

Package ‘aptg’

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Type Package

Title Automatic Phylogenetic Tree Generator

Version 0.1.0

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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	<i>Hierarchical Tree Generator</i>
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Description

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

Usage

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

Arguments

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

species	a list of species that is to be included in the phylogenetic tree.
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