# Highlights

* We provide the first automated procedure to check species names, construct phylogenetic trees and calculate Darwinian shortfalls for ray-finned fishes (Actinopterygii) by the R package FishPhyloMaker.
* This package provides functions to assemble phylogenies through a fast, reliable, and reproducible method, allowing its use and replicability by specialists and non-specialists in fish systematics.
* The package also provides an interactive procedure that gives more flexibility to the user when compared with other existing tools that construct phylogenetic trees for other highly speciose groups.
* The package includes a new method to compute Darwinian shortfalls for ray-finned fishes, but the rationale of the provided algorithm can be extended in future studies to be used in other groups of organisms