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>.
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R topics documented:

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

**Usage**

```r
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**

*Children of a node.*

**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**

*Distribution of five taxa.*

**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)
IndexI  

Author(s)
Miranda-Esquivel Daniel R.

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

\( W \) index value for a single topology.

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

\[
\text{IndexW}(\text{tree} = \text{tree})
\]

Arguments

tree

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

Author(s)

Miranda-Esquivel Daniel R.

Examples

\[
\begin{align*}
\text{library(jrich)} \\
\text{data(tree)} \\
\text{plot(tree)} \\
\text{indexw} & \leftarrow \text{IndexW(tree)} \\
\text{newTree} & \leftarrow \text{tree} \\
\text{newTree}\$\text{tip.label} & \leftarrow \text{indexw} \\
\text{plot(newTree)}
\end{align*}
\]

Multi.Index.Calc

Jack-knife indices in \( n \) topologies one time.

Description

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

Usage

\[
\text{Multi.Index.Calc(MultiData = MultiData, jtip = 0, jtopol = 0)}
\]
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

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

## load the data
data(multitaxon1)

Multi.Index.Calc(multitaxon1, jtip = 0, jtopol = 0)
```

Description

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

Usage

```r
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**: in 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

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

## load the data
data(Multitaxon1)

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

---

Multitaxon1  

*Multitaxon example.*

---

Description

A multitaxon example with two hypothetical taxa/distributions

Usage

```r
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  

*Rank indices.*

---

Description

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

Usage

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

Arguments

- `index.Value`: a table with indices values.
Read.Data

Value

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

Author(s)

Miranda-Esquivel Daniel R.

Examples

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

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

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

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**

```r
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**

```r
# 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)
```
A tree and the distribution of the taxa.

**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.

---

A tree with five terminals.

**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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