

Package ‘jrich’

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Title Jack-Knife Support for Evolutionary Distinctiveness Indices I and W

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Depends ape

Description These functions calculate the taxonomic measures presented in Miranda-Esquivel (2016).

The package introduces Jack-knife resampling in evolutionary distinctiveness prioritization analysis, as a way to evaluate the support of the ranking in area prioritization, and the persistence of a given area in a conservation analysis.

The algorithm is described in: Miranda-Esquivel, D (2016) <[DOI:10.1007/978-3-319-22461-9_11](https://doi.org/10.1007/978-3-319-22461-9_11)>.

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URL <https://github.com/Dmirandae/jrich>

BugReports <https://github.com/Dmirandae/jrich/issues>

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Best . Index	<i>Jack-knife indices in a single topology m times and evaluates a success rule.</i>
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Description

The function jack-knives the terminals and calculates the indices value m (=replicates) times.

Usage

```
Best.Index(tree = tree, distribution = distribution, jtip = jtip,
           replicates = replicates, success = c(success))
```

Arguments

tree	is a single tree with n terminals, an ape phylo object.
distribution	species distributions in n areas, a data.frame
jtip	is the proportion of terminals to delete, real (range 0-1).
replicates	is the number of replicates, an integer.
success	the measure of the success, a vector.

Value

The function returns the success that correspond to obtain the same ranking for X,Y positions, established as the vector success (by default success)).

The function returns the success that corresponds to obtain the same ranking for X,Y positions, established as the vector success (by default success))

Author(s)

Miranda-Esquivel Daniel R.

Examples

```
library(jrich)
data(tree)
data(distribution)
```

```
Best.Index(tree = tree, distribution = distribution, jtip =0.5, replicates =10, success=1)
```

 Calculate.Index

Indices values and Jack-knife indices for a single topology.

Description

The function calculates standard and terminal jack-knifed indices I and W [see Miranda-Esquivel 2016], along with Posadas et al. 2001 modifications.

Usage

```
Calculate.Index(tree = tree, distribution = distribution, jtip = 0,
  verbose = TRUE, standard = "distribution")
```

Arguments

tree	is a single tree with n terminals, an ape phylo object.
distribution	species distributions in n areas, a data.frame
jtip	is the proportion of terminals to delete, real (range 0-1).
verbose	Boolean. If TRUE, the output reports the number of deleted terminals/topologies.
standard	"distribution" or "tree" to standardize by the by the sum of indices in the distribution or the sum of indices in the tree

Author(s)

Miranda-Esquivel Daniel R.

Examples

```
library(jrich)
data(tree)
data(distribution)
## Standardized by the sum of indices in the distribution
Calculate.Index(tree=tree, distribution = distribution, verbose=TRUE, standard = "distribution")

## Standardized by the sum of indices in the tree (as figure 1 in Miranda-Esquivel 2016)
Calculate.Index(tree=tree, distribution = distribution, verbose=TRUE, standard = "tree")
```

Children	<i>Children of a node.</i>
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Description

Get the children of a node in a tree.

Usage

```
Children(tree = tree, node = node)
```

Arguments

tree	is a single tree with n terminals, an ape phylo object.
node	representing the node in APE notation, is an integer.

Value

The children nodes of the internal node; in most cases, two integers.

Author(s)

Miranda-Esquivel Daniel R.

Examples

```
library(jrich)
data(tree)

Children(tree,7)
```

distribution	<i>Distribution of five taxa.</i>
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Description

A data frame with five species distributions in eight areas, following Miranda-Esquivel (2016).

Usage

```
distribution
```

Format

A data.frame object with eight areas (columns) and five species (rows)

Author(s)

Miranda-Esquivel Daniel R.

IndexI

I index value for a single topology.

Description

This function assigns the same weight to sister clades (see Van-Wright et al., 1981). The input tree is reordered in post order.

Usage

```
IndexI(tree = tree)
```

Arguments

`tree` is a single tree with n terminals, an ape phylo object.

Value

Returns a vector with weights.

Author(s)

Miranda-Esquivel Daniel R.

Examples

```
library(jrich)
data(tree)
plot(tree)
indexi      <- IndexI(tree)
newTree     <- tree
newTree$tip.label <- indexi
plot(newTree)
```

IndexW	<i>W index value for a single topology.</i>
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Description

This function assigns the weight according to the ramification patterns (see Van-Wright et al., 1981). The input tree is reordered in post order. Returns a vector with weights.

Usage

```
IndexW(tree = tree)
```

Arguments

tree is a single tree with n terminals, an ape phylo object.

Author(s)

Miranda-Esquivel Daniel R.

Examples

```
library(jrich)
data(tree)
plot(tree)
indexw      <- IndexW(tree)
newTree     <- tree
newTree$tip.label <- indexw
plot(newTree)
```

Multi.Index.Calc	<i>Jack-knife indices in n topologies one time.</i>
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Description

The function calculates the indices values for a MultiData list one time.

Usage

```
Multi.Index.Calc(MultiData = MultiData, jtip = 0, jtopol = 0)
```

Arguments

MultiData is the list of Trees and distributions to evaluate, a list object.
 jtip is the proportion of terminals to delete, real (range 0-1).
 jtopol is the proportion of topologies to delete, real (range 0-1).

Value

Returns the indices values.

Author(s)

Miranda-Esquivel Daniel R.

Examples

```
## get the library
library(jrich)

## load the data
data(Multitaxon1)

Multi.Index.Calc(Multitaxon1, jtip = 0, jtopol = 0)
```

Multi.Jack

Jack-knife indices in n topologies m times.

Description

The function calculates the indices values for a MultiData list m (=replicates) times

Usage

```
Multi.Jack(MultiData = MultiData, times = 100, jtip = 0, jtopol = 0)
```

Arguments

MultiData is the list of Trees and distributions to evaluate, a list object.
 times is the number of times to repeat the process, an integer.
 jtip is the proportion of terminals to delete, real (range 0-1).
 jtopol is the proportion of topologies to delete, real (range 0-1).

Author(s)

Miranda-Esquivel Daniel R.

Examples

```
## get the library
library(jrich)

## load the data
data(Multitaxon1)

Multi.Jack(Multitaxon1, jtip=0.25)
```

Multitaxon1	<i>Multitaxon example.</i>
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Description

A multitaxon example with two hypothetical taxa / distributions

Usage

```
Multitaxon1
```

Format

A list with two objects, each with an APE object, class phylo and the distribution of the terminals.

Author(s)

Miranda-Esquivel Daniel R.

Rank.Indices	<i>Rank indices.</i>
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Description

Rank indices according to the areas' absolute position. If the index value is empty, the function assigns a dummy position "X0X"

Usage

```
Rank.Indices(index.Value = index.Value)
```

Arguments

index.Value a table with indices values.

Value

a table with the decreasing order of the areas It presents the ties alphabetically

Author(s)

Miranda-Esquivel Daniel R.

Examples

```
## get the library  
library(jrich)
```

```
## load the data  
data(tree)  
data(distribution)
```

```
Rank.Indices(Calculate.Index(tree=tree, distrib = distribution, verbose=FALSE))
```

Read.Data

Read distributions.

Description

Read distributions as a csv with two columns species and area

Usage

```
Read.Data(data.File)
```

Arguments

data.File a csv file to read

Value

a data.frame object with the distribution by species

Author(s)

Miranda-Esquivel Daniel R.

Sum.Indices.2.Topologies

Sums two tables with indices values.

Description

You input two tables with indices and it function returns a single table with the sum.

Usage

```
Sum.Indices.2.Topologies(indices1 = indices1, indices2 = indices2)
```

Arguments

indices1 a table of indices values.
indices2 a table of indices values.

Value

a single table with the sum of the two indices.

Author(s)

Miranda-Esquivel Daniel R.

Examples

```
## get the library
library(jrich)

## load the data
data(Multitaxon1)

## calculate indices for two trees and their distributions
temp.Index.Value1 <- Calculate.Index(tree = Multitaxon1[[1]][[1]],
                                     distribution = Multitaxon1[[1]][[2]],0)

temp.Index.Value2 <- Calculate.Index(tree = Multitaxon1[[2]][[1]],
                                     distribution = Multitaxon1[[2]][[2]],0)

## sum the indices values
Sum.Indices.2.Topologies(temp.Index.Value1, temp.Index.Value2)
```

taxon1	<i>A tree and the distribution of the taxa.</i>
--------	---

Description

A list with two objects: Taxon[[1]]: A tree as an APE object with five terminals and Taxon[[2]]: A data frame with five species distributions in eight areas, following Miranda-Esquivel (2016).

Usage

```
taxon1
```

Format

A list with two objects

Author(s)

Miranda-Esquivel Daniel R.

tree	<i>A tree with five terminals.</i>
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Description

A tree as an APE object with five terminals, following Miranda-Esquivel (2016).

Usage

```
tree
```

Format

An APE object, class phylo. A tree dataset with five terminals.

Author(s)

Miranda-Esquivel Daniel R.

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