# geneplast.data

November 11, 2026

| | |
|---|---|
| `make.cogdata` | *Parse orthogroups tabular output from OrthoFinder into a 'cogdata' data frame for geneplast* |

## Description

Parse orthogroups tabular output from OrthoFinder into a 'cogdata' data frame for geneplast

## Usage

```
make.cogdata(file)
```

## Arguments

| | |
|---|---|
| `file` | OrthoFinder orthogroups tabular file |

## Value

cogdata data frame

## Author(s)

Leonardo RS Campos

`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".

## Author(s)

Danilo O Imparato

Leonardo RS Campos

# Index

make.cogdata, 1
make.phyloTree, 2