

Package ‘rusda’

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Type Package

Title Interface to USDA Databases

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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.

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URL <http://www.usda.gov/wps/portal/usda/usdahome>,
<http://nt.ars-grin.gov/fungalatabases/index.cfm>

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rusda-package

Interface to USDA Databases

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

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Author(s)

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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

Downloads associations for input species from SMML Fungus-Host DB

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)
```

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

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". Cleaned 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)

```

literature

Downloads literature from SMML Literature DB

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 list

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

<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>process</code>	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	<i>Downloads substrate data from SMML Nomenclature DB</i>
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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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