Package 'Rveg'

November 22, 2024

Title Digitization of Phytosociological Relevés

Version 0.1.6

Description Simple and fast tool for transforming phytosociological
vegetation data into digital form for the following analysis.
Danihelka, Chrtek, and Kaplan (2012, ISSN:00327786).
Hennekens, and Schaminée (2001) <doi:10.2307/3237010>.
Tichý (2002) <doi:10.1111/j.1654-1103.2002.tb02069.x>.
Wickham, François, Henry, Müller (2022) <https://CRAN.R-project.org/package=dplyr>.

URL https://plant-ecology-lab-czu.com/rveg/

License GPL (>= 3)

Encoding UTF-8

RoxygenNote 7.3.1

Imports dplyr, utils

Suggests knitr, rmarkdown

VignetteBuilder knitr

NeedsCompilation no

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addReleve *addReleve*

Description

Digitizing and editing your releves - Rveg database

Usage

```
addReleve(
  DATABASE = "NEW",
  SAVE = "default",
  checklist = "default",
  extrahead = NULL,
  start = TRUE
)
```

Arguments

DATABASE   name of csv files for releve table and header - database

SAVE   name of exporting database

checklist   custom checklist

extrahead   extra rows in header

start   Boolean to start immediately digitizing first releve

Value

export two csv files, one for releve and one for header (Rveg database)

Examples

```
## NOT RUN
if (interactive()) {
  addReleve()
}
```

CreateChecklist *CreateChecklist*

Description

Create a custom checklist with species ShortNames

Usage

```
CreateChecklist(specieslist, export = "export")
```

Arguments

specieslist	path to list of species
export	name of your exported checklist file

Value

txt file used as checklist in Rveg functions

Examples

```
## NOT RUN
if (interactive()) {
CreateChecklist(specieslist = paste0(path.package("Rveg"),
"/extdata/SpeciesList"))
}
```

RvegCheck *RvegCheck*

Description

Checking your DATABASE for duplicity and allowing to export table with full species name (not Rveg editable anymore).

Usage

```
RvegCheck(
  DATABASE,
  fullnames = FALSE,
  export = "export",
  checklist = "default"
)
```

Arguments

`DATABASE`	name of csv files for releve table and header - database
`fullnames`	logical value if you want to add fullnames to the database
`export`	name of exporting database
`checklist`	checklist used to match shortnames with species name

Value

Export csv file releve table

Examples

```
## NOT RUN
if (interactive()) {
  RvegCheck(DATABASE = paste0(
    path.package("Rveg"),
    "/extdata/example_db"
  ))
}
```

`RvegCombine`	*RvegCombine*

Description

Merging species or layers in the database

Usage

```
RvegCombine(database, export = "export", checklist = "default")
```

Arguments

`database`	name of the loading database
`export`	name of the exported database
`checklist`	checklist to be used

Value

export two csv files, one for releve and one for header

Examples

```
## NOT RUN
if (interactive()) {
  RvegCombine(database = paste0(
    path.package("Rveg"),
    "/extdata/example_db"
  ))
}
```

RvegLoad   *RvegLoad*

Description

Reading your Rveg database

Usage

```
RvegLoad(DATABASE = "default", CustomScale = FALSE, checklist = "default")
```

Arguments

DATABASE   name of Rveg database

CustomScale   logical values if different than predefined scale was used during the database
                creation

checklist   used checklist

Value

read the database in one object

Examples

```
RvegLoad()
```

RvegMerge   *RvegMerge*

Description

Merge two Rveg databases

Usage

```
RvegMerge(x, y, save = "export_merge", head = TRUE)
```

Arguments

x	name of first database
y	name of second database
save	name of exported databes
head	logical value if want to merge header

Value

export two csv files, one for releve and one for header

Examples

```
## NOT RUN
if (interactive()) {
  RvegMerge(x = paste0(
    path.package("Rveg"),
    "/extdata/example_db"
  ), y = paste0(
    path.package("Rveg"),
    "/extdata/example_db"
  ))
  read.csv("export_mergeREL.csv", row.names = 1)
}
```

RvegToJuice   *RvegToJuice*

Description

Export Rveg database to Juice software compatible format

Usage

```
RvegToJuice(Data, checklist = "default", export = "export")
```

Arguments

`Data`	name of your Rveg database
`checklist`	path to your custom species checklist
`export`	name of your exported csv file

Value

csv file which is readible by Juice

Examples

```
## NOT RUN
if (interactive()) {
  RvegToJuice(Data = paste0(
    path.package("Rveg"),
    "/extdata/example_db"
  ))
}
```

RvegToTv   *RvegToTv*

Description

Export Turboveg csv compatible file

Usage

```
RvegToTv(database, export = "export", ver = 3, checklist = "default")
```

Arguments

`database`	path to Rveg database
`export`	name of your exported Tv file
`ver`	version of TURBOVEG
`checklist`	checklist to match Fullnames

Value

csv file

Examples

```
## NOT RUN
if (interactive()) {
  RvegToTv(database = paste0(
    path.package("Rveg"),
    "/extdata/example_db"
  ))
}
```

TvToRveg　　　　　　　　　　　　*TvToRveg*

Description

Export Turboveg csv file to Rveg database compatible format

Usage

```
TvToRveg(tv, export = "export", checklist = "default")
```

Arguments

tv	path to Turboveg csv export
export	name of your exported database
checklist	checklist used to match shortnames with species name

Value

csv file

Examples

```
## NOT RUN
if (interactive()) {
  TvToRveg(tv = paste0(
    path.package("Rveg"),
    "/extdata/tvexport.csv"
  ))
}
```

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