Package 'Triples'

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Title Test your phylogeny

Version 1.0

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Description Calculates resolution of triples from the set of phylogeny trees

Depends ape (>= 2.0)

License GPL (>= 2)

URL https://github.com/Ambuj-UF/Triples

R topics documented:

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triples   *SuperMatrix Rooted Triple (SMRT)*

Description

Calculates triples resolution from the input phylogeny tree file.

Usage

```
triples(input="", auth="", outgroup="", output="Triples.txt")
```

Arguments

input   Phylogeny tree file name specified by either a variable of mode character, or a
                double-quoted string; if input = "" (the default) then the program terminates
                with message

auth   File that contains list of taxa to be included for calculating triples resolution. If
                auth = "" (the default) then the program terminates with message

outgroup	Tree outgroup taxa name. If `outgroup = ""` (the default) then the program terminates with message
output	a file name specified by either a variable of mode character, or a double-quoted string; if `output = ""` (the default) programs generates output in Triples.txt file

Author(s)

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References

DeGiorgio M, Degnan JH. Fast and Consistent Estimation of Species Trees Using Supermatrix Rooted Triples. Mol Biol Evol. 2010 Mar;27(3):552-69. http://mbe.oxfordjournals.org/content/27/3/552.long

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