Package ‘brranching’

June 12, 2020

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 0.6.0

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URL https://docs.ropensci.org/brranching,
https://github.com/ropensci/brranching

BugReports http://github.com/ropensci/brranching/issues

LazyLoad yes

LazyData yes

Encoding UTF-8

VignetteBuilder knitr

Depends R(>= 3.2.1)

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

Suggests testthat, knitr

RoxygenNote 7.1.0

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**brranching-package**  
*brranching*

**Description**

Phylogenies from many sources

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**phylomatic**  
*Query Phylomatic for a phylogenetic tree.*

**Description**

Query Phylomatic for a phylogenetic tree.

**Usage**

```r
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), binindaemons2007 (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 curl::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_specific epithet"

Value

Newick formatted tree as phylo object or nexml character string

Examples

```r
## 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",
```

"Itea daphne 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 collapse 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''
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**

```r
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_specific epithet"

Value

Newick formatted tree as phylo object

Examples

```r
## 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)
**Description**

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

**Usage**

```r
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/2017/11/02/new-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

```r
## 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 \texttt{phylocomr::ph_bladj()} under the hood

Value

Newick formatted tree as \texttt{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)

\begin{longtable}{l}
\texttt{tpl} & \textit{Lookup-table for family, genus, and species names for ThePlantList} \\
& \textit{gymnosperms}
\end{longtable}

Description

These names are from \url{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 \texttt{phylomatic_names()}

Format

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

- family: family name
- genus: genus name
Source

http://www.theplantlist.org/
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