Downscaling metawebs: propagation of uncertainties in species distribution and interaction probability

Gabriel Dansereau [1,2,‡], Ceres Barros [3], Timothée Poisot [1,2,‡]

[1] Université de Montréal; [2] Québec Centre for Biodiversity Sciences; [3] University of British Columbia
[‡] Equal contributions

Correspondance to:
Gabriel Dansereau — gabriel.dansereau@umontreal.ca
Timothée Poisot — timothee.poisot@umontreal.ca

0.1. Methods Fig. **??** shows a conceptual overview of the methodological steps. The components were grouped as the inputs (spatial or non-spatial), the localized steps (divided into single-species-level, two-species-level, and network-level steps), and the final spatial output.

0.1.1 Inputs The inputs were divided into two main categories: the spatial and non-spatial ones (*Inputs* box on Fig. **??**).

The main building block for the interaction data was the metaweb for Canadian mammals from (1), a non-spatial input (represented as nodes and links on Fig. **??**). As stated above, a metaweb contains all the possible interactions between the species found in a given regional species pool (2). The species list for the Canadian metaweb was extracted from the International Union for the Conservation of Nature (IUCN) checklist (1). Briefly, the metaweb was developed using graph embedding and phylogenetic transfer learning based on the metaweb of European mammals, which is itself based on a comprehensive survey of interactions reported in the scientific literature (3). The Canadian metaweb is probabilistic, which has the advantage of taking into account that species do not necessarily interact whenever they co-occur (4). However, the Canadian metaweb is not explicitly spatial: it only gives information on interactions in Canada as a whole and does not represent networks at specific locations. Local networks, on the other hand, are realizations from the metaweb resulting from sorting the species and the interactions (5). A spatial and localized metaweb is not equivalent to the local networks, as it will have a different structure and a higher connectance (6). Therefore, producing a spatial metaweb requires additional steps to account for species composition and interaction variability in space.

The spatial data used to develop the spatial component of the metaweb were species occurrences and environmental data. First, I extracted species occurrences from the Global Biodiversity Information Facility (GBIF; www.gbif.org) for the Canadian mammals using `GBIF.jl` (7). Since GBIF observations represent presence-only data and most predictive models require absence data, I generated pseudo-absence data using the surface range envelope method available in `SimpleSDMLayers.jl` (7). This method generates pseudo-absences by selecting random non-observed locations within the spatial range delimited by the presence data (8). Then, I used environmental data and species distribution models (SDMs, 9) to predict the distribution of Canadian mammals across the whole country. The environmental data I used were the 19 standard BIO-CLIM climate variables from WorldClim 2.0 (10) and the 12 consensus land cover variables from EarthEnv (11). The climate variables represent various measures of temperature and precipitation (e.g., annual ranges, monthly maximum or minimum, seasonality) and are available for land areas across the globe. Therefore, they can be used to capture the climatic tolerance of species and model habitat suitability in new locations. The WorldClim data are available at various resolutions. I decided to use the 2.5 arcmin resolution (around 4.5 km at the Equator) as a compromise to catch potential local variations while limiting computation costs to

a manageable level. The land cover variables represent classes such as Evergreen broadleaf trees, Cultivated and managed vegetation, Urban/Built-up, and Open Water. Values range between 0 and 100 and represent the consensus prevalence of each class in percentage within a pixel at a 1-km resolution. Since this is finer than the resolution for the climate data, I coarsened the land cover ones to the same 2.5 arcmin resolution using (12).

Our selection criteria for choosing an SDM algorithm was to have a method that generated probabilistic results, including both a probability of occurrence for a species in a specific location and the uncertainty associated with the prediction. These were crucial to obtaining a probabilistic version of the metaweb as they were used to create spatial variations in the localized interaction probabilities (see next section). One promising method for this is Gradient Boosted Trees with a Gaussian maximum likelihood from the `EvoTrees.jl` *Julia* package (https://github.com/Evovest/EvoTrees.jl). This method returns a prediction for every pixel with an average value and a standard deviation, which I used as a measure of uncertainty to build a Normal distribution for the probability of occurrence of a given species at all pixels (represented as probability distributions on Fig. **??**).

0.1.2 Localized steps
The next part of the method was the localized steps which produce local metawebs in every pixel. This component was divided into single-species, two-species, and network-level steps (*Localized steps* box on Fig. **??**).

The single-species steps represented four possible ways to account for uncertainty in the species distributions and bring variation to the spatial metaweb. I explored four different options to select a value from the occurrence distributions obtained in the previous steps (Inputs section): 1) taking the mean from the distribution as the probability of occurrence (option 1 on Fig. **??**); 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); 4) converting the random value into a binary result (option 4). The threshold (τ on Fig. **??**) used was the value that maximized Youden's J informedness statistic (13), the same metric used by (1) 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 and reproduce some of the filterings that create the local network realizations (5). I 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 (14). Meanwhile, I expected random sampling to create spatial heterogeneity compared to the mean probabilities, as including some extreme values should disrupt the potential effects of environmental gradients.

Next, the two-species steps aimed to give the probability of observing a given interaction in a location. For all species pairs, I multiplied the two species' occurrence probability obtained using the sampling options described in the previous paragraph, then multiplied the co-occurrence probability by the interaction probability from the Canadian metaweb.

The network-level steps then created the probabilistic metaweb for the location. I assembled all the local interaction probabilities (from the two-species steps) into a probabilistic network (*sensu* 14). I then sampled several random network realizations to represent the potential local realization process (5). Finally, this resulted in a distribution of localized networks, which I averaged over the number of simulations to obtain a probabilistic network.

0.1.3 Outputs and additional steps
The final output of my method was the spatial probabilistic metaweb, which contains a localized probabilistic metaweb in every cell across the student extent (Outputs box on Fig. **??**). This gives us an idea of the possible networks in all locations as the metaweb essentially serves to set an upper bound on the potential interactions (6), but with the added benefit of accounting for co-occurrence probabilities in this case. From there, I can create maps of network properties (e.g. number of links, connectance) measured on the local realizations, display their spatial distribution, and compute some community-level measures such as species richness. Importantly, I can also calculate the uncertainty associated with the network and community measurements and contrast their spatial distribution. I computed uncertainty for species richness by summing the standard deviations of the species occurrence probabilities. For networks, I computed link variance based on the link probabilities according to (14). I then contrasted their spatial distributions to identify areas where their uncertainty matches. These would either indicate that we should trust the predictions (if the uncertainty is low) or need more sampling (if the uncertainty is high) to improve our current knowledge. On the other hand, identifying areas where the richness and link uncertainty do not match would also be highly informative. It could lead to targeted sampling programs for either component (community or network composition).

I compared the compositional uniqueness of the networks and the communities to verify if they indicated different exceptional areas. I measured uniqueness using the local contributions to beta diversity (LCBD, 15), which identify sites with exceptional composition by quantifying how much one site contributes to the total variance in the community composition. While many studies used LCBD values to evaluate uniqueness on local scales or few study sites (for example, 16,17), recent studies used the measure on predicted species compositions over broad spatial extents and a large number of sites (18,19). LCBD values can also be used to measure uniqueness for networks by computing the values over the adjacency matrix, which has been shown to capture more unique sites and uniqueness variability than through species composition (20). Here, I measured and compared the uniqueness of our localized community and network predictions. I was especially interested in seeing if the sites identified as unique were the same based on the species and the interactions or if this method allowed identifying areas unique for one element (interactions, for instance) but not the other. Sites with such mismatches should warrant more investigation to understand the reasons for this difference.

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