Package ‘brranching’

July 27, 2019

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 0.5.0

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

Suggests testthat, knitr

RoxygenNote 6.1.1

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NeedsCompilation no

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brranching-package  

Phylogenies from many sources

Description
Phylogenies from many sources

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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), nxeml, 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 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
taxa = "family/genus/genus specific 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", 
"Teadaphne 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)
phylomatic_local

## 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), binindaemons2007 (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 phylocom::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)
```

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

```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/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.

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
**rbladj**

**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

```r
## 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)
```

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**tpl**

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

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**Description**

These names are from [http://www.theplantlist.org/](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**