

# Package: FishPhyloMaker (via r-universe)

August 25, 2024

**Type** Package

**Title** Phylogenies for a List of Finned-Ray Fishes

**Version** 0.2.0

**Description** Provides an alternative to facilitate the construction of a phylogeny for fish species from a list of species or a community matrix using as a backbone the phylogenetic tree proposed by Rabosky et al. (2018)  [<doi:10.1038/s41586-018-0273-1>](https://doi.org/10.1038/s41586-018-0273-1).

**License** MIT + file LICENSE

**Encoding** UTF-8

**LazyData** true

**Roxygen** list(markdown = TRUE)

**RoxygenNote** 7.2.3

**Imports** ape, fishtree, geiger, knitr, phytools, progress, rfishbase, rmarkdown, utils

**VignetteBuilder** knitr, rmarkdown

**Depends** R (>= 2.10)

**Suggests** markdown, gh

**Remotes** ropensci/rfishbase

**Repository** <https://phylotastic.r-universe.dev>

**RemoteUrl** <https://github.com/GabrielNakamura/FishPhyloMaker>

**RemoteRef** HEAD

**RemoteSha** 04373d07704296dcf64218dcb9f5afc4f9e06a9f

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FishPhyloMaker	<i>Obtaining fish phylogeny according to a local pool of species</i>
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## Description

Obtaining fish phylogeny according to a local pool of species

## Usage

```
FishPhyloMaker(
  data,
  insert.base.node = FALSE,
  return.insertions = TRUE,
  progress.bar = TRUE
)
```

## Arguments

<code>data</code>	A data frame with three columns containing the name of species (s), the Family (f) and the Order (o). This data frame can be generated with <code>tab_function</code> function.
<code>insert.base.node</code>	Logical argument indicating if the species must be added automatically in the family and order (when needed) nodes. Default is FALSE
<code>return.insertions</code>	Logical, if TRUE (default) the output is a list of length two containing the phylogeny and a dataframe with a column indicating at which level each species was inserted.
<code>progress.bar</code>	Logical argument. If TRUE (default) a progress bar will be shown in console.

## Value

A newick object containing the phylogeny with the species in data object. If `return.insertions = TRUE` the output will be a list of length two containing the newick phylogeny and a data frame equal that provided in data plus a column indicating at which level each species was inserted in the tree.

**Examples**

```
data("taxon_data_PhyloMaker")
res_phylo <- FishPhyloMaker(data = taxon_data_PhyloMaker,
  insert.base.node = TRUE,
  return.insertions = TRUE,
  progress.bar = TRUE)
```

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FishTaxaMaker	<i>Generate a list of species Auxiliary function to obtain taxonomic classification and check the names of species present in species pool</i>
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**Description**

Generate a list of species Auxiliary function to obtain taxonomic classification and check the names of species present in species pool

**Usage**

```
FishTaxaMaker(data, allow.manual.insert = TRUE)
```

**Arguments**

data	A character vector with species names or a community matrix with species names in columns
allow.manual.insert	Logical, if TRUE (default), the user must type the names of Family and Order of species not found in Fishbase

**Value**

List with three elements.

- A data frame containing the taxonomic classification of valid species accordingy to Fishbase
- A data frame with three columns containing the name of species (s), the Family (f) and Order (o) that ca FishPhyloMaker function
- A character vector containing all names of species that was not find in Fishbase

**Examples**

```
## Not run:
data(neotropical_comm)
data_comm <- neotropical_comm[, -c(1, 2)]
taxon_data <- FishTaxaMaker(data_comm, allow.manual.insert = TRUE)
Characidae
Characiformes
Characidae
Characiformes
Characidae
Characiformes
Loricariidae
Siluriformes
Characidae
Characiformes
Cichlidae
Cichliformes
Crenuchidae
Characiformes
Gymnotidae
Gymnotiformes
Loricariidae
Siluriformes
Loricariidae
Siluriformes
Loricariidae
Siluriformes
Loricariidae
Siluriformes
Loricariidae
Siluriformes
Heptapteridae
Siluriformes
Characidae
Characiformes
Loricariidae
Siluriformes
Characidae
Characiformes

## End(Not run)
```

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neotropical\_comm

*Abundance of stream fish species in Parana and Paraguay streams*

---

**Description**

A dataset containing the abundance of stream fish species distributed in streams of Parana and Paraguay river Basins

**Usage**

```
neotropical_comm
```

**Format**

A data frame with 20 rows and 61 variables:

**Source**

Article published in Neotropical Ichthyology [doi:10.1590/1982022420200126](https://doi.org/10.1590/1982022420200126)

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PD\_deficit

*Title Calculate the amount of phylogenetic deficit in assemblages*

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**Description**

Title Calculate the amount of phylogenetic deficit in assemblages

**Usage**

```
PD_deficit(phylo, data, level = "Congeneric_insertion")
```

**Arguments**

phylo	Phylogenetic tree in newick format, can be an object from <a href="#">FishPhyloMaker</a> function
data	A data frame containing the classification informing the level of insertions. This can be obtained from <a href="#">FishPhyloMaker</a> function
level	Character indicating which level must be considered in the calculation of PD deficit. Can be a vector with the levels ("Congeneric_insertion", "Congeneric_Family_level", "Family_insertion", "Order_insertion") which will be considered in the calculation of phylogenetic deficit. default is "Congeneric_insertion".

**Value**

A vector containing four values:

- Amount phylogenetic information present in the tree before insertions (PDintree)
- Amount of phylogenetic information inserted in the tree (PDdeficit)
- Total Phylogenetic information of the tree (PDtotal)
- A ratio calculated as PDdeficit/PDtotal (Darwinian\_deficit)

**See Also**

[FishPhyloMaker](#) for phylogeny and data frame containing the classification of insertions

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spp\_afrotropic *List of fish species with occurrence in Afrotropical ecoregion*

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**Description**

A list of species that occur in basins of Afrotropical ecoregion

**Usage**

spp\_afrotropic

**Format**

A character vector with 767 species names:

**References**

<https://www.nature.com/articles/sdata2017141>

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taxon\_data\_PhyloMaker *Data frame with species names needed to assemble the phylogenetic tree*

---

**Description**

A data frame that can be directly used in FishPhyloMaker to obtain a phylogenetic tree

**Usage**

taxon\_data\_PhyloMaker

**Format**

A data frame with taxonomic classification (species, family and order) of 45 species

**References**

Species that make up the dataset in the paper published in Neotropical Ichthyology [doi:10.1590/1982022420200126](https://doi.org/10.1590/1982022420200126)

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whichFishAdd	<i>Function to inform which species must be added to the mega-tree phylogeny in the insertion process.</i>
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**Description**

Function to inform which species must be added to the mega-tree phylogeny in the insertion process.

**Usage**

```
whichFishAdd(data)
```

**Arguments**

data	A data frame with three column containing the name of species (s), the Family (f) and Order (o). This can be generated with function <a href="#">FishTaxaMaker</a>
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**Details**

This function can be used in order to known which species that must be added in the insertion process made by [FishPhyloMaker](#).

**Value**

A data frame containing a column informing at which level the species in data must be added.

**Examples**

```
data("taxon_data_PhyloMaker")  
res_test <- whichFishAdd(data = taxon_data_PhyloMaker)
```

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