Supplementary Material

Appendix 1 to *Deciphering probabilistic species interaction networks*

Francis Banville [1,2,3]   Tanya Strydom [1,3]   Penelope S. A. Blyth [4]   Chris Brimacombe [5]   Michael Catchen [3,6]
Gabriel Dansereau [1,3]   Gracielle Higino [2]   Thomas Malpas [4]   Hana Mayall [4]   Kari Norman [1]
Dominique Gravel [2,3]   Timothée Poisot [1,3]

[1] Université de Montréal   [2] Université de Sherbrooke   [3] Quebec Centre for Biodiversity Science   [4] University of Sheffield   [5] University of Toronto   [6] McGill University

Host-parasite network data

1.1. Data description We use the collection of tripartite host-parasite networks sampled across Europe of Kopelke *et al.* (2017). This dataset contains well-resolved binary local interactions between willows (52 species), willow-galling sawflies (96 species), and their parasitoids (126 species). Out of a total of 374 local networks, we retained those containing at least 5 species, resulting in a set of 233 georeferenced local networks (networks sampled within areas of 0.1 to 0.3 km² during June and/or July spanning 29 years).

We built a metaweb of binary interactions by aggregating all local interactions, which gave us a regional network composed of 274 species and 1080 interactions.

1.2. Metawebs of probabilistic interactions We converted these binary regional interactions into probabilistic ones using simple assumptions. Our aim is not to estimate precise probability values, but to create plausible metawebs of probabilistic interactions for our illustrative examples.

We created two metawebs of probabilistic interactions by employing constant false positive and false negative rates for all regional interactions. In the first metaweb, we set both false positive and false negative rates to zero to prevent artificially inflating the total number of interactions, enabling a more accurate comparison with binary interaction networks. This gave us a probability of regional interaction of 1 when at least one interaction has been observed locally and of 0 in the absence of any observed interaction between a given pair of species. This metaweb was used in Box 2.

In the second metaweb, we introduced a 5% false positive rate to account for spurious interactions and a 10% false negative rate to address the elevated occurrence of missing interactions in ecological networks (Catchen *et al.* 2023). We believe these rates represent reasonable estimates of missing and spurious potential interactions, but confirming their accuracy is challenging due to the unavailability of data on the actual feasibility of interactions. Observed interactions were thus given a probability of regional interaction of 95%, whereas unobserved ones were assigned a probability of 10%. This metaweb was used in Boxes 3 and 5.

1.3. Local networks of probabilistic interactions We built local networks of probabilistic interactions using the taxa found in the empirical local networks and attributing pairwise interaction probabilities based on the metawebs of probabilistic interactions $P(M_{i \to j})$ and a constant value of $P(L_{i \to j}|M_{i \to j})$ across interactions:

$$P(L_{i \to j}) = P(L_{i \to j}|M_{i \to j}) \times P(M_{i \to j}).$$

We set all values of $P(L_{i \to j}|M_{i \to j})$ to 0.5, 0.75, or 1.0 depending on the simulation, as indicated in the main text. Intermediate values of $P(L_{i \to j}|M_{i \to j})$ around 50% indicate considerable spatiotemporal variability, while higher values close to 1.0 indicate that regional interactions are nearly always realized locally.

Catchen, M.D., Poisot, T., Pollock, L.J. & Gonzalez, A. (2023). The missing link: Discerning true from false negatives when sampling species interaction networks.

Kopelke, J.-P., Nyman, T., Cazelles, K., Gravel, D., Vissault, S. & Roslin, T. (2017). Food-web structure of willow-galling sawflies and their natural enemies across Europe. *Ecology*, 98, 1730–1730.