Package ‘PhySortR’

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Type Package

Title A Fast, Flexible Tool for Sorting Phylogenetic Trees

Version 1.0.9

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Description Screens and sorts phylogenetic trees in both traditional and extended Newick format. Allows for the fast and flexible screening (within a tree) of Exclusive clades that comprise only the target taxa and/or Non-Exclusive clades that includes a defined portion of non-target taxa.

Depends R (>= 3.0.0)

Imports phytools, ape, methods

Repository CRAN

License GPL (>= 3)

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NeedsCompilation no

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Contents

`PhySortR-package` *A Fast, Flexible Tool for Sorting Phylogenetic Trees*

Description

PhySortR provides a quick and highly flexible function for the screening (within a tree) of Exclusive clades that comprise only the target taxa and/or Non-Exclusive clades that includes a defined portion of non-target taxa. Support is also provided for both traditional and extended Newick formatted phylogenetic trees.

A full list of functions can be displayed by `library(help = PhySortR)`.

Details

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Type:	Package
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Author(s)

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References

Stephens TG, Bhattacharya D, Ragan MA, Chan CX. 2016. PhySortR: a fast, flexible tool for sorting phylogenetic trees in R. PeerJ, 4:e2038, DOI:10.7717/peerj.2038

`convert.eNewick` *Converts Extended Newick Format to Traditional Newick Format*

Description

Takes a phylogenetic tree in extended Newick format and converts it to traditional Newick format that can be directly manipulated by packages such as `ape` and `phytools`.

Usage

```
convert.eNewick(eNewick)
```

Arguments

`eNewick`	phylogenetic tree in extended Newick format.

Value

phylogenetic tree in traditional Newick format.

Examples

```
### Converts the phylogenetic tree into traditional Newick format.
tree <- "((A:0.1,(B:0.3,C:0.2):0.2[60]):0.4[100],(E:0.12,F:0.09):0.4[100]);"
new.tree <- convert.eNewick(tree)
new.tree
```

`sortTrees` *Sorts Phylogenetic Trees using Taxa Identifiers*

Description

Reads phylogenetic trees from a directory and sorts them based on the presence of Exclusive and Non-Exclusive clades containing a set of given target leaves at a desired support value. Can interpret trees in both Newick and extended Newick format.

Usage

```
sortTrees(
  target.groups,
  min.support = 0,
  min.prop.target = 0.7,
  in.dir = ".",
  out.dir = "Sorted_Trees",
  mode = "l",
  clades.sorted = "E,NE",
  extension = ".tre",
  clade.exclusivity = 0.9
)
```

Arguments

`target.groups`	a set of one or more terms that represent the target leaves whose membership will be tested in each clade during sorting. Multiple terms are to be separated by a comma (`"Taxon1,Taxon2"`). This process is case sensitive and uses strict string-matching, so the taxa identifiers must be unique i.e. `"plantae"` and `"Viridiplantae"` might not be appropriate as the first is a subset of the second.
`min.support`	the minimum support (i.e. between 0-1 or 0-100) of a clade (Default = 0). Support values missing from phylogenetic trees are interpreted as zero. A vector of values can be provided if multiple support values (e.g., aLRT, UFboot) are present in the tree (i.e., `"75.5/95"`).

`min.prop.target`	the minimum proportion (between 0.0-1.0) of target leaves to be present in a clade out of the total target leaves in the tree (Default = 0.7).
`in.dir`	directory containing the phylogenetic trees to be sorted (Default = current working directory).
`out.dir`	directory to be created within `in.dir` for the trees identified during sorting. If `out.dir` is omitted the default of `Sorted_Trees/` will be used.
`mode`	option to `"m"` (move), `"c"` (copy) or `"l"` (list) trees identified during sorting. In `"l"` mode (default) a list of the sorted trees is returned, in the `"m"` and `"c"` modes a list is returned and the identified trees are moved/copied to the `out.dir`.
`clades.sorted`	option to control if the function will sort for Exclusive (`"E"`) and/or Non-Exclusive (`"NE"`) clades. Specify both options by comma separation `"E,NE"` (Default). Exclusive clades are also sorted into a sub-group of All Exclusive trees.
`extension`	the file extension of the tree files to be analyzed (Default = `".tre"`).
`clade.exclusivity`	the minimum proportion (0.0 <= x < 1.0) of target leaves to interrupting leaves allowed in each non-exclusive clade (Default = 0.9).

Value

Will always return a list containing the names of the trees identified during sorting, irrespective of the `mode` argument.

Examples

```
### Load data ###
extdata <- system.file("extdata", package="PhySortR")
file.copy(dir(extdata, full.names = TRUE), ".")
dir.create("Algae_Trees/")
file.copy(dir(extdata, full.names = TRUE), "Algae_Trees/")

### Examples ###
# (1) Sorting using 3 target terms, all other parameters default.
sortTrees(target.groups = "Rhodophyta,Viridiplantae")

# The function will search in the users current working directory for files
# with the extension ".tre" and check them (using default min.support,
# min.prop.target and clade.exclusivity) for Exclusive, All Exclusive or
# Non-Exclusive clades. A list will be returned with the names of the trees
# identified during sorting.



# (2) Sorting with a target directory and an out directory specified.
sortTrees(target.groups = "Rhodophyta,Viridiplantae",
  in.dir= "Algae_Trees/",
  out.dir="Sorted_Trees_RVG/",
  mode = "c")

# The function will search in "Algae_Trees/" for files with the extension
```

```
# ".tre" and check them (using default min.support, min.prop.target,
# clade.exclusivity) for Exclusive, All Exclusive or Non-Exclusive clades.
# The function will both (a) return a list of the trees identified during
# sorting and (b) copy the files into their respective subdirectories of
# "Algae_Trees/Sorted_Trees_RVG/Exclusive/",
# "Algae_Trees/Sorted_Trees_RVG/Exclusive/All_Exclusive/" and
# "Algae_Trees/Sorted_Trees_RVG/Non_Exclusive/".



# (3) Sorting with in/out directories, min.prop.target and min.support specified.
sortTrees(target.groups = "Rhodophyta,Viridiplantae",
  min.prop.target = 0.8,
  min.support = 90,
  in.dir= "Algae_Trees/",
  out.dir="Sorted_Trees_RVG_95/",
  mode = "c",
  clades.sorted = "NE",
  clade.exclusivity = 0.95)

# The function will search in "Algae_Trees/" for files with the
# extension ".tre" and check them for only Non-Exclusive clades.
# A clade will only be defined if it has support >= 90 and contains at least
# 80% of the total target leaves in the tree. A Non-Exclusive clade must also
# be composed of >= 95% target taxa (i.e. < 5% non-target taxa).
# The function will (a) return a list of the trees identified during
# sorting and (b) copy the trees identified during sorting to the out
# directory "Algae_Trees/Sorted_Trees_RVG/Non_Exclusive/".

# (4) Sorting with multiple min.support values specified.
#sortTrees(target.groups = "Rhodophyta,Viridiplantae",
#  min.prop.target = 0.8,
#  min.support = c(75, 90),
#  in.dir= "Algae_Trees/",
#  out.dir="Sorted_Trees_RVG_75_95/",
#  mode = "c",
#  clades.sorted = "NE",
#  clade.exclusivity = 0.95)

# The function will search in "Algae_Trees/" for files with the
# extension ".tre" and check them for only Non-Exclusive clades.
# A clade will only be defined if it has its first support >= 75
# and its second support >= 90 and contains at least 80% of the
# total target leaves in the tree. A Non-Exclusive clade must also
# be composed of >= 95% target taxa (i.e. < 5% non-target taxa).
# The function will (a) return a list of the trees identified during
# sorting and (b) copy the trees identified during sorting to the out
# directory "Algae_Trees/Sorted_Trees_RVG/Non_Exclusive/".

### Clean up ###
unlink("Algae_Trees", recursive=TRUE)
unlink("Sorted_Trees.log")
unlink(dir(".", ".*.tre$"))
```

Index