

Package ‘aptg’

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Type Package

Title Automatic Phylogenetic Tree Generator

Version 0.1.0

Author Christophe Benjamin

Maintainer Christophe Benjamin <c.chignac.benjamin@gmail.com>

Description Generates phylogenetic trees and distance matrices from a list of species name or from a taxon down to whatever lower taxon. It can do so based on two reference super trees: mammals and angiosperms.

Depends ape, brranching, phytools, taxize, xml2

Suggests paco, vegan, knitr, rmarkdown

VignetteBuilder knitr

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Encoding UTF-8

LazyData true

RoxygenNote 6.0.1

NeedsCompilation no

Repository CRAN

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`downto.tree`*Hierarchical Tree Generator*

Description

Generates a phylogenetic tree from a taxon down to a chosen lower taxon.

Usage

```
downto.tree(taxon, downto, key = NULL)
```

Arguments

<code>taxon</code>	The higher taxon from which the tree will start.
<code>downto</code>	The lowest level of taxonomy wanted. Must be included in the argument <code>taxon</code> .
<code>key</code>	API key.

`taxa.tree`*Tree from taxa*

Description

Generates a tree and distance matrix from a list of species names. There are reference trees for mammals and angiosperms. The input species will be sorted by reference trees.

Usage

```
taxa.tree(species)
```

Arguments

<code>species</code>	a list of species that is to be included in the phylogenetic tree.
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