.e., range contraction) and leading (i.e., range expansion) edges of species distributions are typically documented in response to anthropogenic climate change along spatial gradients such as latitude, elevation (on land), and depth (in the oceans) and reflect both (a) the ecological processes (left panel) and the (b) estimation processes (right panel), which involve a set of intrinsic, extrinsic and methodological factors. Ecological processes may involve complex interaction terms between species traits and either the abiotic or biotic context such that it suggests complex context dependencies. Numbers illustrate a set of recommendations to improve our ability to decipher the mechanisms of range shifts.

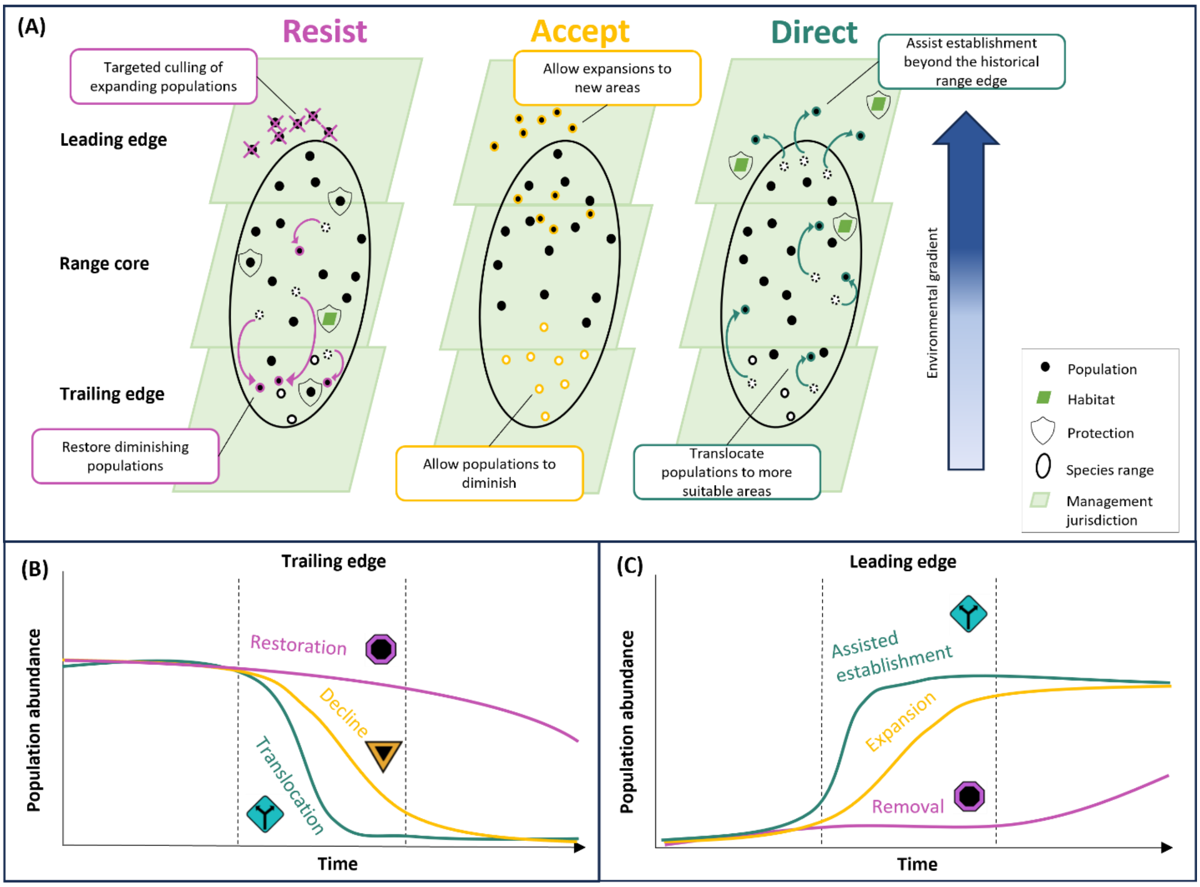


Figure 3. (A) Example of Resist-Accept-Direct (RAD) strategies implemented across multiple management jurisdictions at the trailing edge, leading edge, and core of a species' range along an environmental gradient (e.g., temperature), which is directional along a geographical dimension (e.g., latitude or elevation here). Populations with white centers represent either those that have been extirpated (solid outline) or relocated (dotted outline). Arrows indicate active management actions for the displacement of individuals from the focal populations. Crosses represent population presences that have been actively managed to resist range expansion. Shields represent protection of populations (e.g., harvest regulation) or habitats (e.g., potential refugia or corridors). Shifting environmental gradients (e.g., temperature, soil conditions) can shape demographic or genetic variation of species. Colours correspond to the Resist (purple), Accept (orange), and Direct (teal) strategies of the RAD framework. (B) At the trailing edge, resist may include restoring declining population abundance, accept may include allowing declines to occur, and direct may include facilitating declines by translocating populations to more suitable areas. (C) At the leading edge, resist may include removing unwanted species, accept may include allowing expansions to occur, and direct may include assisting the establishment of populations in new areas that become suitable from climate change.

Database compilation and tool developement

The working group also merged BioShifts (Comte et al. 2020) with the CoRE database (Rubenstein et al. 2024) to consolidate a georeferenced dataset of observed species range shifts from the scientific litterature. It is now including 31,760 observed range shifting rate estimates in marine, freshwater, and terrestrial ecosystems, spanning 12,912 species from 57 taxonomic classes (plants, animals and fungi) since 1770. The database was augmented with methodological variables, trait data, macrogenetic data, climate velocities at a variety of spatial scales, and habitat connectivity metrics specific to the species range shifts. We are currently developing the R package *BioShiftR* with functionalities that would make the database publicly accessible, together with tools that allow to easily manipulate the data for analysis (Figure 4; **Lawlor et al. In Preparation**). This database can provide uniquely comprehensive insights into climate-induced range shift processes, and is expected to increase the capacity of the scientific community to better understand and ultimatly manage biodiversity redistribution under climate change.

Working with the data scientist (Nicolas Casajus) of the CESAB, our group was able to initiate a pipeline for trait integration across multiple physiological, life-history, ecological, and morphological traits (Figure 5). Altough these efforts are still ongoing, they open the door for more in-depth (multi-dimentional) inquiries regarding the influence of species traits on range shifts in the future.

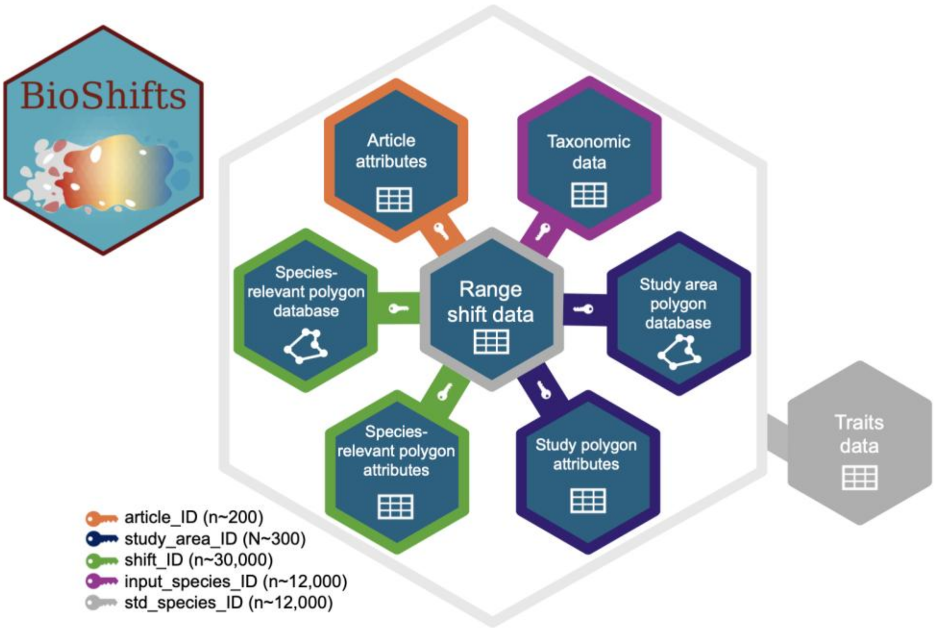


Figure 4. Different elements of the BioShifts database that can be accessed and manipulated through the companion package. The database includes data on species range shifts, associated with information about the articles, species taxonomy and study methodology, as well as spatial data associated with the study irrespective of where species occur within the area (study polygons) or clipped to species ranges (species-relevant study areas) together with a variety of metrics capturing climate velocity over the period of study calculated at different spatial resolutions and for both the study and species relevant polygons. The database will be enriched with trait data at a later stage.

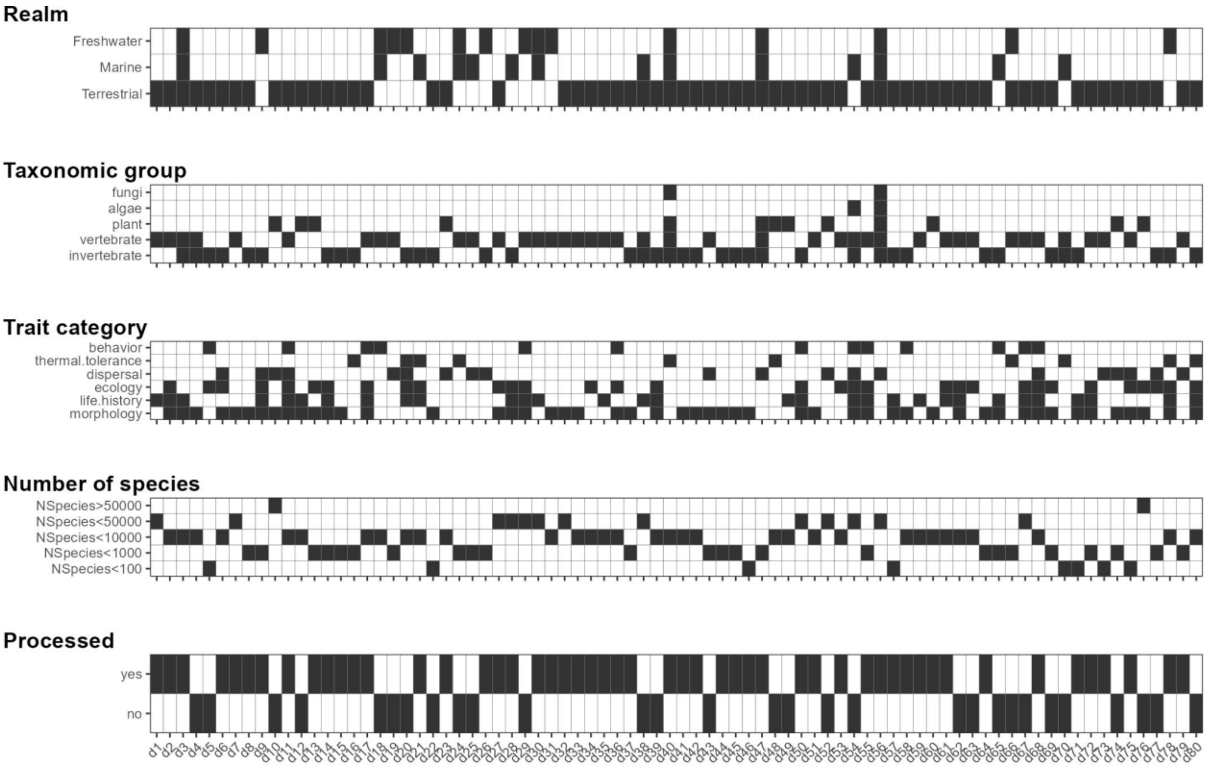


Figure 5. Characteristics of the trait databases (d1 to d80 along the x-axis) included in the compilation. Some of these databases have already been processed (i.e., species names have been harmonized and code to extract and compile targeted traits has been developed, like for d1), some are pending processing, while other more specialized databases will be processed more specifically to fill key gaps in the data (e.g., to support phylogenetic imputation or conduct analyses tailored to a particular taxonomic group). The full table of trait databases are included in Appendix S1.

Empirical research

The working group also engaged in empirical research. Leveraging the BioShifts database, we developed finely-resolved species distribution models tailored to the metadata provided by the original study, such that modeled range shifts covered the same geographical extent and temporal window as the observations used to document range shifts. This unique set of paired documented and modelled range shifts provided us with the opportunity to test the ability of species distribution models to predict range shifts as well as to answer a variety of questions regarding the influence of extrinsic drivers (e.g., climatic changes, habitat fragmentation), intrinsic traits (e.g., dispersal mode) and methodological factors (e.g., spatio-temporal extent and granularity), in explaining the rates of species redistribution (Figure 5; **Oliveira et al. Under Review**). Briefly, we found that whereas the directions of the latitudinal range shifts aligned in the majority of cases (73% for marine and 54% for terrestrial range shifts), documented range shifts were two to four times faster than the modeled expectations. We also demonstrated a higher predictability for studies relying on long-term monitoring data across a restricted spatial extent, in regions with higher habitat connectivity and when interannual variability in climate suitability was low. These results highlight when and where species distribution models work best and under which conditions predictions capture observations, offering a clearer path for improving forecasts of biodiversity redistribution.

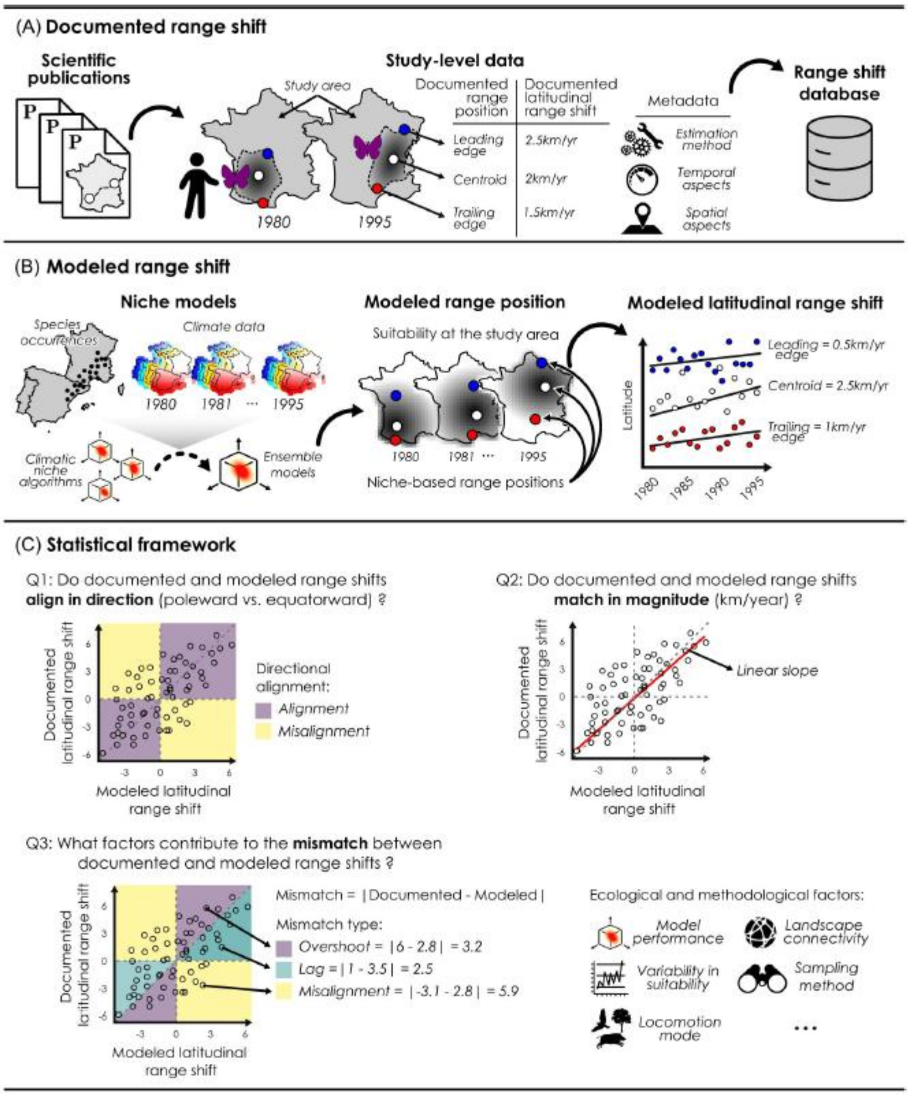


Figure 5. Graphical overview of the methodological approach used to evaluate the ability of climatic niche models to reproduce documented latitudinal species range shifts. This approach was applied globally to 3,552 species across marine and terrestrial systems. Documented latitudinal range shifts (km/year) at different range positions (A) and associated methodological variables were sourced from the BioShifts databases, here illustrated with a hypothetical study using a butterfly species in France. To ensure robust comparisons between modeled and documented shifts, we implemented an ensemble modeling framework specifically designed to match the geographical and temporal parameters of each original empirical study. Modeled range shifts (B) were estimated through linear regressions to calculate latitudinal changes (km/year) for the centroid, leading edge, and trailing edge of each species range, using yearly suitability maps predicted by niche models. The statistical framework (C) included testing the predictive accuracy of modeled range shifts in terms of alignment in direction (Q1) and match in magnitude (Q2) of documented range shifts, and identifying factors influencing the mismatch (Q3) (i.e., absolute differences between documented and modeled shifts), which was categorized as cases of overshoot, lag, or misalignment.

Combining the BioShifts database with a global database of genetic diversity (Fonseca et al. 2023), we also addressed the fundamental question of whether evolutionary potential of species affects the pace of species redistribution. This first large-scale macrogenetic test of adaptive capacity showed that genetic diversity reduces the rates of climate-driven range contraction at the trailing edge, while accelerating range expansion at the leading edge, particularly at intermediate levels of climate velocity (Figure 6; **Oliveira et al. In Preparation**). These results confirm the theoretical hypothesis that genetic diversity favors persistence under rapid climate change at the trailing edge and promotes colonization at the leading edge under specific circumstances. These results have important implications for conservation, by underscoring the value of genetic diversity not only as a long-term evolutionary reservoir but also as a short-term buffer against environmental change. They also demonstrate the potential of macrogenetic data in informing species vulnerability and the pressing need for integrative approaches that combine population genetic data with demographic, ecological, and environmental information across spatial and temporal scales.

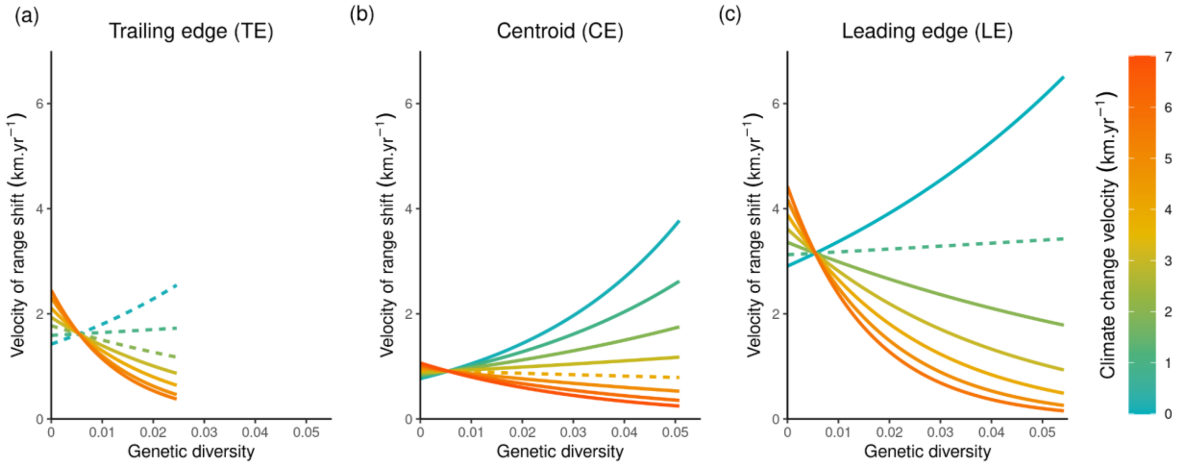


Figure 6. Marginal effects of the interaction between climate change velocity and genetic diversity on species range shifts. Predicted effects of genetic diversity on species range shifts across different magnitudes of climate change velocity at the (a) trailing edges (b) range centroid, and (c) leading edge. Solid and dotted lines indicate significant and non-significant relationships, respectively.

Other ongoing projects of the group include a test of whether fishing pressure influence species range shifts for marine fish by integrating data from the FISHGLOBE database (database developed by another CESAB working group) and the RAM legacy (compilation of stock assessment results for commercially exploited marine populations) database (**Bandara et al. In Preparation**), a detailed analysis of how dispersal influences range shifts for selected groups of plants and insects (**Moore et al. In Preparation**), and an estimation of the temporal changes in the rate of biodiversity change (including potential acceleration) using both the BioShifts (range shifts) and the BioTIME (community turnover) databases (**Chen et al. In Preparation**).

Another project related to phylogenetic signal in the rates of species range shifts was ultimately not pursued due to the confounding effects of methodological variability, which was phylogenetically clustered (Figure 7). Although disappointing, the working group is now considering a methodological publication to alert researchers to this problem: when meta-analyses combine heterogeneous studies, evolutionary history may inadvertently correlate with data collection practices, inflating apparent phylogenetic patterns and underscoring the need for caution in large-scale comparative analyses.

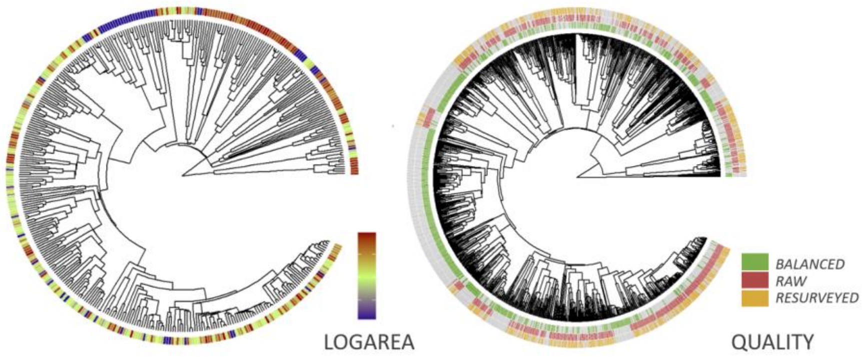


Figure7: Examples of phylogenetic signal in methodological design used to quantify species range shifts in birds, illustrating a strong clustering for two methodological factors (i.e., study area and data quality) from the *BioShifts* database.

References cited

Beissinger, S. R. and Riddell, E. A. (2021). Why are species' traits weak predictors of range shifts? - Annual Review of Ecology, Evolution, and Systematics 52: 47–66.

Comte, L. et al. (2020) BioShifts: a global geo-database of climate-induced species redistribution over land and sea. Figshare https://doi.org/10.6084/m9.figshare.7413365.v1.

Fonseca, E.M., Pelletier, T.A., Decker, S.K., Parsons, D.J. & Carstens, B.C. (2023). Pleistocene glaciations caused the latitudinal gradient of within-species genetic diversity. Evolution Letters, qrad030.

Lenoir, J., Bertrand, R., Comte, L., Bourgeaud, L., Hattab, T., Murienne, J. and Grenouillet, G. (2020). Species better track climate warming in the oceans than on land. Nature Ecology and Evolution 4: 1044–1059.

Rubenstein, M. A. et al. (2023) Climate change and the global redistribution of biodiversity: substantial variation in empirical support for expected range shifts. Environmental Evidence 12, 7781.

Rubenstein, M.A., Weiskopf, S.R., Bertrand, R., Carter, S.L., Comte, L., Eaton, M.E., Johnson, C.G., Lenoir, J., Lynch, A.J., Maslyukova, D.Y., Miller, B.W., Morelli, T.L., Parker, E.J., Poole, C., Rodriguez, M.A., Rudick, T., Terando, A.J., Thompson, L.M., and Turner, K., 2024, CoRE (Contractions or Range Expansions) Database: Global Database of Species Range Shifts from 1802-2019: U.S. Geological Survey data release, https://doi.org/10.5066/P99VP2TW.

Thurman, L. L., Stein, B. A., Beever, E. A., Foden, W., Geange, S. R., Green, N., Gross, J. E., Lawrence, D. J., LeDee, O., Olden, J. D., Thompson, L. M. and Young, B. E. (2020). Persist in place or shift in space? Evaluating the adaptive capacity of species to climate change. Frontiers in Ecology and the Environment 18: 520–528.

III.2.1 Introduction (around 300 characters including spaces): for large audience

Shifts in species distributions are a common ecological response to climate change. Yet, the extent to which the redistribution of biodiversity on Earth is predictable remains an open question. This, in turn can decrease the effectivness of climate change management adaptation strategies.

III.2.2 [FR] Introduction (environ 300 caractères, espaces inclus): pour grand public

Les changements des aires de répartition des espèces constituent une réponse écologique notable aux changements climatiques. Pourtant, la mesure dans laquelle la redistribution de la biodiversité est réellement prévisible demeure une question ouverte. Cela peut à son tour diminuer l'efficacité des stratégies de gestion d'adaptation au changement climatique.

III.3.1 Methods and approaches used for your project (around 700 characters including spaces): for large audience

BIOSHIFTS participated in conceptual developments by synthetizing knowledge on the mechanisms of climate-induced species redistribution, providing a road map for the study of range shifts-traits relationships and recommending a set of best practices to inform the decision making for implementing management strategies in the context of species redistribution. The group also consolidated database of species range shifts from the scientific litterature for more than 12,000 species, that was subsequently leveraged in various projects, including to test the ability of common predictive methods to reliably predict range shifts, and evaluate whether higher evolutionary potential helps species cope with climate change.

III.3.2 [FR] Méthode et approches utilisées pour le projet (environ 700 caractères, espaces inclus): pour grand public

BIOSHIFTS a contribué a des développements conceptuels en synthétisant les connaissances sur les mécanismes de redistribution des espèces induite par le climat, en proposant une feuille de route pour l'étude des relations entre les déplacements de distribution et les traits des espèces, et en formulant un ensemble de recommendations pour la mise en œuvre de stratégies de gestion. Le groupe a également consolidé une base de données unique sur les déplacements de distribution des espèces à partir de la littérature scientifique, couvrant plus de 12 000 espèces. Cette base a ensuite été utilisée dans divers projets, notamment pour tester la capacité de modeles predictif commununement utilises a reproduire les changements de distribution des especes, et pour évaluer si un potentiel évolutif plus élevé permettent aux espèces de mieux faire face au changement climatique.

III.4 Access to data

Describe any data and/or databases created or added to during the course of the project, and components of your data management plan:

(a) the types of data collected and used

We collated data from the scientific literature on species range shifts, including the rates of shifts, the estimation method and underlying data used, as well as the polygons describing the spatial area(s) where the study was conducted. This database is an integration of the BioShifts (Comte et al. 2020) and the CoRE database (Rubenstein et al. 2024).

(b) standards used to document the data

The metadata will be documented following the Federal Geographic Data Committee (FGDC) Content Standard for Digital Geospatial Metadata.

(c) policy for access and re-use, short- and long-term storage and management

The database will be integrated in an R package (*BioShiftR*; Lawlor et al. In Preparation) and publicly accessible under an open non-commercial CC BY-NC license.

(d) people to contact after the end of the project.

Jake Lawlor (jake.lawlor@mail.mcgill.ca); Lise Comte (lcgcomte@gmail.com); Jonathan Lenoir (jonathan.lenoir@u-picardie.fr)

III.5 Scientific outcomes of the project

- List of ALL publications (articles, books, book chapters …) published, submitted or planned (with planned deadlines for submission). Highlight the 3 most significant in your view (***).

Published

Lawlor, J. A., Comte, L., Grenouillet, G, Lenoir, J., Baecher, J.A., Bandara, R.M.W.J., Bertrand, R., Chen, I-C, Diamond, S.E., Lancaster, L.T., Moore, N., Murienne, J., Oliveira, B.F., Pecl, G.T., Pinsky, M.L., Rolland, J., Rubenstein, M., Scheffers, B.R., Thompson, L.M., van Amerom, B., Villalobos, F., Weiskopf, S.R. & Sunday, J. 2024. Mechanisms, detection and impacts of species redistributions under climate change. *Nature Reviews Earth and Environment* 5: 351–368.

***Comte, L., Bertrand, R., Diamon, S., Lancaster, L. T., Pinsky, M. L., Scheffers, B. R., Baecher, J. A., Bandara, R. M. W. J., Chen, I., Lawlor, J. A., Moore, N. A., Oliveira, B. F., Murienne, J., Rolland, J., Rubenstein, M. A., Sunday, J., Thompson, L. M., Villalobos, F., Weiskopf, S. R. & Lenoir, J. (2024). Bringing traits back into the equation: A roadmap to understand species redistribution. *Global Change Biology*, 30(4), e17271.

Lenoir, J. & Comte, L. (2024) Rapid range shifters show unexpected population dynamics. *Nature Ecology and Evolution* 8, 850–851. [Invited Commentary]

Lenoir J (2024) The continental divide in range-shifting birds of North America. *Proceedings of the National Academy of Sciences*, 121, e2401808121. [Invited Commentary]

Submitted

***Oliveira, B., Bertrand, R., Pinsky, M.L., Casajus, N., Wolf, B.W., Scheffers, B., Villalobos, F., Grenouillet, G., Pecl, G., Chen, I-C., Diamond, S., Baecher, A., Lawlor, J.A., Sunday, J., Murienne, J., Rolland, J., Thompson, L.M., Lancaster, L., Rubenstein, M.A., Moore, N.A., Bandara, R.M.W.J, Diamond, S.E., Weiskopf, S., Lenoir J. & Comte L. (Under Review) Species range shifts often speed ahead of their climatic niches. Submitted to *Proceedings of the National Academy of Sciences*.

In Preparation

Oliveira, B., Bertrand, R., Comte, L., Lenoir, J., Grenouillet, G., Lancaster, L.T., Murienne, J., Diamond, S., Baecher, J.A., Bandara, R.M.W.J., Chen, I-C., Lawlor, J.A., Moore, N.A., Pecl, G.T., Rubenstein, M.A., Scheffers, B.R., Sunday, J., Thompson, L.M., Villalobos, F., Weiskopf, S.R., Wolfe, B.W., Pinsky M.L. &

Rolland, J. (In Preparation) Genetic diversity impacts climate-induced range shifts. In preparation for *Ecology Letters*. Target submission: July 2025 (inquiry for the Synthesis section sent).

Thompson, L.M., Weiskopf, S., Rubenstein, M.A., Valler J., Lynch, A., Carter, S., Comte, L., Lenoir, J., Rolland, J., Bandara, R.M.W.J, Pinsky, M.L., Diamond, S., Rodriguez, M., Bertrand, R., Moore, N.A., Scheffers, B.R., Lawlor, J.A., Lancaster, L., Grenouillet, G., Baecher, A., & Oliveira, B. (In Preparation) RAD (Resist-Accept-Direct) management of species redistribution under climate change. In preparation for *Frontiers in Ecology and the Environment*. Target submission: July 2025.

***Lawlor, J. A., Oliveira, B.F., Weiskopf, S.R., Moore, N., Lenoir, J., Grenouillet, G, Bertrand, R., Chen, I-C, Pinsky, M.L., Diamond, S., Bandara, R.M.W.J, Rolland, J., Lancaster, L., Rubenstein, M., Scheffers, B.R., Thompson, L.M., Villalobos, F., Krippel, J., Johnson C.G., Rodriguez M.A., Comte, L. & Sunday, J. (In Preparation) BioShifts – A database of geographical range shifts to study species on the move. In preparation for *Methods in Ecology and Evolution*. Target submission: September 2025.

Planned

R.M.W.J Bandara, John Wiedenmann, Brunno F. Oliveira […] & Malin L. Pinsky (Planned) The effects of fishing pressure on marine range shifts. Target: fall/winter 2025.

Yi-Wen Chen, Jonathan Lenoir, Malin L. Pinsky, Brett Scheffers […] & I-Ching Chen (Planned) Acceleration of biological responses in the Anthropocene. Target: fall/winter 2025.

Nikki Moore, Brunno F. Oliveira […] & Jennifer Sunday (Planned) Informed expectations reveal relationships between dispersal ability and range shifts. Target: fall/winter 2025.

- List of oral communications and posters in conferences, past or planned (please, give the dates of these conferences)

Oral communications

Jonathan Lenoir J. (2025) BioShifts – A database of species range under anthropogenic climate change. The 72nd annual meeting of the Ecological Society of Japan (ESJ) (invited keynote), 15-18 March 2025, Sapporo, Hokkaido, Japan.

Brunno F. Oliveira, Jonathan Lenoir J., Alex Baecher, R.M.W.J Bandara, Bertrand R., I-Ching Chen, Sarah E. Diamond, Lesley T. Lancaster, Jake A. Lawlor, Nikki Moore, Jerome Murienne, Gretta Pecl, Malin L. Pinsky, Jonathan Rolland, Madeleine Rubenstein, Brett Scheffers, Jennifer Sunday, Laura M. Thompson, Fabricio Villalobos, Sarah R. Weiskopf, Gaël Grenouillet & Lise Comte (2023) How well species distribution models predict species range shifts? Species on The Move conference, 14-18 Mai, Bonita Spring, USA.

I-Ching Chen, Yi-Wen Chen, Malin L. Pinsky, Brett Scheffers & Jonathan Lenoir (2023) Acceleration of biological responses in the Anthropocene. Species on The Move conference, 14-18 Mai, Bonita Spring, USA.

Nikki Moore & Jennifer Sunday (2023) Informed expectations reveal relationships between dispersal ability and range shifts. Species on The Move conference, 14-18 Mai, Bonita Spring, USA.

Jonathan Lenoir J. & BIOSHIFTS working group (2023) BioShifts – A database of species range under anthropogenic climate change. Online seminar at the Faculty of Environmental Sciences (FZP), Czech University of Life Sciences (CZU) (invited talk), 2 February 2023, Prague, Czech Republic.

Jonathan Lenoir J. & BIOSHIFTS working group (2023) BioShifts – A database of species range under anthropogenic climate change. Online seminar at the University of Basel (invited talk), 16 March 2023, Basel, Swizerland.

Jonathan Lenoir J. (2023) Biodiversity redistribution & microclimatic processes under climate change. Macroecology & Biogeography meeting (invited keynote), 04-05 May 2023, Bayreuth, Germany.

Lise Comte & BIOSHIFTS working group (2022) Can species traits explain climate-induced range shifts across taxa and realms? Ecological Society of America Annual Meeting (invited talk), 14-19 August, Montreal, Canada.

Jonathan Lenoir J., Alex Baecher, R.M.W.J Bandara, Bertrand R., I-Ching Chen, Sarah E. Diamond, Lesley T. Lancaster, Jake A. Lawlor, Nikki Moore, Jerome Murienne, Brunno F. Oliveira, Gretta Pecl, Malin L. Pinsky, Jonathan Rolland, Madeleine Rubenstein, Brett Scheffers, Jennifer Sunday, Laura M. Thompson, Fabricio Villalobos, Sarah R. Weiskopf, Gaël Grenouillet & Lise Comte (2022) A database of geographic range shifts for terrestrial and marine taxa under anthropogenic climate change. International conference in Ecology & Evolution (Sfe2, GfÖ, EEF) (invited talk), 21-25 November 2022, Metz, France.

- Other outcomes (databases, software, R-code, web sites, etc).
  - BioShifts – A database of geographical range shifts and R package to study species on the move. Target: database & R package to be submitted with article (Fall 2025).
  - Pipeline for trait compilation – R-code to compile trait databases that include code to perform taxonomic, structure and unit harmonization based on open-source trait databases, that is transferable to other efforts.
  - R-code associated with the empirical analyses that will be released with the associated articles.

- List of grant proposal submitted or planned (with planned deadlines for submission).
  - NCEAS working group (National Center for Ecological Analysis & Synthesis) – The MORPHO initiative. Mechanisms and impacts of climate-driven species range shifts at global scales. PIs: Sarah Weiskopf, Sarah Diamond, Brett Scheffers, Lise Comte. Submitted April 2025 (pending).
  - Powell Center working group (U.S. Geological Survey). Understanding mechanisms and impacts of climate-driven species range shifts. PIs: Sarah Weiskopf, Sarah Diamond, Brett Scheffers, Lise Comte. Submitted January 2025 (not funded).
  - sDiv working group (Synthesis Centre for Biodiversity Sciences). Mechanisms and impacts of climate-driven species range shifts at global scales. PIs: Sarah Weiskopf & Sarah Diamond. Submitted March 2025 (not funded).

IV. Principal conclusions (publishable)

IV. 1 Principal conclusions (around 1000 characters including spaces): for large audience

By comparing predictions from climatic niche models that are widely used by the scientific community to actual observations of range shifts for thousands of species across land and sea, we found that while niche models tend to get the direction right, especially for marine species, they often fail to predict the pace of biodiversity redistribution (Figure 7). Range shifts are more predictable when they are estimated across small areas and with long-term monitoring data, in regions where habitat connectivity is high and when interannual climate variability is low. This work provides the first global evaluation of the capacity of climatic niche models to predict observed range shift rates. In doing so, it also identifies key factors associated with model–data mismatches, offering new insights into the mechanisms driving range shift dynamics and informing the development of more robust predictive tools for biodiversity management under ongoing climate change.

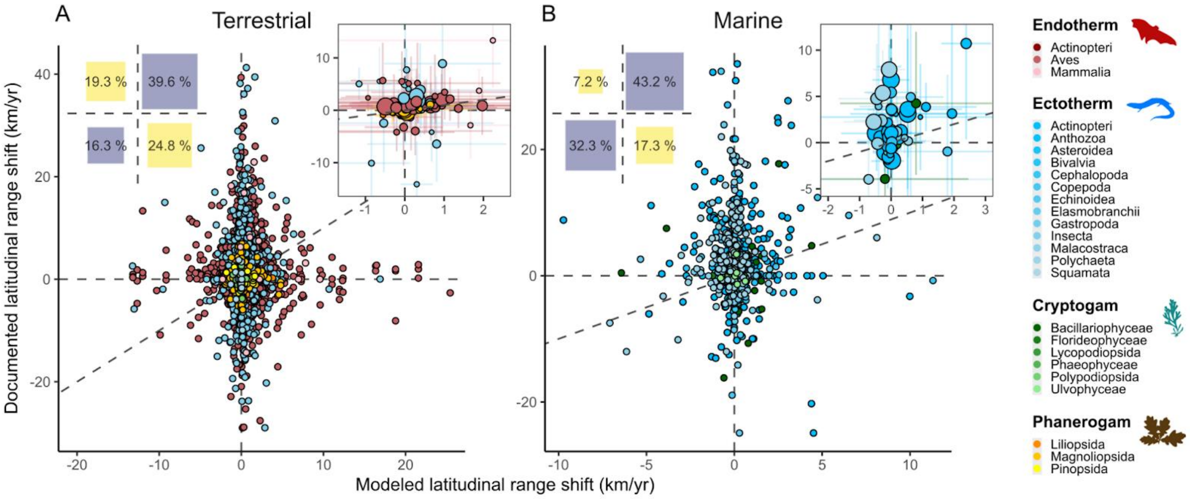


Figure 7. Relationship between documented and modelled latitudinal range shifts in the terrestrial (A) and marine (B) realms. The large panels illustrate relationships at the observation-level (i.e., one dot being a single observation of latitudinal range shift for a single species, study area and range position) and the small right panel to data aggregated by taxonomic class, study and range position, with dot size proportional to the number of range shift observations used to calculate the mean. The diagonal dashed lines indicate the 1:1 line, where modelled and documented shifts are equal. The upper-left insets show the percentage of the observation-level data, distributed across four quadrants, where purple boxes represent alignment (i.e., poleward or equatorward) and yellow boxes misalignment in direction, with box sizes proportional to the number of range shifts per quadrant. Species are color-coded by taxonomic class into four life-form categories: endotherms and ectotherm animals, and phanerogam and cryptogam plants.

IV. 2 [FR] Principales conclusions (environ 1000 caractères, espaces inclus): pour grand public

En comparant les prédictions issues des modèles de niche climatique largement utilisés avec des observations réelles de déplacements d'aires de répartition pour des milliers d'espèces terrestres et marines, nous avons constaté que, bien que ces modèles parviennent généralement à prédire correctement la direction des déplacements — en particulier pour les espèces marines — ils échouent souvent à en prévoir la vitesse (Figure 7). La précision des prédictions est plus élevée pour les études reposant sur des données de suivi à long terme couvrant une étendue spatiale restreinte, dans des régions présentant une plus grande connectivité des habitats et lorsque la variabilité climatique interannuelle est faible. Cette étude constitue la première évaluation à l'échelle mondiale de la capacité des modèles de niche climatique à prédire les vitesses observées de déplacement des aires de répartition des espèces, apportant de nouvelles connaissances sur les mécanismes à l'origine des dynamiques de déplacement des espèces et contribuant au développement d'outils prédictifs plus robustes pour la gestion de la biodiversité face aux changements climatiques en cours.

V. Result's impact

V. 1 Anticipated (or actual) impact of theses results for science, society, public and private decision making (around 1500 characters including spaces): for large audience

By assembling a team of scientists in the nascent field of species redistribution with expertise in terrestrial, freshwater and marine ecological systems, temperate and tropical biomes as well as for plant and animal groups, BIOSHIFTS has been an incubator of new ideas to advance the methodological and conceptual approaches needed to improve our ability to understand and predict climate-induced species redistribution. By providing a synthesis of the field of species redistribution as well as contributing novel research and guidelines to develop a more predictive science, these results contribute knowledge on the challenges and opportunities associated with the management of species redistribution within socio-ecological systems, thereby having a broad impact on the scientific community, society and ultimatly help develop adapted tools to guide the decision making in response to one of the greatest challenges of our time. The working group also consolidated and enriched a database of documented range shifts that has no equivalent. By making the database publicly accessible and developing tools that allow to easily manipulate the data for analysis, these efforts will increase the capacity of the scientific community and managers to identify range shifts in the present, anticipate range shifts in the future, and use this knowledge to inform strategies for preserving biodiversity through climate change. Although funding agencies can be hesitant to prioritize monitoring programmes since their benefits largely accrue over longer time frames, the work of the working group raise awarness on the need for increased support for data collection.

IV. 2 [FR] Impact pour la science, la société et la décision publique et privé (environ 1500 caractères, espaces inclus): pour grand public

En réunissant une équipe de scientifiques spécialisés dans le domaine émergent de la redistribution des espèces, avec une expertise couvrant les écosystèmes terrestres, d'eau douce et marins, les biomes tempérés et tropicaux, ainsi que les groupes de plantes et d'animaux, BIOSHIFTS a servi d'incubateur à idées visant à faire progresser les approches méthodologiques et conceptuelles nécessaires pour améliorer notre capacité à comprendre et à prédire la redistribution des espèces induite par le climat. En effectuant une synthèse du domaine de la redistribution des espèces et en contribuant à une recherche innovante ainsi qu'à l'élaboration de lignes directrices pour développer une science plus prédictive, ces résultats visent à sensibiliser davantage aux défis et opportunités liés à la gestion de la redistribution des espèces au sein des socioécosystèmes, exerçant ainsi un impact large sur la communauté scientifique, la société, et contribuant, *in fine*, à développer des outils adaptés pour guider la prise de décision face à l'un des plus grands défis de notre époque.

Le groupe de travail a également consolidé et enrichi une base de données sur les déplacements de répartition d'especes documentés dans la littérature scientifique, sans équivalent à ce jour. En rendant cette base de données accessible au public et en développant des outils permettant d'accéder facilement aux données à des fins d'analyse, ces efforts renforceront la capacité de la communauté scientifique et des gestionnaires à identifier les déplacements de répartition actuels, anticiper ceux à venir, et utiliser ces connaissances pour mieux orienter les stratégies de préservation de la biodiversité face aux changements climatiques. Bien que les agences de financement puissent être réticentes à prioriser les programmes car leur bénéfices s'inscrivent souvent sur le long terme, les travaux du groupe de travail viennent appuyer la nécessité d'un soutien accru à ces initiatives.

VI. Outreach and dissemination activities (if relevant)

- Please describe any dissemination and knowledge transfer activities that have been conducted toward policy makers, managers, socio-economic actors (or any other stakeholder) in relation to the project.
  Not applicable.

- Let us know about any media articles, interviews, educational projects, etc. in relation with the research conducted in the project.
  - Movie. (2025) Our New World (90 min; link: https://vimeo.com/1079299952; password: newworld). Version française intitulée « Notre Nouveau Monde », diffusée le 8 juillet 2025 sur France 2 à 21H10. https://www.francetvpro.fr/contenu-de-presse/73798484
  - Media Article. (2024) How climate change is affecting where species live. https://www.mcgill.ca/newsroom/channels/news/how-climate-change-affecting-where-species-live-357786
  - Media Article. (2024) From mountains to oceans: Climate change and ecosystem dynamics. https://www.thetribune.ca/sci-tech/from-mountains-to-oceans-climate-change-and-ecosystem-dynamics-17092024/
    Media Article. (2024) Mieux comprendre la redistribution du vivant en réponse aux changements climatiques (Actualités Scientifiques CNRS Ecologie & Environnement). https://www.inee.cnrs.fr/fr/cnrsinfo/mieux-comprendre-la-redistribution-du-vivant-en-reponse-aux-changements-climatiques
  - Outreach paper. (2024) Lenoir J., « A la conquête des zones froides », Le Courrier de la Nature (n°343), parution en Novembre 2024, Société nationale de protection de la nature (SNPN). https://www.snpn.com/produit/le-courrier-de-la-nature-n-343-novembre-2024/

   - Outreach paper. (2022) Lenoir J., « Avec le changement climatique, la migration silencieuse des espèces », The Conversation. https://theconversation.com/avec-le-changement-climatique-la-migration-silencieuse-des-especes-189017

- Are there any management or decision-making tools which have been developed as a result of the project (e.g. design/implementation of biodiversity indicators)?
  Not applicable.

- Are there any activities planned (or that could be planned) to expand the utilization or application of the results?
  As mentioned in the previous sections, we are still in the process of compiling a large number of trait databases related to the physiology, life-history strategies, ecology and morphology of the species included in the BioShifts database. Preliminary results show a high degree of match, especially for vertebrate groups. Finalizing the trait compilation will open the door for a large project of synthesis regarding the traits-range shifts relationships. This could be done by implementing the conceptual framework developed in **Comte et al. 2024**, to uncover the mechanistic bases for responses at leading and trailing edges and range centroids. We are also planning to examine how range shifts may differ for species of importance to human society (e.g., ecosystem engineers, species that interact with humans, species of conservation concern) and how species redistribution can impact ecosystem functions and services.

  One of the former participants of BIOSHIFTS (I-Ching Chen) is the organizer of the conference *Species on The Move*, that will take place in April 2026 in Taiwan. That would be the opportunity for our group to organize a workshop to demonstrate the utility of the BioShifts database and associated R package, thus increasing the awareness and utilization of the data.

  In connection with the BIOSHIFTS group, we benefited extra funding from a SYNERGIE grant, also funded by the FRB, on the influence of human pressures on the speed and direction of forest plant species redistribution along mountain slopes within the French mountains (FRAGSHIFTS). This project, albeit officially finished since February 2025, is still ongoing with preliminary analyses showing a significant acceleration of the velocity at which 100 understory forest plant species have shifted their elevational distribution upslope, switching from an average velocity of 1.13 m/yr ($p < 0.05$) over the period 1905-2005 to an average velocity of 3.82 m/yr ($p < 0.05$) over the period 2005-2022, which corresponds to an increase of +2.69 m/yr ($p < 0.05$) over the last two decades. At the moment, one Master Student (Sarah Orth, ENS Lyon) is doing a 6-months internship in Toulouse (from March until August 2025), under the supervision of one the BIOSHIFTS member (Romain Bertrand), to confirm the results of this preliminary analysis with the aim to write a research article. We can also report that Sarah Orth received a PhD grant from the ENS Lyon to start a PhD, in October 2025, under the supervision of Romain Bertrand, Jonathan Lenoir & Gaël Grenouillet, to work on the BioShifts database to investigate the link between species range shifts and biotic interactions. During her PhD, Sarah will work in close collaboration with all the members of the BIOSHIFTS group.

VII Next steps – the legacy of the CESAB project

We have submitted three project proposals to pursue the activities of the working group, with over one third of the extended group being new members who bring new expertise in ecosystem services, quantitative analysis, and conservation policy. However, two of the proposals haven't been selected for funding (sDiv and Powell Center); the results for the NCEAS working group proposal are still pending.

The postdoctoral researcher affiliated with the project, Brunno Oliveira, is actively prospecting for another full-time position but is currently unemployed (contracting work part time). Since the end of the project, he got interviewed for two Assistant Professor positions in Brazil and applied to several post-doctoral positions, with no success so far. He has other targets in mind in the coming months, both post-doctoral and Assistant Professor positions. We have been doing our best lately to push two of the ongoing projects towards paper submission, one is now submitted and under review in PNAS and the second one is nearly ready for submission to Ecology Letters, with Brunno Oliveira as the first and lead author on both papers, which should help him boost his CV for future applications.

VIII CESAB AFTER

We are interested by the organization of a CESABAFTER meeting, more specifically to implement the traits-based framework discussed above and set the bases for an analysis looking at the effects of species redistribution on ecosystem services. This would be particulalry interesting to add an extra meeting in Montpellier for our working group if we receive a positive response from the NCEAS, especially as half of the BIOSHIFTS members are located in Europe. We would be happy to discuss this potential funding mechanism if our proposal gets selected. We are also willing to present our work during a full day of conference, either in person at CESAB or remotely during a CESABINAR, or even in hybrid format if technically possible.

IX Comments on the execution of the project

Overall, we feel that the activities of the working group have been broadly consistent with the objectives described in the original proposal, despite a few difficulties encountered, that led to modifications of some of the original sub-objectives (detailed below).

First, the project relied on the BioShifts database, a database of range shifts compiled from the scientific literature. We had planned to update a previous version of the database (Comte et al. 2020) at the beginning of the project as part of an ongoing collaboration with a team of researchers from the U.S. Geological Survey (USGS) Climate Adaptation Science Center (CASC) who developed a similar database: the CoRE database (Rubenstein et al. 2024). This task was planned to take 4 months prior to our first in-person meeting by merging the two databases. However, we rapidly realized that there were many mismatches in terms of the information available in the two different databases (rates of species range shift and methodological variables). We subsequently formed a data management task force to systematically check the information from the two databases and harmonize the methodological variables (Lise Comte, Brunno Oliveira, Jake A. Lawlor, Yi-Wen Chen, Jessica Krippel, Ciara G. Johnson, Ailey Linderman, Mari Angel Rodriguez, Elly Spongdale, Sarah R. Weiskopf, Madeleine Rubenstein), a task that spanned almost the entire lifespan of the project. Although the update of the range shift database took more time and human resources than initially planned, we had been able to work on the prior version of the database to develop preliminary results and analytical pipelines. As such, this unexpected delay did not impair too much the progress on the different sub-projects but divert some attention from other data management tasks.

Second, the sub-project intended to provide a test of common modelling methods to reliably forecast species range shifts relied on the implementations of species distribution models at a fine temporal (yearly) and spatial (1 km^2 for terrestrial species; 5 km^2 for marine species) resolution for about 10,000 species at the global scale. This created technical challenges as the workflow requires large processing and storage computing capacity. Indeed, the project resulted in approximately 85 terabytes of data and required a wall time of approximately 200 days (computation time distributed across many cores in a high-performance computing facility), justifying the need for substantial computational resources. Brunno Oliveira (postdoctoral researcher on the project) had to explore several high-performance computing (HPC) options outside of the CESAB, including at the Illinois State University, University of Florida, the University of Toulouse and the University of Montpellier. Various limitations (storage capacity or restricted access) created some delays in the project until a stable solution was found at the Jules Verne University of Picardy (UPJV). Brunno created an account on the MatriCs platform hosted by UPJV. His account has been recently further extended until September 2025, in case some of the models need to be rerun. However, a more permanent solution needs to be found to store and secure the 85 terabytes of model outputs that are still sitting on a server at UPJV. The MatriCs platform at UPJV offered to keep the space open until we can transfer it to a more secure and long-term repository, such as InDoRES. We (Lise Comte and Jonathan Lenoir) have had several email exchanges and Zoom meetings with the InDoRES team to archive the data with a dedicated DOI.

Third, we reframed the focus of the work package focusing on the macroevolutionary approach to include tests of evolutionary potential using contemporary genetic diversity data, which was not part of the original proposal. Initial analyses revealed significant phylogenetic signal in species range shifts for many taxonomic groups (i.e., closely related species tended to exhibit similar responses). However, closer inspection revealed a critical complication: while the *BioShifts* database compiles many different studies that vary in methodological design to quantify range shifts, these methodological factors were not randomly distributed across phylogenies. In fact, many of these methodological covariates also exhibited phylogenetic signal (e.g., closely related species tended to have been studied using similar methods). This raised the concern that observed phylogenetic patterns in range shifts could be confounded by phylogenetically structured study bias. After extensive discussion, the group concluded that observed patterns could not be confidently interpreted as biological, given the confounding influence of methodological factors.

Fourth, the working group explored the influence of traits in various projects but without developing the synthesis framework presented in **Comte et al. 2024** due to delays in the trait compilation pipeline (as no group member had enough time to allocate on the sub-project). We are hopeful that these analyses would take place next year once we finalize the trait compilation.

Fifth, we did not explore the role of biotic constraints through additional focused case studies using detailed biotic interaction networks as first anticipated, mainly because none of the group members had shown a particular interest for that project. This said, the forthcoming PhD project of Sarah Orth, under the supervision of three of the BIOSHIFTS members (see above), will specifically focus on this topic, which will allow us to develop those ideas while keeping the BIOSHIFTS group in close contact through Sarah Orth’s PhD.

In conclusion, we enjoyed our time at the CESAB and the fantastic atmosphere and support from the CESAB staff.

Appendix S1 – Trait databases included in the trait compilation.

Trait databases (details on trait characteristics are presented in Figure S1)				
amniota	R package	R package traitdata	https://doi.org/10.1890/15-0846R.1	none
AmphiBIO	R package	R package traitdata	https://doi.org/10.1038/sdata.2017.123	none
AnAge	R package	R package traitdata	https://doi.org/10.1093/nar/gkx1042	none
AnimalTraits	csv	10.6 Mb	https://doi.org/10.1038/s41597-022-01364-9	none
aphid	csv	4.9 Mb	https://doi.org/10.1017/S0007485308005919	none
arthropodtraits	R package	R package traitdata	https://doi.org/10.1038/sdata.2015.13	none
AVONET	R package	R package traitdata	https://doi.org/10.1111/ele.13898 [in press]	none
Beerli et al. 2019	csv	< 1 Mb	https://doi.org/10.1111/jbi.13583	none
Benedetti et al. 2015	csv	< 1 Mb	https://doi.org/10.1093/plankt/fbv096	none
BIEN	R package	R package BIEN	https://doi.org/10.32614/CRAN.package.BIEN	none
bird_behav	R package	R package traitdata	http://doi.org/10.1098/rstb.2019.0012	none
BROT	R package	R package BROT	https://doi.org/10.1038/sdata.2018.135	none
BryForTrait	csv	< 1 Mb	https://onlinelibrary.wiley.com/doi/full/10.1111/jvs.12646	none
butterflytraits	csv	1.9 Mb	https://doi.org/10.1038/s41597-020-00697-7	none
carabids	R package	R package traitdata	https://doi.org/10.1111/icad.12045	none
climber	R package	R package traitdata	http://dx.doi.org/10.3897/zookeys.367.6185	none
COMBINE	csv	22.5 Mb	http://dx.doi.org/10.1002/ecy.3344	none
Comte & Olden 2017	csv	< 1 Mb	http://dx.doi.org/10.1038/nclimate3382	none
Comte & Olden 2018	csv	< 1 Mb	https://doi.org/10.1111/faf.12312	none
CONUS_freshwater	csv	261.0 Mb	https://doi.org/10.1111/geb.13257	none
Coral Species traits	csv	14.4 Mb	https://doi.org/10.1038/sdata.2016.17	none
Cueva del Castillo et al. 2011	csv	< 1 Mb	https://doi.org/10.1002/ece3.65	none
D3	csv	1.6 Mb	https://doi.org/10.1016/j.ppees.2013.02.001	none
Dahlke et al. 2020	csv	< 1 Mb	https://doi.org/10.1126/science.aaz3658	none
Di Stefano et al. 2024	csv	38.9 Mb	https://doi.org/10.17882/91148	none
DISPERSE	R package	R package traitdata	https://doi.org/10.1038/s41597-020-00732-7	none
EltonTraits	R package	R package traitdata	https://doi.org/10.1890/13-1917.1	none
ESSD - Brun 2017	csv	1.8 Mb	https://doi.org/10.5194/essd-9-99-2017	none

Fishbase*	R package	R package rfishbase	https://docs.ropensci.org/rfishbase/	none
FISHLIFE	R package	R package FishLife	https://doi.org/10.1111/2041-210X.14076	none
fishmorph	R package	R package traitdata	https://doi.org/10.1111/geb.13395	none
GARD	csv	4.9 Mb	https://doi.org/10.1111/geb.12491	none
Feldman et al. 2015	csv	2.1 Mb	https://doi.org/10.1111/geb.12398	none
Novosolov et al. 2017	csv	< 1 Mb	https://doi.org/10.1111/geb.12617	none
Meiri et al. 2020	csv	4.9 Mb	https://doi.org/10.1111/geb.13124	none
lizard_traits - Meiri et al. 2018	R package	R package traitdata	https://doi.org/10.1111/geb.12773	none
Gillepsie et al. 2017	csv	< 1 Mb	https://dx.doi.org/10.1002%2Fece3.2732	none
Ginther et al. 2022**	csv	9.8 Mb	https://doi.org/10.5061/dryad.2547d7wts	none
GLAD[GlobalAnts]	csv	3.1 Mb	https://doi.org/10.1111/icad.12211	none
GlobTherm	R package	R package traitdata	https://doi.org/10.5061/dryad.1cv08	none
Gossner et al. 2015	csv	< 1 Mb	https://doi.org/10.1038/sdata.2015.13	none
Haarstad et al. 2018	csv	< 1 Mb	https://doi.org/10.6073/pasta/b08092e42516f07fe8f17a1054eba989	none
Heinen et al. 2017	csv	< 1 Mb	https://doi.org/10.1111/ecog.03462	none
heteroptera	R package	R package traitdata	https://dx.doi.org/10.1890/14-2159.1	none
Horne et al. 2017	csv	2.3 Mb	https://doi.org/10.1111/1365-2435.13031	none
Javois et al. 2019	csv	< 1 Mb	https://doi.org/10.1111/jeb.13422	none
Jenkins et al. 2007	csv	< 1 Mb	https://doi.org/10.1111/j.1466-8238.2007.00312.x	none
Landcaster & Humphreys 2020	csv	< 1 Mb	https://doi.org/10.1073/pnas.1918162117	none
LEDA	R package	R package leda	https://doi.org/10.1111/j.1365-2745.2008.01430.x	none
LepTraits 1.0	csv	58.9 Mb	https://doi.org/10.1038/s41597-022-01473-5	none
AvianBodySize - Lislevand et al 2007	R package	R package traitdata	https://esajournals.onlinelibrary.wiley.com/doi/abs/10.1890/06-2054	none
Lososova et al. 2023	csv	1.9 Mb	https://onlinelibrary.wiley.com/doi/10.1111/geb.13712	none
mammalDIET2	R package	R package traitdata	https://doi.org/10.1002/ece3.1136	none
Marine Species Traits	API	-	http://www.marinespecies.org/traits	none
marsupials - Fisher et al. (2001)	R package	R package traitdata	https://doi.org/10.2307/2680170	none
Mobility_BioShifts	csv	< 1 Mb	Oliveira et al. in prep	internal dataset, t yet published
Neff et al. 2020	csv	< 1 Mb	https://doi.org/10.1002/eap.2133	none

OPDB	csv	1.7 Mb	https://doi.org/10.1038/s41597-019-0318-9	none
Pacifici et al. 2014	csv	< 1 Mb	https://doi.org/10.3897/natureconservation.5.5734	none
PalmTraits	csv	10.0 Mb	https://doi.org/10.10...38/s41597-019-0189-0	none
PanTHERIA	R package	R package traitdata	https://doi.org/10.1890/08-1494.1	none
PHYLACINE 1.2	csv	240 Mb	https://doi.org/10.1002/ecy.2443	none
Pigot et al. 2020	csv	2.3 Mb	https://doi.org/10.1038/s41559-019-1070-4	none
Pincebourde et al. 2021	csv	< 1 Mb	https://doi.org/10.5061/dryad.4qrfj6q9c	none
Polytraits	API	-	http://biodiversitydatajournal.com/articles.php?id=1024	none
Pottier et al. 2022	csv	2.3 Mb	https://www.nature.com/articles/s41597-022-01704-9	none
reptile_lifehist	R package	R package traitdata	https://doi.org/10.3897/natureconservation.9.8908	none
ReptTraits	csv	17.7 Mb	https://doi.org/10.6084/m9.figshare.24572683	none
Rzanny and Voigt 2012	csv	< 1 Mb	https://doi.org/10.1111/j.1365-2656.2012.01951.x	none
Shanks et al. 2009	csv	< 1 Mb	https://doi.org/10.1086/BBLv216n3p373	none
Slade et al. 2013	csv	< 1 Mb	https://doi.org/10.1890/12-1366.1	none
eubirds - Storchova & Horak 2018	R package	R package traitdata	https://doi.org/10.1111/geb.12709	none
Sutherland 2000	csv	< 1 Mb	https://doi.org/10.1046/j.1365-2656.1998.00215.x	none
Tamme et al. 2014	csv	< 1 Mb	https://doi.org/10.6084/m9.figshare.c.3306522.v1	none
TetrapodTraits	csv	16.8 Mb	https://zenodo.org/records/10582070	none
amphi_lifehist - Trochet et al. 2014	R package	R package traitdata	https://doi.org/10.3897/BDJ.2.e4123	none
TRY**	csv	17.5 Gb	https://www.try-db.org/TryWeb/Home.php	none
Vergnes et al. 2012	csv	< 1 Mb	https://doi.org/10.1016/j.biocon.2011.11.002	none
Vieira et al. 2006	csv	5.6 Mb	https://pubs.usgs.gov/ds/ds187/	none
Whitmee & Orme 2013	csv	< 1 Mb	https://doi.org/10.1111/j.1365-2656.2012.02030.x	none
World Spider Trait Database	API	-	https://spidertraits.sci.muni.cz/	none

**can be used as a complement of FISHLIFE database (as needed)*

***compilation of reproductive trait databases, can be used as a complement of other databases (as needed)*

***can be used as a complement to BIEN and LEDA databases (and other more specific plant trait databases)*