

# Package ‘Rveg’

March 31, 2024

**Title** Digitization of Phytosociological Relevés

**Version** 0.1.4

**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

**Author** Přemysl Král [aut, cre] (<<https://orcid.org/0000-0002-2887-651x>>),

Jan Douša [aut] (<<https://orcid.org/0000-0002-1205-364X>>)

**Maintainer** Přemysl Král <kralp@fzpz.czu.cz>

**Repository** CRAN

**Date/Publication** 2024-03-31 20:10:08 UTC

## R topics documented:

addReleve . . . . .	2
CreateChecklist . . . . .	3
RvegCheck . . . . .	3
RvegCombine . . . . .	4
RvegMerge . . . . .	5
RvegToJuice . . . . .	6
RvegToTv . . . . .	6
tvToRveg . . . . .	7

---

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)
}
```



# Index

[addReleve](#), [2](#)

[CreateChecklist](#), [3](#)

[RvegCheck](#), [3](#)

[RvegCombine](#), [4](#)

[RvegMerge](#), [5](#)

[RvegToJuice](#), [6](#)

[RvegToTv](#), [6](#)

[tvToRveg](#), [7](#)