

# Supplementary ecoregion-level and site-level figures

Supplementary material to *Spatially explicit predictions of food web structure from regional level data*

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## Supplementary ecoregion-level figure

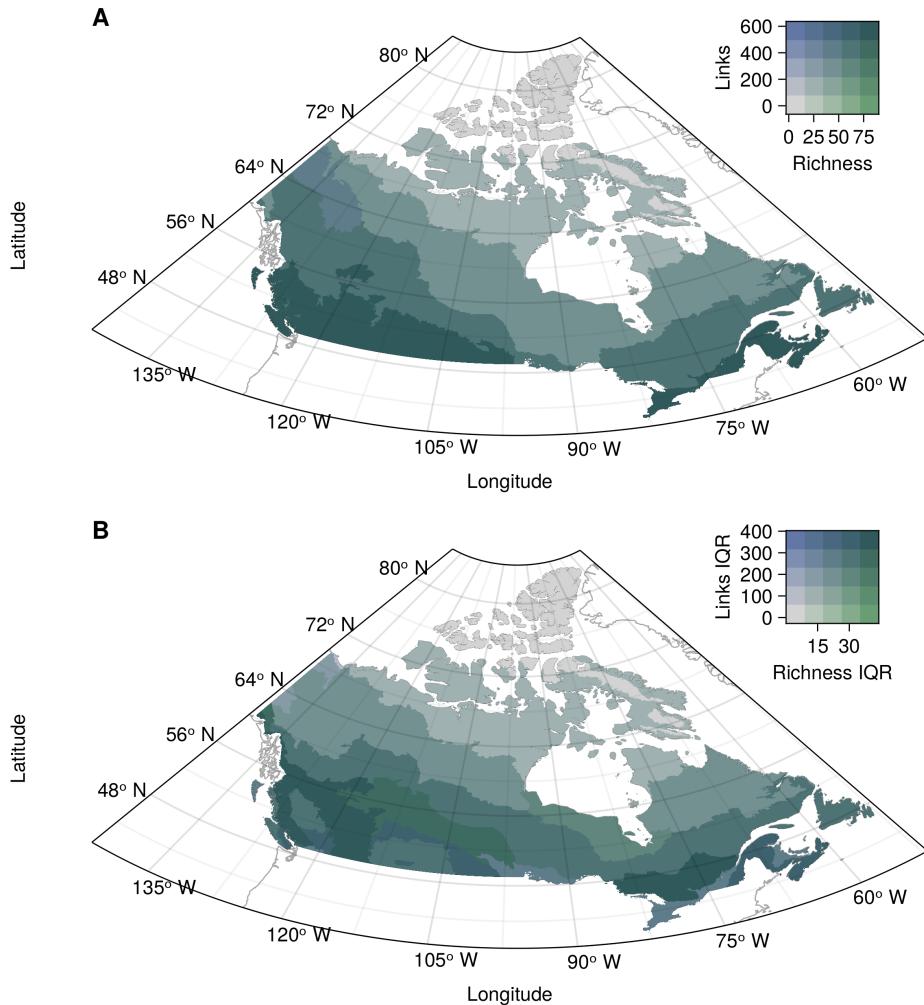


Figure S1: Bivariate relationship between community and network measures for the median ecoregion value (A) and the within-ecoregion 89% interquartile range (B). Values are grouped into five quantiles separately for each variable. The colour combinations represent the nine possible combinations of quantiles. 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).

## Supplementary site-level figures

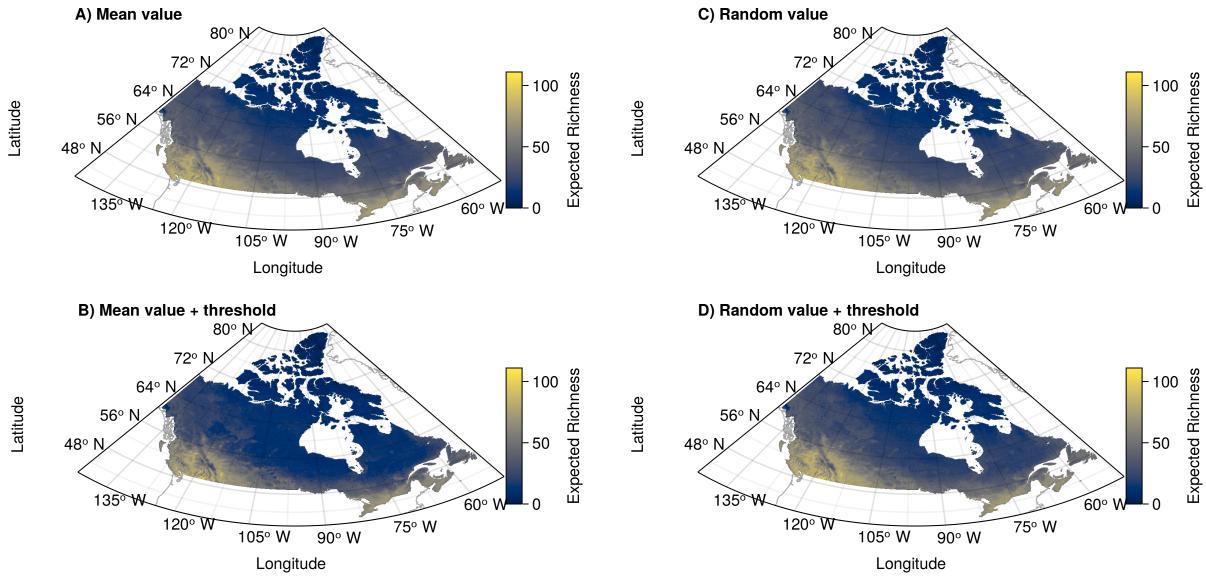
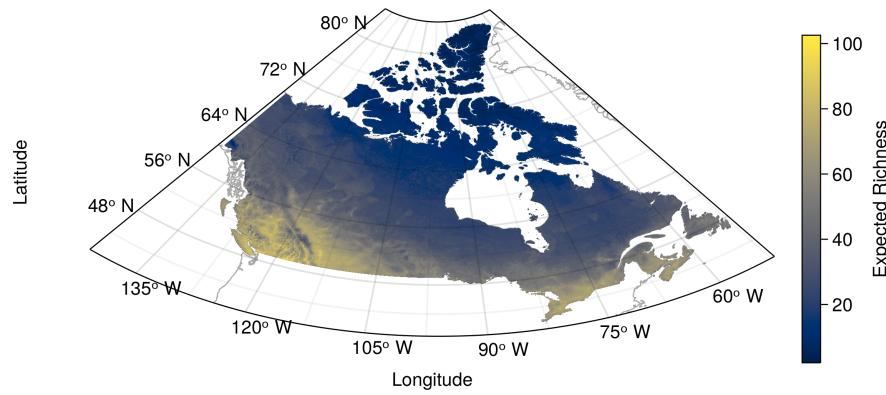
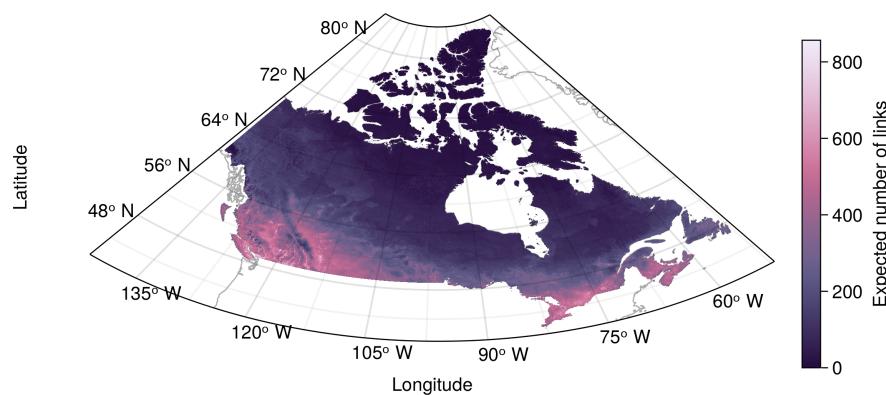


Figure S2: Illustration of the effect of changing the sampling options for the species occurrence probabilities: a) taking the mean from the distribution as the probability of occurrence; b) converting the mean value to a binary one using a specific threshold per species; c) sampling a random value within the Normal distribution; d) converting the random value into a binary result.

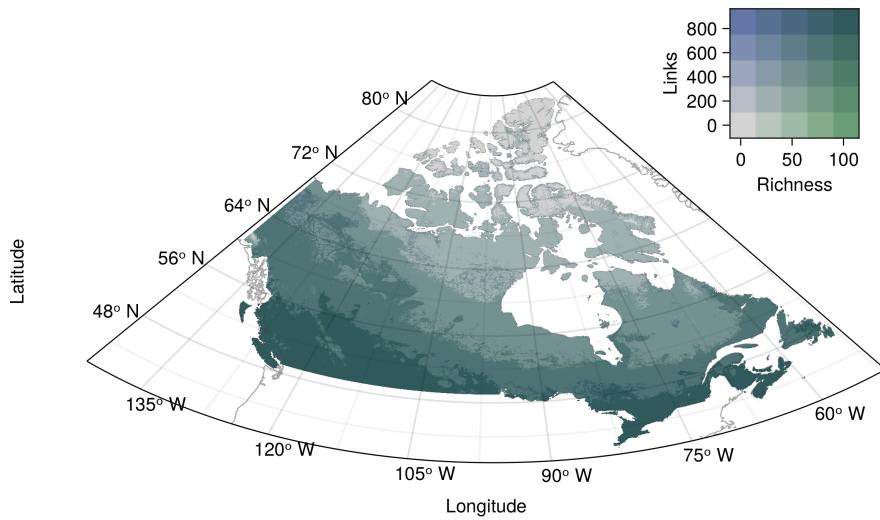


(a) Expected richness

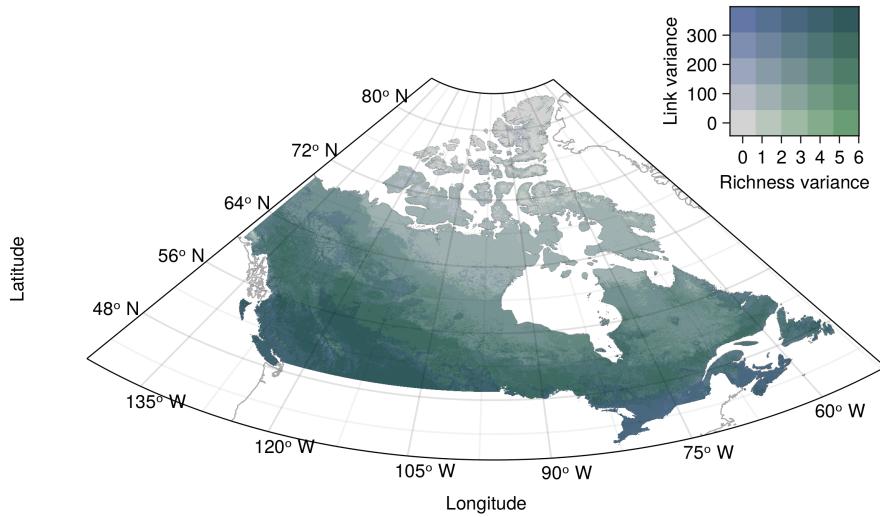


(b) Expected number of links

Figure S3: Site-level examples 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 measured separately for all sites and represented directly unlike in the main text where they are later summarized by ecoregion.



(a) Comparison of the estimates



(b) Comparison of the estimates' uncertainty

Figure S4: Bivariate representation of the estimates (a) and uncertainty (b) of species richness and the number of links. Values are grouped into five quantiles separately for each variable. The colour combinations represent the nine possible combinations of quantiles. The richness (horizontal axis) goes left to right from low richness (light grey, bottom left) to high richness (green, bottom right). The number of links goes bottom-up from low (light grey, bottom left) to high (blue, top left). Uncertainty values (b) are computed for every site as the sum of the standard deviations returned for each species by the Gradient Boosted Trees with Gaussian maximum likelihood (for richness uncertainty) and as link variance measured on the local probabilistic networks (for links uncertainty).

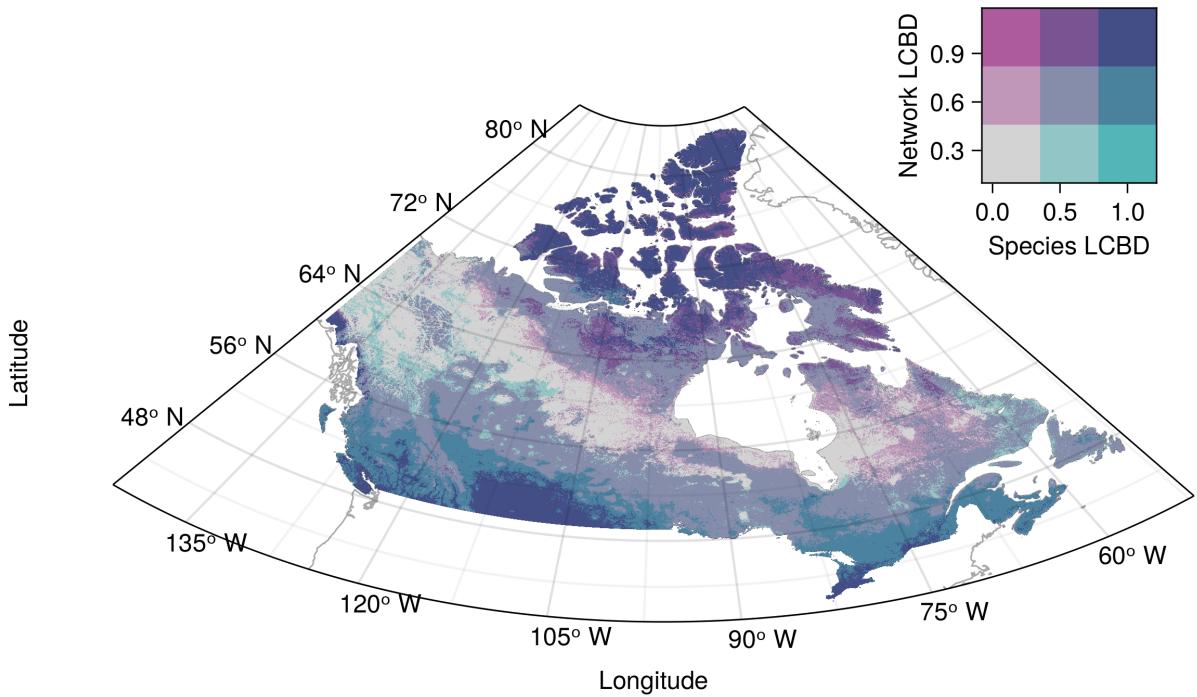
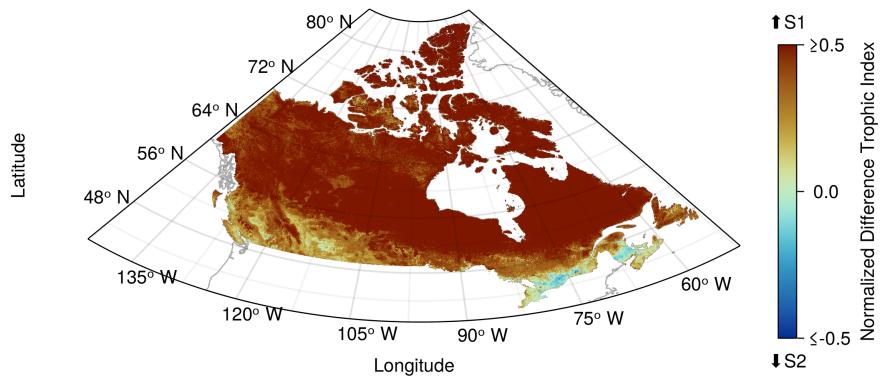
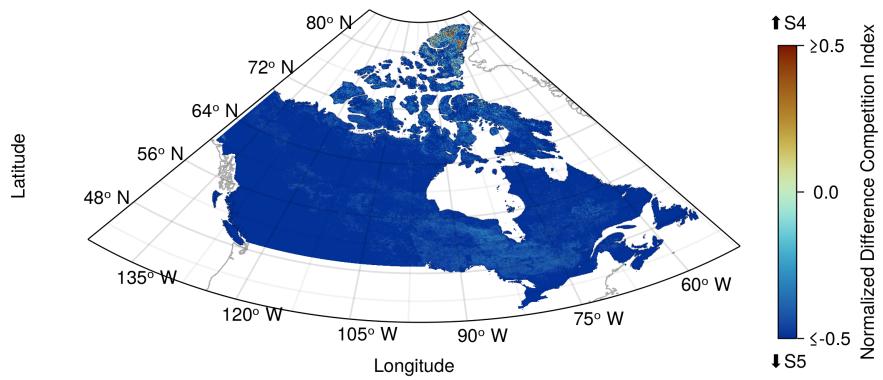


Figure S5: Bivariate representation of species and network composition uniqueness. Values are grouped into three quantiles separately for each variable. The colour combinations represent the nine possible combinations of quantiles. The species composition uniqueness (horizontal axis) goes left to right from low uniqueness (light grey, bottom left) to high uniqueness (cyan, bottom right). The network uniqueness (vertical axis) goes bottom-up from low uniqueness (light grey, bottom left) to high uniqueness (pink, top left).



(a) Normalized Difference Trophic Index (NDTI)



(b) Normalized Difference Competition Index (NDCI)

Figure S6: Comparison of the dominant ecological motifs across ecoregions. a) Normalized Difference Index (NDTI) comparing the trophic motifs S1 (tri-trophic food chains) and S2 (omnivory). Positive values indicate a dominance of S1 while negative values indicate a dominance of S2. Values equal or superior to  $|0.5|$  are shown with the same color as they indicate a high dominance of one motif. b) Normalized Difference Index (NDCI) comparing the competition motifs S4 (exploitative competition) and S5 (apparent competition). Positive values indicate a dominance of S4 while negative values indicate a dominance of S5.