

# geneplast.data

January 14, 2026

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| <code>make.cogdata</code> | <i>Parse orthogroups tabular output from OrthoFinder into a 'cogdata' data frame for geneplast</i> |
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## Description

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

## Usage

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

## Arguments

|                   |                                      |
|-------------------|--------------------------------------|
| <code>file</code> | OrthoFinder orthogroups tabular file |
|-------------------|--------------------------------------|

## Value

cogdata data frame

## Author(s)

Leonardo RS Campos

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| <code>make.phyloTree</code> | <i>Build a 'phyloTree' object for geneplast</i> |
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## 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**

|                      |                                                                                |
|----------------------|--------------------------------------------------------------------------------|
| <code>sspids</code>  | a vector or data frame containing NCBI Taxon IDs from the species of interest. |
| <code>newick</code>  | a phylogenetic tree in Newick format.                                          |
| <code>verbose</code> | 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

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