

## **Beyond where species go: integrating SDMs, functional traits, and the Tree of Life to anticipate climate-driven change in ecosystem functioning**

Bruno Eleres Soares<sup>1,2\*</sup>, Romullo G. Lima<sup>1</sup>, Jessica E. Reemeyer<sup>1</sup>, Thais A. Bernos<sup>3</sup>, Christophe Brabant<sup>4</sup>, Rikki Gumbs<sup>5</sup>, Nicholas E. Mandrak<sup>6</sup>, Luciano F. A. Montag<sup>7</sup>, Carla F. Rezende<sup>8</sup>, Janaína Serrano<sup>4</sup>, Zohra Zahir<sup>9</sup>

<sup>1</sup>Institute of Environmental Change & Society, University of Regina, Regina, Canada

<sup>2</sup>Programa de Pós-Graduação em Ecologia, Universidade Federal do Rio de Janeiro, Rio de Janeiro, Brazil

<sup>3</sup>University of Vermont, Burlington, United States

<sup>4</sup>McGill University, Montréal, Canada

<sup>5</sup>Zoological Society of London, London, United Kingdom

<sup>6</sup>Department of Biological Sciences, University of Toronto Scarborough, Toronto, Canada

<sup>7</sup>Universidade Federal do Pará, Belém, Brazil

<sup>8</sup>Programa de Pós-Graduação em Ecologia e Recursos Naturais, Universidade Federal do Ceará, Fortaleza, Brazil

<sup>9</sup>University of Toronto, Toronto, Canada

\*Corresponding author: BES - [bruno.soares@uregina.ca](mailto:bruno.soares@uregina.ca)

### **Abstract**

Forecasting biodiversity under climate-change scenarios typically involves applying species distribution models (SDMs) to project shifts in the areas where abiotic conditions are suitable for a given species under future climates, often interpreted as gains or losses in species ranges. Although the impacts of species loss are often quantified using measures of functional or evolutionary irreplaceability, SDM outputs are rarely translated into changes in ecosystem functioning or evolutionary diversity. If climate change reshapes species distribution non-randomly, disproportionately affecting particular functional groups or phylogenetic lineages, the consequences might extend beyond species occurrence and result in the erosion of ecosystem services, functional redundancy, and adaptive potential. SDMs implicitly forecast changes in community composition, and such changes can be directly translated into shifts in functional and phylogenetic structure when paired with additional ecological information. We advocate linking

SDMs with functional traits and phylogenetic information to create two complementary tools that can support decision-making and policy: i) a species-level indicator summarizing the net effects of a species' distributional shift to the pool of functional and phylogenetic services; and, ii) scalable site-based indicators summarizing the net changes in the functional and phylogenetic pool. This framework supports the implementation of the Kunming–Montreal Global Biodiversity Framework (KMGBF) by linking climate-driven SDMs to changes in ecosystem functioning, resilience, and evolutionary diversity, which are the dimensions central to Targets 4, 8, and 10 of KMGBF. This approach moves from *where species go* to *what might change* in ecosystem functioning, directly supporting a climate adaptation to the global commitments of protecting nature's contributions to people and safeguarding Earth's evolutionary history, which would help bridge the gap between biodiversity policy goals and current monitoring approaches.

**Key-words:** Climate change; community reassembly; functional traits; phylogenetic diversity; ecosystem functioning.

### Highlights

- Species distribution models implicitly forecast community reassembly under climate change
- Climate-driven range shifts can erode ecosystem functioning and evolutionary history
- Connecting SDMs with traits and phylogenies can reveal non-random losses in ecosystem structure and dynamics
- We propose species- and site-level indicators directly relevant for managing ecosystem under future climates
- The framework supports monitoring and implementation of the KMGBF

## **The overlooked risk: climate change might affect how communities function**

Species distribution models (SDMs) have transformed conservation planning by projecting how climate change might affect species' ranges across space and time (Özkan Tümer et al., 2026). They have offered critical insights for planning protected areas resilient to climate change, implementing management strategies that consider species future climatic suitabilities, and identifying climate refugia and priority areas for conservation under future environmental scenarios (Eckert et al., 2023; Gumbs et al., 2023; Hannah et al., 2020). However, focusing on the potential range of species in a given area conceals a critical reality: species are not ecologically interchangeable units. If climate-driven environmental changes disproportionately shifts the range of, say, large-bodied herbivorous fishes targeted by artisanal fishery, communities may retain similar richness but lose key functions (e.g., seed dispersal, top-down control), redundancy (buffering against temporal variations), and evolutionary option value (the diversity of features and potentials encoded across branches of the Tree of Life).

Global syntheses reveal that range shifts under climate-change scenarios are largely heterogeneous and not uniformly expansions or retractions latitudinally poleward or elevationally upslope. In addition, factors beyond temperature and precipitation, including dispersal limits, land use, habitat fragmentation, and biotic interactions, affect species distributions and, consequently, the expectations under future climates (Abdel Moniem et al., 2025; Diniz et al., 2020; Medina-Madariaga et al., 2026). This heterogeneity in response to climate change implies non-random reassembly of communities that, in turn, may lead to non-random changes in trait diversity (Benone et al., 2022; Leitão et al., 2016) even in areas where species richness might seem stable.

Although numerous studies have combined species distribution models with functional traits or phylogenetic information to explore climate-driven biodiversity change, these efforts have largely focused on ecological inference within specific taxa or regions (Buisson et al., 2013; Cabral et al., 2024; Cancellario et al., 2022; Thuiller et al., 2011, 2011). Here, we synthesize these approaches into a policy-oriented framework that translates SDM-derived projections of community reassembly into species- and site-level indicators of ecosystem functioning, resilience, and evolutionary diversity. Based on previous advances, we expect to clarify how existing tools can be consistently interpreted and applied to support conservation prioritization and monitoring under global biodiversity commitments.

## **Why distributions alone are not enough**

SDMs provide rich projections of how climate change may reorganize the presence and overlap of species across landscapes and waterscapes. These outputs are generally interpreted in a strictly spatial sense, in which species may gain or lose potential habitat, as often characterized by suitable abiotic variables (e.g., climate suitability). This may obfuscate deeper ecological meaning embedded in the same projections. SDMs predicting the distribution of individual species can then be assembled, or stacked, to reconstruct species that may co-occur in specific regions and thereby forecast spatiotemporal changes in community composition. Such changes can be directly translated into expected shifts in functional and phylogenetic structure when paired with additional ecological information.

Although SDMs are typically used for individual species, they can also be used to draw inferences about entire ecological communities. They can forecast which species are likely to co-occur in the future, which functional groups or lineages will expand or contract, and where turnover will be highest. Then, if we consider species not as interchangeable units but as carriers of functional roles and branches of the Tree of Life, we can reinterpret SDM outputs to predict future ecosystem functioning, functional redundancy, and expected loss of evolutionary history. Rather than producing maps of distributional change independent of traits or phylogenetic information, the same outputs can be directly integrated with them. This results in more informative forecasting: not only where species will be, but the ecological services ecosystems will provide, and which evolutionary lineages are most at risk as communities reorganize under climate change.

## **An integrative framework**

In Figure 1, we outline a general framework that uses SDM outputs as the foundation for downstream functional and phylogenetic indicators. Note that the SDMs themselves remain unchanged and at the discretion of the user depending on their specific study cases; what changes is how we interpret the projections.

The required information for integration comes from three different sources:

- 1) SDM projections under climate scenarios (presence or abundance). When multiple SDMs are combined, they produce a community-level model often used to understand regional

species pools under climate scenarios. These outputs themselves are already an integration of multiple open-sourced information, such as distributional data, current environmental information, and future environmental projections.

- 2) Functional traits. Functional traits are individual, population, or species-specific ecological information related to how species respond to environmental variation or have direct effects on the ecosystem they inhabit (Jiang et al., 2023; Villéger et al., 2017). For example, these may include, the role of birds and fishes in seed dispersal, bioturbation by some benthic macroinvertebrates, trophic roles in a mammal community, and more. These types of data are being increasingly compiled in large databases (Brosse et al., 2021; Daché et al., 2025; Fraser, 2020). Functional traits are often important determinants of ecosystem functions and can vary across a species range, mediating species responses to changing environments (Bayliss et al., 2022).
- 3) Phylogenetic hypotheses. Evolutionary relationships within the current and projected communities allow us to calculate site-level metrics that describe the amount of divergence in evolutionary history contained in a given pool of species, and species-level metrics that describe how evolutionarily distinct a given organism is (Tucker et al., 2017). Comprehensive phylogenies are readily available for plants and vertebrate taxa, but still in construction for other taxa; evidence suggests that supertrees, where actual phylogenetic information is merged with taxonomic categories, are useful for community-level metrics (Li et al., 2019; Nakamura et al., 2021). When combined with SDM-derived projections of community composition, phylogenetic information allows the identification of areas and species whose projected climate exposure would result in disproportionate losses of evolutionary history, providing a direct basis for prioritization under conservation targets aimed at safeguarding the Tree of Life.

Integrating these three sources of information can generate conservation outputs that are complementary as species-level and site-based indicators. At the species level, SDM projections of future climatic suitability can be combined with measures of functional or evolutionary distinctiveness to identify unique species whose climate space contracts most severely and, thus, represent disproportionately large potential losses of functional or evolutionary diversity. The Zoological Society of London's EDGE of Existence Programme has combined evolutionary

distinctiveness, trait-based distinctiveness, and extinction risk, to prioritize species whose extinction would result in the greatest losses of evolutionary history for conservation action (Gumbs et al., 2023; Webster et al., 2024).

At the site-level, functional and phylogenetic diversity metrics can be calculated to summarize community structure and, consequently, axes of ecosystem structure and function under climate change. These include: community-weighted means (CWM) that track shifts in dominant traits such as trophic level, seed dispersal, and size; functional richness (FRic) that captures the volume of trait space occupied by the community and signals potential losses of functional roles; functional diversity, reflected in whether multiple species provide similar trait combinations, indicating buffering capacity against disturbances; and, phylogenetic diversity (PD) that captures the amount of evolutionary history in the pool of species. Given that SDM outputs already allow understanding of potential co-occurrence scenarios, these metrics can be easily generated at any spatial unit (from 1-km pixels to large protected areas), providing managers with locally interpretable indicators of future functional structure, ecosystem-process vulnerability, and Tree-of-Life risks directly linked to the nature's contributions to people and global conservation goals.

### **What managers can do with this knowledge**

- 1) Prioritize areas or communities for management actions: these tools can identify areas where functional diversity or PD might decline dramatically, and areas with the least net change in ecosystem functioning from present to future. Together, these outputs can inform priority areas for adaptive planning efforts and for the long-term maintenance of ecosystem functions and evolutionary diversity, respectively. For example, projecting not only the future range of invasive species, but their net effects in the functional traits related to key ecosystem services. It can also be used to locate and safeguard areas combining species, functional, and phylogenetic diversity.
- 2) Species-focused strategies: EDGE-like metrics identify species that are also functionally or phylogenetically distinct, and whose suitable climate space is projected to reduce substantially. This information is directly relevant for national Red Lists and prioritization on species-focused conservation programs. These tools can potentially

define management problems, by identifying key species that might impact ecosystem functioning given their projected distributions.

### **Anticipating how ecosystems will change**

Across terrestrial, marine, and freshwater systems, SDM projections provide an opportunity to tell us far more than where species may move: by inference, they allow us to forecast how communities are likely to reorganize, which functional roles may weaken or disappear, and which branches of the Tree of Life are most exposed to climate-driven contraction. By interpreting SDM-derived community compositions through the lenses of functional traits and phylogenetic diversity, we gain the ability to anticipate changes in ecosystem functioning, the capacity of communities to buffer species loss without major functional change, adaptive potential, and evolutionary history. The Kunming–Montreal Global Biodiversity Framework sets 23 targets to be achieved by 2030 (Convention on Biological Diversity, 2022). By integrating SDM projections with functional traits and phylogenetic information, our proposed approach enables the assessment and monitoring of climate-driven changes in ecosystem functioning, resilience, and evolutionary history. These can be central to Targets 4, 8, and 10 of the Kunming–Montreal Global Biodiversity Framework, which respectively emphasize preventing species and lineage loss, reducing climate-related impacts on biodiversity, and managing biodiversity to sustain ecosystem functions and services. By identifying where functional roles and evolutionary history are most at risk, or most likely to persist, this framework supports evidence-based prioritization of conservation actions aligned with these targets.

Examples from all ecological realms showcase the potential of such integration. In terrestrial systems, asynchronous shifts between herbivores and carnivores may destabilize food webs; in marine ecosystems, ocean warming can have synergistic effects with overfishing, directly affecting species important for fishery and ecosystem stability; and, in freshwaters, the loss of long-living, large-sized species may shift secondary productivity and food web functioning. Because SDM outputs can be combined with traits and phylogeny at any management-relevant scale, these insights have the potential to become actionable for spatial prioritization, adaptive management, and the maintenance of ecosystem functioning and resilience under climate change.

Realizing this potential requires the scientific community to focus on four priorities. First, expand the coverage of trait and phylogenetic information of species, which still exhibit knowledge shortfalls for several clades (Gonçalves-Souza et al., 2023; Nakamura et al., 2025; Soares et al., 2023). Second, tackle the geographical and taxonomic biases in the available information on species distribution (Serrano et al., 2023; Vergara-Asenjo et al., 2023), which can distort species forecasting (Van Proosdij et al., 2016; Whitford et al., 2024). Third, co-design indicators of functional and phylogenetic diversity with practitioners, ensuring outputs that fit the scales and decision windows—that is, the planning and action time horizons—used by agencies, Indigenous governments, water authorities, and protected-area planners. Finally, clearly communicate uncertainty, particularly because SDM-based projections may underestimate climate impacts when physiological constraints are ignored (Cavalcante et al., 2026) or misrepresent the pace of species redistribution (Oliveira et al., 2026), and the framework compounds these uncertainties with those arising from ecological and evolutionary information.

As conservation shifts toward maintaining ecosystem processes and safeguarding evolutionary history, integrating SDMs with available information on functional traits and the Tree of Life offers an immediately applicable pathway forward: both the tools and the data exist. What is needed now is a broadly applicable framework that recognizes that the future of biodiversity is not only about where species will go, but about what ecosystems will become as the climate reshapes the functional and evolutionary diversity on Earth.

## **Acknowledgements**

This work was supported by a Working Group Award from the Canadian Institute of Ecology and Evolution (CIEE). RGL was supported by a postdoctoral fellowship funded by the National Council for Scientific and Technological Development (CNPq, Brazil) and the Natural Sciences and Engineering Research Council of Canada (NSERC).

## **References**

Abdel Moniem, H. E., Mallon, C., Allen, B., Littlefair, C., Leston, L., Azeria, E., Petty, A., & Pendlebury, D. (2025). Thresholding species distribution models: Simple approaches for land-use planning in multifunctional landscapes. *Methods in Ecology and Evolution*, 2041-210x.70226. <https://doi.org/10.1111/2041-210x.70226>

Bayliss, S. L. J., Mueller, L. O., Ware, I. M., Schweitzer, J. A., & Bailey, J. K. (2022). Stacked distribution models predict climate-driven loss of variation in leaf phenology at continental scales. *Communications Biology*, 5(1), 1213. <https://doi.org/10.1038/s42003-022-04131-z>

Benone, N. L., Soares, B. E., Lobato, C. M. C., Seabra, L. B., Bauman, D., & De Assis Montag, L. F. (2022). How modified landscapes filter rare species and modulate the regional pool of ecological traits? *Hydrobiologia*, 849(20), 4499–4514. <https://doi.org/10.1007/s10750-020-04405-9>

Brosse, S., Charpin, N., Su, G., Toussaint, A., Herrera-R, G. A., Tedesco, P. A., & Villéger, S. (2021). FISHMORPH: A global database on morphological traits of freshwater fishes. *Global Ecology and Biogeography*, 30(12), 2330–2336. <https://doi.org/10.1111/geb.13395>

Buisson, L., Grenouillet, G., Villéger, S., Canal, J., & Laffaille, P. (2013). Toward a loss of functional diversity in stream fish assemblages under climate change. *Global Change Biology*, 19(2), 387–400. <https://doi.org/10.1111/gcb.12056>

Cabral, H., Piatti, L., & Santana, D. (2024). Impacts of climate change in taxonomic, phylogenetic and functional diversity in snakes in largest dry forest ecoregion, the Gran Chaco. *Journal of Arid Environments*, 224, 105214. <https://doi.org/10.1016/j.jaridenv.2024.105214>

Cancellario, T., Miranda, R., Baquero, E., Fontaneto, D., Martínez, A., & Mammola, S. (2022). Climate change will redefine taxonomic, functional, and phylogenetic diversity of Odonata in space and time. *Npj Biodiversity*, 1(1), 1. <https://doi.org/10.1038/s44185-022-00001-3>

Cavalcante, V. H. G. L., Caetano, G. H. O., Godinho, L. B., Sinervo, B. R., Miles, D. B., & Colli, G. R. (2026). Ecophysiological constraints outperform environmental predictors in forecasting climate-driven extinction risk of a Cerrado endemic lizard. *Frontiers in Amphibian and Reptile Science*, 4, 1762750. <https://doi.org/10.3389/famrs.2026.1762750>

Convention on Biological Diversity. (2022). *Kunming-Montreal Global Biodiversity Framework: Decision/adopted by the Conference of the Parties to the Convention on Biological Diversity*. (CBD/COP/DEC/15/4).

Daché, E., Zeppilli, D., Sarrazin, J., Singh, R., Baldrighi, E., Miljutin, D., & Boyé, A. (2025). MarNemaFunDiv: A first comprehensive dataset of functional traits for marine nematodes. *Scientific Data*, *12*(1), 752. <https://doi.org/10.1038/s41597-025-05105-6>

Diniz, M. F., Cushman, S. A., Machado, R. B., & De Marco Júnior, P. (2020). Landscape connectivity modeling from the perspective of animal dispersal. *Landscape Ecology*, *35*(1), 41–58. <https://doi.org/10.1007/s10980-019-00935-3>

Eckert, I., Brown, A., Caron, D., Riva, F., & Pollock, L. J. (2023). 30×30 biodiversity gains rely on national coordination. *Nature Communications*, *14*(1), 7113. <https://doi.org/10.1038/s41467-023-42737-x>

Fraser, L. H. (2020). TRY—A plant trait database of databases. *Global Change Biology*, *26*(1), 189–190. <https://doi.org/10.1111/gcb.14869>

Gonçalves-Souza, T., Chaves, L. S., Boldorini, G. X., Ferreira, N., Gusmão, R. A. F., Perônico, P. B., Sanders, N. J., & Teresa, F. B. (2023). Bringing light onto the Raunkiaeran shortfall: A comprehensive review of traits used in functional animal ecology. *Ecology and Evolution*, *13*(4), e10016. <https://doi.org/10.1002/ece3.10016>

Gumbs, R., Gray, C. L., Böhm, M., Burfield, I. J., Couchman, O. R., Faith, D. P., Forest, F., Hoffmann, M., Isaac, N. J. B., Jetz, W., Mace, G. M., Mooers, A. O., Safi, K., Scott, O., Steel, M., Tucker, C. M., Pearse, W. D., Owen, N. R., & Rosindell, J. (2023). The EDGE2 protocol: Advancing the prioritisation of Evolutionarily Distinct and Globally Endangered species for practical conservation action. *PLOS Biology*, *21*(2), e3001991. <https://doi.org/10.1371/journal.pbio.3001991>

Hannah, L., Roehrdanz, P. R., Marquet, P. A., Enquist, B. J., Midgley, G., Foden, W., Lovett, J. C., Corlett, R. T., Corcoran, D., Butchart, S. H. M., Boyle, B., Feng, X., Maitner, B., Fajardo, J., McGill, B. J., Merow, C., Morueta-Holme, N., Newman, E. A., Park, D. S., ... Svenning, J. (2020). 30% land conservation and climate action reduces tropical extinction risk by more than 50%. *Ecography*, *43*(7), 943–953. <https://doi.org/10.1111/ecog.05166>

Jiang, S., Zhang, J., Tang, Y., Li, Z., Liu, H., Wang, L., Wu, Y., & Liang, C. (2023). Plant functional traits and biodiversity can reveal the response of ecosystem functions to grazing. *Science of The Total Environment*, *899*, 165636. <https://doi.org/10.1016/j.scitotenv.2023.165636>

Leitão, R. P., Zuanon, J., Villéger, S., Williams, S. E., Baraloto, C., Fortunel, C., Mendonça, F. P., & Mouillot, D. (2016). Rare species contribute disproportionately to the functional structure of species assemblages. *Proceedings of the Royal Society B: Biological Sciences*, 283(1828), 20160084. <https://doi.org/10.1098/rspb.2016.0084>

Li, D., Trotta, L., Marx, H. E., Allen, J. M., Sun, M., Soltis, D. E., Soltis, P. S., Guralnick, R. P., & Baiser, B. (2019). For common community phylogenetic analyses, go ahead and use synthesis phylogenies. *Ecology*, 100(9), e02788. <https://doi.org/10.1002/ecy.2788>

Medina-Madariaga, G., He, F., Domisch, S., Wang, Y., & Jähnig, S. C. (2026). Incorporating Biotic Interactions and Dispersal Processes in Modelling Species Distributions of Freshwater Organisms: A Review. *Diversity and Distributions*, 32(3), e70163. <https://doi.org/10.1111/ddi.70163>

Nakamura, G., Corvalán, L. C. J., Paula-Souza, L. B., Frateles, L. E. F., Tavares, G. R. G., Pereira, J. C., Silva, D. O. D., Barragán-Ruiz, C., Breseghello, F. D. P., Suzigan, N. M., Targueta, C. P., Tessarolo, G., Teresa, F. B., Dias, M. S., Jardim, L., Barbosa Pinto, R., Nunes, R., Telles, M. P. D. C., & Diniz-Filho, J. A. F. (2025). Darwinian shortfall and macroecological patterns in genetic data of Tocantins-Araguaia basin fishes. *Neotropical Ichthyology*, 23(1), e240047. <https://doi.org/10.1590/1982-0224-2024-0047>

Nakamura, G., Richter, A., & Soares, B. E. (2021). FishPhyloMaker: An R package to generate phylogenies for ray-finned fishes. *Ecological Informatics*, 66, 101481. <https://doi.org/10.1016/j.ecoinf.2021.101481>

Oliveira, B. F., Bertrand, R., Pinsky, M. L., Casajus, N., Wolfe, B. W., Scheffers, B. R., Villalobos, F., Grenouillet, G., Pecl, G. T., Chen, I.-C., Baecher, J. A., Lawlor, J. A., Sunday, J., Muriene, J., Rolland, J., Thompson, L. M., Lancaster, L. T., Rubenstein, M. A., Moore, N. A., ... Comte, L. (2026). Species range shifts often speed ahead of their modeled climatic niches. *Proceedings of the National Academy of Sciences*, 123(14), e2515903123. <https://doi.org/10.1073/pnas.2515903123>

Özkan Tümer, Y., Caglayan, İ., Yeşil, A., & Iverson, L. (2026). Two decades of species distribution modeling: A systematic review of methods and applications. *Ecological Modelling*, 513, 111441. <https://doi.org/10.1016/j.ecolmodel.2025.111441>

Serrano, F. C., Vieira-Alencar, J. P. D. S., Díaz-Ricaurte, J. C., Valdujo, P. H., Martins, M., & Nogueira, C. D. C. (2023). The Wallacean Shortfall and the role of historical distribution records in the conservation assessment of an elusive Neotropical snake in a threatened landscape. *Journal for Nature Conservation*, *72*, 126350. <https://doi.org/10.1016/j.jnc.2023.126350>

Soares, B. E., Nakamura, G., Freitas, T. M. S., Richter, A., & Cadotte, M. (2023). Quantifying and overcoming Darwinian shortfalls to conserve the fish tree of life. *Biological Conservation*, *285*, 110223. <https://doi.org/10.1016/j.biocon.2023.110223>

Thuiller, W., Lavergne, S., Roquet, C., Boulangeat, I., Lafourcade, B., & Araujo, Miguel B. (2011). Consequences of climate change on the tree of life in Europe. *Nature*, *470*(7335), 531–534. <https://doi.org/10.1038/nature09705>

Tucker, C. M., Cadotte, M. W., Carvalho, S. B., Davies, T. J., Ferrier, S., Fritz, S. A., Grenyer, R., Helmus, M. R., Jin, L. S., Mooers, A. O., Pavoine, S., Purschke, O., Redding, D. W., Rosauer, D. F., Winter, M., & Mazel, F. (2017). A guide to phylogenetic metrics for conservation, community ecology and macroecology. *Biological Reviews*, *92*(2), 698–715. <https://doi.org/10.1111/brv.12252>

Van Proosdij, A. S. J., Sosef, M. S. M., Wieringa, J. J., & Raes, N. (2016). Minimum required number of specimen records to develop accurate species distribution models. *Ecography*, *39*(6), 542–552. <https://doi.org/10.1111/ecog.01509>

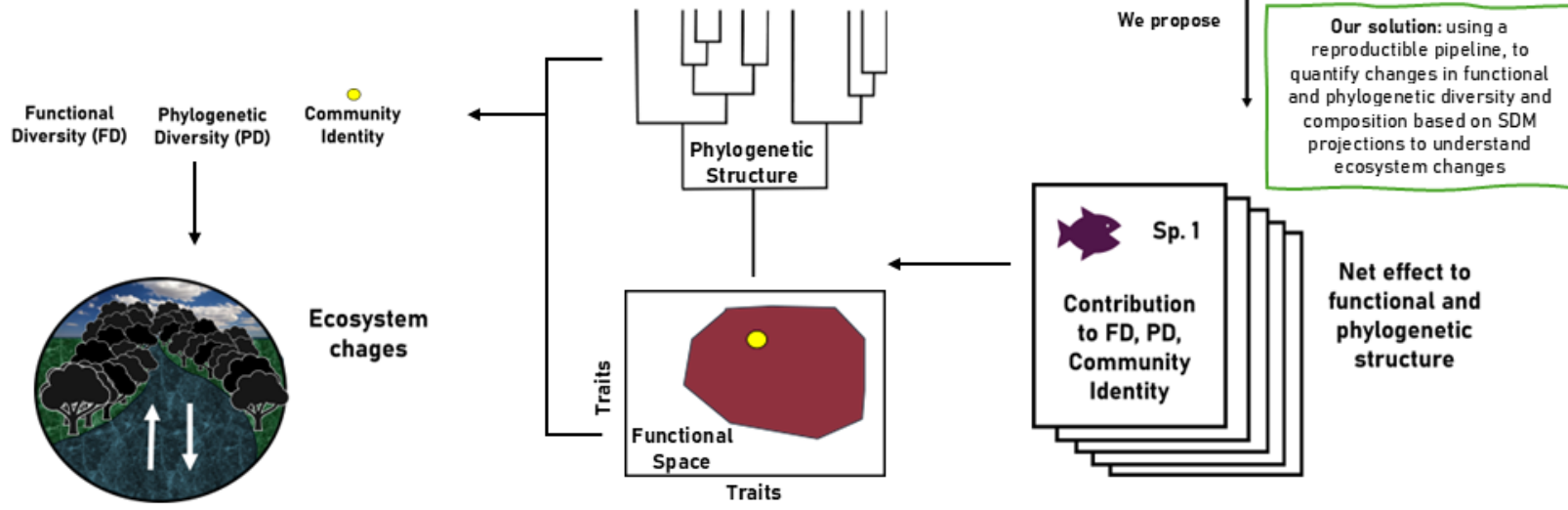
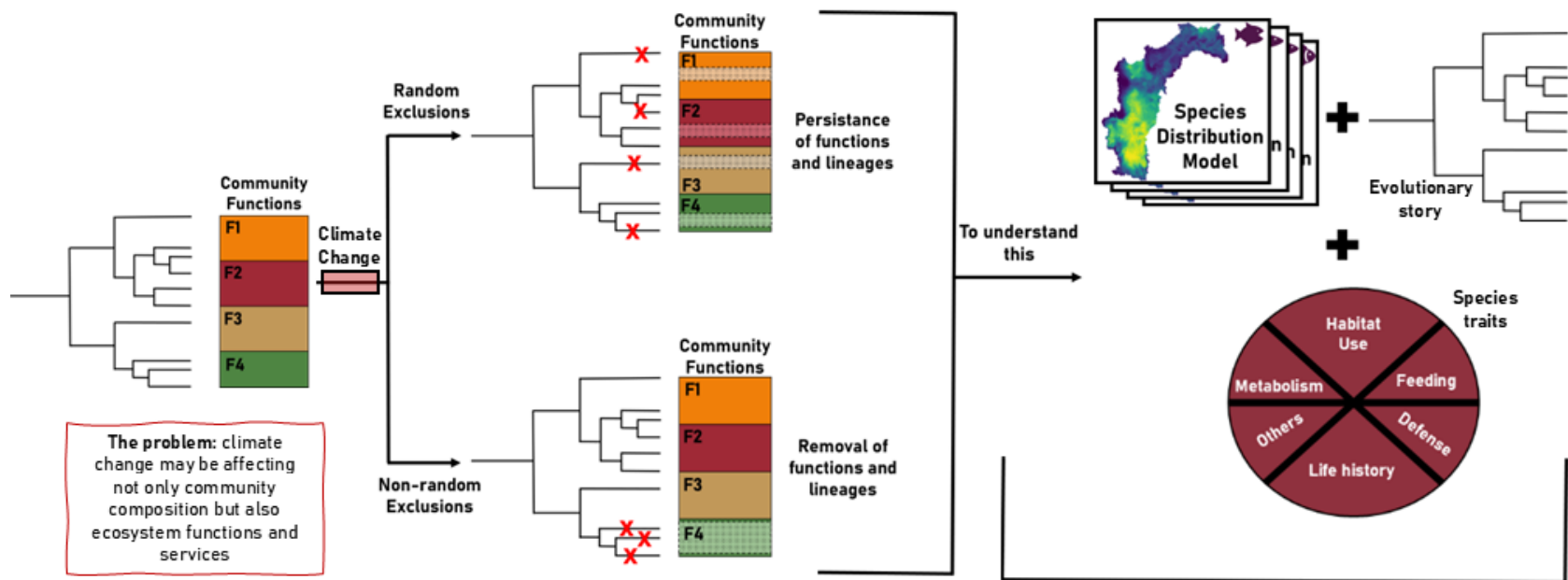
Vergara-Asenjo, G., Alfaro, F. M., & Pizarro-Araya, J. (2023). Linnean and Wallacean shortfalls in the knowledge of arthropod species in Chile: Challenges and implications for regional conservation. *Biological Conservation*, *281*, 110027. <https://doi.org/10.1016/j.biocon.2023.110027>

Villéger, S., Brosse, S., Mouchet, M., Mouillot, D., & Vanni, M. J. (2017). Functional ecology of fish: Current approaches and future challenges. *Aquatic Sciences*, *79*(4), 783–801. <https://doi.org/10.1007/s00027-017-0546-z>

Webster, C., Barker, J., Curnick, D., Gollock, M., Hansford, J., Hoffmann, M., Martin, T. E., Matthews, T. J., Pettorelli, N., Tobias, J. A., Turvey, S. T., Walkden, P. A., Wang, J., Wayman, J. P., Rosindell, J., & Gumbs, R. (2024). *A trait-based metric to prioritise the conservation of functionally irreplaceable species at risk of extinction*. *Ecology*. <https://doi.org/10.1101/2024.06.05.597292>

Whitford, A. M., Shipley, B. R., & McGuire, J. L. (2024). The influence of the number and distribution of background points in presence-background species distribution models. *Ecological Modelling*, 488, 110604.

<https://doi.org/10.1016/j.ecolmodel.2023.110604>



**Figure 1** - Framework for translating climate-driven changes in species distributions into functional and phylogenetic indicators. Species distribution models (SDMs) project changes in species occurrence or abundance under future climate scenarios, implicitly forecasting shifts in community composition. When combined with functional traits and phylogenetic relationships, these projections can be summarized using complementary indicators. Functional space and functional diversity (FD) describe the range and redundancy of trait combinations present in a community, indicating potential losses of ecological roles. Phylogenetic structure and phylogenetic diversity (PD) capture the amount and distribution of evolutionary history represented by the projected species pool. Community functional identity (represented by the yellow dot) reflects the trait centroid or community-weighted mean, indicating shifts in dominant functional strategies even when overall diversity is maintained. Together, these indicators provide distinct but complementary information on how climate-driven community reassembly may alter ecosystem functioning, resilience, and evolutionary history.