

Package ‘FishPhyloMaker’

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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)>.

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Encoding UTF-8

LazyData true

RoxygenNote 7.1.1

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

VignetteBuilder knitr, rmarkdown

Depends R (>= 2.10)

Suggests markdown, gh

NeedsCompilation no

Author Gabriel Nakamura [aut, cre] (<<https://orcid.org/0000-0002-5144-5312>>),
Aline Richter [aut],
Bruno Soares [aut]

Maintainer Gabriel Nakamura <gabriel.nakamura.souza@gmail.com>

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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

data	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.
insert.base.node	Logical argument indicating if the species must be added automatically in the family and order (when needed) nodes. Default is FALSE
return.insertions	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.
progress.bar	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)
```

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)
```

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)

PD_defict

Title Calculate the amount of phylogenetic deficit in assemblages

Description

Title Calculate the amount of phylogenetic deficit in assemblages

Usage

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

Arguments

phylo	Phylogenetic tree in newick format, can be an object from FishPhyloMaker function
data	A data frame containing the classification informing the level of insertions. This can be obtained from FishPhyloMaker function
level	Character indicating which level must be considered in the calculation of PD deficit. default is "Congeneric_insertion"

Value

A scalar containing the value of PD deficit for the level chosen

See Also

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

spp_afrotropic *List of fish species with occurrence in Afrotropical ecoregion*

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>

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)

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 FishTaxaMaker
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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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