Package ‘TotalCopheneticIndex’
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Title An R Package to Quantify Tree Balance
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Description For a given phylogenetic tree, calculates the Total Cophenetic Index.
A new balance index for phylogenetic trees.
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BugReports https://github.com/ms609/tci/issues
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list.ancestors  List ancestors

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**
```r
tci(tree)
```

**Arguments**
- `tree` a tree of class `phylo`.

**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**

**See Also**
The CollessLike package (https://github.com/LuciaRotger/CollessLike) now provides an alternative implementation of this index, and its predecessors. See `cophen.index`.

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**
```r
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)
  tci.context.n(n)

Arguments

  tree  a tree of class phylo;
  n      integer specifying the number of tips in a tree.

Details

For a tree with n tips, the Total Cophenetic Index can take values of 0 to \( \text{choose}(n+2, 3) \) 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


See Also

  tci, the Total Cophenetic Index for a given tree
Examples

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