

# Package ‘aptg’

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**Type** Package

**Title** Automatic Phylogenetic Tree Generator

**Version** 0.1.1

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**Description** Generates phylogenetic trees and distance matrices ('brranching', <<https://CRAN.R-project.org/package=brranching>>) from a list of species name or from a taxon down to whatever lower taxon ('taxize', <<https://github.com/ropensci/taxize>>). It can do so based on two reference super trees: mammals (Bininda-Emonds et al., 2007; <[doi:10.1038/nature05634](https://doi.org/10.1038/nature05634)>) and angiosperms (Zanne et al., 2014; <[doi:10.1038/nature12872](https://doi.org/10.1038/nature12872)>).

**Depends** ape,brranching, phytools, taxize, xml2

**Suggests** paco, vegan, knitr, rmarkdown, qpdf

**VignetteBuilder** knitr

**License** MIT + file LICENSE

**Encoding** UTF-8

**LazyData** true

**RoxygenNote** 7.1.1

**NeedsCompilation** no

**Repository** CRAN

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 downto.tree

*Hierarchical Tree Generator*


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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, db = "ncbi")
```

### Arguments

taxon	The higher taxon from which the tree will start. (i.e. Family, Genus)
downto	The lowest level of taxonomy wanted. Must be lower than the one in taxon argument. Only species can be outputted from the Mammals tree.
key	API key. To create one use <code>taxize::use_entrez()</code> .
db	Database used. Default is "ncbi". For possible databases see <code>?taxize::downstream</code>

### Examples

```
## Not run:
#Choose a certain taxon and the level you want the tree to stop
downto.tree("Cervidae", "species")

## End(Not run)
```

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 taxa.tree

*Tree from taxa*


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### 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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### Examples

```
## Not run:  
#Choose a list of string of species that you want to have in a phylogenetic tree.  
taxa.tree(species = c("Canis lupus", "Canis latrans", "Acer saccharum", "Castor canadensis",  
"Alces alces", "Acer rubrum",  
"Vulpes vulpes", "Salix babylonica", "Odocoileus virginianus", "Betula alleghaniensis",  
"Rangifer tarandus", "Juniperus occidentalis"))  
## End(Not run)
```

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