Package ‘vegtable’

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'as.list.R' 'merge_taxa.R' 'add_releves.R' 'header.R'
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'aspect_con-data.R' 'braun_blanquet-data.R' 'dune_veh-data.R'
'Kenya_veh-data.R' 'Wetlands-data.R' 'StartMessage.R'
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Addition of plot observations into existing data sets may implicate merging data frames with vegtable 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_releves(vegtable, releves, ...)

## S4 method for signature 'vegtable, data.frame'
add_releves(
  vegtable,
  releves,
  header,
  abundance,
  split_string,
  usage_ids = FALSE,
  layers = FALSE,
  layers_var,
  format = "crosstable",
  preserve_ids = FALSE,
  ...
)

Arguments

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

Author(s)

Miguel Alvarez <kamapu78@gmail.com>

See Also

cross2db()
aggregate

Description

This function aggregates information contained in `vegtable` objects to a summarizing data frame. This function works in a similar way as `crosstable()`.

Usage

```r
## 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

Description

Coerce an S4 object to a list.

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**

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

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

**Arguments**

- `x`  
an object of class `coverconvert` or `vegetable`
- `...`  
further arguments passed from or to other methods.

**Value**

An object of class `list`.

**Author(s)**

Miguel Alvarez &lt;kamapu78@gmail.com&gt;

**Examples**

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

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

---

**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")]

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).

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 orphaned records in vegetable object

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 vegetable objects. This function should be applied to optimise the allocated size of a vegetable 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 Count taxa included in vegetable objects

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

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

## S4 method for signature 'formula,vegtable'
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

```r
## Different alternatives
count_taxa(Kenya_veg)
head(count_taxa(~ ReleveID, Kenya_veg))
head(count_taxa(species ~ ReleveID, Kenya_veg))
head(count_taxa(species ~ ReleveID, Kenya_veg, TRUE))
head(count_taxa(family ~ ReleveID, Kenya_veg, TRUE))
```
**coverconvert**

*Cover conversion tables*

**Description**

Cover conversion tables for `vegetable` 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**

```r
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 `vegetable`, 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,vegtable'
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 vegtable.
... 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

```r
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 ~ ReleveID + 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**

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

**Arguments**

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

**Value**

A `vegtable` object.

**Author(s)**

Miguel Alvarez <kamapu78@gmail.com>
### Examples

```r
## 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**

*Dutch dune meadows as vegtable Data set from the package vegan::vegan, converted to a vegtable object.*

---

**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 CJE, van Tongeren OFR (1987).** *Data analysis in community and landscape ecology.* Pudoc, Wageningen, NL.
Examples

summary(dune_veg)

Description

Methods for quick access to slot header of `vegtable` objects or for access to single cover scales in `coverconvert` objects. Also replacement methods are implemented.

Usage

## S4 method for signature 'vegtable'

```r
x$name
```

## S4 replacement method for signature 'vegtable,ANY'

```r
x$name <- value
```

## S4 method for signature 'coverconvert'

```r
x$name
```

## S4 replacement method for signature 'coverconvert,list'

```r
x$name <- value
```

## S4 method for signature 'vegtable,ANY,ANY'

```r
x[i, j, ..., drop = FALSE]
```

## S4 replacement method for signature 'vegtable,ANY,ANY,ANY'

```r
x[i, j] <- value
```

Arguments

- `x`: Object of class `vegtable`.
- `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

```r
## 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 vegtable objects*

Description

Retrieve or replace the content of slot header in vegtable objects.

Usage

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

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

header(x) <- value

## S4 replacement method for signature 'vegtable,data.frame'
header(x) <- value
```

Arguments

- `x` Object of class vegtable.
- `...` 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

```r
head(header(Kenya_veg))
```
**Description**

A subset of [http://www.givd.info/ID/AF-00-006SWEA-Dataveg](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 `vegtable`.

**Author(s)**

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

**Source**

[http://www.givd.info/ID/AF-00-006](http://www.givd.info/ID/AF-00-006)

**References**


**Examples**

`summary(Kenya_veg)`
layers2samples

Add information from slot `layers` into slot `samples`.

**Description**

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

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

**Usage**

```r
layers2samples(object, layer, variable, ...)
```

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

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

**Arguments**

- `object`  
  An object of class `vegtable`.
- `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>.
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,vegtable,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",

### S4 method for signature 'shaker, vegetable, character'

```r
call = set_pseudo(shaker, companion, pseudo, ...)
```

### S4 method for signature 'shaker, taxlist, character'

```r
call = set_formula(shaker, companion, formula, ...)
```

### S4 method for signature 'shaker, vegetable, character'

```r
call = make_cocktail(shaker, vegetable, ...)
```

### S4 method for signature 'shaker, vegetable'

```r
call = make_cocktail(shaker, vegetable, ...)
```

#### 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.
make_cocktail

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.

vegtable
An object of class vegtable 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 vegtable.

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 vegtable, including the results of Cocktail classification for the respective plots.
A shaker object.

Author(s)
Miguel Alvarez <kamapu78@gmail.com>

References


See Also
shaker vegtable 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:\/\"Var\"
                               Species:     \/\"Var\"
                                "Cyperus papyrus > 50"
                                \"Var\"")

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

match_names

Search matchings between character and taxlist objects.

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'
momat_names(x, object, ...)

Arguments

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

Author(s)

Miguel Alvarez <kamapu78@gmail.com>

See Also

taxlist::match_names() stringdist::stringsim()
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 addes as columns in samples and taxon traits if indicated in argument add_traits.

Usage

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

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

taxa2samples(object, ...)

## S4 method for signature 'vegtable'
taxa2samples(object, merge_to, add_traits, ...)
```

Arguments

- `object`: Object of class `vegtable`.
- `concepts`: Numeric (integer) vector including taxon concepts to be merged.
- `level, merge_to`: Character value indicating the level to which the taxa have to be merged.
- `...`: Further arguments passed to `taxlist::merge_taxa()`.
- `add_traits`: A character vector indicating variables in the slot `taxonTraits` to be added in slot `samples`.

Value

An object of class `vegtable`.

Author(s)

Miguel Alvarez <kamapu78@gmail.com>
Examples

```r
## 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 vegtable 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 vegtable objects.

Usage

```r
## S4 method for signature 'vegtable'
names(x)

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

## S4 method for signature 'vegtable'
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 vegtable.
- `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**

```r
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**

```r
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, 
  ...
)

Arguments

x A vegetable object for subset.
subset Logical vector or operation for subset.
slot Slot to be applied for subset.
keep_children Argument passed to taxlist::subset().
keep_parents Argument passed to taxlist::subset().
... Further arguments passed from or to other methods.

Value

A S4 object of class vegetable.

Author(s)

Miguel Alvarez <kamapu78@gmail.com>
**Examples**

```r
summary(dune_veg)

## Select plots used as pastures
Pastures <- subset(dune_veg, Use == "Pasture", slot="header")
summary(Pastures)
```

---

**Summary (Summary method for vegtable objects)**

**Description**

Display summaries for `vegtable` objects.
Those methods are implemented for objects of the classes `vegtable`, `coverconvert` and `shaker`.
The method for class `vegtable` 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 `vegtable` object.

**Usage**

```r
## S4 method for signature 'vegtable'
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 `format()`).

- **...**  
  Further arguments to be passed to or from other methods.

- **companion**  
  Companion object (either a `taxlist` or a `vegtable` object).

- **authority**  
  Logical value indicating whether authors should be displayed or not.

**Author(s)**

Miguel Alvarez <kamapu78@gmail.com>
Examples

```r
## 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**

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

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

... )

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

trait_proportion(trait, object, ...)

## S4 method for signature 'character,vegtable'
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,vegtable'
trait_proportion(trait, object, in_header = FALSE, ...)

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>trait</td>
<td>Either a character value indicating the name of trait variable or a formula including both arguments, trait and head_var.</td>
</tr>
<tr>
<td>object</td>
<td>A vegtable object.</td>
</tr>
<tr>
<td>...</td>
<td>Further arguments passed among methods. In the case of the formula method, arguments are passed to the character method.</td>
</tr>
<tr>
<td>FUN</td>
<td>A function usually defined as foo(x,...) or as foo(x,w,...) for weighted statistics.</td>
</tr>
<tr>
<td>head_var</td>
<td>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.</td>
</tr>
<tr>
<td>taxon_level</td>
<td>Character value indicating a selected taxonomic rank for the output.</td>
</tr>
<tr>
<td>merge_to</td>
<td>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.</td>
</tr>
<tr>
<td>weight</td>
<td>Character value indicating the name of the variable at slot samples used as weight for the proportions. Usually the numeric abundance.</td>
</tr>
<tr>
<td>suffix</td>
<td>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.</td>
</tr>
</tbody>
</table>
transform

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.

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 vegtable 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

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

x Either a factor or character vector, or a vegtable object.
conversion An object of class vegtable.
... Further arguments passed from or to other methods.
from Scale name of values in x 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 vegtable 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))
```

---

**tv2vegtable**  
*Import of vegetation data from Turboveg databases*

### Description

Import function for **Turboveg** databases into an object of class **vegtable**. 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

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

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

```r
## 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)
```

Description

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

This function will only retrieve synonyms that are used in plot records.

Usage

```r
used_synonyms(x, ...)
```

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

x A `vegtable` object.

... Further arguments to be passed from or to another methods.

Value

A data frame with following columns:

- **SynonymsID** Usage ID of synonyms.
- **Synonym** The synonym itself.
- **SynonymAuthor** Author of synonym.
- **TaxonConceptID** ID of the taxon concept.
- **AcceptedNameID** Usage ID of the accepted name.
- **AcceptedName** The respective accepted name.
- **AcceptedNameAuthor** The author of the accepted name.

Author(s)

Miguel Alvarez <kamapu78@gmail.com>

See Also

- `accepted_name()`

Examples

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

---

**vegtable-class**

*Class vegtable.*

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("vegtable",...).`
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

tv2vegtable()

Examples

showClass("vegtable")

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

vegtable2kml(obj, ...)

## S4 method for signature 'data.frame'
vegtable2kml(
  obj,
  file,
  coords = ~Longitude + Latitude,
  srs = CRS("+proj=longlat +datum=WGS84")
)

## S4 method for signature 'vegtable'
vegtable2kml(
  obj,
Arguments

obj Input object containing coordinate values.
...
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: vegtable2kml(Kenya_veg, "Podocarpus.kml")

vegtable_stat

General statistics from vegtable 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

vegtable_stat(vegtable)
veg_relation

Arguments

vegtable An object of class vegtable.

Author(s)

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

Examples

## Statistics for GIVD
vegtable_stat(Kenya_veg)

---

### veg_relation

Retrieve or replace relations in vegtable objects

Description

Tables providing information about levels of categorical variables in the header of a Turboveg database are called popups in Turboveg, but relations in vegtable::vegtable. 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(vegtable, relation, ...)

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

veg_relation(vegtable, relation) <- value

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

relation2header(vegetable, relation, ...)

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

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

---
Arguments

- **vegtable**: An object of class `vegtable`.
- **relation**: A character value indicating the relation table to be retrieved or replaced.
- **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 `vegtable`, including `value` in the slot `relations`.

Author(s)

Miguel Alvarez <kamapu78@gmail.com>

Examples

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

Description

A subset of [http://www.givd.info/ID/AF-00-006SWEA-Dataveg](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>
write_juice

Source

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

References


Examples

summary(Wetlands)
summary(Wetlands_veg)

---

**write_juice**

*Exporting tables for Juice*

**Description**

This function produces txt files as import formats for Juice ([http://www.sci.muni.cz/botany/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 may start with the table following in the menu File -> Import -> Table -> from Spreadsheet File (e.g. EXCEL Table) and then follow the wizard. You further import the header table following in the menu File -> Import -> Header Data -> From Comma Delimited File. Notice that the vegetation is a semi-colon delimited file, while the header is a comma delimited file.

For a properly import, you may strictly follow the export steps in Juice:

1. In menu File -> Export -> Table -> to Spreadsheet Format File and
2. check the option Export covers in %.

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

**Usage**

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

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

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