Dear editor of Ecological Informatics,

Phylogenies are an essential source of information to reveal the role of Ecological and Evolutionary mechanisms acting on the distribution of species and lineages through space and time. Studies untangling the importance of these mechanisms demand phylogenetic hypotheses, but comprehensive phylogenies for local (or regional) pools of species are rarely available. Building a phylogenetic hypothesis for all species in the species pool can be a laborious task. When achievable, it can not be fully reproducible due to the lack of formal and standardized approaches to fill the phylogenetic gaps.

That is the situation for ray-finned fishes, the most speciose lineage of vertebrates, especially in megadiverse regions. Despite their taxonomic and ecological diversity that addresses important ecological and evolutionary questions, no single phylogenetic hypothesis includes all known species. Therefore, a standardized tool to acquire a phylogenetic hypothesis for local/regional fish assemblages is crucial to make those studies feasible.

We fill this gap by proposing in this manuscript an R package that solves the problem associated with the phylogenetic gaps of fish species through a standardized and user-friendly procedure. Further, we developed a new metric to quantify Darwinian shortfalls. We illustrate all the functionalities of our package by constructing phylogenies for the four most speciose freshwater ecoregions of the world, besides to map the Darwinian shortfalls for all the assemblages in freshwater basins in the world. We hope that this tool allows specialists and nonspecialists in fish taxonomy to obtain phylogenetic hypotheses, which will ultimately boost the understanding of evolutionary and ecological factors acting on the distribution of ray-finned fishes.

The authors