Package 'algaeClassify'

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Title Determine phytoplankton functional groups based on functional traits

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URL http://github.com/vppatil/GEISHA_phytoplankton

BugReports https://github.com/vppatil/GEISHA_phytoplankton/issues

Description The algaeClassify package contains functions designed to facilitate the assignment of morpho-functional group (MFG) classifications to phytoplankton species based on a combination of taxonomy (Class,Order) and a suite of 7 binomial functional traits. MFG classifications are derived from Salmaso, Nico, Luigi Naselli-Flores, and Judit Padisak. ``Functional classifications and their application in phytoplankton ecology.'' Freshwater Biology 60.4 (2015): 603-619, and this reference should be cited when using the package. The algaeClassify package is a product of the GEISHA (Global Evaluation of the Impacts of Storms on freshwater Habitat and Structure of phytoplankton Assemblages), funded by CESAB (the Centre for Synthesis and Analysis of Biodiversity) and the USGS John Wesley Powell Center, with data and other support provided by members of GLEON (the Global Lake Ecology Observation Network). This software is preliminary or provisional and is subject to revision. It is being provided to meet the need for timely best science. The software has not received final approval by the U.S. Geological Survey (USGS). No warranty, expressed or implied, is made by the USGS or the U.S. Government as to the functionality of the software and related material nor shall the fact of release constitute any such warranty. The software is provided on the condition that neither the USGS nor the U.S. Government shall be held liable for any damages resulting from the authorized or unauthorized use of the software.

Depends R (>= 3.4.0)

License GPL (>=3)

Encoding UTF-8

LazyData true

RoxygenNote 6.1.0

R topics documented:

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traits_to_mfg | *Assign a morphofunctional group based on binary functional traits and higher taxonomy*

Description

Assign a morphofunctional group based on binary functional traits and higher taxonomy

Usage

```
traits_to_mfg(flagella = NA, size = NA, colonial = NA,
  filament = NA, centric = NA, gelatinous = NA, aerotopes = NA,
  class = NA, order = NA)
```

Arguments

flagella	1 if flagella are present, 0 if they are absent.
size	Character string: 'large' or 'small'. Classification criteria is left to the user.
colonial	1 if typically colonial growth form, 0 if typically unicellular.
filament	1 if dominant growth form is filamentous, 0 if not.
centric	1 if diatom with centric growth form, 0 if not. NA for non-diatoms.
gelatinous	1 mucilagenous sheath is typically present, 0 if not.
aerotopes	1 if aerotopes allowing buoyancy regulation are typically present, 0 if not.
class	Character string: The taxonomic class of the species
order	Character string: The taxonomic order of the species

Value

A character string of the species' morphofunctional group

See Also

http://www.algaebase.org for up-to-date phytoplankton taxonomy, https://powellcenter.usgs.gov/geisha for project information

Examples

```
traits_to_mfg(1,"large",1,0,NA,0,0,"Euglenophyceae","Euglenales")
```

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traits_to_mfg_df	*Assign morphofunctional groups to a dataframe of functional traits and higher taxonomy*

Description

Assign morphofunctional groups to a dataframe of functional traits and higher taxonomy

Usage

```
traits_to_mfg_df(dframe, arg.names = c("flagella", "size", "colonial",
  "filament", "centric", "gelatinous", "aerotopes", "class", "order"))
```

Arguments

dframe	An R dataframe containing functional trait information and higher taxonomy
arg.names	Character string of column names corresponding to arguments for traits_to_mfg()

Value

A character vector containing morpho-functional group (MFG) designations

Examples

```
#create a two-row example dataframe of functional traits
func.dframe=data.frame(flag=1,size=c("large","small"),col=0,fil=0,cent=NA,gel=0,
                       aer=0,cl="Euglenophyceae",or="Euglenales",stringsAsFactors=FALSE)

#check the dataframe
print(func.dframe)

#run the function to produce a two-element character vector
traits_to_mfg_df(func.dframe,c("flag","size","col","fil","cent","gel","aer","cl","or"))
```

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