

Package ‘geneplast.data’

December 10, 2025

Title Input data for the geneplast package via AnnotationHub

Version 0.99.9

Description The package geneplast.data provides
datasets from different sources via AnnotationHub to use in geneplast pipelines.
The datasets have species, phylogenetic trees, and orthology relationships
among eukaryotes from different orthologs databases.

Depends R (>= 4.0)

Imports ape, treeio, tibble, tidyr, dplyr, readr, purrr, igraph,
geneplast, BiocFileCache

Suggests geneplast, BiocGenerics, BiocStyle, knitr, rmarkdown

VignetteBuilder knitr

License Artistic-2.0

biocViews Genetics, GeneRegulation, SystemsBiology, AnnotationData,
AnnotationHub

Encoding UTF-8

RoxygenNote 7.2.3

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make.cogdata	<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

file OrthoFinder orthogroups tabular file

Value

cogdata data frame

Author(s)

Leonardo RS Campos

make.phyloTree	<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>sspid</code> s	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".

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