

Package ‘brranching’

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Title Fetch 'Phylogenies' from Many Sources

Description Includes methods for fetching 'phylogenies' from a variety of sources, currently includes 'Phylomatic' (<<http://phylodiversity.net/phyloomatic>>), with more in the future.

Version 0.3.0

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URL <https://github.com/ropensci/brranching>

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

LazyLoad yes

LazyData yes

Depends R(>= 3.2.1)

Imports crul (>= 0.4.0), curl (>= 1.2), ape, taxize, phytools

Suggests testthat

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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), 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 HttpClient

Details

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

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 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 \code{get='GET'},
# when that happens use \code{get='POST'}
library("taxize")
spp <- names_list("species", 5000)
# phylomatic(taxa = spp, get = "GET")
(out <- phylomatic(taxa = spp, get = "POST"))
plot(out)

# Pass in a tree from a URL on the web
spp <- c("Abies_nordmanniana", "Abies_bornmuelleriana", "Abies_cilicica", "Abies_cephalonica",
"Abies_numidica", "Abies_pinsapo", "Abies_alba")
url <- "http://datadryad.org/bitstream/handle/10255/dryad.8791/final_tree.tre?sequence=1"
phylomatic(taxa=spp, treeuri=url)
```

```
## End(Not run)
```

```
phyloomatic_local      Use Phyloomatic locally - ideal for large queries
```

Description

Use Phyloomatic locally - ideal for large queries

Usage

```
phyloomatic_local(taxa = NULL, taxaurl = NULL, taxnames = TRUE,
  informat = "newick", method = "phyloomatic", storedtree = "R20120829",
  treeurl = NULL, taxaformat = "slashpath", outformat = "newick",
  clean = TRUE, db = "apg", verbose = TRUE, outfile = "out.new",
  cleanup = TRUE, path = "phyloomatic-ws")
```

Arguments

taxa	(character) Phyloomatic format input of taxa names.
taxaurl	(character) URL of a taxa list online
taxnames	If TRUE (default), we get the family names for you to attach to your species names to send to Phyloomatic API. If FALSE, you have to provide the strings in the right format.
informat	(character) One of newick (default), nexml, or cdaordf. If using a stored tree, informat should always be newick.
method	(character) One of 'phyloomatic' (default) or 'convert'
storedtree	One of R20120829 (Phyloomatic tree R20120829 for plants), smith2011 (Smith 2011, plants), binindaemonds2007 (Bininda-Emonds 2007, mammals), or zanne2014 (Zanne et al. 2014, plants). Default: R20120829
treeurl	(character) URL for a phylogenetic tree in newick format.
taxaformat	(character) Only option is slashpath for now. Leave as is.
outformat	(character) One of newick, nexml, or fyt.
clean	(logical) Return a clean tree or not. Default: TRUE
db	(character) One of "ncbi", "itis", or "apg". Default: apg
verbose	(logical) Print messages. Default: TRUE
outfile	(character) output file for the tree, cleaned up after
cleanup	(logical) Remove the output file. Default: TRUE
path	(character) Path to the phyloomatic-ws folder

Value

Newick formatted tree as phylo object or nexml character string

Fetch Phylomatic code

Download the code by doing `git clone https://github.com/camwebb/phyloomatic-ws` which will result in a folder `phyloomatic-ws` (or download a zip file, and uncompress it). Then give the path to that folder in the `path` parameter

Examples

```
## Not run:
# Input taxonomic names
taxa <- c("Poa annua", "Phlox diffusa", "Helianthus annuus")
(tree <- phyloomatic_local(taxa, path = "~/github/play/phyloomatic-ws"))
plot(tree, no.margin=TRUE)

taxa <- c("Poa annua", "Collomia grandiflora", "Lilium lankongense", "Phlox diffusa",
"Iteadaphne caudata", "Gagea sarmentosa", "Helianthus annuus")
(tree <- phyloomatic_local(taxa, path = "~/github/play/phyloomatic-ws"))
plot(tree, no.margin=TRUE)

# Don't clean - clean=TRUE is default
(tree <- phyloomatic_local(taxa, path = "~/github/play/phyloomatic-ws", 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)

library("taxize")
spp <- names_list("species", 1000)
length(spp)
(tree <- phyloomatic_local(spp, path = "~/github/play/phyloomatic-ws", outfile="my.new"))

## End(Not run)
```

phyloomatic_names	<i>Phylomatic names</i>
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Description

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

Usage

```
phyloomatic_names(taxa, format = "isubmit", db = "ncbi")
```

Arguments

taxa	quoted tsn number (taxonomic serial number)
format	output format, <code>isubmit</code> (you can paste in to the Phylomatic website), or <code>rsubmit</code> to use in fxn <code>phyloomatic_tree</code>
db	One of <code>"ncbi"</code> , <code>"itis"</code> , or <code>"apg"</code>

Value

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

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)
```

rbladj

Run Phylocom's bladj from R

Description

Run Phylocom's bladj from R

Usage

```
rbladj(tree = NULL, ages = NULL, path = NULL, fixroot = FALSE)
```

Arguments

tree	(phylo/character) If left NULL, it is expected that you already have a phylo file with your newick tree in your directory with your phylocom executable
ages	(data.frame) If left NULL, it is expected that you already have an ages file with your node names and ages in your directory with your Phylocom executable
path	(character) Path to the folder with at least the Phylocom executable
fixroot	(logical) If TRUE root name is changed to the oldest root in your ages file. If FALSE (default),

Details

Download Phylocom <http://phylodiversity.net/phylocom/phylocom-4.2.zip>

Examples

```
## Not run:
library("taxize")
taxa <- names_list("species", 15)
tree <- phylomatic(taxa=taxa, get = 'POST')

path <- "~/Mac/Courses_Rice/EcolJClub563/Fall10/phylometa_stuff/R_tutorial/bladjing/"
(tree2 <- rbladj(tree, path = path, fixroot = TRUE))
```

```
plot(tree)
plot(tree2)

## End(Not run)
```

tpl	<i>Lookup-table for family, genus, and species names for ThePlantList gymnosperms</i>
-----	---

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/>

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