Package: Rveg (via r-universe)

September 25, 2024

Title Digitization of Phytosociological Relevés

Version 0.1.5

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

Author Přemysl Král [aut, cre] (<https://orcid.org/0000-0002-2887-651X>), Jan Douda [aut] (<https://orcid.org/0000-0002-1205-364X>)

Maintainer Přemysl Král <kralp@fzp.czu.cz>

Repository CRAN

Date/Publication 2024-06-26 15:10:02 UTC

Contents

`addReleve` *addReleve*

Description

Writing and editing your releves

Usage

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

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

Value

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

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

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 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"
  ))
  read.csv("exportREL.csv", row.names = 1)
}
```

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"
  ))
  read.csv("exportREL.csv", row.names = 1)
}
```

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"
  ))
  read.csv("export.csv", header = FALSE)
}
```

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"
  ))
  read.csv("exportREL.csv", row.names = 1)
}
```

Index