

geneplast.data

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make.phyloTree *Build a 'phyloTree' object for geneplast*

Description

This function has two optional arguments that define its behavior depending on which one is provided. Given a list of species' NCBI Taxonomy IDs, 'make.phyloTree()' builds a phylogenetic tree by merging the TimeTree and NCBI Taxonomy databases. If given a newick file, it simply forwards the argument to [treeio::read.newick()].

Usage

```
make.phyloTree(sspids = NULL, newick = NULL, verbose = TRUE)
```

Arguments

sspids	a vector or data frame containing NCBI Taxon IDs from the species of interest.
newick	a phylogenetic tree in Newick format.
verbose	a logical value specifying whether or not to display detailed messages.

Value

An object of class "phylo".

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