FishPhyloMaker: An R package to generate phylogenies for ray-finned fishes

Authors: Gabriel Nakamura1, 2, \*, Aline Richter1, Bruno E. Soares3

1 – Universidade Federal do Rio Grande do Sul, Departamento de Ecologia, Bento Gonçalves Avenue, 9500, CP

2 – INCT Ecology, Evolution, and Biodiversity Conservation

3 – Universidade Federal do Rio de Janeiro, Programa de Pós-Graduação em Ecologia

\*correspondence author: gabriel.nakamura.souza@gmail.com

# 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 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 rationale of the provided algorithm can be extended in future studies to be used in other groups of organisms.

# Abstract

Phylogenies summarize evolutionary information that is essential in the investigation of ecological and evolutionary causes of diversity patterns. They allow investigating hypotheses from trait evolution to the relationship between evolutionary diversity and ecosystem functioning. However, obtaining a comprehensive phylogenetic hypothesis can be difficult for some groups, especially those with a high number of species, that is the case for fishes, particularly tropical ones. The lack of species in phylogenetic hypotheses, called Darwinian shortfalls, can hinder ecological and evolutionary studies involving this group. To tackle this problem, we developed FishPhyloMaker, an R package that facilitates the generation of phylogenetic trees through a reliable and reproducible procedure, even for a large number of species. The package adopts well-known rules of insertion based on cladistic hierarchy, allowing its use by specialists and non-specialists in fish systematics. We exemplified the use of the FishPhyloMaker package by constructing complete phylogenies for fishes inhabiting the four richest freshwater ecoregions of the world. Furthermore, we proposed a new method to calculate Darwinian shortfalls and mapped this information for the major freshwater drainages of the world. FishPhyloMaker will expand the range of evolutionary and ecological questions that can be addressed using ray-finned fishes as study models, mainly in the field of community phylogenetics, by providing an easy and reliable way to obtain comprehensive phylogenies. Further, FishPhyloMaker presents the potential to be extended to other taxonomic groups that suffer from the same difficulty in the obtention of comprehensive phylogenetic hypothesis.

# Introduction

Phylogenies have been widely explored in ecology in the last decades due to the development of theoretical frameworks, numerical methods, and software (*e.g.,* Webb et al. 2008; Felsenstein 1985). The research agenda in ecology and evolution encompasses phylogenetic approaches from organismal to macroecological-scale, including trait evolution, invasion ecology, metacommunity ecology, and ecosystem functioning (Cavender-Bares et al., 2009). Hence, comprehensive phylogenetic trees must be available to address those topics.

Well-established phylogenies for most of the known species are available for some groups, such as terrestrial vertebrates (birds (Jetz et al., 2012), mammals (Upham et al., 2019), amphibians (Jetz and Pyron, 2018), squamates (Tonini et al., 2016), sharks (Stein et al., 2018), and plants (Magallón et al., 2015), which also have powerful tools to generate phylogenetic trees for local/regional pools of species (*e.g.,* Webb & Donoghue 2005 for mammals and plants; Jin & Qian 2019 for plants, to the others see http://vertlife.org/phylosubsets/). Inversely, available phylogenies for bony fishes (Betancur et al., 2017; Rabosky et al., 2018) display issues related to the taxonomic position of some clades (e.g., non-monophyletic groups) and the lack of species representativeness. The latter issue hampers answering some questions on the ecology and evolution of ray-finned fishes by generating inaccuracy in estimates of phylogenetic signal, trait evolution, and phylogenetic diversity (Seger et al. 2010; Boettiger et al., 2012a), or even impeding their calculation.

Ray-finned fishes (Actinopterygii) exhibit a complex evolutionary history and high ecological diversity (Albert et al., 2020), making them an interesting group to address questions in the interface of ecology and evolution (*e.g.*, Roa-Fuentes et al. 2019; Nakamura et al. 2020). The difficulty in obtaining phylogenetic information can hinder our efforts to understand fish ecology and evolution. Additionally, the lack of phylogenetic information for species, *i.e*., Darwinian shortfalls, is currently investigated in few lineages (*e.g.*, Freitas et al., 2021), which impedes the mapping of the relative demand of additional efforts needed in entire regions or clades to uncover the phylogenetic history of fishes. This problem urges a rapid solution in the context of the accelerated loss of species (ref aqui).

when did "by hand" proceduresAn alternative would be the use of to . However,it shigh investment, limiting factors for several institutionscomprehensive using the information from cladistic hierarchy, as suggested by Diniz-Filho et al (2013),, accessible,. The technique produces reliable phylogenetic information for community phylogenetics (Li et al., 2019)

In order to tackle the problem of obtention of comprehensive fish phylogenies in a reliable and reproducible way, we developed the FishPhyloMaker. This freely available R package facilitates the obtention of phylogenetic trees for ray-finned fishes. FishPhyloMaker automates the insertion procedure of species in the most comprehensive phylogeny (Rabosky et al., 2018) of ray-finned fishes following their taxonomic hierarchy. We illustrated how the FishPhyloMaker package solves the problem of obtaining comprehensive phylogenies by constructing phylogenetic trees for species inhabiting the four major freshwater ecoregions (Afrotropics, Australasia, Indo-Malay, Nearctic and Neotropics, sensu Tedesco et al., (2017)). Further, we developed a new method to quantify the Darwinian shortfalls and illustrate the use of this method by mapping the Darwinian shortfalls of all the major freshwater drainages in the world. Our package overcomes the main problems associated with manually building phylogenies for ray-finned fishes by following a specific and documented procedure and reducing the manual labor in large phylogenies.

**Methods**

# Inside the Fish(PhyloMaker): an overview of the package

FishPhyloMaker is a freely available R package containing three main functions, *FishTaxaMaker*, *FishPhyloMaker,* and *Darwinian\_deficit*. Below, we describe the functions to generate phylogenetic trees, highlighting the input data, intermediate steps, and output objects. Brief descriptions of the package functions are available in Table 1.

*FishTaxaMaker*

The *FishTaxaMaker* function checks the validity of species names provided by the user and prepares a formatted data frame for the *FishPhyloMaker* function. The input data must be a string vector or a data frame containing a list of species from the regional pool or an occurrence matrix (sites x species). The genus and specific epithet (or subspecies) must be separated by underline (e.g., *Genus*\_*epithet*). The function first classifies the provided species names as valid or synonymies based on Fishbase (Froese & Pauly, 2006) using the *rfishbase* package (Boettiger et al., 2012b). A new column summarizes names initially valid and the current valid names substituting identified synonymies. Unknown species to Fishbase are printed in the command line, and the user must manually inform the Family and the Order of the species. The output of the function is a list containing three elements: 1) a data frame displaying the taxonomic information (Valid name, Subfamily, Family, Order, Class, and SuperClass) for each provided species; 2) a data frame displaying the taxonomic information (Species, Family, and Order), only for the valid species; 3) a character vector displaying the species names not found in Fishbase.

Table 1: Functions presented in the package FishPhyloMaker and their descriptions.

|  |  |
| --- | --- |
| **Function** | **Description** |
| *FishTaxaMaker*() | Checks species names according to Fishbase and prepares the species list for the other functions in the package. |
| *whichFishAdd*() | Identifies the species already included in the mega-tree and in which taxonomic level each remaining species will be inserted. |
| *FishPhyloMaker*() | Builds the phylogeny and may return a data frame identifying step-by-step the performed insertions. |
| *Darwinian\_deficit*() | Calculates the Darwinian shortfall for the provided species list through a Phylogenetic Diversity (PD Faith (1992)) ratio |

*FishPhyloMaker*

*FishPhyloMaker* is the core function of the package. This function builds a phylogenetic hypothesis for the provided species list by inserting in and pruning species from the Rabosky's et al. (2020) phylogenetic tree (Figure 1) downloaded by the fishtreeoflife R package (Chang et al. 2019). This phylogeny is the most up-to-date and comprehensive phylogenetic hypothesis for ray-finned fishes.

The input for the *FishPhyloMaker* function can be the second element in the list returned by the *FishTaxaMaker* function or a manually constructed data frame with the same configuration (species, family, and order names for each taxon). The function also contains three logical arguments: insert.base.node, return.insertions and progress.bar. These three arguments are set by default as FALSE, TRUE, and TRUE, respectively, and allow the user to choose if the species must be inserted at the base node of families/orders, if the insertions made by each species must be shown in the output and if a progress bar must be shown in the console.

The function works sequentially, first identifying which of the provided species are in the backbone phylogenetic tree. If all of them are already present in the backbone tree, the function returns a pruned one. If any of the provided species is not in the backbone tree, the function performs a four-level insertion routine. First, species from genera already included in the backbone tree are inserted as polytomies at the most recent ancestral node that links all congeneric species (or as the sister species of the only species representing a genus in the backbone tree, as shown in *i* in Figure 1). Second, species not inserted in the previous step are then inserted at the family level by an interactive procedure using a returned list of all the genera within the same family of the target species. The user has the option to insert the target species as a sister taxon to a genus (*ii* in Figure 1, option 1, near to *Loricaria* genus), between two genera (*ii* in Figure 1, option 2, between genus *Loricaria* and *Hypostomus*), or at the node of the family (*ii* in Figure 1, option 3). If the user enters a single genus from the list, the function splits its branch and inserts the target species as a sister taxon (option 1). If the user enters two genera separated by a blank space, the function inserts the target species as a polytomy at the most recent node that links the selected genera (option 2). If the user enters the family name, the function inserts the target species at the family node as a polytomy (option 3). Third, if any remaining species can now be inserted at the genus level, the function repeats the first procedure but records it as a Congeneric family-level insertion (*iii* in Figure 1). Fourth, remnant species are inserted at the order level following similar to the second step, by an interactive procedure using a returned list of all the families within the order of the target species. Hence, the user may specify a family to insert the target species as sister taxon (option 1), two families to insert it as a polytomy at the most recent node linking them (option 2), or the order to insert it as a sister taxon (option 3). The function will not perform insertions steps beyond the order level because it would add too much uncertainty to the phylogenetic tree.

Setting the argument insert.base.node as TRUE automatically inserts the target species from the second and fourth steps in the family and order nodes, respectively. This setting facilitates the insertion of a large number of species or species with the phylogenetic position unknown. The default output is a list with two objects: (i) the pruned tree including only the provided species list (Final tree in Figure 1); (ii) a data frame identifying if each provided species was initially present in the backbone tree, in which step it was inserted, or not inserted at all. This data frame will tag each species with one of the four classification based on the insertion procedure: 1 – Present in tree will indicate species that were already present in the backbone tree; 2 -



Figure 1: Schematic representation of insertion and subsetting procedure performed by the FishPhyloMaker() function. Here we used a hypothetical phylogeny containing ten species and four families (silhouettes inside the tree) as the backbone phylogeny. Step (i) represents the congeneric level of insertion. Step (ii) represents the three options that the user may choose in the Family-level round of insertions (Option 1 – near to a genus; Option 2 – between two genera; Option 3 – at the family node). (iii) represents the congeneric insertions at the family level and, finally, the final pruned tree containing only the species of interest.

*Darwinian\_deficit*

The *Darwinian\_deficit* function calculates a measure of Darwinian shortfalls following Equation 1:

Equation 1

In this function, PDinserted is the sum of the branch lengths of species in the phylogenetic tree before the insertion procedure. PDpresent in tree is the sum of branch lengths of the species inserted in the tree. The Darwinian deficit ranges from 0 (most species already present in the tree before the insertion procedure) to 1 (all the species in the phylogenetic tree were inserted). To calculate the Darwinian shortfall through the *Darwinian\_deficit* function, the user must provide a phylogenetic tree and a table of insertions, both obtained from the *FishPhyloMaker* function.

*Illustrating the use of FishPhyloMaker package*

We provide an example of the usage of the *FishPhyloMaker* package by creating phylogenetic trees using a global dataset of freshwater fishes inhabiting 3,119 drainage basins that cover more than 80% of the Earth surface (Tedesco et al., 2017). This dataset allowed in-depth investigation on the global patterns of species distribution and their evolutionary determinants (*e.g.*, Miller & Román-Palácios, 2021). We built phylogenetic trees for the four major freshwater ecoregions based on species richness: Afrotropics, Indo-Malay, Nearctic, and Neotropics. Moreover, we used this same dataset to demonstrate how to map the Darwinian shortfalls, calculated following Equation 1 and *Darwinian\_deficit* function, for all the drainage basins in the Tedesco et al. (2017) dataset.

First, the user must download the package from the online GitHub repository, using the following command line:

devtools::install\_github("GabrielNakamura/FishPhyloMaker", ref = "main", build\_vignettes = TRUE)

We recommend that the user updates all the requested packages to avoid errors related to packages versions. We prepared the fish occurrence by checking the validity of its names by using the function *FishTaxaMaker*. The occurrence matrix encompassed 2,478 species, from which 2,477 were valid names. We applied the *FishPhyloMaker* function separately for each ecoregion using the valid names retrieved from the *FishTaxaMaker* (Figure 2). For simplicity and reproducibility, we set the argument insert.base.node as TRUE, thus, inserting all species at the base node of its corresponding family and order. We also set the argument return.insertions = TRUE for retrieving the insertion information of each species. Then, we applied the *Darwinian\_deficit* functional to calculate the Darwinian shortfall for all the freshwater basins of the world harboring at least three species (Tedesco et al. 2017). The *Darwinian\_deficit* function may also include other levels of phylogenetic insertion, like family and order insertions.

All the codes need to reproduce this analysis fully is provided at GitHub (GabrielNakamura/MS\_FishPhyloMaker). Further analysis exploring the usage of the package is available at <https://gabrielnakamura.github.io/FishPhyloMaker/index.html>.

**Results**

The entire insertion procedure lasted approximately two hours using one core from a computer machine with an i5 processor. A total of 821 species were inserted, with the Afrotropics exhibiting the largest number of insertions (359 from 767, Figure 2). On the contrary, the Nearctic displayed the least number of insertions, being only six species inserted at the genus level (2.7% of missing species in the phylogenetic tree). Indo-Malay and Neotropics presented 30.3% and 30% of insertions, respectively. Except for the Nearctic, all the remaining ecoregions exhibited insertions in all considered taxonomic levels (Figure 2).

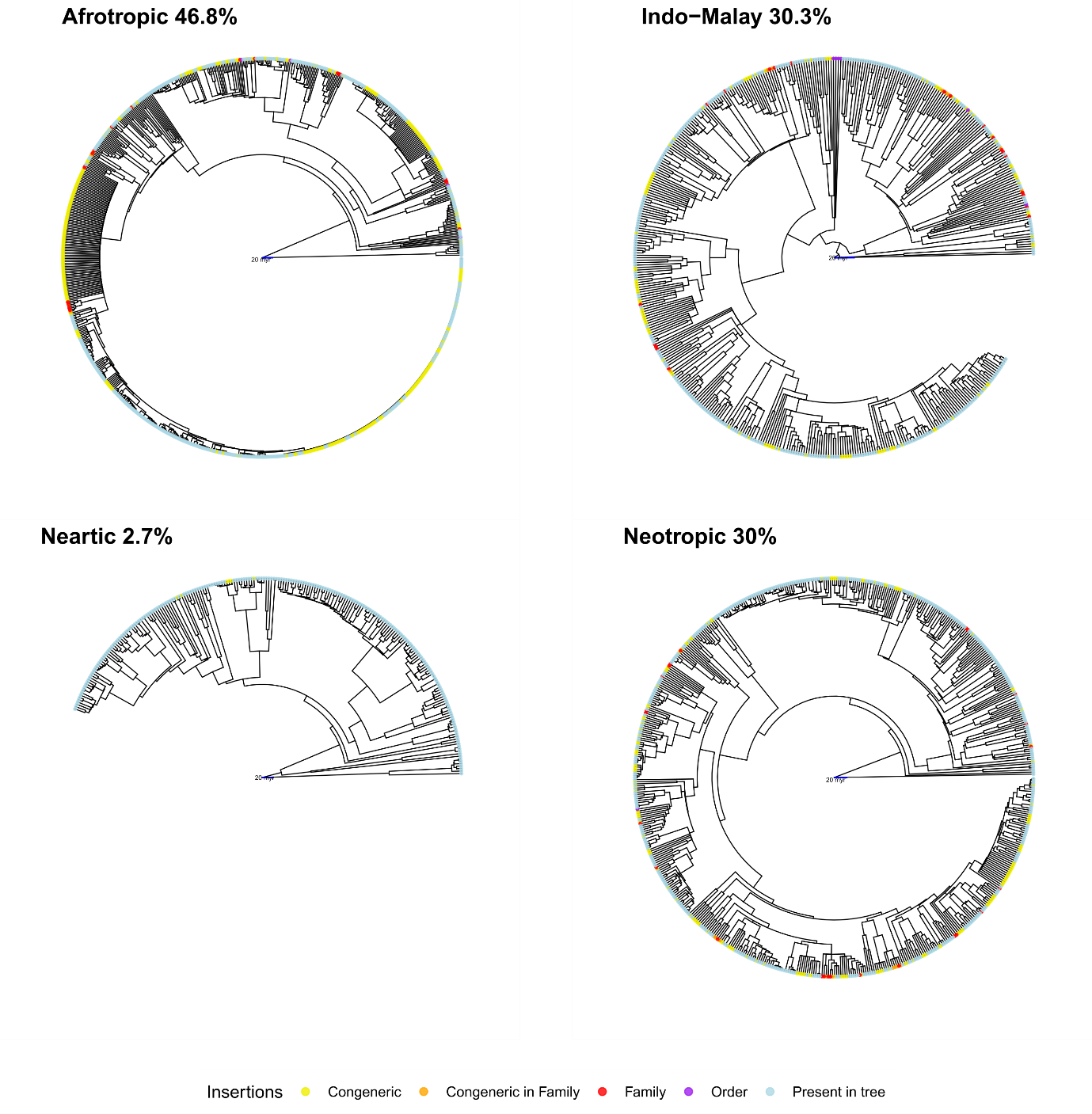


Figure 2: Phylogenetic trees generated with the FishPhyloMaker package for freshwater fishes inhabiting four ecoregions (Afrotropics, Indo-Malay, Nearctic, and Neotropic). The colored tip-points indicate if species were present in the backbone tree (Present in tree) or at which level they were inserted. The percentages of insertions over the total number of species for each ecoregion are shown.

We observed that tropical regions exhibited larger Darwinian shortfalls, while northern sites had lower values of shortfalls (Figure 3). The highest values of Darwinian shortfalls were found in Afrotropics and Neotropics, as some drainages did not harbor any (or few) species in the original Rabosky's phylogeny.

aa Darwinian a congeneric insertionsa Gunsampled areas

**Discussion**

, efficients.These features include for inserting species in given phylogeniesing. The latter option allows a better systematization of building supertrees and calculating the first, to our knowledge, quantitative measure of the Darwinian shortfall

Whereas Phylomatic allows the insertion of absent species only as congeneric or at the node corresponding to the family of the focal species (Webb and Donoghue, 2005), the FishPhyloMaker package delivers options through an interactive procedure of insertion. The performed insertions can be easily recorded in an R script, providing flexibility and the same level of reproducibility as other algorithms designed for similar purposes (*e.g.*, Jin and Qian, 2019). This interactive option is a novelty when compared to similar insertion algorithms (*e.g.*, Phylomatic).

Understanding the spatial distribution of the Darwinian shortfall is paramount to guide our future efforts to understand the history of life. The phylogenetic gaps in the knowledge of ray-finned fishes are geographically biased, with tropical basins presenting the higher levels of Darwinian shortfalls. This gap in evolutionary knowledge could lead to a bias in evaluating evolutionary history or macroecological patterns for fish assemblages in these regions. Some factors can be pointed to explain this bias. First, the lack of biodiversity knowledge is related to the rate of formation of new species, which we can not describe at the same speed (Hortal et al., 2015). Besides that, the regions with the largest number of species require more sampling effort and research investment to access reliable representativeness of total biodiversity.

*Limitations and possible applications*

Future developments of the package should consider the Catalog of Fishes (Fricke & Eschemeyer, 2021) to improve the nomenclature checking procedures. Despite Fishbase being a widely used database to check for the taxonomic classification of fishes, it may present delays in updating taxonomic information because it is not its primary purpose. Inversely, the Catalog of Fishes is an authoritative taxonomic list frequently updated.

An inherent limitation of the phylogenetic hypothesis produced by FishPhyloMaker is the large number of polytomies resulting from the insertion procedures. We recommend that users directly assess how the phylogenetic uncertainty affects further analysis when not using a fully solved phylogenetic tree (Martins et al., 2013).

These limitations do not preclude the package applicability for studies in phylogenetic community ecology since synthesis phylogenies do not significantly impact phylogenetic diversity indices (Li et al., 2019). Moreover, this is the only automated tool able to provide a complete phylogenetic tree that can easily handle large datasets. FishPhyloMaker can be relevant for addressing several critical questions in ecology and evolution by facilitating the obtention of phylogenetic hypotheses for local pools of ray-finned fishes. This facilitation can be essential for regions with a large gap in the phylogenetic knowledge of fishes, such as the Neotropical region (Albert et al., 2020). Such phylogenetic hypotheses allow understanding how ecological traits evolved or how the current and past environmental conditions selected the lineages in different areas.

Biogeographical studies are usually restricted to one or a few lineages at larger scales due to the availability of molecular phylogenies. The FishPhyloMaker package facilitates large-scale investigations on the biogeographic history of the most diverse group of vertebrates on Earth, the Actinopterygians, helping us understand the processes that drive this high diversity. Finally, we can map where the lack of phylogenetic information is the most critical once the function returns the insertion level of species. This information can directly elucidate the patterns of the Darwinian shortfalls for ray-finned fishes, contributing not only to direct sampling and studying efforts but also to evidence the need for increased efforts to decolonize science (Trisos et al., 2021). Therefore, we expect that the FishPhyloMaker package reduces the gaps and barriers to addressing ecological and evolutionary questions due to the difficulty or lack of a reliable phylogenetic hypothesis for local and regional pools of ray-finned fishes.

**Contributions**

GN conceived the idea of R package. GN and AR wrote the package. GN and BES lead the writing. All authors contributed to reviwew all versions of this work.

**Acknowledgements**

GN is member of the National Institutes for Science and Technology (INCT) in

Ecology, Evolution and Biodiversity Conservation, supported by MCTIC/CNPq (proc.

465610/2014-5). BES and AR are grateful to FAPERJ and CAPES for their postdoctoral and doctoral grants, respectively. The Brazilian science resists.

# References

Albert, J.S., Tagliacollo, V.A., Dagosta, F., 2020. Diversification of Neotropical Freshwater Fishes. Annu. Rev. Ecol. Evol. Syst. 51, 27–53. https://doi.org/10.1146/annurev-ecolsys-011620-031032

Betancur, R.R., Wiley, E.O., Arratia, G., Acero, A., Bailly, N., Miya, M., Lecointre, G., Ortí, G., 2017. Phylogenetic classification of bony fishes. BMC Evol. Biol. 17, 1–40. https://doi.org/10.1186/s12862-017-0958-3

Boettiger, C., Coop, G., Ralph, P., 2012. Is your phylogeny informative? Measuring the power of comparative methods. Evolution (N. Y). 66, 2240–2251. https://doi.org/10.1111/j.1558-5646.2011.01574.x

Cavender-Bares, J., Kozak, K.H., Fine, P.V.A., Kembel, S.W., 2009. The merging of community ecology and phylogenetic biology. Ecol. Lett. 12, 693–715. https://doi.org/10.1111/j.1461-0248.2009.01314.x

Chang, J., Rabosky, D.L., Smith, S.A., Alfaro, M.E., 2019. An r package and online resource for macroevolutionary studies using the ray-finned fish tree of life. Methods Ecol. Evol. 10, 1118–1124. https://doi.org/10.1111/2041-210X.13182

Diniz-Filho, J.A.F., Loyola, R.D., Raia, P., Mooers, A.O., Bini, L.M., 2013. Darwinian shortfalls in biodiversity conservation. Trends Ecol. Evol. 28, 689–695. https://doi.org/10.1016/j.tree.2013.09.003

Faith, D.P., 1992. Conservation evaluation and phylogenetic diversity. Biol. Conserv. 61, 1–10. https://doi.org/10.1016/0006-3207(92)91201-3

Felsenstein, J., 1985. Phylogenies and the comparative method. Am. Nat. 125, 1–15. https://doi.org/0003-0147/85/2501-0001

Freitas, T.M. da S., Stropp, J., Calegari, B.B., Calatayud, J., De Marco, P., Montag, L.F. de A., Hortal, J., 2021. Quantifying shortfalls in the knowledge on Neotropical Auchenipteridae fishes. Fish Fish. 22, 87–104. https://doi.org/10.1111/faf.12507

Hortal, J., De Bello, F., Diniz-Filho, J.A.F., Lewinsohn, T.M., Lobo, J.M., Ladle, R.J., 2015. Seven Shortfalls that Beset Large-Scale Knowledge of Biodiversity. Annu. Rev. Ecol. Evol. Syst. 46, 523–549. https://doi.org/10.1146/annurev-ecolsys-112414-054400

Jetz, W., Pyron, R.A., 2018. The interplay of past diversification and evolutionary isolation with present imperilment across the amphibian tree of life. Nat. Ecol. Evol. 2, 850–858. https://doi.org/10.1038/s41559-018-0515-5

Jetz, W., Thomas, G.H., Joy, J.B., Hartmann, K., Mooers, A.O., 2012. The global diversity of birds in space and time. Nature 491, 444–448. https://doi.org/10.1038/nature11631

Jin, Y., Qian, H., 2019. V.PhyloMaker: an R package that can generate very large phylogenies for vascular plants. Ecography (Cop.). 42, 1353–1359. https://doi.org/10.1111/ecog.04434

Li, D., Trotta, L., Marx, H.E., Allen, J.M., Sun, M., Soltis, D.E., Soltis, P.S., Guralnick, R.P., Baiser, B., 2019. For common community phylogenetic analyses, go ahead and use synthesis phylogenies. Ecology 100, 1–15. https://doi.org/10.1002/ecy.2788

Magallón, S., Gómez-Acevedo, S., Sánchez-Reyes, L.L., Hernández-Hernández, T., 2015. A metacalibrated time-tree documents the early rise of flowering plant phylogenetic diversity. New Phytol. 207, 437–453. https://doi.org/10.1111/nph.13264

Martins, W.S., Carmo, W.C., Longo, H.J., Rosa, T.C., Rangel, T.F., 2013. SUNPLIN: Simulation with Uncertainty for Phylogenetic Investigations. BMC Bioinformatics 14. https://doi.org/10.1186/1471-2105-14-324

Nakamura, G., Vicentin, W., Súarez, Y.R., Duarte, L., 2020. A multifaceted approach to analyzing taxonomic, functional, and phylogenetic β‐diversity. Ecology. https://doi.org/10.1002/ecy.3122

Rabosky, D.L., Chang, J., Title, P.O., Cowman, P.F., Sallan, L., Friedman, M., Kaschner, K., Garilao, C., Near, T.J., Coll, M., Alfaro, M.E., 2018. An inverse latitudinal gradient in speciation rate for marine fishes. Nature 559, 392–395. https://doi.org/10.1038/s41586-018-0273-1

Roa-Fuentes, C.A., Heino, J., Cianciaruso, M. V., Ferraz, S., Zeni, J.O., Casatti, L., 2019. Taxonomic, functional, and phylogenetic β-diversity patterns of stream fish assemblages in tropical agroecosystems. Freshw. Biol. 64, 447–460. https://doi.org/10.1111/fwb.13233

Roa-Fuentes, C.A., Heino, J., Zeni, J.O., Ferraz, S., Cianciaruso, M.V., Casatti, L., 2020. Importance of local and landscape variables on multiple facets of stream fish biodiversity in a Neotropical agroecosystem. Hydrobiologia 7. https://doi.org/10.1007/s10750-020-04396-7

Roquet, C., Thuiller, W., Lavergne, S., 2013. Building megaphylogenies for macroecology: Taking up the challenge. Ecography (Cop.). 36, 13–26. https://doi.org/10.1111/j.1600-0587.2012.07773.x

Stein, R.W., Mull, C.G., Kuhn, T.S., Aschliman, N.C., Davidson, L.N.K., Joy, J.B., Smith, G.J., Dulvy, N.K., Mooers, A.O., 2018. Global priorities for conserving the evolutionary history of sharks, rays and chimaeras. Nat. Ecol. Evol. 2, 288–298. https://doi.org/10.1038/s41559-017-0448-4

Tedesco, P.A., Beauchard, O., Bigorne, R., Blanchet, S., Buisson, L., Conti, L., Cornu, J.F., Dias, M.S., Grenouillet, G., Hugueny, B., Jézéquel, C., Leprieur, F., Brosse, S., Oberdorff, T., 2017. Data Descriptor: A global database on freshwater fish species occurrence in drainage basins. Sci. Data 4, 1–6. https://doi.org/10.1038/sdata.2017.141

Tonini, J.F.R., Beard, K.H., Ferreira, R.B., Jetz, W., Pyron, R.A., 2016. Fully-sampled phylogenies of squamates reveal evolutionary patterns in threat status. Biol. Conserv. 204, 23–31. https://doi.org/10.1016/j.biocon.2016.03.039

Trisos, C.H., Auerbach, J., Katti, M., 2021. Decoloniality and anti-oppressive practices for a more ethical ecology. Nat. Ecol. Evol. https://doi.org/10.1038/s41559-021-01460-w

Upham, N.S., Esselstyn, J.A., Jetz, W., 2019. Inferring the mammal tree: Species-level sets of phylogenies for questions in ecology, evolution, and conservation. PLOS Biol. 17, e3000494. https://doi.org/10.1371/journal.pbio.3000494

Webb, C.O., Ackerly, D.D., Kembel, S.W., 2008. Phylocom: Software for the analysis of phylogenetic community structure and trait evolution. Bioinformatics 24, 2098–2100. https://doi.org/10.1093/bioinformatics/btn358

Webb, C.O., Donoghue, M.J., 2005. Phylomatic: Tree assembly for applied phylogenetics. Mol. Ecol. Notes 5, 181–183. https://doi.org/10.1111/j.1471-8286.2004.00829.x