Package 'OReillyEtAl2016'

January 17, 2019

Version 1.0.0

Date 2019-01-10

Title Distance metrics for trees generated by O'Reilly et al. 2016

Description Includes the datasets simulated by O'Reilly et al. (2016)
<doi:10.1111/pala.12236>, and analyes of their partition and quartet distance
from the generative tree, as analysed by Smith (2019).

URL <https://github.com/ms609/OReillyEtAl2016>

BugReports <https://github.com/ms609/Quartet/issues>

Copyright Data from O'Reilly et al. (2016) released uncer a CCO license <doi:10.5061/dryad.10qf3>.

License GPL (>= 2)

Encoding UTF-8

Language en-GB

Depends R (>= 3.4.0)

Suggests ape,
bookdown,
CongreveLamsdell2016,
knitr,
Quartet,
Rdpack,
rmarkdown,
testthat,
usethis

Remotes ms609/CongreveLamsdell2016

RdMacros Rdpack

LazyData true

ByteCompile true

VignetteBuilder knitr

RoxygenNote 6.1.1

Roxygen list(markdown = TRUE)

R **topics documented:**

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orQuartets	*Partition and Quartet similarity counts for trees generated from the datasets of O'Reilly* et al.

Description

For each of the 3000 matrices simulated by O'Reilly *et al.* (2016),, I conducted phylogenetic analysis under different methods:

Usage

```
orQuartets

orPartitions
```

Format

An object of class list of length 3.

Details

- markovUsing the Markov K model in MrBayes.
- equalUsing equal weights in TNT.
- implied1,implied2,implied3,implied5,implied10Using implied weights in TNT, with the concavity constant (*k*) set to 1, 2, 3, 5, or 10
- impliedCBy taking the strict *c*onsensus of all trees recovered by implied weights parsimony analysis under the *k* values 2, 3, 5 and 10 (but not 1).

For each analysis, I recorded the strict consensus of all optimal trees, and also the consensus of trees that were suboptimal by a specified degree.

I then calculated, of the total number of < reference tree, how many were the *s*ame or *d*ifferent in the tree that resulted from the phylogenetic analysis, and how many were not resolved in this tree (*r2*).

The data object contains a list whose elements are named after the methods, as listed above.

Each list entry is a three-dimensional array, whose dimensions are:

- 1The suboptimality of the tree: for *markov*, the consensus at a 50 52.5 all trees that are 0, 1, ... 19, 20 steps less optimal than the optimal tree; for *implied*, the consensus of all trees that are 0.73^(19:0) less optimal than the optimal tree.
- 2The number of < in the estimated tree but not the generative tree (= 0), resolved in the generative tree but not the estimated tree
- 3The number of the matrix, from 1 to 100.

Source

Adummy A (2019). "Not avalable." Failed to insert reference with key = Congreve2016 from package = 'Quartet'. Possible cause — missing or misspelled key.

See Also

[clMatrices](#), [clReferenceTree](#).

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orReferenceTree	*O'Reilly et al. reference tree*

Description

The tree topology used to generate the matrices in O'Reilly *et al.* 2016

Usage

```
orReferenceTree
```

Format

A single phylogenetic tree saved as an object of class `phylo`

Source

Adummy A (2019). "Not avalable." Failed to insert reference with key = OReilly2016 from package = 'Quartet'. Possible cause — missing or misspelled key.

References

Adummy A (2019). "Not avalable." Failed to insert reference with key = OReilly2016 from package = 'Quartet'. Possible cause — missing or misspelled key.

Examples

```
library('ape') # Contains tree plotting functions
data(orReferenceTree)
plot(orReferenceTree)
```

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