Package 'brranching'

May 11, 2021

Title Fetch 'Phylogenies' from Many Sources

Description Includes methods for fetching 'phylogenies' from a variety
of sources, including the 'Phylomatic' web service
(<http://phylodiversity.net/phylomatic/>), and 'Phylocom'
(<https://github.com/phylocom/phylocom/>).

Version 0.7.0

License MIT + file LICENSE

URL <https://docs.ropensci.org/brranching/> (documentation)

    <https://github.com/ropensci/brranching> (source)

BugReports <https://github.com/ropensci/brranching/issues>

LazyLoad yes

LazyData yes

Encoding UTF-8

Depends R(>= 3.2.1)

Imports crul (>= 0.4.0), curl, ape, taxize (>= 0.9.97), phytools,
phylocomr (>= 0.1.4), conditionz

Suggests testthat

RoxygenNote 7.1.1

X-schema.org-applicationCategory Phylogenetics

X-schema.org-keywords phylogeny, tree, phylomatic, molecular, plants

X-schema.org-isPartOf ``https://ropensci.org''

NeedsCompilation no

Author Scott Chamberlain [aut, cre] (<https://orcid.org/0000-0003-1444-9135>)

Maintainer Scott Chamberlain <myrmecocystus@gmail.com>

Repository CRAN

Date/Publication 2021-05-11 05:22:14 UTC

R topics documented:

Index **10**

---

brranching-package   *brranching*

Description

Phylogenies from many sources

Author(s)

Scott Chamberlain myrmecocystus@gmail.com

---

phylomatic   *Query Phylomatic for a phylogenetic tree.*

Description

Query Phylomatic for a phylogenetic tree.

Usage

```
phylomatic(
  taxa,
  taxnames = TRUE,
  get = "GET",
  informat = "newick",
  method = "phylomatic",
  storedtree = "R20120829",
  treeuri = NULL,
  taxaformat = "slashpath",
  outformat = "newick",
  clean = TRUE,
  db = "apg",
  mssgs = TRUE,
  ...
)
```

Arguments

taxa	Phylomatic format input of taxa names.
taxnames	If TRUE (default), we get the family names for you to attach to your species names to send to Phylomatic API. If FALSE, you have to provide the strings in the right format.
get	'GET' (default) or 'POST' format for submission to the website.
informat	One of newick (default), nexml, or cdaordf. If using a stored tree, informat should always be newick.
method	One of phylomatic (default) or convert
storedtree	One of R20120829 (Phylomatic tree R20120829 for plants), smith2011 (Smith 2011, plants), binindaemonds2007 (Bininda-Emonds 2007, mammals), or zanne2014 (Zanne et al. 2014, plants). Default: R20120829
treeuri	URL for a phylogenetic tree in newick format.
taxaformat	Only option is slashpath for now. Leave as is.
outformat	One of newick, nexml, or fyt.
clean	Return a clean tree or not. Default: TRUE
db	One of "ncbi", "itis", or "apg". Default: apg
mssgs	Print messages. Default: TRUE
...	curl options passed on to crul::HttpClient

Details

Use the web interface at <http://phylodiversity.net/phylomatic/>

If you set taxnames = FALSE, you need to pass in a character vector, with each element like this example: "asteraceae/taraxacum/taraxacum_officinale", of the form "family/genus/genus_specfic epithet"

Value

Newick formatted tree as phylo object or nexml character string

Examples

```
## Not run:
# Input taxonomic names
taxa <- c("Poa annua", "Phlox diffusa", "Helianthus annuus")
tree <- phylomatic(taxa=taxa, get = 'POST')
plot(tree, no.margin=TRUE)

# Genus names
taxa <- c("Poa", "Phlox", "Helianthus")
tree <- phylomatic(taxa=taxa, storedtree='R20120829', get='POST')
plot(tree, no.margin=TRUE)

# Lots of names
taxa <- c("Poa annua", "Collomia grandiflora", "Lilium lankongense", "Phlox diffusa",
```

```
"Iteadaphne caudata", "Gagea sarmentosa", "Helianthus annuus")
tree <- phylomatic(taxa=taxa, get = 'POST')
plot(tree, no.margin=TRUE)

# Don't clean - clean=TRUE is default
(tree <- phylomatic(taxa=taxa, clean = FALSE))
## with clean=FALSE, you can get non-splitting nodes, which you
## need to collpase before plotting
library('ape')
plot(collapse.singles(tree), no.margin=TRUE)

# Output NeXML format
taxa <- c("Gonocarpus leptothecus", "Gonocarpus leptothecus", "Lilium lankongense")
out <- phylomatic(taxa=taxa, get = 'POST', outformat = "nexml")
cat(out)

# Lots of names, note that when you have enough names (number depends on length of individual
# names, so there's no per se rule), you will get an error when using `get='GET'`,
# when that happens use `get='POST'`
library("taxize")
spp <- names_list("species", 500)
# phylomatic(taxa = spp, get = "GET")
(out <- phylomatic(taxa = spp, get = "POST", db = "itis"))
plot(out)

## End(Not run)
```

---

phylomatic_local   *Use Phylomatic locally - ideal for large queries*

Description

Use Phylomatic locally - ideal for large queries

Usage

```
phylomatic_local(
  taxa,
  taxnames = TRUE,
  storedtree = "R20120829",
  db = "apg",
  lowercase = FALSE,
  nodes = FALSE,
  verbose = TRUE
)
```

Arguments

taxa   (character) Phylomatic format input of taxa names. required

taxnames	If TRUE (default), we get the family names for you to attach to your species names to send to Phylomatic API. If FALSE, you have to provide the strings in the right format. See Details.
storedtree	One of R20120829 (Phylomatic tree R20120829 for plants), smith2011 (Smith 2011, plants), binindaemonds2007 (Bininda-Emonds 2007, mammals), or zanne2014 (Zanne et al. 2014, plants). Default: R20120829
db	(character) One of "ncbi", "itis", or "apg". Default: apg
lowercase	(logical) Convert all chars in taxa file to lowercase. Default: FALSE
nodes	(logical) label all nodes with default names. Default: FALSE
verbose	(logical) Print messages. Default: TRUE

Details

uses phylocomr::ph_phylomatic() under the hood

This function uses Phylomatic via Phylocom using the **phylocomr** package. The interface is slightly different from phylomatic(): there's no tree by URL available, and some of the parameters are not included here.

If you set taxnames = FALSE, you need to pass in a character vector, with each element like this example: "asteraceae/taraxacum/taraxacum_officinale", of the form "family/genus/genus_specfic epithet"

Value

Newick formatted tree as phylo object

Examples

```
## Not run:
library('ape')

# Input taxonomic names
taxa <- c("Poa annua", "Phlox diffusa", "Helianthus annuus")
(tree <- phylomatic_local(taxa))
plot(collapse.singles(tree), no.margin=TRUE)

taxa <- c("Poa annua", "Collomia grandiflora", "Lilium lankongense",
"Phlox diffusa", "Iteadaphne caudata", "Gagea sarmentosa",
"Helianthus annuus")
(tree <- phylomatic_local(taxa))
plot(collapse.singles(tree), no.margin=TRUE)

library("taxize")
spp <- names_list("species", 500)
length(spp)
(tree <- phylomatic_local(spp))

## End(Not run)
```

---

phylomatic_names   *Phylomatic names*

Description

Get family names to make Phylomatic input object, and output input string to Phylomatic for use in the function phylomatic

Usage

```
phylomatic_names(taxa, format = "isubmit", db = "ncbi", ...)
```

Arguments

taxa   quoted tsn number (taxonomic serial number)

format   output format, isubmit (you can paste in to the Phylomatic website), or 'rsubmit'
              to use in fxn phylomatic_tree

db   One of "ncbi", "itis", or "apg". if you use "apg", no HTTP requests are made (no
              internet connection needed), whereas if you use "ncbi" or "itis" you do need an
              internet connection. IMPORTANT: see **Authentication** below if using "ncbi".

...   curl options passed on to [taxize::tax_name()]

Value

string (e.g., "pinaceae/pinus/pinus_contorta"), in Phylomatic submission format

Authentication

NCBI Entrez doesn't require that you use an API key, but you get higher rate limit with a key, from 3 to 10 requests per second, so do get one. Run taxize::use_entrez() or see https://ncbiinsights.ncbi.nlm.nih.gov/2017/11/0 api-keys-for-the-e-utilities/ for instructions.

NCBI API key handling logic is done inside of the taxize package, used inside this function.

Save your API key with the name ENTREZ_KEY as an R option in your .Rprofile file, or as environment variables in either your .Renviron file or .bash_profile file, or .zshrc file (if you use oh-my-zsh) or similar. See [Startup] for help on R options and environment variables. You cannot pass in your API key in this function.

Remember to restart your R session (and to start a new shell window/tab if you're using the shell) to take advantage of the new R options or environment variables.

We strongly recommend using environment variables over R options.

Note that if you don't have an ENTREZ_KEY set, you'll get a message about it, but only once during each function call. That is, there can be of these messages per R session, across function calls.

Examples

```
## Not run:
mynames <- c("Poa annua", "Salix goodingii", "Helianthus annuus")
phylomatic_names(taxa = mynames, format='rsubmit')
phylomatic_names(mynames, format='rsubmit', db="apg")
phylomatic_names(mynames, format='isubmit', db="ncbi")
phylomatic_names(mynames, format='isubmit', db="apg")

## End(Not run)
```

---

phylomatic_trees   *Phylogenies to use with phylomatic*

Description

Phylogenies to use with phylomatic

Format

A list with 4 character strings:

- R20120829 - 2401 tips, 1801 internal nodes
- binindaemonds2007 - 4510 tips, 2108 internal nodes
- zanne2014 - 31749 tips, 31748 internal nodes
- smith2011 - 55473 tips, 55338 internal nodes

Source

phylocom

---

rbladj   *Run Phylocom's bladj from R*

Description

Run Phylocom's bladj from R

Usage

```
rbladj(tree, ages)
```

Arguments

tree	(character/phylo) One of: phylogeny as a newick string (will be written to a temp file) - OR path to file with a newick string - OR a an **ape** phylo object. required.
ages	(data.frame/character) ages data.frame, or path to an ages file. required.

Details

uses phylocomr::ph_bladj() under the hood

Value

Newick formatted tree as phylo object

Examples

```
## Not run:
library("phylocomr")

# make an ages data.frame
ages_df <- data.frame(
  a = c('malpighiales','eudicots','ericales_to_asterales','plantaginaceae',
        'malvids', 'poales'),
  b = c(81, 20, 56, 76, 47, 71)
)

# read phylogeny file as a string
phylo_file <- system.file("examples/phylo_bladj", package = "phylocomr")
phylo_str <- readLines(phylo_file)

# Run Bladj, returns phylo object
(x <- rbladj(tree = phylo_str, ages = ages_df))

# load ape and plot tree
library(ape)
plot(x)

## End(Not run)
```

---

tpl   *Lookup-table for family, genus, and species names for ThePlantList*
                                             gymnosperms

Description

These names are from http://www.theplantlist.org/, collected on 2015-11-11, and are from
version 1.1 of their data. This data is used in the function phylomatic_names()

Format

A data frame with 23,801 rows and 2 variables:

- family: family name
- genus: genus name

Source

http://www.theplantlist.org/

Index