

Package ‘rphylotastic’

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Title Interface to 'Phylotastic' Web Services

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Description This wraps the 'Phylotastic' services APIs <https://github.com/phylotastic/phylo_services_docs/tree/master/ServiceDescription>. The main use case is to turn a phylogenetic tree for a set of species, but the services also include ways to extract species names from web pages, perform taxonomic name resolution, retrieve a list of all descendant species of a taxon, find images of a species, and more.

URL <https://github.com/phylotastic/rphylotastic>

Depends R (>= 3.3.0)

Imports httr, jsonlite, ape, utils, phylobase, methods, rentrez (>= 1.0.4)

Suggests testthat

License GPL-2

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R topics documented:

get_base_url	2
get_list_server_url	2
get_species_from_list	3
insert_species_in_list	4
newick_compare	5

remove_species_from_list	5
replace_species_in_list	6
species_get_image_data	7
species_get_info	8
taxa_get_otol_tree	8
taxa_get_phylomatic_tree	9
taxa_get_taxonomic_tree	10
taxa_resolve_names_with_gnr	10
taxa_resolve_names_with_otol	11
taxon_get_species	12
taxon_get_species_and_country	12
taxon_get_species_with_genome	13
taxon_separate_dark_taxa_using_genbank	14
taxon_separate_dark_taxa_using_otol	14
text_get_scientific_names	15
update_species_in_list	16
url_get_scientific_names	17

Index **18**

<code>get_base_url</code>	<i>Get Phylotastic base URL return The URL for the phylotastic server</i>
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Description

Get Phylotastic base URL return The URL for the phylotastic server

Usage

`get_base_url()`

<code>get_list_server_url</code>	<i>Return Species List server URL</i>
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Description

Return Species List server URL

Usage

`get_list_server_url()`

get_species_from_list *Get existing list/lists of species*

Description

Get existing list/lists of species

Usage

```
get_species_from_list(userid, access_token, list_id, verbose = FALSE,  
  content = TRUE)
```

Arguments

userid	A valid gmail address of the user
access_token	Access token of the gmail address
list_id	An integer id of the list to retrieve
verbose	(optional)By default FALSE and shows minimal meta-data of the list.
content	(optional)By default TRUE and shows the species collection of the list

Value

An existing list with metadata and content based on parameters

See Also

https://github.com/phylostatic/phylo_services_docs/tree/master/ServiceDescription

Examples

```
# This gives you the syntax, but since the access token expires after one hour,  
# this particular example will not work.  
## Not run:  
userid = "abusalehmdtayeem@gmail.com"  
access_token = "ya29..zQLmLjbyujJjwV6RVSM2sy-mkeaKu-9"  
list_id = 12  
verbose = TRUE  
content = FALSE  
get_species_from_list(userid, access_token, list_id, verbose, content)  
  
## End(Not run)
```

 insert_species_in_list

Insert list of species

Description

Insert list of species

Usage

```
insert_species_in_list(userid, listObj)
```

Arguments

userid	A valid gmail address of the user
listObj	A list object

Value

A list with the id of the new list created

See Also

https://github.com/phylostatic/phylo_services_docs/tree/master/ServiceDescription

Examples

```
userid = "abusalehmdtayeen@gmail.com"
listObj = list(list_extra_info="", list_description="A sublist on the bird species added",
  list_keywords=c("bird", "endangered species", "Everglades"),
  list_curator="HD Laughinghouse", list_origin="webapp",
  list_curation_date="02-24-2016", list_source="des", list_focal_clade="Aves",
  list_title="Bird Species List", list_author=c("Bass", "O. & Cunningham", "R."),
  list_date_published="01-01-2017", is_list_public=TRUE,
  list_species=list(list(family="", scientific_name="Aix sponsa",
    scientific_name_authorship="", vernacular_name="Wood Duck",
    phylum="", nomenclature_code="ICZN", order="Anseriformes", class=""),
    list(family="", scientific_name="Anas strepera",
    scientific_name_authorship="", vernacular_name="Gadwall",
    phylum="", nomenclature_code="ICZN",
    order="Anseriformes", class="") ))
insert_species_in_list(userid, listObj)
```

newick_compare *Compare two phylogenetic trees*

Description

Compare two phylogenetic trees

Usage

```
newick_compare(trees)
```

Arguments

trees A multiphylo object of two newick trees

Value

A named list with are_same_tree property set to either TRUE or FALSE

See Also

https://github.com/phylostatic/phylo_services_docs/tree/master/ServiceDescription

Examples

```
are_same <- newick_compare(c(ape::rcoal(5), ape::rcoal(5)))
```

remove_species_from_list
Remove an existing list of species

Description

Remove an existing list of species

Usage

```
remove_species_from_list(userid, access_token, list_id)
```

Arguments

userid A valid gmail address of the user
access_token Access token of the gmail address
list_id An integer id of the list to retrieve

Value

A list with the id of the list removed

See Also

https://github.com/phylostatic/phylo_services_docs/tree/master/ServiceDescription

Examples

```
# This gives you the syntax, but since the access token expires after one hour,
# this particular example will not work.
## Not run:
userid = "abusalehmdtayeen@gmail.com"
access_token = "ya29..zQLmLjbyujJjwV6RVSM2sy-mkeaKu-9"
list_id = 12
remove_species_from_list(userid, access_token, list_id)

## End(Not run)
```

replace_species_in_list

Replace a list of species

Description

Replace a list of species

Usage

```
replace_species_in_list(userid, access_token, list_id, speciesObj)
```

Arguments

userid	A valid gmail address of the user
access_token	Access token of the gmail address
list_id	An integer id of the list to be modified
speciesObj	A species object to replace with

Value

A list with the old species and new species list

See Also

https://github.com/phylostatic/phylo_services_docs/tree/master/ServiceDescription

Examples

```
# This gives you the syntax, but since the access token expires after one hour,  
# this particular example will not work.  
## Not run:  
userid = "abusalehmdtayeen@gmail.com"  
access_token = "ya29..zQLmLjbyujJjwV6RVSM2sy-mkeaKu-9"  
list_id = 12  
speciesObj = list( list(family="",scientific_name="Aix sponsa",scientific_name_authorship="",  
vernacular_name="Wood Duck",phylum="",nomenclature_code="ICZN",order="Anseriformes",class=""))  
replace_species_in_list(userid, access_token, list_id, speciesObj)  
  
## End(Not run)
```

species_get_image_data

Get image metadata of a list of species

Description

Get image metadata of a list of species

Usage

```
species_get_image_data(species)
```

Arguments

species A vector of names

Value

A data frame of image metadata(image urls, license info etc.) of species

See Also

https://github.com/phylostatic/phylo_services_docs/tree/master/ServiceDescription
or <https://eol.org/api/>

species_get_info *Get information of a list of species*

Description

Get information of a list of species

Usage

```
species_get_info(species)
```

Arguments

species A vector of names

Value

A data frame of info about species

See Also

https://github.com/phylostatic/phylo_services_docs/tree/master/ServiceDescription
or <https://eol.org/api/>

taxa_get_otol_tree *Get OTOL induced subtree*

Description

Get OTOL induced subtree

Usage

```
taxa_get_otol_tree(taxa)
```

Arguments

taxa The vector of names, already resolved to match OTOL taxa

Value

A phylo object

See Also

https://github.com/phylostatic/phylo_services_docs/tree/master/ServiceDescription
or the rotl package, another interface to Open Tree of Life

Examples

```
taxa <- c("Crabronidae", "Ophiocordyceps", "Megalyridae",  
         "Formica polycтена", "Tetramorium caespitum",  
         "Pseudomyrmex", "Carebara diversa", "Formicinae")  
phy <- taxa_get_otol_tree(taxa)  
plot(phy)
```

`taxa_get_phylomatic_tree`*Get phylomatic subtree*

Description

Get phylomatic subtree

Usage

```
taxa_get_phylomatic_tree(taxa)
```

Arguments

`taxa` The vector of names, already resolved

Value

A phylo object

See Also

https://github.com/phylostatic/phylo_services_docs/tree/master/ServiceDescription
or the interface of phylomatic <http://phylodiversity.net/phylomatic/>

Examples

```
phy <- taxa_get_phylomatic_tree(c("Panthera leo", "Panthera onca",  
                                "Panthera tigris", "Panthera uncia"))  
plot(phy)
```

`taxa_get_taxonomic_tree`*Get taxonomic tree from the NCBI*

Description

Get taxonomic tree from the NCBI

Usage

```
taxa_get_taxonomic_tree(taxa)
```

Arguments

`taxa` The vector of names, already resolved

Value

A phylo object

See Also

https://github.com/phyloTastic/phylo_services_docs/tree/master/ServiceDescription
or the interface of phyloT <http://phyloT.biobyte.de/>

Examples

```
taxa <- c("Setophaga striata", "Setophaga magnolia",  
         "Setophaga angelae", "Setophaga plumbea",  
         "Setophaga virens")  
phy <- taxa_get_taxonomic_tree(taxa)  
plot(phy)
```

`taxa_resolve_names_with_gnr`*Resolve Scientific Names with GNR TNRS*

Description

Resolve Scientific Names with GNR TNRS

Usage

```
taxa_resolve_names_with_gnr(taxa)
```

Arguments

taxa The vector of names

Value

A vector of corrected names. THE ORDER MAY NOT CORRESPOND TO YOUR INPUT ORDER.

See Also

https://github.com/phylotastic/phylo_services_docs/tree/master/ServiceDescription or the `rotl` package, another interface to Open Tree of Life, or the `taxize` package for name resolution in general.

taxa_resolve_names_with_otol

Resolve Scientific Names with Open Tree TNRS

Description

Resolve Scientific Names with Open Tree TNRS

Usage

```
taxa_resolve_names_with_otol(taxa)
```

Arguments

taxa The vector of names

Value

A vector of corrected names. THE ORDER MAY NOT CORRESPOND TO YOUR INPUT ORDER.

See Also

https://github.com/phylotastic/phylo_services_docs/tree/master/ServiceDescription or the `rotl` package, another interface to Open Tree of Life, or the `taxize` package for name resolution in general.

Examples

```
my.species.raw <- c("Formica polyctena", "Formica exsectoides", "Formica pecefica")
my.species.corrected <- taxa_resolve_names_with_otol(my.species.raw)
print(my.species.corrected)
```

taxon_get_species *Get all species from a taxon*

Description

Get all species from a taxon

Usage

```
taxon_get_species(taxon, filters = c("environmental", "sp\\.\"", "cf\\.\""))
```

Arguments

taxon A taxon to get all species for
filters A character vector of strings to exclude

Value

A vector of names

See Also

https://github.com/phylostatic/phylo_services_docs/tree/master/ServiceDescription
or the rotl package, another interface to Open Tree of Life

Examples

```
print(taxon_get_species("Vulpes"))
```

taxon_get_species_and_country
 Get all species filtered by country from a taxon

Description

Get all species filtered by country from a taxon

Usage

```
taxon_get_species_and_country(taxon, country, filters = c("environmental",  
"sp\\.\"", "cf\\.\""))
```

Arguments

taxon A taxon to get subset of species that are established in a particular country
country A country name where species of the input taxon are established.
filters A character vector of strings to exclude

Value

A vector of names

See Also

https://github.com/phylostatic/phylo_services_docs/tree/master/ServiceDescription
or the `rotl` package, another interface to Open Tree of Life

taxon_get_species_with_genome

Get all species that have genome sequence in NCBI from a taxon

Description

Get all species that have genome sequence in NCBI from a taxon

Usage

```
taxon_get_species_with_genome(taxon, filters = c("environmental", "sp\\.",  
"cf\\."))
```

Arguments

taxon	A taxon to get subset of species having genome sequence
filters	A character vector of strings to exclude

Value

A vector of names

See Also

https://github.com/phylostatic/phylo_services_docs/tree/master/ServiceDescription
or the `rotl` package, another interface to Open Tree of Life

taxon_separate_dark_taxa_using_genbank

Separate dark from known taxa on another database

Description

Separate dark from known taxa on another database

Usage

```
taxon_separate_dark_taxa_using_genbank(taxon, filters = c("environmental",
  "sp\\.\"", "cf\\.\"", "uncultured", "unidentified", " clone", " enrichment"),
  verbose = TRUE, sleep = 0)
```

Arguments

taxon	A taxon to get all species for
filters	A character vector of strings to exclude
verbose	Update on how many are done
sleep	How many seconds to sleep between calls (on top of rentrez's defaults)

Value

A list containing a vector of dark names, a vector of known names, and fraction.dark

taxon_separate_dark_taxa_using_otol

Separate dark from known taxa on OpenTree of Life

Description

Separate dark from known taxa on OpenTree of Life

Usage

```
taxon_separate_dark_taxa_using_otol(taxon, filters = c("environmental",
  "sp\\.\"", "cf\\.\"", "uncultured", "unidentified", " clone", " enrichment"))
```

Arguments

taxon	A taxon to get all species for
filters	A character vector of strings to exclude

Value

A list containing a vector of dark names, a vector of known names, and fraction.dark

See Also

https://github.com/phylostatic/phylo_services_docs/tree/master/ServiceDescription
or the rotl package, another interface to Open Tree of Life

text_get_scientific_names

Function to pull scientific names from text

Description

Function to pull scientific names from text

Usage

```
text_get_scientific_names(text, search_engine = 0)
```

Arguments

text The text string to extract names from
search_engine 1 to use TaxonFinder, 2 to use NetiNeti, 0 to use both

Value

A vector of scientific names

See Also

https://github.com/phylostatic/phylo_services_docs/tree/master/ServiceDescription

Examples

```
text <- "Formica polyctena is a species of European red wood ant in  
the genus Formica. The pavement ant, Tetramorium caespitum  
is an ant native to Europe."  
print(text_get_scientific_names(text))
```

`update_species_in_list`*Update metadata of a list of species*

Description

Update metadata of a list of species

Usage

```
update_species_in_list(userid, access_token, list_id, listObj)
```

Arguments

<code>userid</code>	A valid gmail address of the user
<code>access_token</code>	Access token of the gmail address
<code>list_id</code>	An integer id of the list to be modified
<code>listObj</code>	A list object to update with

Value

A list with modified list metadata

See Also

https://github.com/phylostatic/phylo_services_docs/tree/master/ServiceDescription

Examples

```
# This gives you the syntax, but since the access token expires after one hour,  
# this particular example will not work.  
## Not run:  
userid = "abusalehmdtayeen@gmail.com"  
access_token = "ya29..zQLmLjbyujJjwV6RVSM2sy-mkeaKu-9"  
list_id = 12  
listObj = list(list_description="A sublist on the bird species",  
              list_keywords=c("bird", "Everglades"))  
update_species_in_list(userid, access_token, list_id, listObj)  
  
## End(Not run)
```

`url_get_scientific_names`*Function to pull scientific names from web pages*

Description

Function to pull scientific names from web pages

Usage

```
url_get_scientific_names(URL, search_engine = 0)
```

Arguments

URL The URL to extract names from
search_engine 1 to use TaxonFinder, 2 to use NetiNeti, 0 to use both

Value

A vector of scientific names

See Also

https://github.com/phylostatic/phylo_services_docs/tree/master/ServiceDescription

Examples

```
URL <- "https://en.wikipedia.org/wiki/Plain_pigeon"  
print(url_get_scientific_names(URL))
```

Index

[get_base_url](#), [2](#)
[get_list_server_url](#), [2](#)
[get_species_from_list](#), [3](#)

[insert_species_in_list](#), [4](#)

[newick_compare](#), [5](#)

[remove_species_from_list](#), [5](#)
[replace_species_in_list](#), [6](#)

[species_get_image_data](#), [7](#)
[species_get_info](#), [8](#)

[taxa_get_otol_tree](#), [8](#)
[taxa_get_phylomatic_tree](#), [9](#)
[taxa_get_taxonomic_tree](#), [10](#)
[taxa_resolve_names_with_gnr](#), [10](#)
[taxa_resolve_names_with_otol](#), [11](#)
[taxon_get_species](#), [12](#)
[taxon_get_species_and_country](#), [12](#)
[taxon_get_species_with_genome](#), [13](#)
[taxon_separate_dark_taxa_using_genbank](#),
[14](#)
[taxon_separate_dark_taxa_using_otol](#),
[14](#)
[text_get_scientific_names](#), [15](#)

[update_species_in_list](#), [16](#)
[url_get_scientific_names](#), [17](#)