

# Package ‘brranching’

August 29, 2016

**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** 0.2.0

**Date** 2016-04-13

**License** MIT + file LICENSE

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

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

**LazyLoad** yes

**LazyData** yes

**Depends** R(>= 3.2.1)

**Imports** httr (>= 1.1.0), curl, ape, taxize, phytools

**Suggests** testthat, covr

**RoxygenNote** 5.0.1

**NeedsCompilation** no

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**Repository** CRAN

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brranching-package      *Phylogenies from many sources*

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**Description**

Phylogenies from many sources

**Author(s)**

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phylomatic      *Query Phylomatic for a phylogenetic tree.*

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**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", verbose = 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   |
| verbose    | Print messages. Default: TRUE   |
| ...        | curl options passed on to <a href="#">GET</a> or <a href="#">POST</a>   |

**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)
```

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phylomatic\_local      *Use Phylomatic locally - ideal for large queries*

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## Description

Use Phylomatic locally - ideal for large queries

## Usage

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

## Arguments

|            |   |
|------------|---|
| taxa       | (character) Phylomatic 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 Phylomatic 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 '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 |
| 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 phylomatic-ws folder  |
| ...        | curl options passed on to <a href="#">GET</a> or <a href="#">POST</a>   |

**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/phylomatic-ws` which will result in a folder `phylomatic-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 <- phylomatic_local(taxa, path = "~/github/play/phylomatic-ws"))
plot(tree, no.margin=TRUE)

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

# Don't clean - clean=TRUE is default
(tree <- phylomatic_local(taxa, path = "~/github/play/phylomatic-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 <- phylomatic_local(spp, path = "~/github/play/phylomatic-ws", outfile="my.new"))

## End(Not run)
```

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|                  |                         |
|------------------|-------------------------|
| phylomatic_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 `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 <code>phylomatic_tree</code> |
| db     | One of "ncbi", "itis", or "apg"  |

**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)
```

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

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**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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