

Spatially explicit predictions of food web structure from regional level data

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Abstract: Knowledge about how ecological networks vary across global scales is currently limited given the complexity of acquiring repeated data for species interactions. Yet, recent developments of metawebs highlight efficient ways to first document possible interactions within regional species pools. Downscaling metawebs towards local network predictions is a promising approach to use current data to investigate the variation of networks across space. However, issues remain in how to represent the spatial variability and uncertainty of species interactions, especially for large scale food webs. Here, we present a probabilistic framework to downscale a metaweb based on the Canadian mammal metaweb and species occurrences from GBIF. We investigate how our approach can be used to represent the variability of networks and communities between ecoregions in Canada. Our results highlighted mismatches in the distribution of species richness and interactions, especially in their within-ecoregion variability, indicating that interactions vary differently than species distributions over continental-scale gradients. Results summarized by ecoregion showed non-constant variation within and between ecologically meaningful biogeographic boundaries and identified contrasting diversity hotspots. Our method offers the potential to bring global predictions down to a more actionable local scale, and increases the diversity of ecological networks that can be projected in space.

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1 Introduction

2 Because species interactions vary in time and space, and because species show high turnover over larger spatial
3 extents, adequately capturing the diversity of ecological networks is a challenging task (Jordano 2016). Most
4 studies on food webs have previously focused on local networks limited in size and extent, and are rarely
5 replicated in space or time (Mestre *et al.* 2022). Interactions can show important variations in space (Poisot *et*
6 *al.* 2015; Zarnetske *et al.* 2017), yet available network data also show important geographical bias by focusing
7 sampling efforts in a few areas or biomes, limiting our ability to answer questions in many biomes and over
8 broad spatial extents (Poisot *et al.* 2021). Moreover, global monitoring of biotic interactions is insufficient to
9 properly describe and understand how ecosystems are reacting to global change (Windsor *et al.* 2023).

10 Approaches to predict species interactions (Desjardins-Proulx *et al.* 2017; e.g., Morales-Castilla *et al.* 2015) are
11 increasingly used as an alternative to determine potential interactions; they can handle limited data to
12 circumvent data scarcity (Strydom *et al.* 2021), but are still rarely used to make explicitly spatial predictions.
13 As a result, there have been repeated calls for globally distributed interaction and network data coupled to
14 repeated sampling in time and space (Mestre *et al.* 2022; Windsor *et al.* 2023), which will help understand the
15 macroecological variations of food webs (Baiser *et al.* 2019).

16 Despite these limitations, food web ecologists often can infer a reasonable approximation of the network
17 existing within a region. This representation, called a metaweb, contains all possible interactions between
18 species in a given regional species pool (Dunne 2006), and provides a solid foundation to develop approaches to
19 estimate the structure of networks at finer spatial scales.

20 When assembled by integrating different data sources (and potentially with additional predictive steps), the
21 metaweb allows to overcome sampling limitations and to raise network data to a global scale. For example,
22 Albouy *et al.* (2019) coupled data on fish distributions with a statistical model of trophic interactions to provide
23 estimates of the potential food web structure at the global scale. Recent studies have focused on assembling
24 metawebs for various taxa through literature surveys and expert elicitation (European terrestrial tetrapods,
25 Maiorano *et al.* 2020) or using predictive tools (marine fishes, Albouy *et al.* 2019; Canadian mammals,
26 Strydom *et al.* 2022a). At a finer spatial scale, the local food webs (i.e. the local “realization” of the metaweb
27 when combined with species distributions, Poisot *et al.* 2012) reflect local environmental conditions but still
28 retain the signal of the metaweb to which they belong (Saravia *et al.* 2022). Given this, Strydom *et al.* (2022b)
29 defended that predicting the metaweb’s structure should be the core goal of predictive network ecology, as if

30 there is a strong link between the metaweb and its local realizations, more accurate predictions of the metaweb
31 will have the potential to bring us closer to producing accurate local (downscaled) predictions. Therefore,
32 establishing or predicting the metaweb should be the first target in systems lacking information about local
33 realizations. This is not the same as using interactions to improve predictions of species distributions, as recent
34 studies have done (Lucas *et al.* 2023; Moens *et al.* 2022; Poggiato *et al.* 2022), although these are incredibly
35 relevant and answer long-standing calls to include interactions within such models (Wisz *et al.* 2013). Instead,
36 predicting networks in space is a different task, and it serves a different goal: focusing first on the distribution of
37 network structures and its drivers rather than on the distribution of species.

38 Explicit spatial predictions (such as downscaled metaweb predictions) are essential as they will allow
39 comparisons with extant work for species-rich communities. Recent approaches to metaweb downscaling
40 combined a regional metaweb with species distribution maps to generate local assemblages for European
41 tetrapods (Braga *et al.* 2019; Galiana *et al.* 2021; Gaüzère *et al.* 2022; O'Connor *et al.* 2020), Barents Sea
42 marine taxa (Kortsch *et al.* 2019), and North Sea demersal fishes and benthic epifauna (Frelat *et al.* 2022).
43 These downscaled assemblages allowed studying network structures in novel ways, for instance, assessing
44 changes in food web structure across space (Braga *et al.* 2019), describing the scaling of network area
45 relationships (Galiana *et al.* 2021). Other examples have shown that the metaweb can be used to investigate
46 large-scale variation in food web structure, indicating high geographical connections and heterogeneous
47 robustness against species extinctions (Albouy *et al.* 2019), which are only apparent when the local and global
48 networks are both available. Further comparisons between network structure and other community properties
49 are relevant as they may highlight new and surprising elements regarding network biogeography. For instance,
50 Frelat *et al.* (2022) found a strong spatial coupling between community composition and food web structure, but
51 a temporal mismatch depending on the spatial scale. Poisot *et al.* (2017) found that interaction uniqueness
52 captures more composition variability than community uniqueness, and that sites with exceptional compositions
53 might differ for networks and communities, because species distributions and species interactions had different
54 bioclimatic drivers. Spatialized network data will allow these comparisons, identifying important conservation
55 targets for networks and whether they differ geographically from areas currently prioritized for biodiversity
56 conservation.

57 A key challenge remains in how to downscale a regional metaweb towards local network predictions that reflect
58 the spatial variability of interactions. Even when the metaweb is known, local networks may vary substantially
59 and differ both amongst themselves and from the metaweb (McLeod *et al.* 2021), emphasizing the need for

60 methods to generate local, downscaled network predictions. A potential limitation to previous downscaling
61 approaches is that they assume interactions are constant across space, which ignores well-documented
62 interaction variability, and masks the effect of environmental conditions on interaction realization (Braga *et al.*
63 2019). In contrast, recent studies argued that seeing interactions as probabilistic (rather than binary) events
64 allows us to account for their variability in space (Poisot *et al.* 2016) and that this should also be reflected at the
65 metaweb level (Strydom *et al.* 2022b). Gravel *et al.* (2019) introduced a probabilistic framework describing
66 how the metaweb can generate local realizations and showed how it could be used for modelling interaction
67 distributions. This approach to downscaling is relevant when combined with *in situ* observations of interactions
68 and local networks to train interaction models (in this case, with willow-galler-parasitoid networks). However,
69 such data is rarely available across broad spatial extents (Hortal *et al.* 2015; Poisot *et al.* 2021; Windsor *et al.*
70 2023). Spatially replicated interaction data required for such models are especially challenging to document
71 with large food web systems such as European tetrapod and Canadian mammal metawebs (Maiorano *et al.*
72 2020; Strydom *et al.* 2022a), where hundreds of species result in tens of thousands of species pairs that may
73 potentially interact. We currently lack a downscaling framework that is both probabilistic and can be trained
74 without replicated *in situ* interaction data. Additionally, a probabilistic view can allow propagating uncertainty,
75 which can play a key role in evaluating the quality of the predictions. Assessing model uncertainty would
76 enable us to determine to which degree we should trust our predictions and to identify what to do to improve the
77 current knowledge.

78 Here, we present a workflow to downscale a metaweb in space, and illustrate it by spatially reconstructing local
79 instances of a probabilistic metaweb of Canadian mammals. We do so using a probabilistic approach to both
80 species distributions and interactions in a system without spatially replicated interaction data. We then explore
81 how the spatial structure of the downscaled metaweb varies in space and how the uncertainty of interactions can
82 be made spatially explicit. We further show that the downscaled metaweb can highlight important biodiversity
83 areas and bring novel ecological insight compared to traditional community measures like species richness.

84 **Methods**

85 Fig. 1 shows a conceptual overview of the methodological workflow leading to the downscaled metaweb. Its
86 components were grouped as non-spatial and spatial data, localized site steps (divided into single-species-level,
87 two-species-level, and network-level steps), and the final downscaled and spatialized metaweb. Throughout

88 these steps, we highlight the importance of presenting the uncertainty of interactions and their distribution in
89 space. We argue that this requires adopting a probabilistic view and incorporating variation between scales.

90 [Figure 1 about here.]

91 **Data**

92 **Metaweb**

93 The main source of interaction data was the metaweb for Canadian mammals from Strydom *et al.* (2022a),
94 which is a-spatial, i.e., it represents interactions between mammals that can occur anywhere in Canada. The
95 species list for the Canadian metaweb was extracted from the International Union for the Conservation of
96 Nature (IUCN) checklist (Strydom *et al.* 2022a). Briefly, the metaweb was developed using graph embedding
97 and phylogenetic transfer learning based on the metaweb of European terrestrial mammals, which is itself based
98 on a comprehensive survey of interactions reported in the scientific literature (Maiorano *et al.* 2020). The
99 Canadian metaweb is probabilistic, which has the advantage of reflecting the likelihood of an interaction taking
100 place given the phylogenetic and trait match between two species. This allows incorporating interaction
101 variability between species (i.e., taking into account that two species may not always interact whenever or
102 wherever they occur); however, we highlight that other factors beyond trait and phylogenetic matching (e.g.,
103 population densities) will also contribute to observed interaction frequencies.

104 **Species occurrences**

105 The downscaling of the metaweb involved combining it with species occurrence and environmental data. First,
106 we extracted species occurrences from the Global Biodiversity Information Facility (GBIF; www.gbif.org) for
107 the Canadian mammals after reconciling species names between the Canadian metaweb and GBIF using the
108 GBIF Backbone Taxonomy (GBIF Secretariat 2021). This step removed potential duplicates by combining
109 species listed in the Canadian metaweb which were considered as a single entity by GBIF. We collected
110 occurrences for the updated species list (159 species) using the GBIF download API on October 21st 2022
111 (GBIF.org 2022). We restricted our query to occurrences with coordinates between longitudes 175°W to 45°W
112 and latitudes 10°N to 90°N. This was meant to collect training data covering a broader range than our prediction
113 target (Canada only) and include observations in similar environments. Then, since GBIF observations

114 represent presence-only data and most predictive models require absence data, we generated pseudo-absence
115 data using the surface range envelope method, which selects random non-observed sites within the spatial range
116 delimited by the presence data (Barbet-Massin *et al.* 2012).

117 **Environmental data**

118 We used species distribution models (SDMs, Guisan & Thuiller 2005) to project Canadian mammal habitat
119 suitability across the country, which we treated as information on potential distribution. For each species, we
120 related occurrences and pseudo-absences with 19 bioclimatic variables from CHELSA (Karger *et al.* 2017) and
121 12 consensus land-cover variables from EarthEnv (Tuanmu & Jetz 2014). The CHELSA bioclimatic variables
122 (*bio1-bio19*) represent various measures of temperature and precipitation (e.g., annual averages, monthly
123 maximum or minimum, seasonality) and are available for land areas across the globe. We used the most recent
124 version, the CHELSA v2.1 dataset (Karger *et al.* 2021), and subsetting it to land surfaces only using the
125 CHELSA v1.2 (Karger *et al.* 2018), which does not cover open water. The EarthEnv land-cover variables
126 represent classes such as Evergreen broadleaf trees, Cultivated and managed vegetation, Urban/Built-up, and
127 Open Water. Values range between 0 and 100 and represent the consensus prevalence of each class in
128 percentage within a pixel (hereafter called sites). We coarsened both the CHELSA and EarthEnv data from their
129 original 30 arc-second resolution to a 2.5 arc-minute one (around 4.5 km at the Equator) using GDAL
130 (GDAL/OGR contributors 2021). This resolution compromised capturing both local variations and broad-scale
131 patterns while limiting computation costs to a manageable level as memory requirements rapidly increase with
132 spatial resolution.

133 **Analyses**

134 **Species distribution models**

135 Our selection criteria for choosing an SDM algorithm was to have a method that generated probabilistic results
136 (similar to Gravel *et al.* 2019), including both a probability of occurrence for a species in a specific site and the
137 uncertainty associated with the prediction. These were crucial to obtaining a probabilistic version of the
138 metaweb as they were used to create spatial variations in the localized interaction probabilities (see next
139 section). One suitable method for this is Gradient Boosted Trees with a Gaussian maximum likelihood from the
140 `EvoTrees.jl` *Julia* package (<https://github.com/EvoVest/EvoTrees.jl>). This method returns a prediction

for every site with an average value and a standard deviation, which we used as a measure of uncertainty to build a Normal distribution for the probability of occurrence of a given species at all sites (represented as probability distributions on Fig. 1). We trained models across the extent chosen for occurrences (longitudes 175°W to 45°W and latitudes 10°N to 90°N), then predicted species distributions only for Canada. We used the 2021 Census Boundary Files from Statistics Canada (Statistics Canada 2022) to set the boundaries for our predictions, which gave us 970,698 sites in total. Performance evaluation for the single species SDMs are available on [GitHub](#).

Building site-level instances of the metaweb

The next part of the workflow was to produce local metawebs for every site (*Localized steps* box on Fig. 1). This component was divided into single-species, two-species, and network-level steps.

The single-species steps represented four possible ways to account for uncertainty in the species distributions and bring variation to the spatial metaweb. We explored four different options to select a value ($P(\text{occurrence})$; Fig. 1) from the occurrence distributions obtained in the previous steps: 1) taking the mean from the distribution as the probability of occurrence (option 1 in Fig. 1); 2) converting the mean value to a binary one using a specific threshold per species (option 2); 3) sampling a random value within the Normal distribution (option 3); or 4) converting a random value into a binary result (option 4, using a separate draw from option 3 and the same threshold as in option 2). The threshold (τ in Fig. 1) used was the value that maximized Youden's J informedness statistic (Youden 1950), the same metric used by Strydom *et al.* (2022a) at an intermediate step while building the metaweb. The four sampling options were intended to explore how uncertainty and variation in the species distributions can affect the metaweb result. We expected thresholding to have a more pronounced effect on network structure as it should reduce the number of links by removing many of the rare interactions (Poisot *et al.* 2016). On the other hand, we expected random sampling to create higher spatial heterogeneity compared to the mean probabilities, as including some extreme values should confound the potential effects of environmental gradients. We chose option 1 to present our results as it is intuitive and essentially represents the result of a probabilistic SDM (as in Gravel *et al.* 2019), but results obtained with other sampling strategies are available in Supplementary Material, Fig. S1.

Next, the two-species steps were aimed at assigning a probability of observing an interaction between two species in a given site. For each species pair, we multiplied the product of the two species' occurrence probabilities ($P(\text{co-occurrence})$; Fig. 1) (obtained using one of the sampling options above) by their interaction probability in the Canadian metaweb. For cases where species in the Canadian metaweb were considered as the

170 same species by the GBIF Backbone Taxonomy (the reconciliation step mentioned earlier), we used the highest
171 interaction probabilities involving the duplicated species.

172 The network-level steps then created the probabilistic metaweb for the site. We assembled all the local
173 interaction probabilities (from the two-species steps) into a probabilistic network (Poisot *et al.* 2016). We then
174 sampled several random network realizations to represent the potential local realization process (Poisot *et al.*
175 2015). This resulted in a distribution of localized networks, which we averaged over the number of simulations
176 to obtain a single probabilistic network for the site.

177 **Downscaled metaweb**

178 The final output of our workflow was the downscaled metaweb, which contains a localized probabilistic
179 metaweb in every site across the study area (*Outputs* box in Fig. 1). The metaweb sets an upper bound on the
180 potential interactions (Strydom *et al.* 2022b), therefore, the downscaled metaweb is a refined upper boundary at
181 the local scale that takes into account co-occurrences. It is still potential in nature and differs from a local
182 realization, from which it should have a different structure. Nonetheless, from the downscaled metaweb, we can
183 create maps of network properties (e.g. number of links, connectance) measured on the local probabilities of
184 species interactions and occurrences, and compute some traditional community-level measures such as species
185 richness. We chose to compute and display the expected number of links (measured on probabilistic networks
186 following Poisot *et al.* 2016; see Gravel *et al.* 2019 for a similar example) as its relationship with species
187 richness has been highlighted in a spatial context in recent studies (Galiana *et al.* 2021, 2022). We also
188 computed the uncertainty associated with the community and network measurements (richness variance and
189 link variance, respectively) and compared their spatial distribution (see Supplementary Material).

190 **Analyses of results by ecoregions**

191 Since both species composition and network summary values display a high spatial variation and complex
192 patterns, we simplified the representation of their distribution by grouping sites by ecoregion, as species and
193 interaction composition have been shown to differ between ecoregions across large spatial scales (Martins *et al.*
194 2022). To do so, we rasterized the Canadian subset of the global map of ecoregions from (Dinerstein *et al.*
195 2017; also used by Martins *et al.* 2022), which resulted in 44 different ecoregions. For every measure we report
196 (e.g. species richness, number of links), we calculated the median site value for each ecoregion, as a way to

197 avoid bias due to long tails in the distributions. We also measured within-ecoregion variation as the 89%
198 interquantile range of the site values in each ecoregion (threshold chosen to avoid confusion with conventional
199 significance tests; McElreath 2020).

200 **Analyses of ecological uniqueness**

201 We compared the compositional uniqueness of the networks and the communities to assess whether they
202 indicated areas of exceptional composition. We measured uniqueness using the local contributions to beta
203 diversity (LCBD, Legendre & De Cáceres 2013), which identify sites with exceptional composition by
204 quantifying how much one site contributes to the total variance in the community composition. While many
205 studies used LCBD values to evaluate uniqueness on local scales or few study sites (for example, da Silva &
206 Hernández 2014; Heino & Grönroos 2017), recent studies used the measure on predicted species compositions
207 over broad spatial extents and a large number of sites (Dansereau *et al.* 2022; Vasconcelos *et al.* 2018). LCBD
208 values can also be used to measure uniqueness for networks by computing the values over the adjacency matrix,
209 which has been shown to capture more unique sites and uniqueness variability than through species
210 composition (Poisot *et al.* 2017). Here, we measured and compared the uniqueness of our localized community
211 and network predictions. For species composition, we assembled a site-by-species community matrix with the
212 probability of occurrence at every site from the species distribution models. For network composition, we
213 assembled a site-by-interaction matrix with the localized interaction values from the spatial probabilistic
214 metaweb. We applied the Hellinger transformation on both matrices and computed the LCBD values from the
215 total variance in the matrices (Legendre & De Cáceres 2013). High LCBD values indicate a high contribution
216 to the overall variance and a unique species or interaction composition compared to other sites. Since the values
217 themselves are very low given our high number of sites (as in Dansereau *et al.* 2022), what matters primarily is
218 the magnitude of the difference between the sites. Given this, we divided values by the maximum value in each
219 matrix (species or network) and suggest that these should be viewed as relative contributions compared to the
220 highest observed contribution. As with other measures, we then summarized the local uniqueness values by
221 ecoregion by taking the median LCBD value and measuring the 89% interquantile range.

222 We used *Julia* v1.9.0 (Bezanson *et al.* 2017) to implement all our analyses. We used packages `GBIF.jl`
223 (Dansereau & Poisot 2021) to reconcile species names using the GBIF Backbone Taxonomy,
224 `SpeciesDistributionToolkit.jl` (<https://github.com/PoisotLab/SpeciesDistributionToolkit.jl>) to
225 handle raster layers, species occurrences and generate pseudoabsences, `EvoTrees.jl`

(<https://github.com/EvoVest/EvoTrees.jl>) to perform the Gradient Boosted Trees, EcologicalNetworks.jl (Poisot *et al.* 2019) to analyze network and metaweb structure, and Makie.jl (Danisch & Krumbiegel 2021) to produce figures. Our data sources (CHELSA, EarthEnv, Ecoregions) were all unprojected, and we did not use a projection in our analyses. However, we displayed the results using a Lambert conformal conic projection more appropriate for Canada using GeoMakie.jl (<https://github.com/MakieOrg/GeoMakie.jl>). All the code used to implement our analyses is archived on Zenodo (<https://doi.org/10.5281/zenodo.8350065>) and includes instructions on how to run a smaller example at a coarser resolution. Note that running our analyses at full scale is resource and memory-intensive and required the use of computer clusters provided by Calcul Québec and the Digital Research Alliance of Canada. Full-scale computations required 900 CPU core-hours and peaked at 500 GB of RAM.

Results

Our workflow allowed us to display the spatial distribution of ecoregion-level community measures (here, expected species richness) and network measures (expected number of links; Fig. 2). We highlight that the community and network-level measures presented here are not actual predictions of the measure itself (e.g., we do not present a prediction of actual species richness at each location). Instead, they are the reflection of these metrics from the localized predictions of the communities and networks obtained from the downscaling of the metaweb, then summarized for the ecoregions (using the median value). Expected ecoregion richness (Fig. 2A) and expected number of links (Fig. 2B) displayed similar distributions with a latitudinal gradient and higher values in the south. However, within-ecoregion variability was distributed differently, as some ecoregions along the coast displayed higher interquantile ranges, while ecoregions around the southern border displayed narrower ones (Fig. 2C-D). All results shown are based on the first sampling strategy (option 1) mentioned in the *Building site-level instances of the metaweb* section, where we used the mean value of the species distributions as the species occurrence probabilities (results for other sampling strategies are shown in Supplementary Material, Fig. S1). Site-level results (before summarizing by ecoregion) are also provided in Supplementary Material (Figs. S2-S5).

[Figure 2 about here.]

Direct comparison of the spatial distributions of species richness and expected number of links showed some

253 areas with mismatches, both regarding the median estimates and regarding the within-ecoregion variability
254 (Fig. 3). Median values for the ecoregions showed a similar bivariate distribution, with ecoregions in the south
255 mostly displaying high species richness and a high number of links (Fig. 3A). The northernmost ecoregions
256 (Canadian High Arctic Tundra and Davis Highlands Tundra) displayed higher richness (based on the quantile
257 rank) compared to the number of links. Inversely, ecoregions further south (Canadian Low Arctic Tundra,
258 Northern Canadian Shield Taiga, Southern Hudson Bay Taiga) ranked higher for the number of links than for
259 species richness. On the other hand, within-ecoregion variability showed different bivariate relationships and a
260 less constant latitudinal gradient (Fig. 3B). This indicates that richness and links do not co-vary completely
261 (i.e. their variability is not highly correlated) although they may show similar distributions for median values.

262 [Figure 3 about here.]

263 Our results also indicate a mismatch between the uniqueness of communities and networks (Fig. 4). Uniqueness
264 was higher mostly in the north and along the south border for communities, but only in the north for networks
265 (Fig. 4A-B). Consequently, ecoregions with both unique community composition and unique network
266 composition were mostly in the north (Fig. 4C). Meanwhile, some areas were unique for one element but not the
267 other. For instance, the New England-Acadian forests ecoregion (south-east, near 70°W and 48°N) had a highly
268 unique species composition but a more common network composition (Fig. 4C). Opposite areas with unique
269 network compositions only were observed at higher between latitudes 52°N and 70°N (Eastern Canadian Shield
270 Taiga, Northern Canadian Shield Taiga, Canadian Low Arctic Tundra). Also, network uniqueness values for
271 ecoregions spanned a narrower range between the 44 ecoregions than species LCBD values (Fig. 4D, left).
272 Within-ecoregion variation was also lower for network values with generally lower 89% interquantile ranges
273 among the site-level LCBD values (Fig. 4D, right). Moreover, mismatched sites (unique for only one element)
274 formed two distinct groups when evaluating the relationship between species richness and the number of links
275 (see Supplementary Material, Fig. S5). The areas only unique for their species composition had both a high
276 richness and number of links. On the other hand, the sites only unique for their networks had both lower
277 richness and a lower number of links, although they were not the sites with the lowest values for both.

278 [Figure 4 about here.]

279 Discussion

280 Our approach presents a way to downscale a metaweb, produce localized predictions using probabilistic
281 networks as inputs and outputs, and incorporate uncertainty, as called for by Strydom *et al.* (2022b). It gives us
282 an idea of what local metawebs or networks could look like in space, given species distributions and their
283 variability, as well as the uncertainty around species interactions. We also provide the first spatial representation
284 of the metaweb of Canadian mammals (Strydom *et al.* 2022a) and a probabilistic equivalent to how the
285 European tetrapod metaweb (Maiorano *et al.* 2020) was used to predict localized networks in Europe (Botella *et*
286 *al.* 2023; Braga *et al.* 2019; Galiana *et al.* 2021; Gaüzère *et al.* 2022; O'Connor *et al.* 2020). Therefore, our
287 approach could open similar possibilities of investigations on the variation of structure in space (Braga *et al.*
288 2019) and on the effect of land-use intensification (Botella *et al.* 2023) on North American food webs,
289 particularly Canadian mammal food webs. Other interesting research applications include assessing climate
290 change impacts on network structure (e.g., Kortsch *et al.* 2015) or investigating linkages between network
291 structure and stability (Windsor *et al.* 2023).

292 As our approach is probabilistic, it does not assume species interact whenever they co-occur and incorporates
293 variability based on environmental conditions (via projected species distributions), which could lead to different
294 results by introducing a different association between species richness and network properties. Galiana *et al.*
295 (2021) found that species richness had a large explanatory power over network properties, but mentioned this
296 could potentially be due to interactions between species being constant across space. Here, we found
297 mismatches in the distribution of species richness and interactions that were especially apparent in their
298 within-ecoregion variability (Fig. 3), highlighting that interactions might vary differently than species
299 distributions even over continental-scale gradients. Network density (links on Fig. 3A) were also lower in the
300 north, contrarily to what was observed for all European terrestrial tetrapods (Braga *et al.* 2019; Galiana *et al.*
301 2021) and for willow-galler-parasitoid networks (Gravel *et al.* 2019), where connectance was higher in northern
302 regions. Further research should investigate why these results might differ between the two continents and
303 whether it is due to the methodology, data, or biogeographical processes.

304 Our LCBD and uniqueness results highlighted that areas with unique network composition differ from sites
305 with unique species composition. In other words, the joint distribution of community and network uniqueness
306 highlights different diversity hotspots. Poisot *et al.* (2017) showed a similar result with host-parasite
307 communities of rodents and ectoparasitic fleas. Our results further show how these differences could be

distributed across ecoregions and in a broad spatial extent. Areas unique for only one element (species or network composition) differed in their combination of species richness and number of links (Supplementary Material, Fig. S5), with species-unique sites displaying high values of both measures, and network-unique sites displaying low values. Moreover, LCBD scores essentially highlight variability hotspots and are a measure of the variance of community or network structure. Here, they also serve as an inter-ecoregion variation measure, which can be compared to the within-ecoregion variation highlighted by the interquartile ranges. The narrower range of values for network LCBD values and the lower IQR values indicate that both the inter-ecoregion and within-ecoregion variation are lower for networks than for species (Fig. 4). Additionally, higher values for network LCBD also indicate that most ecoregions can hold ecologically unique sites.

When to use the workflow we presented here will depend on the availability of interaction data or existing metawebs, and on the intent to incorporate interaction variability, as well as ecoregion-level variability. In systems where *in situ* interaction and complete network data are available, the approach put forward by Gravel *et al.* (2019) achieves a similar purpose as we attempted here, but is more rigorous and allows modelling the effect of the environment on the interactions themselves. Without such data, establishing or predicting the metaweb should be the first step toward producing localized predictions (Strydom *et al.* 2022b).

Well-documented binary metawebs such as the European tetrapod metaweb could be partly combined with our approach if used with probabilistic SDMs and summarized by ecoregions (as they would only lack an initial probabilistic metaweb, but would still obtain a more probabilistic output). Our approach will essentially differ from previous attempts in how it perceives uncertainty and variability. For instance, rare interactions should not be over-represented (Poisot *et al.* 2016) and should have lesser effects over computed network measures. Furthermore, summarizing results by ecoregion allows for showing variation within and between ecologically meaningful biogeographic boundaries (Martins *et al.* 2022), which, as our results showed, is not constant across space and can help identify contrasting diversity hotspots.

The recent shift in focus towards building metawebs opens many opportunities for projections of networks in space through probabilistic downscaling, as we suggested here. Metawebs have been documented in many systems, allowing us to build new ones from predictions. How the European tetrapod metaweb (Maiorano *et al.* 2020) was used to predict the Canadian mammal metaweb (Strydom *et al.* 2022a) is one such case, but recent examples also extend to other systems. Metawebs have been compiled for many marine food webs (e.g., Barents Sea, Kortsch *et al.* 2019; North Scotia Sea, López-López *et al.* 2022; Gulf of Riga, Kortsch *et al.* 2021) and used to predict the probability of novel interactions (Arctic food web of the Barents sea, Pecuchet *et al.* 2020).

Olivier *et al.* (2019) built a temporally resolved metaweb of demersal fish and benthic epifauna but also suggested combining their approach with techniques estimating the probability of occurrence of trophic relationships to describe spatial and temporal variability more accurately. Lurgi *et al.* (2020) built a metaweb and probabilistic (occurrence-based) networks for rocky intertidal communities (and also showed that environmental factors do not affect the structure of binary and probabilistic networks in different ways). Albouy *et al.* (2019) predicted the global marine fish food web using a probabilistic model, showing the potential to describe networks across broad spatial scales. Similarly, predictive approaches are also increasingly used with other interaction types to highlight interactions hotspots on global scales (e.g. mapping geographical hotspots of predicted host-virus interactions between bats and betacoronaviruses, Becker *et al.* 2022; predicting the distribution of hidden interactions in the mammalian virome, Poisot *et al.* 2023). Our workflow offers the potential to bring these global predictions down to the local scale where they can be made more actionable, and vastly increases the diversity of ecological networks that can be projected in space.

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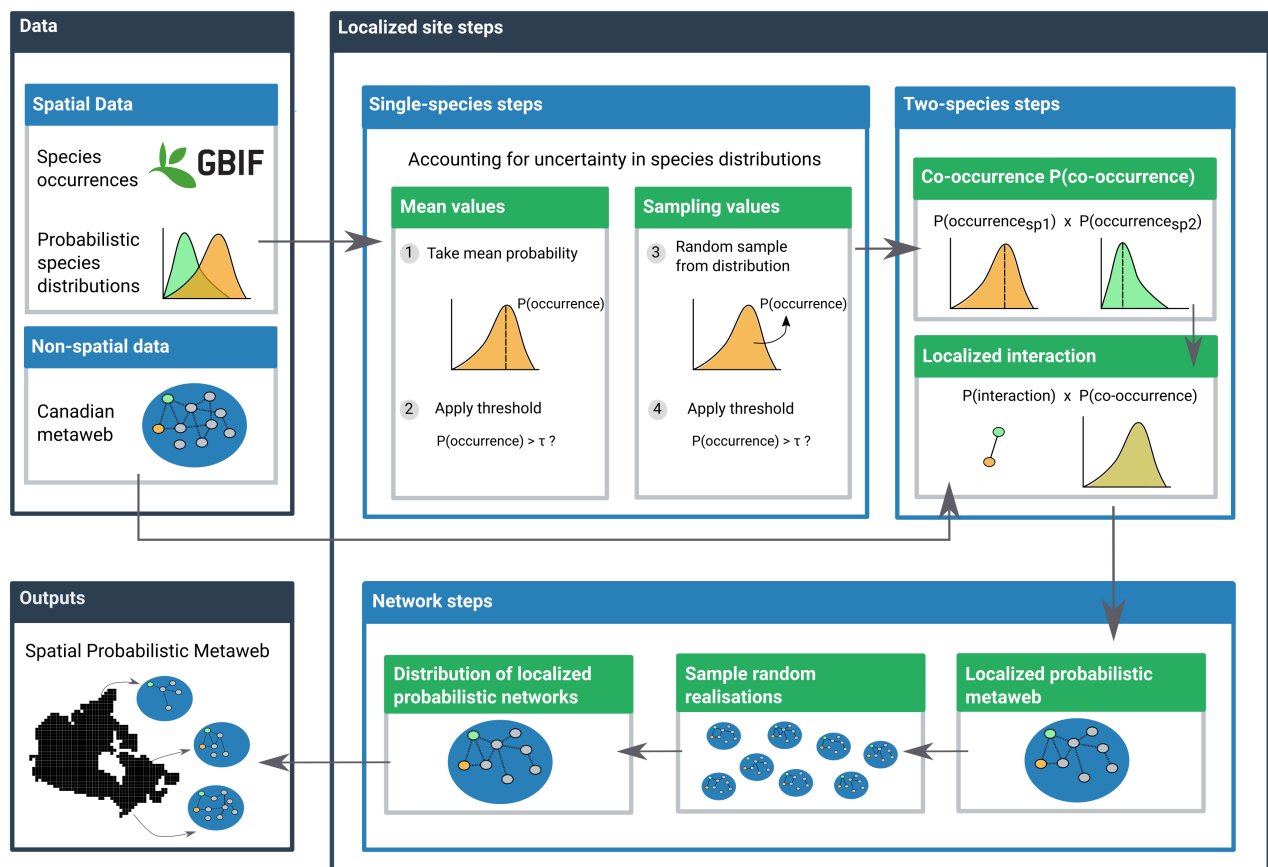


Figure 1: Conceptual figure of the proposed workflow used to downscale the probabilistic metaweb in space. The workflow has three components: the data, the localized steps, and the final spatial output. The data are composed of spatial data (with information in every cell) and non-spatial data (constant for all of Canada). The localized steps use these data and are performed separately in every cell, first at a single-species level (using distribution data), then for every species pair (adding interaction data from the metaweb), and finally at the network level by combining the results of all species pairs. The final output of the network-level steps contains a downscaled probabilistic metaweb for every cell across the study extent.

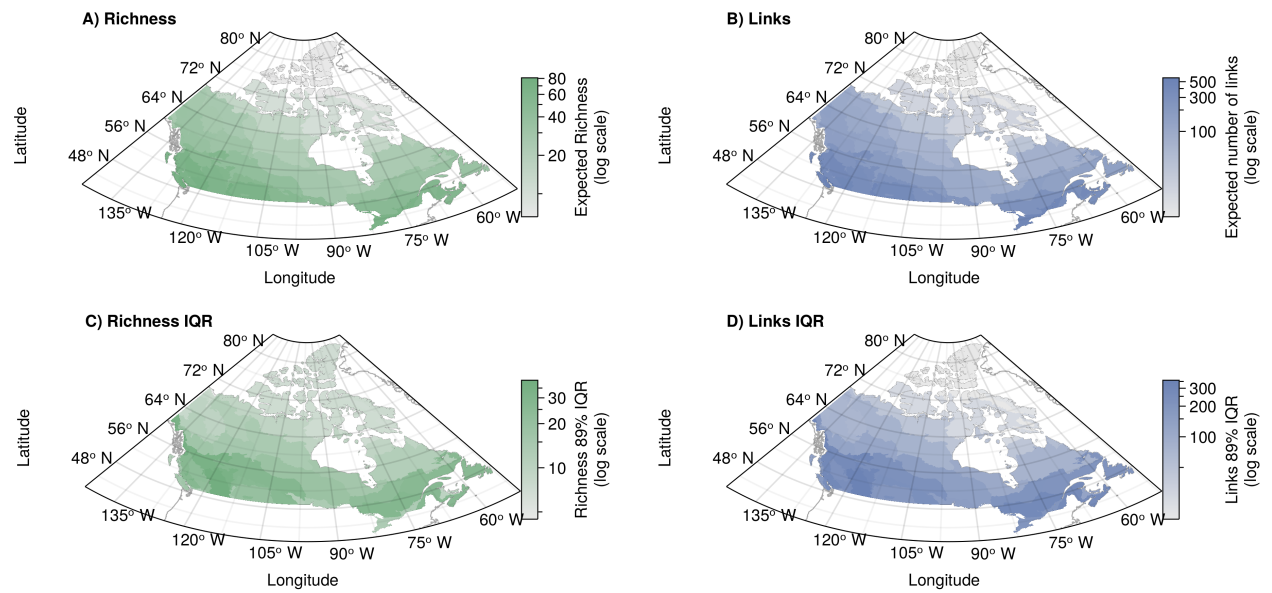


Figure 2: (A-B) Example of a community measure (A, expected species richness) and a network one (B, expected number of links). Both measures are assembled from the predicted probabilistic communities and networks, respectively. Values are first measured separately for all sites; then, the median value within each ecoregion was taken to represent the ecoregion-level value. (C-B) Representation of the 89% interquartile range of values within the ecoregion for expected richness (C) and expected number of links (D).

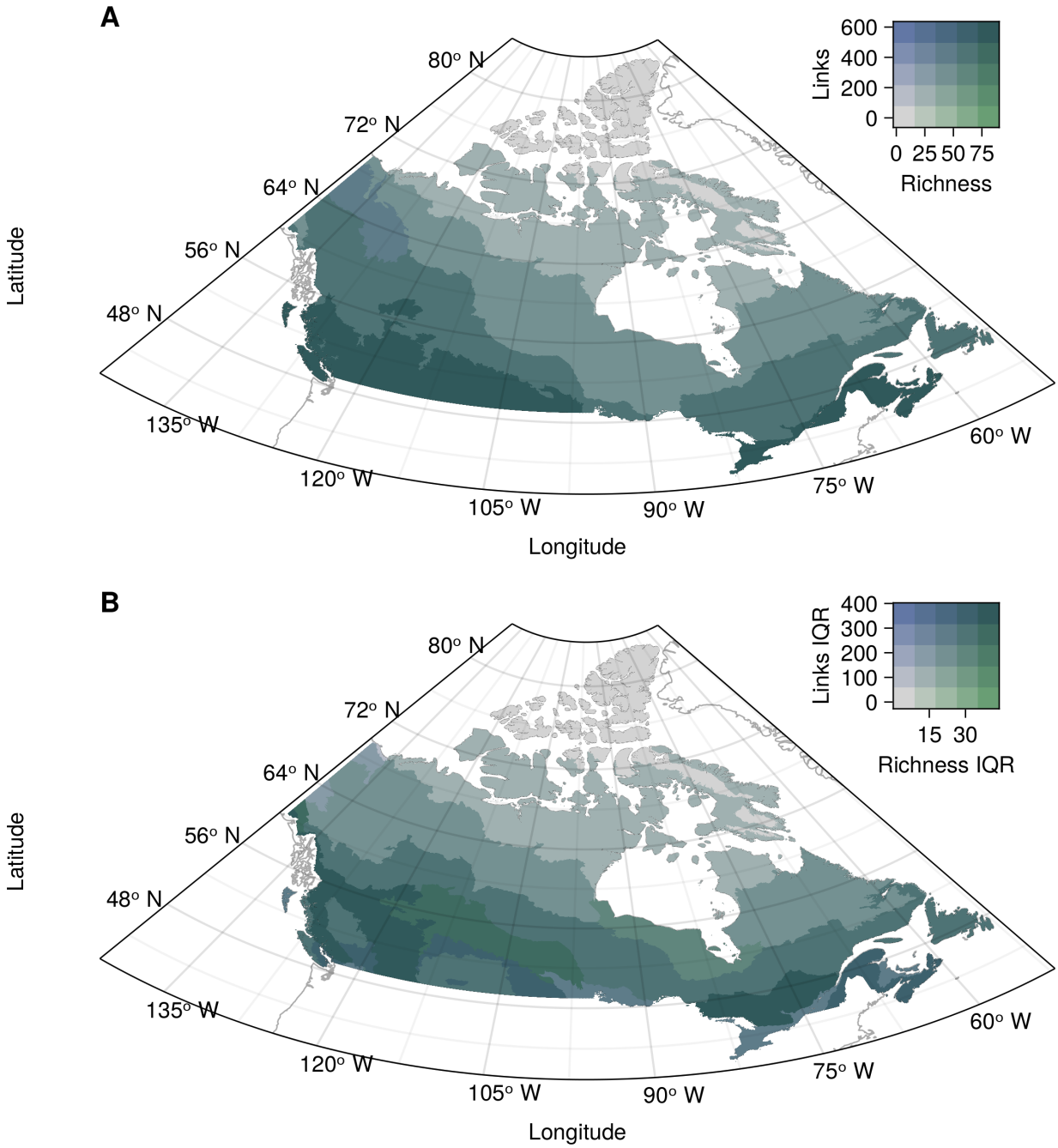


Figure 3: Bivariate relationship between community and network measures for the median ecoregion value (A) and the within-ecoregion 89% interquantile range (B). Values are grouped into three quantiles separately for each variable. The colour combinations represent the nine possible combinations of quantiles. Species richness (horizontal axis) goes left to right from low (light grey, bottom left) to high (green, bottom right). The number of links goes bottom-up from low (light grey, bottom left) to high (blue, top left).

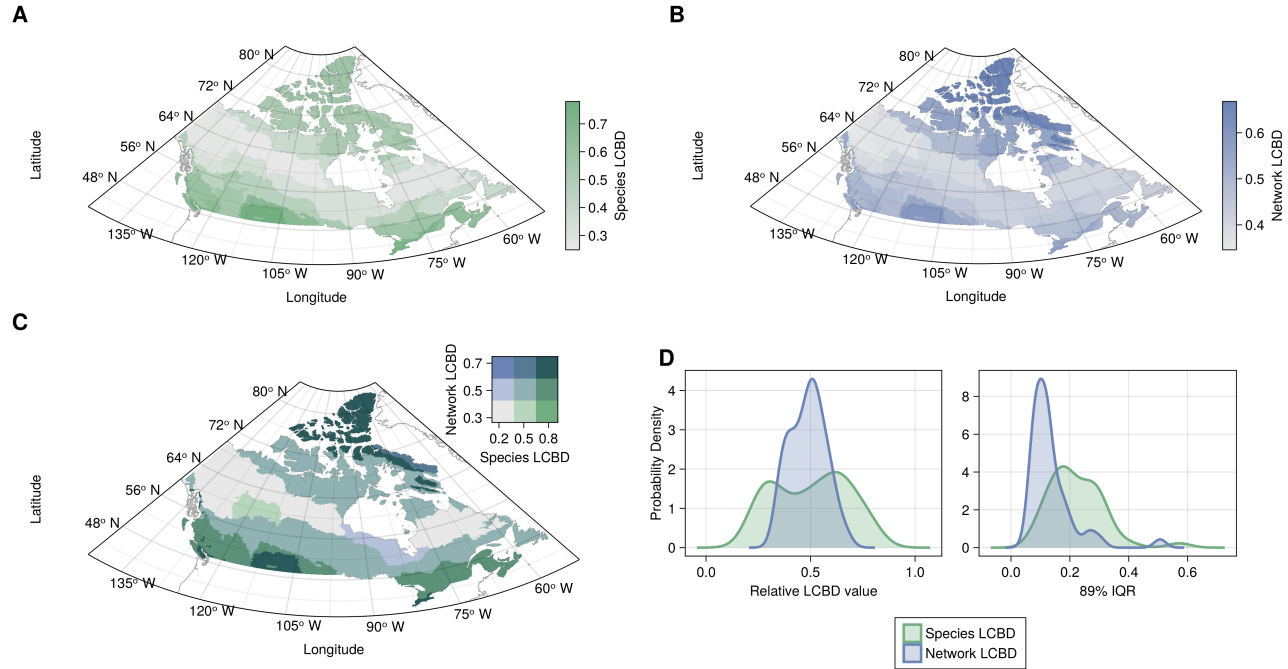


Figure 4: (A-B) Representation of the ecoregion uniqueness values based on species composition (a) and network composition (b). LCBD values were first computed across all sites and scaled relative to the maximum value observed. The ecoregion LCBD value is the median value for the sites in the ecoregion. (C) Bivariate representation of species and network composition LCBD. Values are grouped into three quantiles separately for each variable. The colour combinations represent the nine possible combinations of quantiles. The species uniqueness (horizontal axis) goes left to right from low uniqueness (light grey, bottom left) to high uniqueness (green, bottom right). The network composition uniqueness goes bottom-up from low uniqueness (light grey, bottom left) to high uniqueness (blue, top left). (D) Probability densities for the ecoregion LCBD values for species and network LCBD (left), highlighting the variability of the LCBD between ecoregions, and the 89% interquartile range of the values within each ecoregion (right), highlighting the variability within the ecoregions.