

# Package: jrich (via r-universe)

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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>.

**License** GPL-3

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

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

**LazyData** false

**RoxygenNote** 5.0.1

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

**RemoteUrl** <https://github.com/dmirandae/jrich>

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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 m 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 standarize 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)

## Standarized by the sum of indices in the distribution
Calculate.Index(tree=tree, distribution = distribution, verbose=TRUE, standard = "distribution")

## Standarized 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")
```

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Children	<i>Children of an internal node.</i>
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**Description**

Get the children of an internal 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, 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,node=7)
```

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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 [1]. The input tree is reordered in post order.

**Usage**

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

**Arguments**

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

**Value**

Returns a vector with weights.

**Author(s)**

Miranda-Esquivel Daniel R.

**References**

[1] Van-Wright et al., 1991. What to Protect? Systematics and the Agony of Choice. *Biological Conservation* 55 (1991) 235-254

**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 weights according to the ramification pattern [1]. The input tree is re-ordered 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.

#' @references [1] Van-Wright et al., 1991. What to Protect? Systematics and the Agony of Choice. Biological Conservation 55 (1991) 235-254

### Examples

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

---

 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

```
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)
```

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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.

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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 labeled "species" and "area"

**Usage**

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

**Arguments**

data.File      a csv file to read, with two columns labeled "species" and "area"

**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)
```

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

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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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