

Package: rusda (via r-universe)

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Type Package

Title Interface to USDA Databases

Version 1.0.8

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Author Franz-Sebastian Krah

Maintainer Franz-Sebastian Krah <f.krah@mailbox.org>

Imports XML, httr (>= 0.6.1), plyr, foreach, stringr, testthat, taxize, RCurl

Description An interface to the web service methods provided by the United States Department of Agriculture (USDA). The Agricultural Research Service (ARS) provides a large set of databases. The current version of the package holds interfaces to the Systematic Mycology and Microbiology Laboratory (SMML), which consists of four databases: Fungus-Host Distributions, Specimens, Literature and the Nomenclature database. It provides functions for querying these databases. The main function is `associations`, which allows searching for fungus-host combinations.

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RoxygenNote 6.1.1

Suggests knitr, rmarkdown

VignetteBuilder knitr

URL <https://docs.ropensci.org/rusda>,
<http://www.usda.gov/wps/portal/usda/usdahome>,
<http://nt.ars-grin.gov/fungalDATABASES/index.cfm>,
<https://github.com/ropensci/rusda>

BugReports <https://github.com/ropensci/rusda/issues>

Repository <https://ropensci.r-universe.dev>

RemoteUrl <https://github.com/ropensci/rusda>

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rusda-package	<i>Interface to USDA Databases</i>
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Description

An interface to the web service methods provided by the United States Department of Agriculture (USDA). The Agricultural Research Service (ARS) provides a large set of databases. The current version of the package holds interfaces to the Systematic Mycology and Microbiology Laboratory (SMML), which consists of four databases: Fungus-Host Distributions, Specimens, Literature and the Nomenclature database. It provides functions for querying these databases. The main function is `associations`, which allows searching for fungus-host combinations.

Details

Package: rusda
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Author(s)

Franz-Sebastian Krah
 Maintainer: Franz-Sebastian Krah <f.krah@mailbox.org>

References

Farr, D.F., & Rossman, A.Y. Fungal Databases, Systematic Mycology and Microbiology Laboratory, ARS, USDA
<http://nt.ars-grin.gov/sbmlweb/fungi/databases.cfm>, <http://www.usda.gov/wps/portal/usda/usdahome>

associations	<i>Downloads associations for input species from SMML Fungus-Host DB</i>
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Description

Searches and downloads associations from SMML Fungus-Hosts Distributions and Specimens database for fungus or plant species input vector

Usage

```
associations(x, database = c("FH", "SP", "both"),
  spec_type = c("plant", "fungus"), clean = TRUE, syn_include = TRUE,
  process = TRUE, db = "ncbi")
```

Arguments

x	a vector of class character containing fungal or plant species names or a genus name (see Details)
database	a character string specifying the databases that should be queried. Valid are "FH" (Fungus-Host Distributions), "SP" (Specimens) or "both" databases
spec_type	a character string specifying the type of x. Can be either "plant" or "fungus"
clean	logical, if TRUE a cleaning step is run of the resulting associations list
syn_include	logical, if TRUE associations for synonyms are searched and added. For a complete synonyms list check <code>rusda::synonyms</code>
process	logical, if TRUE downloading and extraction process is displayed
db	if x is higher than species level, all species for the higher taxon are retrived using the function <code>taxize::downstream</code> . Here one of ITIS (<code>itis</code>), Catalogue of Life (<code>col</code>), GBIF (<code>gbif</code>), or NCBI (<code>ncbi</code>) has to be selected. NCBI is default.

Details

The Fungus-Hosts distributions database 'FH' comprises data compiled from Literature. In the uncleaned output all kinds of unspecified substrates are documented like "submerged wood". Cleanded data displays Linnean names only and species names with either "subsp.", "f. sp." "f.", "var.". The Specimens database comprises entries from field collections.

If genera names are supplied, then species are derived from the NCBI taxonomy.

Value

an object of class `list`.

First is `synonyms`, second is `associations`. `Synonyms` is a vector of mode `list` with synonyms for x. Notice: This is not a complete list of synonym data in the database. This is the list of synonyms that contain data for the input x. For a complete synonyms list check `rusda::synonyms` or (if needed) for fungi R package `rmycobank`.

`Associations` is a vector of mode `list` of associations for x

Author(s)

Franz-Sebastian Krah

Examples

```
## Not run:
## Example for species name(s) as input
x <- "Fagus sylvatica"
pathogens <- associations(x, database = "both", clean = TRUE, syn_include = TRUE,
spec_type = "plant", process = TRUE)
x <- "Rosellinia ligniaria"
hosts <- associations(x, database = "both", clean = TRUE, syn_include = TRUE,
spec_type = "fungus", process = TRUE)
is.element("Rosellinia ligniaria", pathogens$association[[1]])
is.element("Fagus sylvatica", hosts$association[[1]])

## Example for genus/genera name(s) as input
x <- "Zehneria"
# or
x <- c("Zehneria", "Momordica")
hosts <- associations(x, database = "both", clean = TRUE, syn_include = TRUE,
spec_type = "plant", process = TRUE)

## End(Not run)
```

getBPI

Downloads specimens records for input study BPI accession number

Description

Downloads specimens records for input study BPI accession number

Usage

```
getBPI(BPI, sep = "; ")
```

Arguments

BPI	a single study BPI or a vector of study BPIs
sep	separator how to collapse output literature references

Value

an object of class `data.frame` with studies

Author(s)

Franz-Sebastian Krah

getStudy	<i>Downloads studies for input study IDs</i>
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Description

Downloads studies for study IDs which are output of associations

Usage

```
getStudy(id, sep = "; ")
```

Arguments

id	a single study id or a vector of study ids
sep	separator how to collapse output literature references

Value

an object of class `data.frame` with studies

Author(s)

Franz-Sebastian Krahl

literature	<i>Downloads literature from SMML Literature DB</i>
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Description

Searches and downloads literature entries from the SMML Literature database

Usage

```
literature(x, spec_type = c("plant", "fungus"), process = TRUE)
```

Arguments

x	a vector of class character containing fungal or plant species names
spec_type	a character string specifying the type of spec. Can be either "plant" or "fungus"
process	logical, if TRUE downloading and extraction process is displayed an object of class <code>list</code>

Value

a vector of mode `list` with literature entries for x

Author(s)

Franz-Sebastian Krahl

Examples

```
## Not run:  
x <- "Polyporus badius"  
lit <- literature(x, process = TRUE, spec_type = "fungus")  
lit  
  
## End(Not run)
```

meta_smml

Downloads and evaluate species presence in SMML DBs

Description

Searches, downloads and evaluates presence/absence of data in the SMML databases

Usage

```
meta_smml(x, spec_type = c("plant", "fungus"), process = TRUE)
```

Arguments

x	a vector of class character containing fungal or plant species or genus names
spec_type	a character string specifying the type of x. Can be either "plant" or "fungus"
process	logical, if TRUE downloading and extraction process is displayed

Details

Use this function before deriving data from one of the databases in order to prune your input species vector. With pruned species vectors the functions will run faster. This is important if x is some hundred species long.

Value

an object of class data.frame: presence/absence

Author(s)

Franz-Sebastian Krahl

Examples

```
## Not run:
fungus.meta <- meta_smml(x = "Picea abies", process = TRUE, spec_type = "plant")
fungus.meta
hosts.meta <- meta_smml(x = "Antrodiella citrinella", process = TRUE, spec_type = "fungus")
hosts.meta

## End(Not run)
```

substrate*Downloads substrate data from SMML Nomenclature DB*

Description

Searches and downloads substrate data from SMML Nomenclature database

Usage

```
substrate(x, process = TRUE)
```

Arguments

x a vector of class character containing fungal or plant species names
process logical, if TRUE downloading and extraction process is displayed

Details

Don't be disappointed. Not much data there. But depends on the study group, so give it try.

Value

an object of mode list containing substrate for fungus species

Author(s)

Franz-Sebastian Krah

Examples

```
## Not run:
x <- c("Polyporus_rhizophilus", "Polyporus_squamosus")
subs.poly <- substrate(x, process=TRUE)
subs.poly

## End(Not run)
```

`synonyms_smml`*Downloads synonym data from SMML Nomenclature DB*

Description

Searches and downloads synonym data from SMML Nomenclature database

Usage

```
synonyms_smml(x, spec_type = c("plant", "fungus"), clean = TRUE,  
              process = TRUE)
```

Arguments

<code>x</code>	a vector of class character containing fungal or plant species or genus names
<code>spec_type</code>	a character string specifying the type of <code>x</code> . Can be either "plant" or "fungus"
<code>clean</code>	logical, if TRUE a cleaning step is run of the resulting associations list
<code>process</code>	logical, if TRUE downloading and extraction process is displayed

Value

an object of class `list` containing synonyms for `x`

Author(s)

Franz-Sebastian Krahl

Examples

```
## Not run:  
x <- "Solanum tuberosum"  
synonyms_usda(x, spec_type = "plant", process = TRUE, clean = TRUE)  
x <- c("Phytophthora infestans", "Polyporus badius")  
synonyms_usda(x, spec_type = "fungus", process = TRUE, clean = TRUE)  
  
## End(Not run)
```


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