

# Package ‘TotalCopheneticIndex’

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**Version** 1.0.1

**Date** 2019-01-28

**Title** An R Package to Quantify Tree Balance

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**Description** For a given phylogenetic tree, calculates the Total Cophenetic Index.

Reference: 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>.

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

**BugReports** <https://github.com/ms609/tci/issues>

**Depends** R (>= 3.2.0)

**Imports** memoise

**Suggests** ape, CollessLike, knitr, testthat

**License** Unlimited

**Language** en-GB

**Encoding** UTF-8

**ByteCompile** true

**RoxygenNote** 6.1.1

**NeedsCompilation** no

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**Repository** CRAN

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## R topics documented:

list.ancestors . . . . .	2
tci . . . . .	3
tci.context . . . . .	4

<b>Index</b>	<b>6</b>
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list.ancestors	<i>List ancestors</i>
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**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)
```

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tci	<i>Total Cophenetic Index</i>
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**Description**

Calculate the Total Cophenetic Index for any tree.

**Usage**

```
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**

A. Mir, F. Rossello, L. A. Rotger, *A new balance index for phylogenetic trees*. *Math. Biosci.* 241, 125-136 (2013).

**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**

```
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
```

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`tci.context`*Contextualize Total Cophenetic Index value*

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### 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

<code>tree</code>	a tree of class <a href="#">phylo</a> ;
<code>n</code>	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 `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).

### 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)
tci.context.n(5) # For any tree with 5 tips
```

# Index

choose, [4](#)

cophen.index, [3](#)

list.ancestors, [2](#)

nodelabels, [2](#)

phylo, [3](#), [4](#)

tci, [3](#), [4](#)

tci.context, [3](#), [4](#)

tiplabels, [2](#)