Dimensions of diversity mediated by habitat preference

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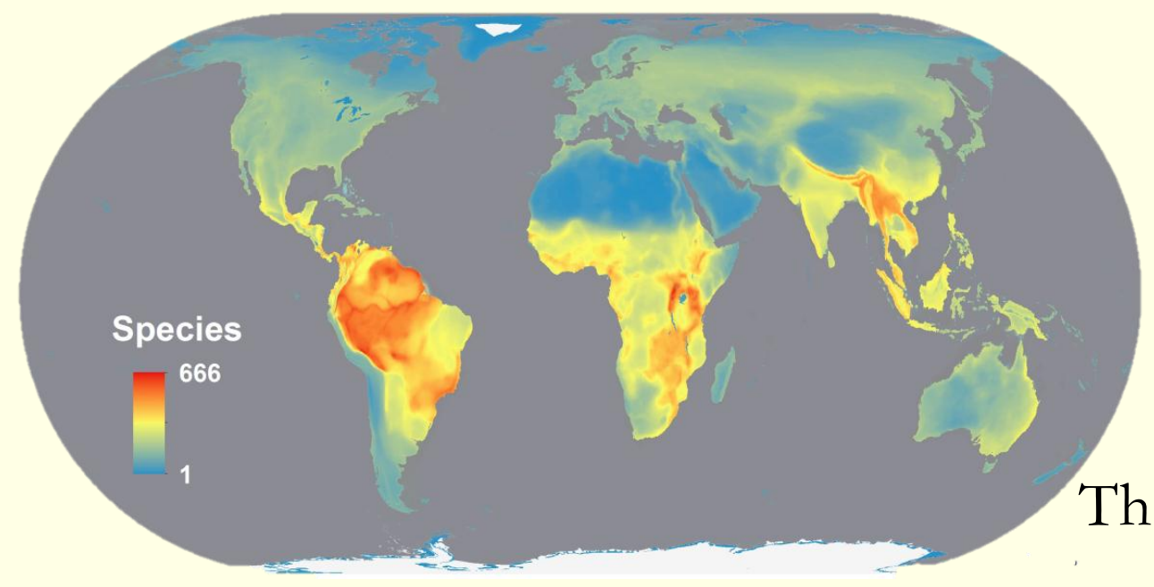
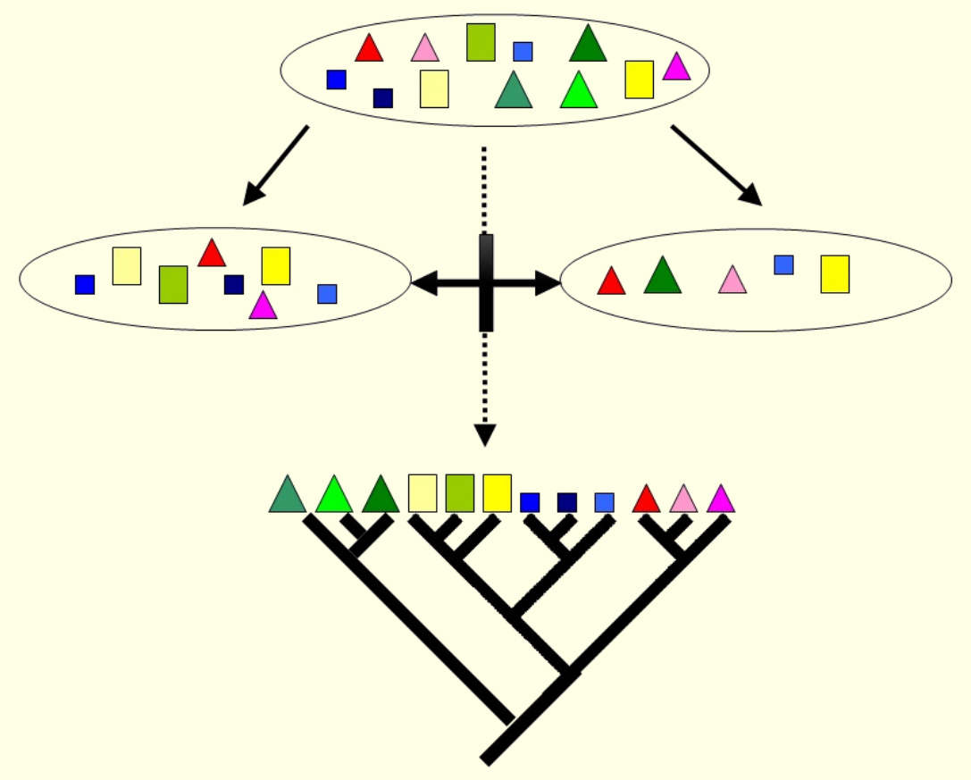
Introduction

The concept of regional community highlights how sets of populations of species are distributed across potential ecological and geographical gradients.



The distributions of 9927 bird species globally.



Neotropical regional communities harbor the highest number of species; to address the patterns of such high species richness, we examined bird diversity in three ecoregions in terms of taxonomic and phylogenetic turnover between local communities based on habitat preference of species.

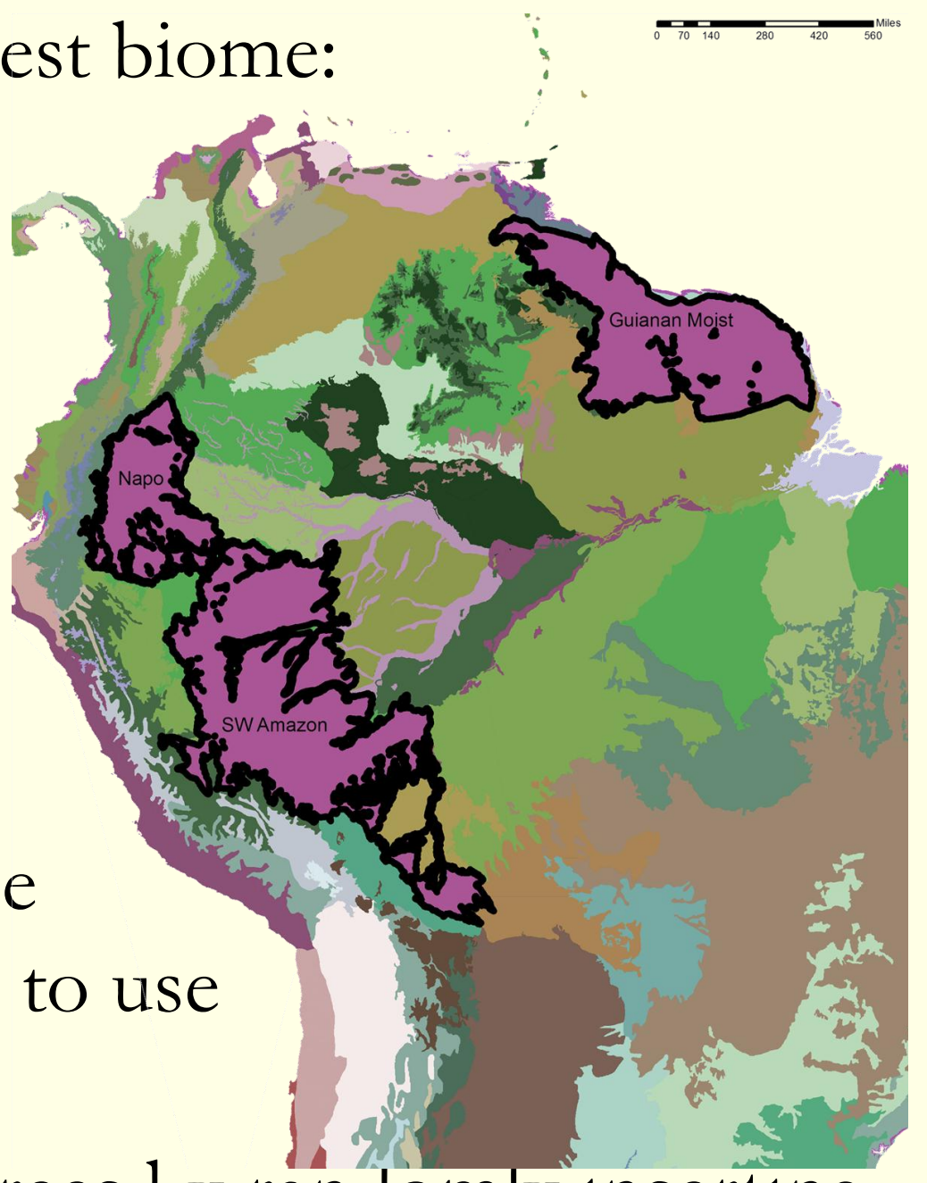
This study was framed around 4 hypotheses and specific predictions for beta-diversity (taxonomic turnover) and phylobetadiversity (turnover based on phylogenetic distance).

Hypothesis	**Beta-diversity Prediction**	**Phylobetadiversity Prediction**
Stochastic processes (drift)	Random	Random
Speciation/Biogeography	High within ecoregions High between ecoregions	Low/random within ecoregions High between ecoregions
Dispersal	Low within ecoregion High between ecoregions Low between habitats	Low within ecoregion Low between ecoregions Low between habitats
Environmental filtering	High within ecoregions High between ecoregions High between habitats	Low within ecoregions Low between ecoregions context dependent High between habitats

Methods

To create regional species pools, species lists (764 spp) were compiled for three lowland ecoregions within the tropical moist broadleaf forest biome:

- Napo Moist Forest
- Southwestern Amazonian Moist Forest
- Guianan Moist Forest



- Assembled local communities based on habitat choice (33 habitat types) based on publications(see refs).
- Compared species composition using pairwise Bray-Curtis Dissimilarity (BCD) - 10,000 replicates
- Built phylogenetic tree by pruning the Burleigh et al. tree including 641 spp (29-locus supermatrix using RAxML) to use pairwise UniFrac distance (PBD) - 1000 permutations
- Accounted for missing species, by generating 100 new trees by randomly inserting missing taxa into the ML tree.
- Analyzed the result by calculating distance matrices in R packages vegan and igraph. All statistical analyses were run within the R environment, or using custom scripts on the UF HPC cluster.

References

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Robinson, S. & Terborgh, J. (1990). Bird Communities of the Cocha Cashu Biological Station in Amazonian Peru. Four Neotropical Forests, 199-216.
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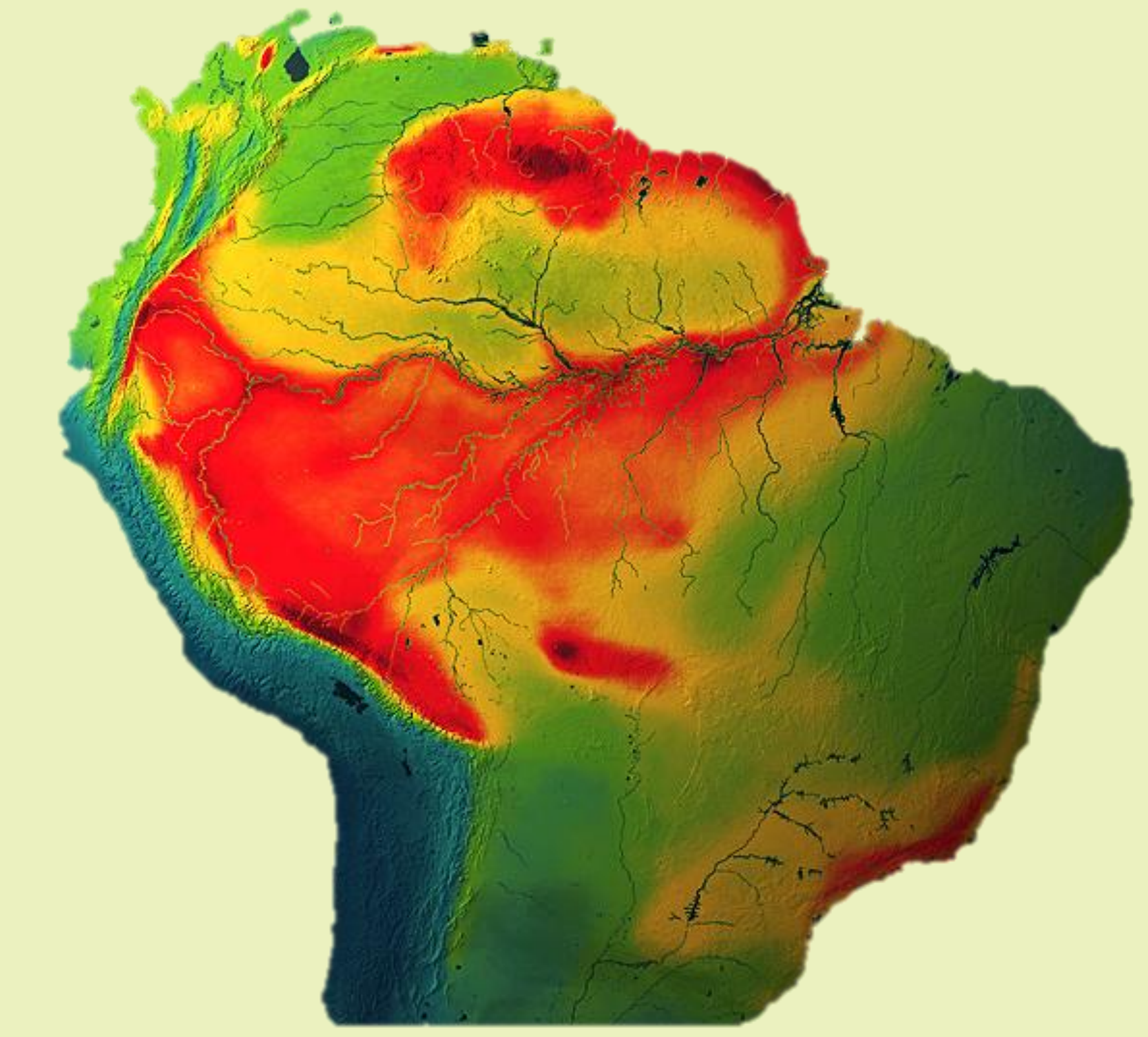
Results

Species Richness

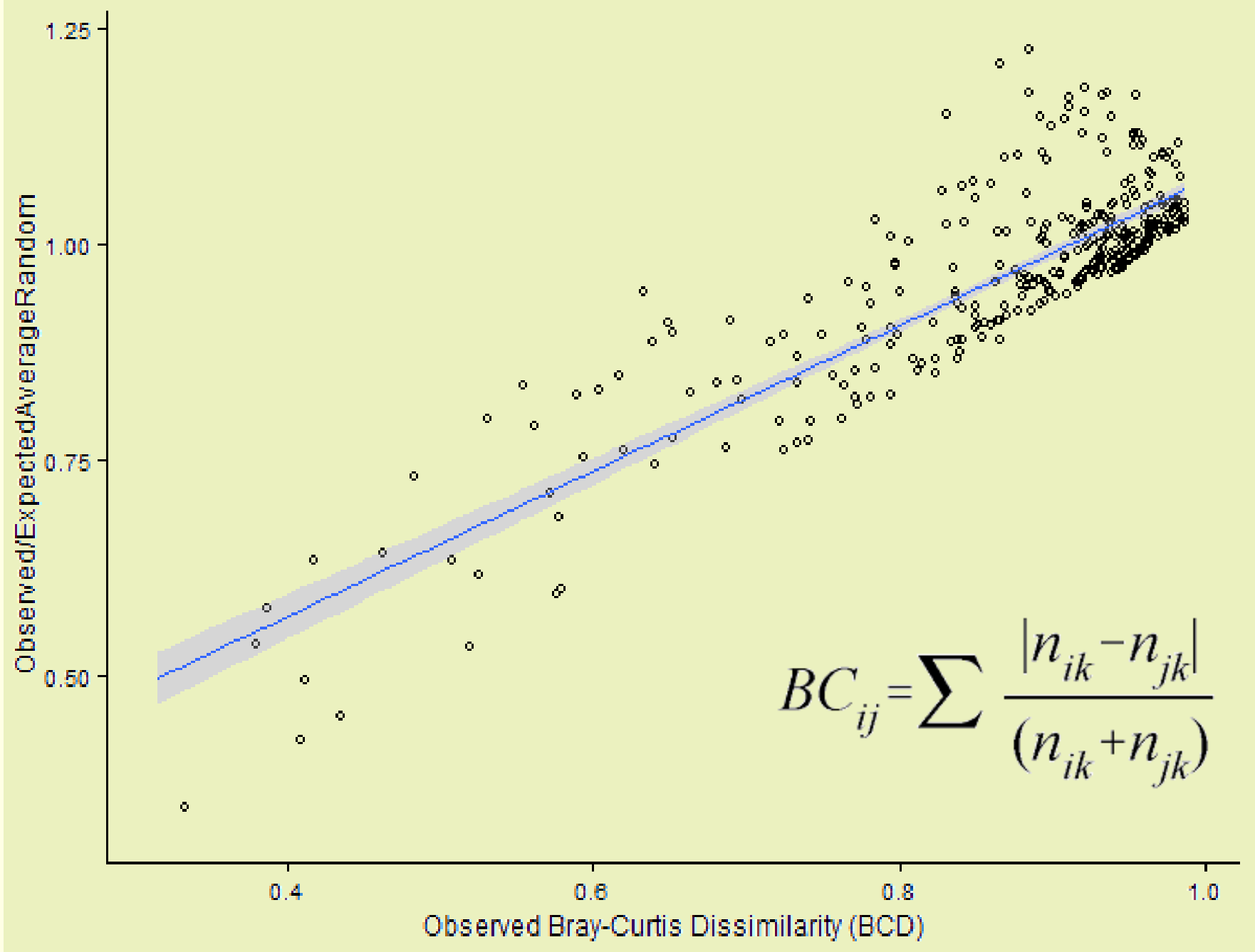
The three ecoregions in our analysis had mean species richness of >900 species. Ecoregions had as many as 1194 species, not accounting for elevational ranges, presence of migrants and vagrant records as well. When restricting our species lists to the exhaustively sampled lowland sites, we accounted for 472 species in SW Amazon, 496 species in the Napo, and 420 species in the Guianan Moist Forests.

Highest species richness in all 3 ecoregions was in mature primary forest ~226 ±5.8 species.



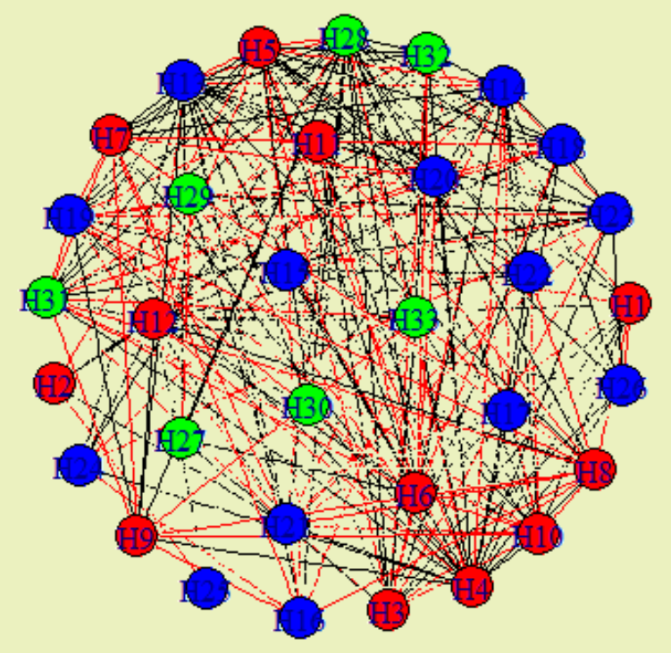
By Félix Pharand-Deschenes at Globaia

Beta-Diversity



$$BC_{ij}=\sum \frac{|n_{ik}-n_{jk}|}{(n_{ik}+n_{jk})}$$

We performed 528 pairwise comparisons of different habitat types.
Only 96 pairs of communities were more similar to each other than expected by chance (>9500 replicates had significant similarities), and 232 comparisons were significantly different.

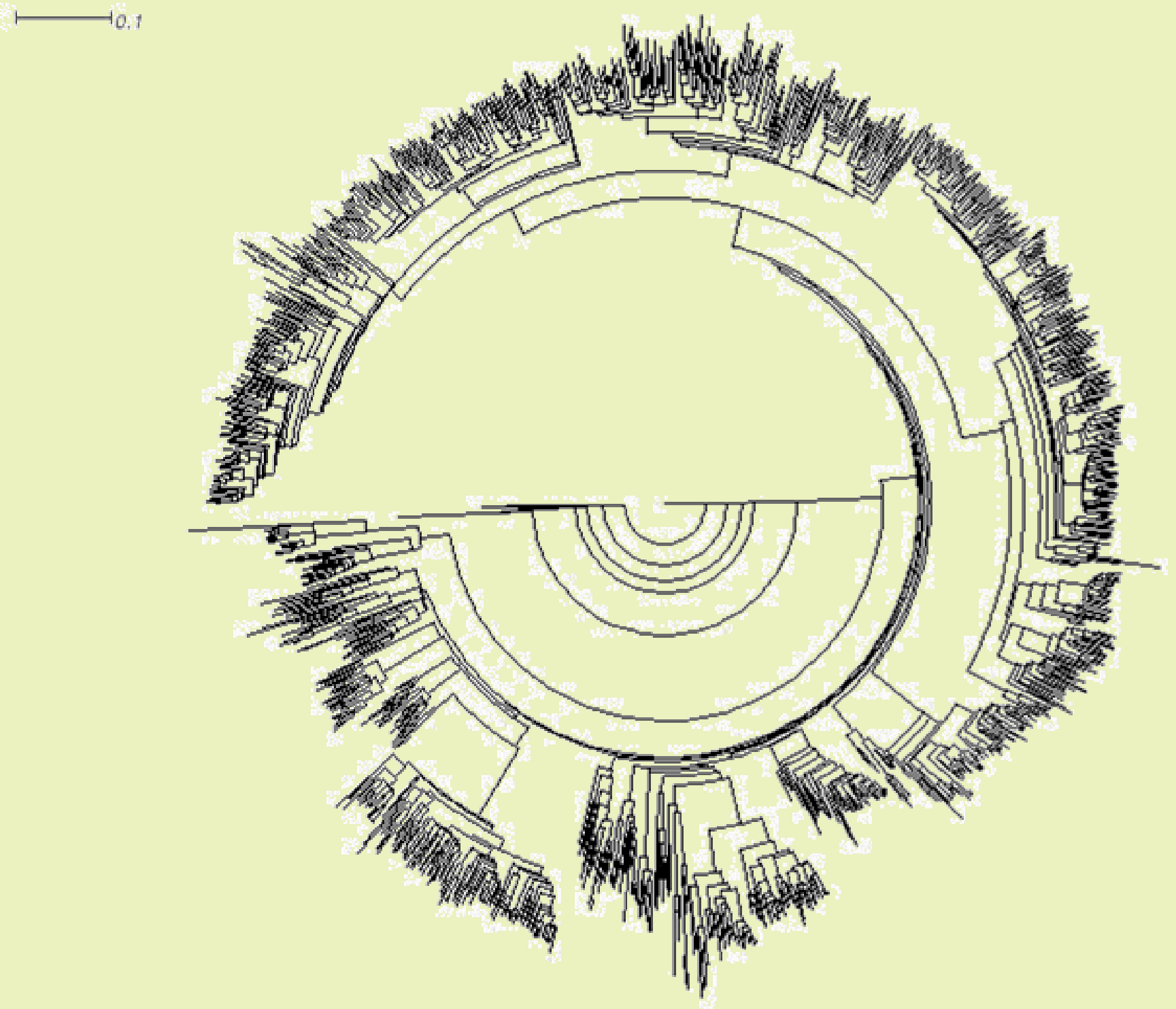


Links:
Black = similarity
Red = dissimilarity

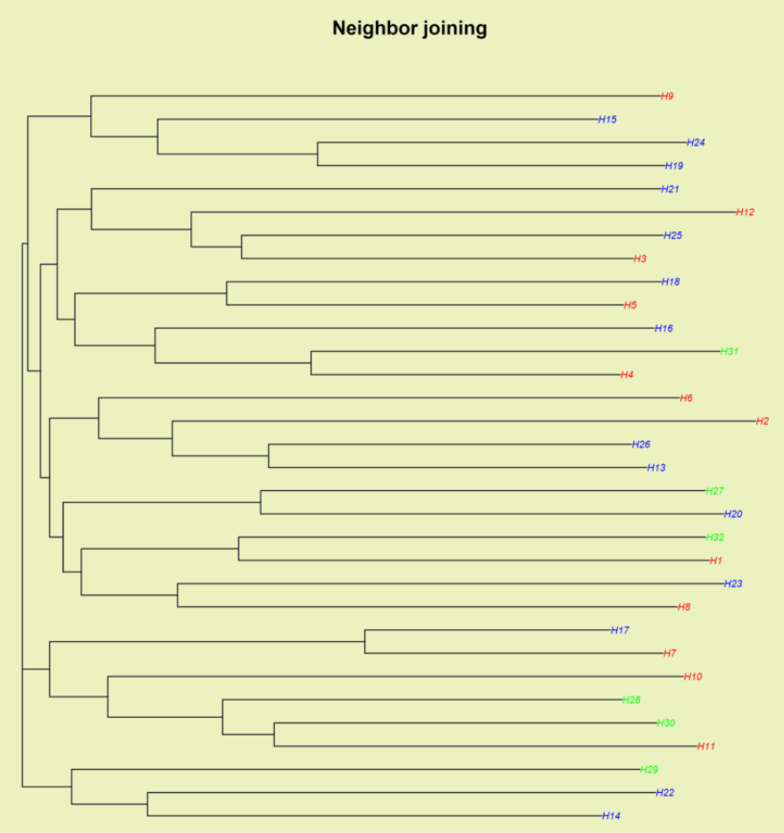
Ecoregions:
Napo = red
SW Amazon = blue
Guianan Moist = green

Network of pairwise Bray-Curtis distances between habitats

Phylobetadiversity



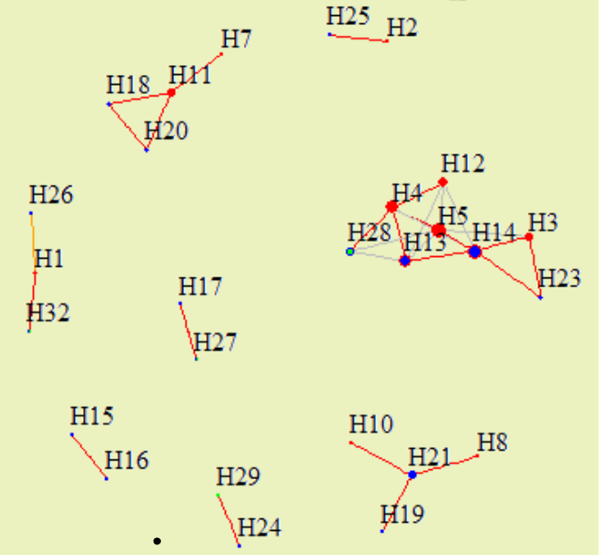
Our ultrametric phylogenetic tree included 83.9% of the species in the analysis.



30 pairs of local communities based on habitats were statistically more similar to each other than expected by chance.

We found three larger clusters of habitat type:

- mature forested habitats
- open water habitats
- water edge habitats



There was no clustering by ecoregions.

Discussion & Conclusions

Biodiversity is usually measured as taxonomic richness of a geographic area described by a certain index in reference to species richness. Phylogenetic diversity measures include information on phylogenetic relationships among species as well. Phylogenies serve as a great tool to generate hypotheses about processes, but they do not necessarily allow us to test these directly. We found:
-no support for the hypothesis that biogeographic barriers, and local speciation are effecting biodiversity (no strong clustering within ecoregions)
-patterns supporting dispersal limitation and environmental filtering
-similar habitats in ecoregions separated by thousands of miles show similar patterns of beta-diversity and phylobetadiversity.
Limitations:
Some of the habitats had very low species counts in comparison to other habitats within and between ecoregions. Depauperate local communities can often lead to patterns of observed overdispersion in the community, due to large phylogenetic distances between community members, as well as few representatives per taxonomic unit in the community.

Future directions

Each of these ecoregions included habitats that are unique for the particular regional community (white sand forest, bamboo, inselbergs). These habitats often contribute to the high levels of observed species richness within regions, even though the alpha-diversity at the particular site may be lower than in other habitats.
Some of these habitats are more ephemeral (such as bamboo), but most occur on more permanent soil formations, some form isolated patches within a larger matrix of a different habitat.
We want to explore the patterns of gene flow across isolated and more connected habitats.