

Package ‘vegtable’

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Encoding UTF-8

Title Handling Vegetation Data Sets

Depends R(>= 3.0.0),
taxlist

Imports foreign,
methods,
plotKML,
qdapRegex,
sp,
stringi,
vegdata

Suggests devtools,
roxygen2,
rmarkdown,
vegan

Description Import and handling data from vegetation-plot databases, especially data stored in 'Turboveg' (<<https://www.synbiosys.alterra.nl/turboveg>>). Also import/export routines for exchange of data with 'Juice' (<<http://www.sci.muni.cz/botany/juice>>) are implemented.

LazyData true

Roxygen list(markdown = TRUE)

License GPL (>= 2)

URL <https://github.com/kamapu/vegtable>

BugReports <https://github.com/kamapu/vegtable/issues>

Collate 'imports.R'
'NULLing.R'
'coverconvert-class.R'
'vegtable-class.R'
'shaker-class.R'
'transform.R'
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 'trait_stats.R'
 'aspect_conv-data.R'
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RoxygenNote 7.1.1

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add_relevés	<i>Merge relevés from data frames into vegetable objects</i>
-------------	--

Description

Addition of plot observations into existing data sets may implicate merging data frames with [vegetable](#) objects.

Since this function will only update slots **samples** and **header**, consistency with slots **layers**, **relations** and **species** have to be checked and accordingly updated in advance.

Usage

```
add_relevés(vegetable, relevés, ...)

## S4 method for signature 'vegetable,data.frame'
add_relevés(
  vegetable,
  relevés,
  header,
  abundance,
  split_string,
  usage_ids = FALSE,
  layers = FALSE,
  layers_var,
  format = "crosstable",
  preserve_ids = FALSE,
  ...
)
```

Arguments

<code>vegetable</code>	An object of class vegetable .
<code>releves</code>	A data frame including plot observations to be added into <code>vegetable</code> .
<code>...</code>	Further arguments passed to function cross2db() (i.e. <code>na_strings</code>).
<code>header</code>	A data frame (optional) including header information for plots.
<code>abundance</code>	A character value (or vector of length 2) indicating the names of abundance variable in <code>vegetable</code> .
<code>split_string</code>	Character value used to split mixed abundance codes.
<code>usage_ids</code>	Logical value indicating whether species are as taxon usage ids (integers) or names in <code>releves</code> .
<code>layers</code>	Logical value indicating whether layers are included in <code>releves</code> or not.
<code>layers_var</code>	Name of the layer variable in <code>vegetable</code> .
<code>format</code>	Character value indicating input format of <code>releves</code> (either <code>"crosstable"</code> or <code>"databaselist"</code>).
<code>preserve_ids</code>	A logical value, whether IDs in input data set should used as <code>ReleveID</code> or not. Those IDs have to be integers and if one of those already exists in <code>vegetable</code> , an error will be retrieved.

Author(s)

Miguel Alvarez <kamapu78@gmail.com>

See Also

[cross2db\(\)](#)

aggregate

Aggregating information into a data frame

Description

This function aggregates information contained in [vegetable](#) objects to a summarizing data frame.

This function works in a similar way as [crosstable\(\)](#).

Usage

```
## S4 method for signature 'formula'
aggregate(x, data, FUN, use_nas = TRUE, ...)
```

Arguments

x	A formula indicating the variables used for the summary.
data	Either a data frame or an object of class vegtable .
FUN	Function used to aggregate values.
use_nas	Logical value indicating whether NA's should be included in categorical variables or not.
...	Further arguments passed to the function stats::aggregate() .

Value

An object of class [data.frame](#).

Author(s)

Miguel Alvarez <kamapu78@gmail.com>

See Also

[stats::aggregate\(\)](#)

as.list	<i>Coerce an S4 object to a list</i>
---------	--------------------------------------

Description

Coercion used to explore content in S4 objects.

S4 objects will be coerced to lists, where each slot in the input object becomes a member of the output list. This way allows to explore content and solve problems when validity checks fail.

Usage

```
## S4 method for signature 'vegtable'
as.list(x, ...)

## S4 method for signature 'coverconvert'
as.list(x, ...)
```

Arguments

x	an object of class coverconvert or vegtable
...	further arguments passed from or to other methods.

Value

An object of class `list`.

Author(s)

Miguel Alvarez <kamapu78@gmail.com>

Examples

```
## Head of slot 'taxonNames'
class(Easplist)
head(Easplist@taxonNames)

## The same after coercing to list
Easplist <- as.list(Easplist)
class(Easplist)
head(Easplist$taxonNames)
```

aspect_conv-data	<i>Conversion of aspect classes to azimuth</i>
------------------	--

Description

Conversion table required to transform values of aspect to azimuth in degrees.

Usage

```
aspect_conv
```

Format

A numeric vector of values in degrees for the symbols used as names.

Author(s)

Miguel Alvarez <kamapu78@gmail.com>

Examples

```
aspect_conv[c("N", "S", "ENE", "SSW")]
```

braun_blanquet-data	<i>Conversion of Braun-Blanquet codes to cover percentage Cover values conversion as <code>coverconvert</code> object. Object of class <code>coverconvert</code> contains conversion tables usually from a categorical variable (a cover scale) to a numerical one (equivalent percentage cover value). Cover values are stored as range for each level in the scale (minimum and maximum cover value).</i>
---------------------	---

Description

Conversion of Braun-Blanquet codes to cover percentage
Cover values conversion as `coverconvert` object.
Object of class `coverconvert` contains conversion tables usually from a categorical variable (a cover scale) to a numerical one (equivalent percentage cover value). Cover values are stored as range for each level in the scale (minimum and maximum cover value).

Usage

braun_blanquet

Format

An object of class `coverconvert`.

See Also

`coverconvert transform()`

Examples

```
names(braun_blanquet)
summary(braun_blanquet)
summary(braun_blanquet$b_bbds)
```

clean	<i>Clean orphaned records in vegtable object</i>
-------	--

Description

Delete entries in slots header and species orphaned by manipulation of slots.
Orphaned records generated by modifications in some slots may cause a loss on the validity of `vegtable` objects. This function should be applied to optimise the allocated size of a `vegtable` object, as well. Since running cleaning only once does not assure the deletion of all orphaned entries, it is recommended to run it at least twice. This repetition of cleaning is controlled by the argument `times`.

Usage

```
clean_once(object)

## S4 method for signature 'vegetable'
clean(object, times = 2, ...)
```

Arguments

object	A vegetable object.
times	Numeric value indicating how many times should be the cleaning be repeated.
...	Further arguments passed from or to other methods.

Value

A clean [vegetable](#) object.

Author(s)

Miguel Alvarez <kamapu78@gmail.com>

count_taxa	<i>Count taxa included in vegetable objects</i>
------------	---

Description

Counting number of taxa within [taxlist](#) objects or character vectors containing taxon names.

This function provides a quick calculation of taxa in [vegetable](#) objects, considering only records in slot samples. Such records can be also merged from lower ranks.

For the formula method, units without any requested taxa will not appear in the output data frame. If no taxa at all is occurring at the requested level in any unit, an error message will be retrieved.

Usage

```
## S4 method for signature 'vegetable,missing'
count_taxa(object, level, include_lower = FALSE, ...)

## S4 method for signature 'formula,vegetable'
count_taxa(
  object,
  data,
  include_lower = FALSE,
  suffix = "_count",
  in_header = FALSE,
  ...
)
```


Arguments

object	An object of class vegtable or a formula.
level	Character value indicating the taxonomic rank of counted taxa.
include_lower	Logical value, whether lower taxonomic ranks should be included at the requested level.
...	further arguments passed among methods.
data	An object of class vegtable .
suffix	Character value used as suffix on the calculated variable.
in_header	Logical value, whether the result should be included in the slot header of the input vegtable object or not. A warning message is provided if the calculation is not done for every plot observation.

Value

An data frame with the number of taxa from requested level at requested units for the formula method, or just an integer value.

Author(s)

Miguel Alvarez <kamapu78@gmail.com>

Examples

```
## Different alternatives
count_taxa(Kenya_veg)
head(count_taxa(~ ReveleID, Kenya_veg))
head(count_taxa(species ~ ReveleID, Kenya_veg))
head(count_taxa(species ~ ReveleID, Kenya_veg, TRUE))
head(count_taxa(family ~ ReveleID, Kenya_veg, TRUE))
```

coverconvert	<i>Cover conversion tables</i>
--------------	--------------------------------

Description

Cover conversion tables for [vegtable](#) objects.

This class implements conversions from different cover scales in percentage cover. For transformations to percentage cover, the function [transform\(\)](#) should be than used.

Slots

value List containing the levels of each scale.
 conversion List with the respective start and end cut levels for the scale levels.

Author(s)

Miguel Alvarez <kamapu78@gmail.com>

See Also

[tv2coverconvert\(\)](#) [braun_blanquet](#).

Examples

```
showClass("coverconvert")

## Add a custom scale
Scale <- new("coverconvert")
Scale$my_scale <- list(
  value=factor(c("low","medium","high"), levels=c("low","medium","high")),
  conversion=c(0,50,75,100))
summary(Scale)
```

crosstable

Generating cross tables from database lists

Description

This function is generating cross tables, which are the most common format used by statistical packages analysing vegetation data (e.g. [vegan::vegan](#)).

Most applications and displays of vegetation data use preferentially the cross table format. For convenience, the formula has the form abundance ~ plot + species + ...{ }. Additional variables used for rows (...{ }) can be for instance the layers.

For objects of class [vegtable](#), the formula can also include variables from the species list (for example AcceptedName, AuthorName) or even taxon traits.

Usage

```
crosstable(formula, data, ...)

## S4 method for signature 'formula,data.frame'
crosstable(
  formula,
  data,
  FUN,
  na_to_zero = FALSE,
  use_nas = TRUE,
  as_matrix = FALSE,
  ...
)
```

```
## S4 method for signature 'formula,vegetable'
crosstable(formula, data, FUN, na_to_zero = FALSE, use_nas = TRUE, ...)

cross2db(object, layers = FALSE, na_strings)
```

Arguments

formula	A formula indicating the variables used in the cross table.
data	Either a data frame or an object of class vegetable .
...	Further arguments passed to the function stats::aggregate() .
FUN	Function used to aggregate values.
na_to_zero	A logical value indicating whether zeros should be inserted into empty cells or not.
use_nas	Logical value indicating whether NAs should be considered as levels for categorical variables or not.
as_matrix	A logical value, whether output should be done as matrix or data frame.
object	A data frame including a cross table.
layers	Logical value, whether the cross table includes a layer column or not.
na_strings	Character vector indicating no records in the cross table.

Value

An object of class [data.frame](#).

Author(s)

Miguel Alvarez <kamapu78@gmail.com>

Examples

```
Kenya_veg <- subset(Kenya_veg, REFERENCE == 2331, slot="header")

## transform cover to percentage
Kenya_veg <- transform(Kenya_veg, to="cover_perc", rule="middle")

## cross table of the first 5 plots
Cross <- crosstable(cover_perc ~ RelveID + AcceptedName + AuthorName,
  Kenya_veg[1:5,], mean, na_to_zero=TRUE)
head(Cross)
```

df2vegtable

Convert a data frame into a vegtable object.

Description

Conversion of a data frame containing a cross table of abundance or cover of species in single plots.

This function coerces a data frame containing a vegetation cross table into a [vegtable](#) object. The input data frame `x` may include information on the layers or not.

Usage

```
df2vegtable(x, species, layer, ...)

## S4 method for signature 'data.frame,numeric,numeric'
df2vegtable(x, species, layer, ...)

## S4 method for signature 'data.frame,numeric,missing'
df2vegtable(x, species, layer, ...)
```

Arguments

<code>x</code>	A data frame formatted for a taxlist object.
<code>species</code>	Numeric or integer indicating the position of the column with species names.
<code>layer</code>	Numeric or integer indicating the position of the column with layers.
<code>...</code>	Further arguments passed from or to other methods.

Value

A [vegtable](#) object.

Author(s)

Miguel Alvarez <kamapu78@gmail.com>

Examples

```
## Creating data set 'dune_veg'
library(vegan)

## Load data from vegan
data(dune)
data(dune.env)

## Conversion to vegtable
dune_veg <- data.frame(species=colnames(dune), t(dune),
  stringsAsFactors=FALSE, check.names=FALSE)
dune_veg <- df2vegtable(dune_veg, species=1)
```

```
summary(dune_veg)

## Adding environmental variables
dune.env$ReleveID <- as.integer(rownames(dune.env))
header(dune_veg) <- dune.env

summary(dune_veg)
```

dune_veg-data	<i>Dutch dune meadows as vegtable Data set from the package vegan::vegan, converted to a vegtable object.</i>
---------------	---

Description

Dutch dune meadows as vegtable

Data set from the package [vegan::vegan](#), converted to a [vegtable](#) object.

Usage

```
dune_veg
```

Format

An object of class [vegtable](#).

Source

Original data were imported from [vegan::dune](#).

References

Jongman RHG, ter Braak CJF, van Tongeren OFR (1987). *Data analysis in community and landscape ecology*. Pudoc, Wageningen, NL.

Examples

```
summary(dune_veg)
```

 Extract

Select or replace elements in objects

Description

Methods for quick access to slot header of [vegetable](#) objects or for access to single cover scales in [coverconvert](#) objects. Also replacement methods are implemented.

Usage

```
## S4 method for signature 'vegetable'
x$name

## S4 replacement method for signature 'vegetable,ANY'
x$name <- value

## S4 method for signature 'coverconvert'
x$name

## S4 replacement method for signature 'coverconvert,list'
x$name <- value

## S4 method for signature 'vegetable,ANY,ANY'
x[i, j, ..., drop = FALSE]

## S4 replacement method for signature 'vegetable,ANY,ANY,ANY'
x[i, j] <- value
```

Arguments

x	Object of class vegetable .
name	A name to access.
value	Either a vectors or a list, used as replacement.
i, j	Indices for access.
...	Further arguments passed to or from other methods.
drop	A logical value passed to Extract .

Author(s)

Miguel Alvarez <kamapu78@gmail.com>

Examples

```
## Range of latitude values in database
range(Kenya_veg$LATITUDE)
```

```
## Summary of countries
summary(Kenya_veg$COUNTRY)
summary(droplevels(Kenya_veg$COUNTRY))

## First 5 samples
summary(Kenya_veg[1:5,])
```

header

Retrieve or replace slot header in vegetable objects

Description

Retrieve or replace the content of slot header in [vegetable](#) objects.

Usage

```
header(x, ...)
```

S4 method for signature 'vegetable'

```
header(x, ...)
```

header(x) <- value

S4 replacement method for signature 'vegetable,data.frame'

```
header(x) <- value
```

Arguments

x	Object of class vegetable .
...	Further arguments passed to or from other methods.
value	Data frame to be set as slot header.

Author(s)

Miguel Alvarez <kamapu78@gmail.com>

Examples

```
head(header(Kenya_veg))
```

Kenya_veg-data

*Vegetation-plots from Kenya***Description**

A subset of <http://www.givd.info/ID/AF-00-006SWEA-Dataveg> including five references providing plots collected in Kenya.

Usage

Kenya_veg

Format

An object of class [vegetable](#).

Author(s)

Miguel Alvarez <kamapu78@gmail.com> and Michael Curran <currmi01@gmail.com>

Source

<http://www.givd.info/ID/AF-00-006>

References

- Bronner G (1990).** *Vegetation and land use in the Mathews Range area, Samburu-District, Kenya*. J. Cramer, Berlin.
- Bussmann RW (1994).** *The forests of Mount Kenya – vegetation, ecology, destruction and management of a tropical mountain forest ecosystem*. Universität Bayreuth.
- Bussmann RW (2002).** Islands in the desert – forest vegetation of Kenya’s smaller mountains and highland areas. *Journal of East African Natural History* 91: 27–79.
- Fujiwara K, Furukawa T, Kiboi SK, Mathenge S, Mutiso P, Hayashi H, Meguro S (2014).** Forest types and biodiversity around the Great Rift Valley in Kenya. *Contributii Botanice* 49: 143–178.
- Schmitt K (1991).** *The vegetation of the Aberdare National Park Kenya*. Universitätsverlag Wagner, Innsbruck.

Examples

```
summary(Kenya_veg)
```

layers2samples	<i>Add information from slot 'layers' into slot 'samples'</i>
----------------	---

Description

Slot layers may include additional information that should be moved to samples in order to use it by `subset()`, `aggregate()` or `crosstable()` methods.

If names of variables are not provided, all variables from the respective layer table will be inserted in slot samples.

Usage

```
layers2samples(object, layer, variable, ...)  
  
## S4 method for signature 'vegtable,character,character'  
layers2samples(object, layer, variable, ...)  
  
## S4 method for signature 'vegtable,character,missing'  
layers2samples(object, layer, variable, ...)
```

Arguments

object	An object of class <code>vegtable</code> .
layer	Character value indicating a target layer.
variable	Character vector with the names of variables to be inserted in slot samples.
...	Further arguments to be passed among methods.

Value

An object of class `vegtable` with variables added to samples.

Author(s)

Miguel Alvarez <kamapu78@gmail.com>.

make_cocktail

*Produce a Cocktail classification***Description**

Classification of [vegetable](#) objects according to **Cocktail** algorithms.

Cocktail algorithms are logical functions selecting plots according to either occurrence of species groups and cover values of single species. A group will be declared as occurring in a plot when at least a half of its members is present in the plot.

This function inserts single columns with logical values indicating whether a plot is classified in the vegetation unit or not. An additional column (name provided in argument syntax) compile all vegetation units, indicating with a + symbol those plots classified in more than one vegetation unit. When only a part of the formulas will be used, it should be specified by the argument *which*.

These functions are implemented for constructing or complementing [shaker](#) objects. Note that construction of those objects will always require a companion object, which is either an object of class [taxlist](#) or [vegetable](#).

Usage

```
set_group(shaker, companion, group, ...)

## S4 method for signature 'shaker,taxlist,character'
set_group(
  shaker,
  companion,
  group,
  group_id,
  authority = FALSE,
  enc_cont = "latin1",
  enc_gr = "utf8",
  ...
)

## S4 method for signature 'shaker,vegetable,character'
set_group(shaker, companion, group, ...)

set_pseudo(shaker, companion, pseudo, ...)

## S4 method for signature 'shaker,taxlist,character'
set_pseudo(
  shaker,
  companion,
  pseudo,
  pseudo_id,
  authority = FALSE,
  enc_cont = "latin1",
```

```

    enc_gr = "utf8",
    ...
)

## S4 method for signature 'shaker,vegetable,character'
set_pseudo(shaker, companion, pseudo, ...)

set_formula(shaker, companion, formula, ...)

## S4 method for signature 'shaker,taxlist,character'
set_formula(
  shaker,
  companion,
  formula,
  formula_id,
  authority = FALSE,
  enc_cont = "latin1",
  enc_gr = "utf8",
  ...
)

## S4 method for signature 'shaker,vegetable,character'
set_formula(shaker, companion, formula, ...)

make_cocktail(shaker, vegetable, ...)

## S4 method for signature 'shaker,vegetable'
make_cocktail(
  shaker,
  vegetable,
  which,
  cover,
  syntax = "Syntax",
  FUN = sum,
  ...
)

```

Arguments

shaker	An object of class shaker containing the respective cocktail definitions.
companion	Either a taxlist or a vegetable object.
...	Further arguments passes from or to other methods.
authority	Logical value indicating whether author names should be included in the taxon name or not.
enc_cont, enc_gr	Encodings used for special characters.
pseudo, group	Character vector with names of taxa included in a pseudo-species or a species group.

pseudo_id, group_id, formula_id	Character value as name of the pseudo-species, species group or defined vegetation unit.
formula	Character vector including a formula as definition of a vegetation unit.
vegetable	An object of class vegetable containing the vegetation observations to be classified.
which	Integer or character indicating the definition to be applied for classification.
cover	Name of the cover variable in vegetable.
syntax	Character value indicating the name of the retrieved variable including the final classification of plots.
FUN	Function used for merging multiple occurrence of species in a single plot.

Value

A data frame corresponding to the slot header of input object `vegetable`, including the results of Cocktail classification for the respective plots.

A [shaker](#) object.

Author(s)

Miguel Alvarez <kamapu78@gmail.com>

References

Alvarez M (2017). Classification of aquatic and semi-aquatic vegetation in two East African sites: Cocktail definitions and syntaxonomy. *Phytocoenologia*.

Bruehlheide H (2000). A new measure of fidelity and its application to defining species groups. *Journal of Vegetation Science* 11: 167–178.

Kočí M, Chytrý M, Tichý L (2003). Formalized reproduction of an expert-based phytosociological classification: a case study of subalpine tall-forb vegetation. *Journal of Vegetation Science* 14: 601–610.

See Also

[shaker](#) [vegetable](#) [Wetlands](#)

Examples

```
## Example from Alvarez (2017)
Wetlands_veg@header <- make_cocktail(Wetlands, Wetlands_veg, cover="percen")
summary(as.factor(Wetlands_veg@header$Syntax))

## Same but only for two vegetation units
Wetlands_veg@header <- make_cocktail(Wetlands, Wetlands_veg,
  which=c("HY1", "HY2"), cover="percen")
summary(as.factor(Wetlands_veg$Syntax))

## Construct the 'shaker' object anew
```

```

Wetlands <- new("shaker")

## Set a pseudo-species
Wetlands <- set_pseudo(Wetlands, Wetlands_veg, c("Cyperus latifolius",
"Cyperus exaltatus"))

## Set a species group
Wetlands <- set_group(Wetlands, Wetlands_veg, group_id="Cyperus papyrus",
group=c(
  "Cyperus papyrus",
  "Cyclosorus interruptus",
  "Lepistemon owariense"))

## Set a formula
Wetlands <- set_formula(Wetlands, Wetlands_veg, formula_id="HE1",
formula="groups:'Cyperus papyrus' | species:'Cyperus papyrus > 50'")

## Summaries
summary(Wetlands)
summary(Wetlands, Wetlands_veg)

```

match_names	<i>Search matchings between character and taxlist objects.</i>
-------------	--

Description

Names provided in a character vector will be compared with names stored in slot `taxonNames` of an object of class `taxlist` by using the function `stringdist::stringsim()`.

This method is applied to the slot `species` in the input `vegetable` object.

Usage

```

## S4 method for signature 'character,vegetable'
match_names(x, object, ...)

```

Arguments

<code>x</code>	A character vector with names to be compared.
<code>object</code>	An object of class <code>vegetable</code> to be compared with.
<code>...</code>	Further arguments passed to <code>taxlist::match_names()</code> .

Author(s)

Miguel Alvarez <kamapu78@gmail.com>

See Also

`taxlist::match_names()` `stringdist::stringsim()`

merge_taxa

*Merge concepts***Description**

Merge taxon concepts form into single ones or insert accepted names to slot samples.

This method is applied to a function defined in the package [taxlist-package](#) and only modify the slot species in the input object.

The use of `taxa2samples()` with `merge_to` argument will produce a similar result as using `merge_taxa` with `level` argument, but `taxa2samples()` will replace the records in slot samples by the respective accepted names without any modification in slot species. Additionally taxon concept IDs will be added as columns in samples and taxon traits if indicated in argument `add_traits`.

Usage

```
## S4 method for signature 'vegetable,numeric,missing'
merge_taxa(object, concepts, level, ...)

## S4 method for signature 'vegetable,missing,character'
merge_taxa(object, concepts, level, ...)

taxa2samples(object, ...)

## S4 method for signature 'vegetable'
taxa2samples(object, merge_to, include_levels, na.rm = FALSE, add_traits, ...)
```

Arguments

<code>object</code>	Object of class vegetable .
<code>concepts</code>	Numeric (integer) vector including taxon concepts to be merged.
<code>level, merge_to</code>	Character value indicating the level to which the taxa have to be merged.
<code>...</code>	Further arguments passed to taxlist::merge_taxa() .
<code>include_levels</code>	Character vector indicating the levels to be considered in the output object. It can be used to exclude some taxonomic ranks.
<code>na.rm</code>	Logical value. Apply to records with missing information on taxonomic rank (i.e. for undetermined specimens).
<code>add_traits</code>	A character vector indicating variables in the slot <code>taxonTraits</code> to be added in slot samples.

Value

An object of class [vegetable](#).

Author(s)

Miguel Alvarez <kamapu78@gmail.com>

Examples

```
## Merge Olea capensis into one
summary(subset(Kenya_veg@species, grepl("Olea capensis", TaxonName),
  slot="names"), "all")
Kenya_veg <- merge_taxa(Kenya_veg, c(52041,50432,50235))

## Check Olea capensis again
summary(subset(Kenya_veg@species, grepl("Olea capensis", TaxonName),
  slot="names"), "all")

## Effect of taxa2samples by counting taxa
count_taxa(Kenya_veg, level="genus")

Kenya_veg <- taxa2samples(Kenya_veg, merge_to="genus")
count_taxa(Kenya_veg, level="genus")
```

names

Retrieve names of vegetable and coverconvert objects

Description

Quick access to column names in slot header and names of conversion codes.

These methods provide a quick display of the contents in [coverconvert](#) and [vegetable](#) objects.

Usage

```
## S4 method for signature 'vegetable'
names(x)

## S4 replacement method for signature 'vegetable'
names(x) <- value

## S4 method for signature 'vegetable'
dimnames(x)

## S4 method for signature 'coverconvert'
names(x)

## S4 replacement method for signature 'coverconvert'
names(x) <- value
```

Arguments

`x` An object of class `coverconvert` or `vegetable`.
`value` A character vector used for replacement methods.

Value

Either a vector or a list (in the case of `dimnames()`) with the names of variables.

Author(s)

Miguel Alvarez <kamapu78@gmail.com>.

Examples

```
names(Kenya_veg@coverconvert)
names(Kenya_veg)
dimnames(Kenya_veg)
```

shaker-class

Class containing Cocktail algorithms.

Description

Objects used for collecting Cocktail definitions.

These objects work as **expert systems** for recognition of defined vegetation units among plots of a `vegetable` object. A shaker object will be always dependent on a `vegetable` object, which is called companion. Since modifications in the companion may affect the functionality of the shaker object, it will be recommended to create the last during a session by a source script instead of recycling them from old R images.

Slots

`pseudos` List containing IDs of taxa that will be merged into pseudo-species.
`groups` List containing IDs of taxa belonging to the same Cocktail group.
`dominants` A data frame including lists of species used as dominant species in Cocktail algorithms, as well as operators and cover values used in the formulas.
`formulas` List with formulas that will be used as definitions for vegetation units.

Author(s)

Miguel Alvarez <kamapu78@gmail.com>

See Also

`make_cocktail()` `set_pseudo()` `set_group()` `set_formula()`

Examples

```
showClass("shaker")
```

subset

Subset functions for vegetable objects

Description

Produce subsets of [vegetable](#) objects.

This function generate subsets of [vegetable](#) objects through logical operations. Such operations can be applied either to the plots, or the relations, which are the main slots in that class.

This method can be referred to the slot species the same way as [taxlist::subset\(\)](#), then the rest of the data will include only references to the subset of species list.

Usage

```
## S4 method for signature 'vegetable'
subset(
  x,
  subset,
  slot = "header",
  keep_children = FALSE,
  keep_parents = FALSE,
  relation,
  ...
)
```

Arguments

x	A vegetable object for subset.
subset	Logical expression for subset.
slot	Character value indicating the slot used as reference for subset. At the moment only the values "taxonNames", "taxonRelations", "taxonTraits", "header", "samples", and "relations" are accepted. The three first values will be applied to the respective slots in the contained taxlist object (slot species).
keep_children	Argument passed to taxlist::get_children() .
keep_parents	Argument passed to taxlist::get_parents() .
relation	Character value indicating the relation (slot relations) to be used as reference for subset.
...	Further arguments passed from or to other methods.

Value

A S4 object of class [vegetable](#).

Author(s)

Miguel Alvarez <kamapu78@gmail.com>

Examples

```
## Subset by taxon name
Kenya_sub <- subset(x=Kenya_veg, subset=TaxonName == "Tagetes",
slot="taxonNames", keep_children=TRUE, keep_parents=TRUE)
summary(Kenya_sub)
summary(Kenya_sub@species)

## Subset by taxon relations
Kenya_sub <- subset(x=Kenya_veg, subset=Level == "species",
slot="taxonRelations")
summary(Kenya_sub)
summary(Kenya_sub@species)

## Subset by taxon traits
Kenya_sub <- subset(x=Kenya_veg, subset=lf_behn_2018 == "obligate_annual",
slot="taxonTraits")
summary(Kenya_sub)
summary(Kenya_sub@species)

## Subset by header
Kenya_sub <- subset(x=Kenya_veg, subset=ALTITUDE <= 1000, slot="header")
summary(Kenya_sub)

## Subset by samples (after converting coverage)
Kenya_veg <- transform(x=Kenya_veg, to="cover_percentage", rule="middle")
Kenya_sub <- subset(x=Kenya_veg, subset=cover_percentage >= 50, slot="samples")
summary(Kenya_sub)

## Subset by relations
Kenya_sub <- subset(x=Kenya_veg, subset=as.integer(YEAR) >= 2000,
slot="relations", relation="REFERENCE")
summary(Kenya_sub)
```

summary

Summary method for vegetable objects

Description

Display summaries for [vegetable](#) objects.

Those methods are implemented for objects of the classes [vegetable](#), [coverconvert](#) and [shaker](#).

The method for class [vegetable](#) retrieves the metadata, the size of the object, its validity and additional statistics on the content of input object.

For objects of class [shaker](#), the function `summary()` will either retrieve general statistics when companion is missing, or a more detailed display when accompanied by a [taxlist](#) or [vegetable](#) object.

Usage

```
## S4 method for signature 'vegetable'
summary(object, units = "Kb", ...)

## S4 method for signature 'coverconvert'
summary(object, ...)

## S4 method for signature 'shaker'
summary(object, companion, authority = FALSE, ...)
```

Arguments

object	Object to be summarized.
units	Units used for object size (passed to <code>format()</code>).
...	further arguments to be passed to or from other methods.
companion	Companion object (either a taxlist or a vegetable object).
authority	Logical value indicating whether authors should be displayed or not.

Author(s)

Miguel Alvarez <kamapu78@gmail.com>

Examples

```
## Summary for 'vegetable' objects
summary(Wetlands_veg)

## Summary for 'coverconvert' objects
summary(braun_blanquet)

## Summary for 'shaker' objects (alone and with companion)
summary(Wetlands, Wetlands_veg)
```

trait_stats

Statistics and proportion for taxon traits

Description

Calculation of statistics and proportions of taxon traits for plot observations or groups of observations, considering data relationships, taxonomic ranks and the handling of not available values.

The function `trait_stats()` calculates statistics for numeric variables, while the function `trait_proportion()` may be used for categorical variables. In the first case, a column with the name of the variable and a suffix will be generated, while in the second case, one additional column per selected trait level will be calculated.

Both mentioned functions offer the alternative weighted and unweighted calculations (e.g. calculations weighted by the abundance of species). In the particular case of `trait_stats()`, customized functions have to be defined as `foo(x,w,...)`, where `w` is the weight.

With the arguments `taxon_level` and `merge_to` the used taxonomic ranks can be defined, where the first one indicates which ranks have to be considered in the calculations and the second one determine the aggregation of taxa from a lower level to a parental one.

Formula methods allow for the calculation of multiple variables at once. The formulas have to be written as `trait_1 + ... + trait_n ~ head_var`.

Usage

```
trait_stats(trait, object, ...)

## S4 method for signature 'character,vegetable'
trait_stats(
  trait,
  object,
  FUN,
  head_var,
  taxon_level,
  merge_to,
  weight,
  suffix = "_stats",
  in_header = FALSE,
  ...
)

## S4 method for signature 'formula,vegetable'
trait_stats(trait, object, weight, suffix = "_stats", in_header = FALSE, ...)

trait_proportion(trait, object, ...)

## S4 method for signature 'character,vegetable'
trait_proportion(
  trait,
  object,
  head_var,
  trait_level,
  taxon_level,
  merge_to,
  include_nas = TRUE,
  weight,
  suffix = "_prop",
  in_header = FALSE,
  ...
)

## S4 method for signature 'formula,vegetable'
```

```
trait_proportion(trait, object, in_header = FALSE, ...)
```

Arguments

trait	Either a character value indicating the name of trait variable or a formula including both arguments, trait and head_var.
object	A vegetable object.
...	Further arguments passed among methods. In the case of the formula method, arguments are passed to the character method.
FUN	A function usually defined as <code>foo(x,...)</code> or as <code>foo(x,w,...)</code> for weighted statistics.
head_var	Character value, the name of the variable at slot header to be used as aggregation level for the calculation of statistics or proportions. If not provided, the function will use ReleveID by default.
taxon_level	Character value indicating a selected taxonomic rank for the output.
merge_to	Character value indicating the taxonomic rank for aggregation of taxa. All ranks lower than the one indicated here will be assigned to the respective parents at the required taxonomic rank.
weight	Character value indicating the name of the variable at slot samples used as weight for the proportions. Usually the numeric abundance.
suffix	A suffix added to the name of the trait variable or to the levels of categorical trait variables. It is meant to avoid homonymous variables within the same object.
in_header	Logical value indicating whether the output should be inserted in the slot header or provided as data frame.
trait_level	Character vector indicating a selection of levels from a trait, in the case that some levels should be ignored in the output. Trait levels that are skipped at output will be still used for the calculation of proportions. This argument gets only applied for the character method.
include_nas	Logical value indicating whether NAs should be considered for the calculation of proportions or not.

Value

A data frame with the proportions of traits levels or statistics for the trait variable, or an object of class [vegetable](#) including those results at the slot header.

Author(s)

Miguel Alvarez <kamapu78@gmail.com>

Examples

```
## Cocktail classification of plots
Wetlands_veg@header <- make_cocktail(Wetlands, Wetlands_veg, cover="percen")

## Calculation of proportion of Cyperaceae species in the plot
```

```
Wetlands_veg <- trait_proportion("FAMILY", Wetlands_veg, trait_level="Cyperaceae",
weight="percen", include_nas=FALSE, in_header=TRUE)

## Display of proportions per plant community
boxplot(Cyperaceae_prop ~ Syntax, Wetlands_veg@header, col="grey")
```

transform

Convert cover scales to percent cover

Description

Convert values of a categorical cover scale to percentage values.

This function requires as input a [coverconvert](#) object which contains the conversion tables.

In the case of [vegtable](#) objects, the conversion is already embedded in the slot `coverconvert`.

Three rules are implemented for transformation, either `top` (values transformed to the top of the range), `middle` (transformation at the midpoint), and `bottom` (conversion at the lowest value of the range). In the later case, transformation ranges starting at 0% of cover can be set to a different value by the argument `zeroto`.

When `replace=FALSE`, existing values of cover in the [vegtable](#) object will be maintained. Since there is not a standard naming of cover values, in the transformation the name of cover variable should be indicated in the argument `to`.

Usage

```
transform(x, conversion, ...)

## S4 method for signature 'character,coverconvert'
transform(x, conversion, from = NULL, rule = "top", zeroto = 0.1, ...)

## S4 method for signature 'factor,coverconvert'
transform(x, conversion, ...)

## S4 method for signature 'numeric,coverconvert'
transform(x, conversion, ...)

## S4 method for signature 'vegtable,missing'
transform(x, to, replace = FALSE, rule = "top", zeroto = 0.1, ...)
```

Arguments

<code>x</code>	Either a factor or character vector, or a vegtable object.
<code>conversion</code>	An object of class vegtable .
<code>...</code>	Further arguments passed from or to other methods.
<code>from</code>	Scale name of values in <code>x</code> as character value.

rule	Rule applied for the conversion (see details).
zeroto	Value used to replace levels with bottom at 0% cover.
to	Name of the column in slot samples for writing converted values.
replace	Logical value indicating whether existing cover values should be replaced or not.

Value

Either a vector or a [vegetable](#) object.

Author(s)

Miguel Alvarez <kamapu78@gmail.com>

Examples

```
## Check the available scales
summary(Kenya_veg@coverconvert)

## Conversion by default 'top' rule
Kenya_veg <- transform(Kenya_veg, to="percent")
summary(as.factor(Kenya_veg@samples$percent))

## Conversion by 'middle' rule
Kenya_veg <- transform(Kenya_veg, to="percent", rule="middle", replace=TRUE)
summary(as.factor(Kenya_veg@samples$percent))

## Conversion by 'bottom' rule
Kenya_veg <- transform(Kenya_veg, to="percent", rule="bottom", replace=TRUE)
summary(as.factor(Kenya_veg@samples$percent))
```

tv2vegetable

Import of vegetation data from Turboveg databases

Description

Import function for **Turboveg** databases into an object of class [vegetable](#). Most of the contents of **Turboveg** databases are included in DBF files and therefore imported by the function `foreign::read.dbf()`. The automatic setting of database path will be done by the function `vegdata::tv.home()` but it can be customised by the argument `tv_home`.

The species list will be imported by using the function `taxlist::tv2taxlist()` and therefore formatted as a [taxlist](#) object. Similarly, conversion tables will be handled as [coverconvert](#) objects.

Empty columns in the header will be deleted in the imported object.

The function `tv2coverconvert()` reads the content of cover conversion tables stored in **Turboveg** and attempts to reformat them in a more comprehensive structure.

This function is used by `tv2vegtable()` to import the respective conversion table from **Turboveg** databases. Note that conversion tables in **Turboveg** have only stored the middle point for each cover class in a scale, thus it will be recommended to rebuild the coverconvert slot or use [braun_blanquet](#).

Usage

```
tv2vegtable(
  db,
  tv_home = tv.home(),
  skip_empty_relations = TRUE,
  skip_scale,
  clean = TRUE
)

tv2coverconvert(file, as.is = TRUE)
```

Arguments

<code>db</code>	Name of Turboveg data base as character value.
<code>tv_home</code>	Turboveg installation path as character value.
<code>skip_empty_relations</code>	Logical value indicating whether empty relations may be excluded from imported database or not.
<code>skip_scale</code>	Character value indicating scales to be excluded in slot coverconvert.
<code>clean</code>	Logical value indicating whether output object should be cleaned or not.
<code>file</code>	A connection to a DBF file containing conversion table in Turboveg .
<code>as.is</code>	A logical value passed to read.dbf() .

Value

A [vegtable](#) object in the case of `tv2vegtable()`. A [coverconvert](#) object in the case of `tv2coverconvert()`.

Author(s)

Miguel Alvarez <kamapu78@gmail.com>

See Also

[taxlist::tv2taxlist\(\)](#) [foreign::read.dbf\(\)](#) [vegdata::tv.home\(\)](#)

Examples

```
## Installed 'Turboveg' version of 'Fujiwara et al. (2014)'
TV_Home <- file.path(path.package("vegtable"), "tv_data")
Veg <- tv2vegtable("Fujiwara_2014", TV_Home)
summary(Veg)

## Installed 'Turboveg' version of "Fujiwara et al. (2014)"
```



```

TV_Home <- file.path(path.package("vegtable"), "tv_data", "popup", "Swea")
Table <- tv2coverconvert(file.path(TV_Home, "tvscale.dbf"))

## First scale have to be deleted from conversion table
Table@value <- Table@value[-1]
Table@conversion <- Table@conversion[-1]
summary(Table)

## Compare the 'Turboveg' version with a vegtable version
data(braun_blanquet)
summary(Table$br_bl)
summary(braun_blanquet$br_bl)

```

used_synonyms

Retrieve synonyms or taxon concepts used in a data set

Description

Plots records are rather linked to plant names than plant taxon concepts. The function `used_synonyms()` provides a quick report about synonyms used in a data set (a [vegtable](#) object) and their respective accepted names.

Additionally, not all taxon concepts included in the taxonomic list (slot **species**) may be recorded in the plot observations. In that case the function `used_concepts()` will optimize the size of the taxonomic list by discarding taxa that are not "in use". Alternatively parents or children of these taxa may be included in the output data set.

Usage

```

used_synonyms(x, ...)

## S4 method for signature 'vegtable'
used_synonyms(x, ...)

used_concepts(x, ...)

## S4 method for signature 'vegtable'
used_concepts(x, keep_children = FALSE, keep_parents = FALSE, ...)

```

Arguments

<code>x</code>	A vegtable object.
<code>...</code>	Further arguments to be passed from or to another methods.
<code>keep_children</code>	Argument passed to taxlist::get_children() .
<code>keep_parents</code>	Argument passed to taxlist::get_parents() .

Value

The function `used_synonyms()` returns a data frame including following variables:

SynonymID ID of the taxon usage name applied as synonym.

Synonym The synonym itself.

SynonymAuthor Author of synonym.

TaxonConceptID ID of the respective taxon concept.

AcceptedNameID ID of the taxon usage name set as accepted name of the taxon concept.

AcceptedName The respective accepted name.

AcceptedNameAuthor The author of the accepted name.

The function `used_concepts()` returns a [taxlist](#) object including only taxa occurring in the plot observations of the input [vegetable](#) object.

Author(s)

Miguel Alvarez <kamapu78@gmail.com>

See Also

[accepted_name\(\)](#)

Examples

```
## Synonyms used in the Kenya_veg
Synonyms <- used_synonyms(Kenya_veg)
head(Synonyms)
```

vegetable-class

Class vegetable.

Description

Class holding vegetation-plot data sets. Designed to content all information stored in **Turboveg** databases in just one object.

This class was designed to include information of relevés, header data and species in just one object. Objects can be created by calls of the form `new("vegetable", ...)`.

Slots

description A named character vector containing metadata.

samples A data frame with samples list.

header A data frame with plots data.

species Species list as a [taxlist](#) object.

layers A list including strata within samples as data frames.

relations A list including popup lists as data frames.

coverconvert A scale conversion object of class [coverconvert](#).

Author(s)

Miguel Alvarez <kamapu78@gmail.com>

See Also

[tv2vegetable\(\)](#)

Examples

```
showClass("vegetable")
```

vegetable2kml	<i>Mapping of plot observations</i>
---------------	-------------------------------------

Description

This function is a wrapper of [plotKML::kml\(\)](#) producing and displaying KML files. Georeferenced plots can be quickly displayed in [Google Earth](#) using this function.

Usage

```
vegetable2kml(obj, ...)

## S4 method for signature 'data.frame'
vegetable2kml(
  obj,
  file,
  coords = ~Longitude + Latitude,
  srs = CRS("+proj=longlat +datum=WGS84")
)

## S4 method for signature 'vegetable'
vegetable2kml(
  obj,
  file,
  coords = ~LONGITUDE + LATITUDE,
  srs = CRS("+proj=longlat +datum=WGS84")
)
```

Arguments

obj	Input object containing coordinate values.
...	Further arguments passed among methods.
file	Character value with the name of output file (including file extension).
coords	Either a character vector or a formula indicating the names of coordinate values.
srs	Spatial reference system as proj4string.

Value

A KML file, which will be automatically opened in **Google Earth**.

Author(s)

Miguel Alvarez <kamapu78@gmail.com>

Examples

```
## Plots containing Podocarpus observations
Kenya_veg@species <- subset(Kenya_veg@species, grepl("Podocarpus", TaxonName),
  slot="names")

Kenya_veg <- subset(Kenya_veg, TaxonUsageID %in%
  Kenya_veg@species@taxonNames$TaxonUsageID, slot="samples")

## Not run: vegetable2kml(Kenya_veg, "Podocarpus.kml")
```

vegetable_stat

General statistics from vegetable objects

Description

This function calculates general statistics of local **Turboveg** databases as required by GIVD (Global Index of Vegetation-Plot Databases, <https://www.givd.info>).

This function is based on a script delivered by GIVD for summarising statistics required in the descriptions of databases (see meta data in the page of the Global Index for Vegetation-Plot Databases).

Usage

```
vegetable_stat(vegetable)
```

Arguments

vegetable An object of class [vegetable](#).

Author(s)

GIVD. Adapted by Miguel Alvarez <kamapu78@gmail.com>

Examples

```
## Statistics for GIVD
vegetable_stat(Kenya_veg)
```

veg_relation	<i>Retrieve or replace relations in vegetable objects</i>
--------------	---

Description

Tables providing information about levels of categorical variables in the header of a **Turboveg** database are called popups in **Turboveg**, but relations in [vegetable](#). Such variables will be converted into factors in the slot header according to the levels and their sorting in the respective relation.

Usage

```
veg_relation(vegetable, relation, ...)

## S4 method for signature 'vegetable,character'
veg_relation(vegetable, relation, match_header = FALSE, ...)

veg_relation(vegetable, relation) <- value

## S4 replacement method for signature 'vegetable,character,data.frame'
veg_relation(vegetable, relation) <- value

relation2header(vegetable, relation, ...)

## S4 method for signature 'vegetable,data.frame'
relation2header(vegetable, relation, by, vars, ...)

## S4 method for signature 'vegetable,character'
relation2header(vegetable, relation, ...)
```

Arguments

vegetable	An object of class vegetable .
relation	A character value indicating the relation table to be retrieved or replaced.
...	Further arguments to be passed among methods.
match_header	A logical vector, whether only levels occurring in slot header should be considered or all.
value	A data frame containing the new veg_relation.
by	Character value indicating the name of the common column used as index for inserting values in slot header.
vars	A character vector with the names of variables to be inserted in slot header.

Value

This function retrieves and object of class `data.frame`. In the replacement method, an object of class [vegetable](#), including value in the slot relations.

Author(s)

Miguel Alvarez <kamapu78@gmail.com>

Examples

```
## overview of references  
veg_relation(Kenya_veg, "REFERENCE")
```

Wetlands-data

Vegetation-plots from Tanzania

Description

A subset of <http://www.givd.info/ID/AF-00-006SWEA-Dataveg> with plots sampled in Tanzania.

Usage

Wetlands

Format

An object of class `shaker` (Wetlands) and the respective companion as `vegtable` object (Wetlands_veg).

Author(s)

Miguel Alvarez <kamapu78@gmail.com>

Source

<http://www.givd.info/ID/AF-00-006>.

References

Alvarez M (2017). Classification of aquatic and semi-aquatic vegetation in two East African sites: Cocktail definitions and syntaxonomy. *Phytocoenologia*.

Examples

```
summary(Wetlands)  
summary(Wetlands_veg)
```

Description

This function produce txt files as inport formats for **Juice** (<http://www.sci.muni.cz/botany/juice/>).

This function produces two output files to be imported into a **Juice** file: A vegetation table produced by `crosstable()` and a header table. Both tables share the file name plus a suffix (table for the vegetation table and header for the header).

For the import in **Juice**, you go to the menu File -> Import -> Table -> from Spreadsheet File (e.g. EXCEL Table) and then follow the wizard. Do not forget to select the proper settings in the wizard: 1) 'Character delimiting columns: Comma' (for default argument values). 2) 'Use the second column as layer information: Unchecked'. 3) 'Cover values: Percentage Values'.

To further import the header table you need to go to the menu File -> Import -> Header Data -> From Comma Delimited File.

In the header (see **Value**), the first column (Table number) corresponds to the plot number assigned by **Juice** at import, while the column (Releve number) is the number originally assigned to the plot (e.g. **Turboveg** ID).

Usage

```
write_juice(data, file, formula, ...)

## S4 method for signature 'vegtable,character,formula'
write_juice(
  data,
  file,
  formula,
  FUN,
  db_name = "Plot Observations",
  header,
  coords,
  sep = ",",
  ...
)

read_juice(file, encoding = "LATIN-1", sep = ";", na = "", ...)
```

Arguments

<code>data</code>	An object of class <code>vegtable</code> .
<code>file</code>	Character value indicating the name of output files (without file extension).
<code>formula</code>	A formula passed to <code>crosstable()</code> .

...	Further arguments. While write_juice() passes them to the function <code>crosstable()</code> , read_juice() passes those arguments to <code>readLines()</code> .
FUN	Funtion passed to <code>crosstable()</code> .
db_name	Name for data set displayed in inport wizard.
header	Variables of header to be exported.
coords	Names of coordinate variables in header of data.
sep	Separator used to split rows into columns.
encoding	Argument passed to <code>readLines</code> .
na	Character used as not available values.

Value

For read_juice(), a list with two elements: A data frame of species by plot (cross_table), and a data frame with header data (header).

Author(s)

Miguel Alvarez <kamapu78@gmail.com>

Examples

```
## Only first 20 observations
Kenya_veg <- Kenya_veg[1:20,]
## Not run:
write_juice(Kenya_veg, "SWEA", FUN=mean)

## End(Not run)

## Installed 'Juice' version of 'Wetlands_veg'
Veg <- file.path(path.package("vegtable"), "juice", "Wetlands_juice.txt")
Veg <- read_juice(Veg)

summary(Veg)
```


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