

Package: Rveg (via r-universe)

June 27, 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](https://doi.org/10.2307/3237010)>. Tichý (2002) <[doi:10.1111/j.1654-1103.2002.tb02069.x](https://doi.org/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 | <i>addReleve</i> |
|-----------|------------------|

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 | <i>CreateChecklist</i> |
|-----------------|------------------------|

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 | <i>RvegCheck</i> |
|-----------|------------------|

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 readable 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)
}
```


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