# geneplast.data

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## `make.cogdata` *Parse orthogroups tabular output from OrthoFinder into a ‘cogdata‘ data frame for geneplast*

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### 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

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## `make.phyloTree` *Build a ‘phyloTree‘ object for geneplast*

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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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# Index