

# Package ‘OReillyEtAl2016’

January 23, 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 analyses 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 under 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)

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orQuartets	<i>Partition and Quartet similarity counts for trees generated from the datasets of O'Reilly et al.</i>
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**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 consensus 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 same or different 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 available.” 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*

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**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 available.” Failed to insert reference with key = OReilly2016 from package = 'Quartet'. Possible cause — missing or misspelled key.

**References**

Adummy A (2019). “Not available.” 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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\*Topic **datasets**

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