

Package ‘distdrawr’

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Title Download Occurrence Data of Vascular Plants in Germany from the FLORKART Database

Version 0.1.3

Description

Download data from the FlorKart database of the floristic field mapping in Germany in a convenient way. The database incorporates distribution data for plants in Germany on the basis of quadrants on a topographical map with a resolution of 1 : 25000 (TK 25). The data is owned and provided by the German Federal Agency for Nature Conservation (BfN) and the Network Phytodiversity in Germany (NetPhyD). For further information please visit <http://www.floraweb.de/pflanzenarten/hintergrundtexte_florkart_organisation.html>. The author of this package is in no way associated with the BfN or NetPhyD.

Depends R (>= 3.3.0)

License GPL-2

Encoding UTF-8

LazyData true

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NeedsCompilation no

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Repository CRAN

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distdrawr-package *The distdrawr package*

Description

Tools for downloading data from the FLORKART-database on the distribution of vascular plants in Germany in a convenient way.

Author(s)

Nicolas Friess

References

Datenbank FLORKART der Floristischen Kartierung Deutschlands, Stand 2013, Bundesamt fuer Naturschutz (BfN) und Netzwerk Phytodiversitaet Deutschland (NetPhyD): <http://www.floraweb.de>

See Also

[get.dist check_species](#)

check_species *Check for available distribution data*

Description

This function will compare the species or genera in your species list with the entries of the FLORKART-database and returns the matching entries.

Usage

```
check_species(x, level = "species")
```

Arguments

x A `data.frame` with one column containing the species names in the format 'genus_epithet'.

level A character string describing whether the check should be conducted on the "species" or "genus" level.

Details

If input data consists only of genus names the function will call `level = "genus"`.

Value

Returns a data frame containing the matching taxon number and species names of x in the FloraWeb database. Mismatches are saved in the attributes of the data frame. The output can be modified and used in `get.dist` with `input = TRUE`.

References

Datenbank FLORKART der Floristischen Kartierung Deutschlands, Stand 2013, Bundesamt fuer Naturschutz (BfN) und Netzwerk Phytodiversitaet Deutschland (NetPhyD): <http://www.floraweb.de>

Examples

```
## Not run:
library("distdraw")
specieslist <- data.frame(c("Bellis_perennis", "Taraxacum_officinale",
                           "Capsella_bursa-pastoris"))
check_species(specieslist, level="species")

## End(Not run)
```

get.dist

Get distribution data for your species list.

Description

This function downloads distribution data from the FloraWeb-database.

Usage

```
get.dist(x, input = FALSE, output = "list", matrix.res = "TK25")
```

Arguments

x	A data.frame with one column containing the species names in the format 'genus_epithet'.
input	logical. If TRUE x is treated as the output of check_species, if FALSE x is treated as the input for check_species with level = "species"
output	A character string describing whether the output format should be a "list" or a "matrix".
matrix.res	A character string describing the resolution of the produced matrix, either "TK25" or "quarterTK".

Details

This function applies functions from the get.dist-family on your species list, depending on the value of output. The default value is list.

Value

Output depends on the output value. `output = "list"` returns a list of one data.frame per taxon, including all information found in the FloraWeb for the particular taxa. `output = "matrix"` returns a presence/absence matrix for the TK25 plane survey sheets, when `matrix.res = "TK25"` or the quarter TK25 plane survey sheets, when `matrix.res = "quarterTK"` including every matching taxon in `x`.

References

Datenbank FLORKART der Floristischen Kartierung Deutschlands, Stand 2013, Bundesamt fuer Naturschutz (BfN) und Netzwerk Phytodiversitaet Deutschland (NetPhyD): <http://www.floraweb.de>

Examples

```
## Not run:
library("distdraw")
specieslist <- data.frame(c("Bellis_perennis", "Abies_alba",
                           "Capsella_bursa-pastoris"))
get.dist(specieslist, output = "list")

## End(Not run)
```

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