

INTEGRATING OPEN PHYLOGENIES AND TAXONOMY TO GENERATE ROBUST PHYLOGENIES FOR COMMUNITY-LEVEL ANALYSIS: A STUDY CASE IN EASTERN AMAZON

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ABSTRACT

At the community-level, biodiversity is often characterized in terms of the composition of species, functional traits, or lineages. The latter encompasses the phylogenetic diversity (PD), which aims to quantify the total amount of phylogenetic history within a given pool of species. Despite multiple evidence of the importance of PD to understand community structure or its relationship with ecosystem functioning, the usage of PD has been rather timid. The use of PD is commonly limited because of the lack of comprehensive phylogenies encompassing all the species in a given region. Herein, we adapted the algorithm provided at the FishPhyloMaker package to create a supertree for a regional pool of species of 20 streams sampled twice in the Guamá River basin, Pará - Brazil, and assess its robustness for community-level ecological analyses. The supertree was generated by taking the open phylogeny available at the Fish Tree of Life and binding the absent species in the tree randomly within the lowest taxonomic rank of the species that displays a representative on the backbone tree. We applied this method using a loop function to generate 1,000 different phylogenetic hypotheses for the species pool, from which we calculated PD (i.e., total branch length connecting species in a given community) for each local pool of species, including 10 artificial communities ranging from low diversity to high diversity and real communities sampled in the area. We observed that PD was consistent, with the rankings from lowest to highest PD remained mostly the same across iterations, with a few potential changes for those communities exhibiting similar community structure. In conclusion, we showcase that the supertree method is adequate for exploring the phylogenetic

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diversity of Amazonian stream fishes whenever more detailed data on the phylogenetic relations of species within a regional pool of species is unavailable.

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