

Package ‘TotalCopheneticIndex’

March 26, 2016

Version 0.1

Date 2016-03-23

Title Total Cophenetic Index

Author Martin R. Smith

Maintainer Martin R. Smith <martins@gmail.com>

Description Quantifies how balanced a phylogenetic tree is, using the Total Cophenetic Index - per A. Mir, F. Rossello, L. A. Rotger (2013), A new balance index for phylogenetic trees. Math. Biosci. 241, 125-136 <DOI:10.1016/j.mbs.2012.10.005>.

Imports ape

License Unlimited

URL <https://github.com/ms609/tci>

NeedsCompilation no

Repository CRAN

Date/Publication 2016-03-26 17:08:55

R topics documented:

list.ancestors	1
tci	2
tci.context	3

Index	5
--------------	----------

list.ancestors	<i>List ancestors</i>
----------------	-----------------------

Description

Reports the ancestors of a given node

Usage

```
list.ancestors(parent, child, node)
```

Arguments

parent	the 'parent' column of the edges property of a tree of class phylo;
child	the 'child' column of the edges property of a tree of class phylo;
node	the number of the node or tip whose ancestors are required.

Details

To observe the number of a node or tip, use `plot(tree); nodelabels(); tiplabels();`

Value

Returns a vector of the numbers of the nodes ancestral to the given node, including the root node.

Author(s)

Martin R. Smith

See Also

`phangorn:::Ancestors`, a less efficient implementation on which this code is based.

Examples

```
tree <- ape::read.tree(text='(1, (2, (3, (4, 5)))));')
edge <- tree$edge
parent <- tree$edge[, 1]
child <- tree$edge[, 2]
list.ancestors(parent, child, 4)
```

tci

Total Cophenetic Index

Description

Calculate the Total Cophenetic Index for any tree.

Usage

```
tci(tree)
```

Arguments

tree	a tree of class <code>phylo</code>
------	------------------------------------

Details

The Total Cophenetic Index is a measure of tree balance - i.e. whether a (phylogenetic) tree comprises symmetric pairs of nodes, or has a pectinate 'caterpillar' shape. The index has a greater resolution power than Sackin's and Colless' indices, and can be applied to trees that are not perfectly resolved. Full details are provided by Mir et al (2013).

Value

Returns the Total Cophenetic Index, a measure of the balance of the tree.

Author(s)

Martin R. Smith

References

A. Mir, F. Rossello, L. A. Rotger, *A new balance index for phylogenetic trees*. Math. Biosci. 241, 125-136 (2013). <DOI:10.1016/j.mbs.2012.10.005>

See Also

The range of possible values for a tree with n tips, and the values expected under simple models of evolution, is provided by [tci.context](#)(tree)

Examples

```
tree12 <- ape::read.tree(text='(1, (2, (3, (4, 5)))));') #Fig. 4, tree 12
tci(tree12) # 10
tree8 <- ape::read.tree(text='((1, 2, 3, 4), 5);') #Fig. 4, tree 8
tci(tree8) # 6
```

tci.context

Contextualize Total Cophenetic Index value

Description

Calculate the range of values that the Total Cophenetic Index can take, and expected values under the Yule and Uniform models of evolution.

Usage

```
tci.context(tree)
```

Arguments

tree a tree of class [phylo](#)

Details

For a tree with n tips, the Total Cophenetic Index can take values of 0 to `choose(nTips, 3)`. The minimum value is higher for a perfectly resolved (i.e. dichotomous) tree (see Lemma 14). Formulae to calculate the expected values under the Yule and Uniform models of evolution are given in Theorems 17 and 23.

Value

A data frame detailing the maximum and minimum value obtainable for the Total Cophenetic Index for dichotomous trees with the number of tips of the given tree, and the expected value under the Yule and Uniform models. The variance of the expected value is given under the Yule model, but cannot be obtained by calculation for the Uniform model.

Author(s)

Martin R. Smith

References

A. Mir, F. Rossello, L. A. Rotger, *A new balance index for phylogenetic trees*. *Math. Biosci.* 241, 125-136 (2013). <DOI:10.1016/j.mbs.2012.10.005>

See Also

`tci`, the Total Cophenetic Index for a given tree

Examples

```
tree12 <- ape::read.tree(text='(1, (2, (3, (4, 5)))));' #Fig. 4, tree 12
tci(tree12)
tci.context(tree12)
```

Index

choose, [4](#)

list.ancestors, [1](#)

nodelabels, [2](#)

phylo, [2](#), [3](#)

tci, [2](#), [4](#)

tci.context, [3](#), [3](#)

tiplabels, [2](#)