

Predicting the spatial structure of St. Lawrence food webs

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Network level evaluation of St. Lawrence networks

“The goal of this document is to combine the use of joint species distribution models (JSDMs) with a machine learning algorithm built to predict biotic interactions in order to predict the spatial structure of interactions networks, effectively bringing to “fruition” the integrated niche concept with predictive tools. At the moment, there are interactions that simply do not make any sense... Like Porifera eating *Gadus morhua*”

Overview

These are essentially the kind of final results we wish to obtain for the 2nd objective of my thesis. The results presented combine the use of joint species distribution models and a biotic interactions prediction machine learning algorithm in order to predict the spatial structure of ecological networks in the St. Lawrence. At the moment, though, there are still many things that need to be finished before we are remotely close to calling these final results and discussing them from an ecological standpoint rather than a purely methodological one:

- There are multiple additional datasets to incorporate to the HMSC model and how this will be achieved is still food for thoughts!
- A new interactions catalogue that includes nutrients and detritus will need to be built to maximize results accuracy and to avoid weird predictions like “Porifera consumes *Gadus morhua*”.
 - Short term, the large groups like Porifera could be split into their constituent species in order to avoid these mistakes.
 - The same could be true for all species groups and they could be reaggregated back at the group level after interactions predictions are performed
- At the moment, I believe that interactions prediction using *iEat* over predicts the amount of links, especially in areas where there are few species. At the moment, maps of taxa richness are the exact opposite of maps for link density and connectance. I believe that the fact that we are using a KNN algorithm forces the predictions to include a minimum number of interactions for taxa, meaning that areas with lower richness will have seemingly higher rates of link. I may be wrong though and results may actually represent a true ecological fact. I need to delve deeper into the results to find out, which I haven’t had time to do.
- Use probabilities instead of binary values for both spatial occurrences and biotic interactions. Ultimately, this could allow us to obtain, for each grid cell, a matrix of length equal to the number of taxa indicating the probability of species interacting based on both interaction and co-occurrence probabilities.
 - At the moment, results from *iEat* are deterministic and obtaining probabilities would be highly valuable (recurring conversation, I haven’t had time to truly get into it)
 - Results from JSDMs are probabilistic, but I transformed them into binary occurrence probabilities using a 0.5 threshold value. This should be modified. In the meantime, we could derive taxa specific threshold values that minimize False Positive Rates and maximize True Positive Rates using ROC curves. I haven’t looked into this yet.

Spatial description of St. Lawrence ecological networks

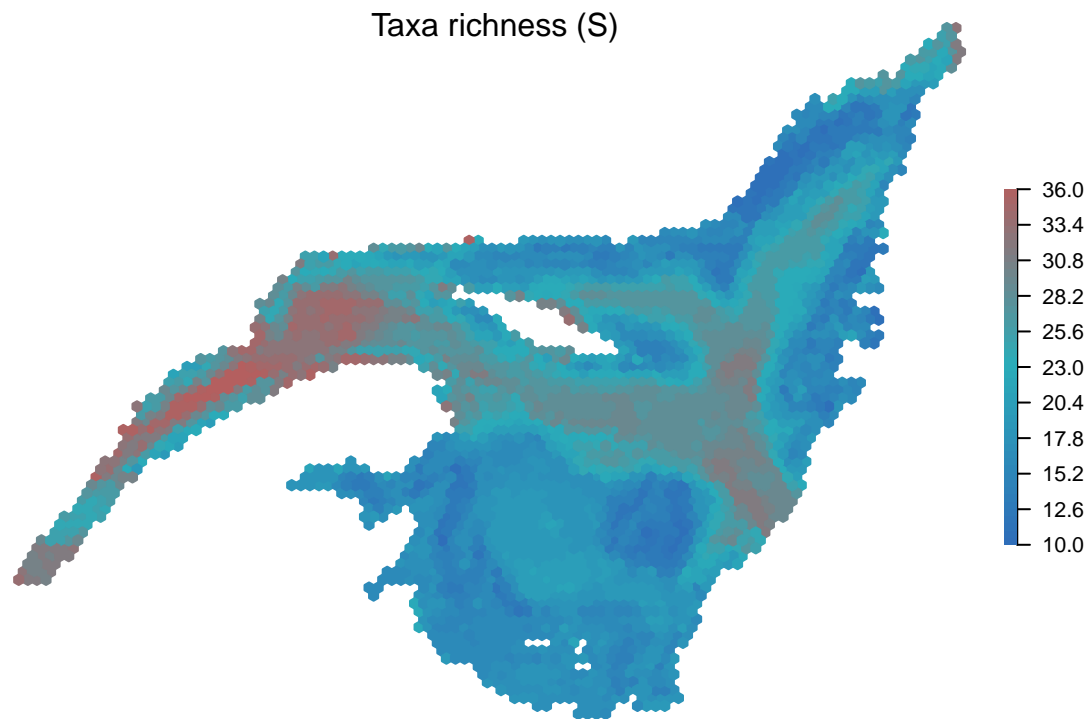


Figure 1. Taxa richness (S) evaluated using a metacommunity of 124 taxa.

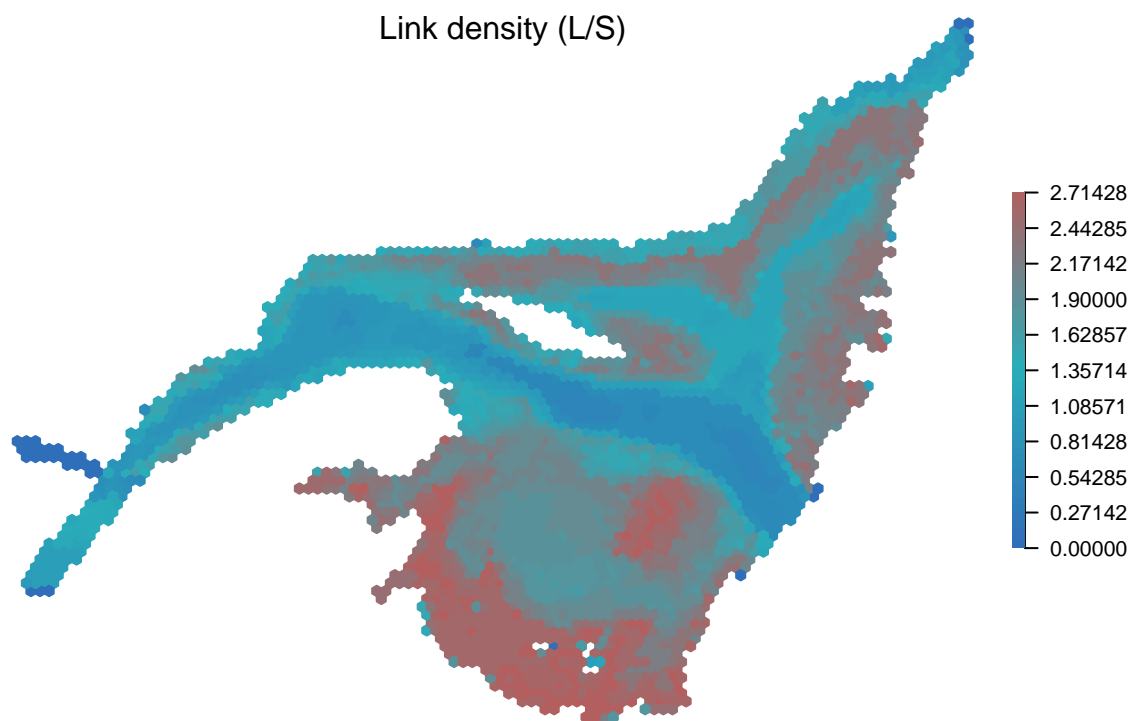


Figure 2. Predicted link density (L/S) evaluated using a metacommunity of 124 taxa.

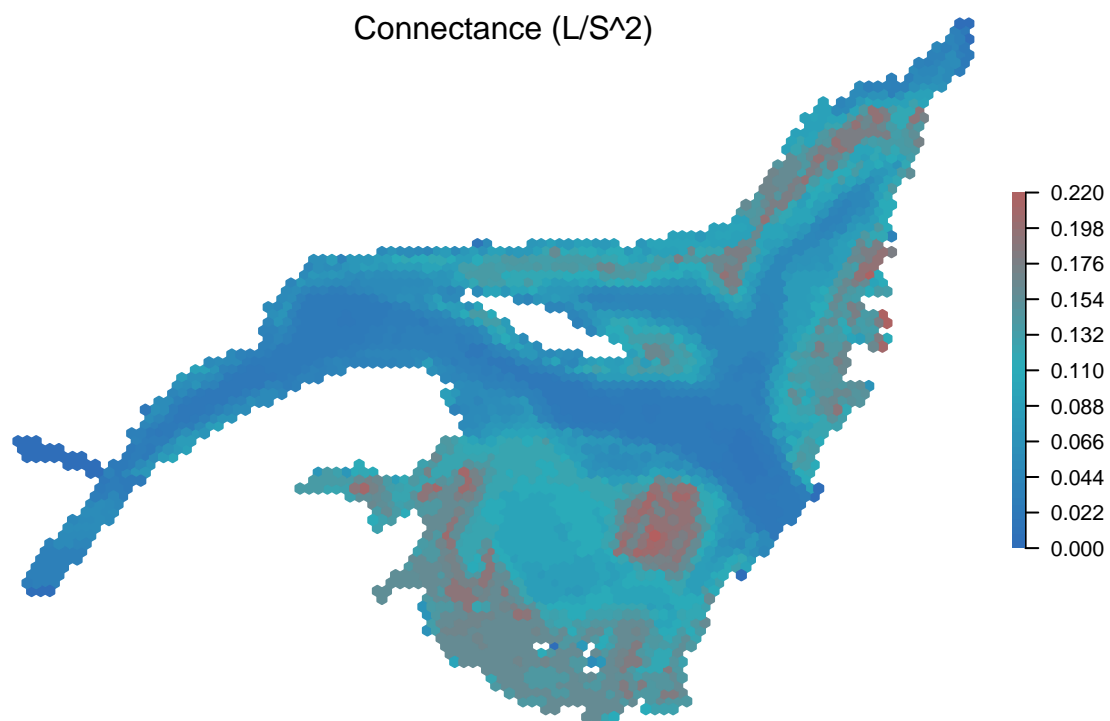


Figure 3. Predicted connectance (L/S^2) evaluated using a metacommunity of 124 taxa.