

# geneplast.data

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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
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## 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**

`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)**

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