# Package ‘taxlist’

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**Description** Handling taxonomic lists through objects of class ‘taxlist’.  
This package provides functions to import species lists from 'Turboveg' (<https://www.synbiosys.alterra.nl/turboveg/>)) and the possibility to create backups from resulting R-objects.  
Also quick displays are implemented as summary-methods.

**License** GPL (>= 2)  
**URL** [https://cran.r-project.org/package=taxlist](https://cran.r-project.org/package=taxlist),  
[https://github.com/ropensci/taxlist](https://github.com/ropensci/taxlist),  
[https://docs.ropensci.org/taxlist/](https://docs.ropensci.org/taxlist/)  
**BugReports** [https://github.com/ropensci/taxlist/issues](https://github.com/ropensci/taxlist/issues)

**Collate**  
'imports.R' 'internal.R' 'levels.R' 'prune_levels.R'  
'deprecated-functions.R' 'id_generator.R' 'replace_x.R'  
'insert_rows.R' 'dissect_name.R' 'clean_strings.R'  
'taxlist-class.R' 'matched_names-class.R' 'clean.R'  
'coerce-methods.R' 'taxon_views.R' 'count_taxa.R'  
'taxon_names.R' 'taxon_relations.R' 'add_concept.R'  
'taxon_traits.R' 'accepted_name.R' 'get_children.R'  
'merge_to_parent.R' 'merge_taxa.R' 'Extract.R' 'subset.R'  
'backup_object.R' 'summary.R' 'df2taxlist.R' 'tv2taxlist.R'  
'tax2traits.R' 'match_names.R' 'print_name.R' 'indented_list.R'  
'Easplist-data.R' 'taxlist-package.R' 'taxlist2df.R'  
'parents.R'

**VignetteBuilder** knitr

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Description

Taxon usage names for a taxon concept can be divided into three categories: accepted names, basionyms and synonyms. Each single taxon concept may at least have an accepted name, while basionym and synonyms are optional.

The function `accepted_name()` retrieves the accepted names for the indicated taxon concepts or for the whole `taxlist` object. By using `show_traits=TRUE`, the respective taxon traits will be displayed as well, providing an overview of taxa included in the object. The replacement method for this function will set the respective usage name IDs as accepted names for the respective taxon concept, provided that these names are already set as synonyms in the respective concepts.

The function `synonyms()` is working in a similar way as `accepted_name()`, but this function does not include taxon traits in the output. Alternatives for inserting new synonyms into a taxon concept are either moving synonyms from other taxa by using `change_concept<-` or inserting new names in the object by using `add_synonym()`.

The function `basionym()` is retrieving and setting basionyms in the respective taxon concepts similarly to `accepted_name`, but this function does not retrieve any information on taxon traits, either.

The function `change_concept<-` replace a taxon usage name (argument 'UsageID') to a different taxonomic concept (argument 'value').

Usage

```
accepted_name(taxlist, ...)  
## S3 method for class 'taxlist'
accepted_name(taxlist, ConceptID, show_traits = FALSE, ...)

accepted_name(taxlist, ...) <- value  
## S3 replacement method for class 'taxlist'
accepted_name(taxlist, ConceptID, ...) <- value

synonyms(taxlist, ...)
## S3 method for class 'taxlist'
synonyms(taxlist, ConceptID, ...)

basionym(taxlist, ...)
## S3 method for class 'taxlist'
basionym(taxlist, ConceptID, ...)
```
```r
accepted_name

basionym(taxlist, ...) <- value

## S3 replacement method for class 'taxlist'
basionym(taxlist, ConceptID, ...) <- value

change_concept(taxlist, ...) <- value

## S3 replacement method for class 'taxlist'
change_concept(taxlist, UsageID, ...) <- value

Arguments

taxlist An object of class taxlist.

... Further arguments passed among methods.

ConceptID Integer containing concept IDs where to request or set names for one category.

show_traits Logical value, whether traits should be included in the output of accepted_name or not.

value Integer containing usage IDs to be set to the respective category in the respective taxon concept.

UsageID Numeric vector with taxon usage IDs that will be changed to a different taxonomic concept.

Value

Most of the methods return information in data frames, while replacement methods do it as taxlist objects.

Author(s)

Miguel Alvarez <kamapu78@gmail.com>

See Also

add_synonym() change_concept-

Examples

## Set a different accepted name for Cyclosorus interruptus
summary(Easplist, "Cyclosorus interruptus")
accepted_name(Easplist, 50074) <- 53097
summary(Easplist, 50074)

## Inserting a new name first
summary(Easplist, "Basella alba")
Easplist <- add_synonym(taxlist = Easplist, ConceptID = 68,
    TaxonName = "Basella cordifolia", AuthorName = "Lam.")
summary(Easplist, 68)
accepted_name(Easplist, 68) <- 56139
```
## Display synonyms

```r
head(synonyms(taxlist = Easplist))
```

## Synonyms for an specific concept

```r
synonyms(taxlist = Easplist, ConceptID = 20)
```

## Basionym for Cyclosrus interruptus

```r
summary(Easplist, 50074)
basionym(Easplist, 50074) <- 53097

summary(Easplist, 50074)
basionym(Easplist, 50074)
```

## Move the name Typha aethiopica to concept 573 (T. latifolia)

```r
summary(Easplist, c(50105, 573))
change_concept(Easplist, 53130) <- 573
summary(Easplist, c(50105, 573))
```

---

### add_concept

**Add new taxonomic concepts into taxlist objects**

#### Description

Alternative methods to add new concepts into existing taxlist objects.

#### Usage

```r
add_concept(taxlist, TaxonName, ...)
```

**# S4 method for signature 'taxlist,data.frame'**

```r
add_concept(taxlist, TaxonName, ...)
```

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

```r
add_concept(taxlist, TaxonName, ...)
```

**# S4 method for signature 'taxlist,taxlist'**

```r
add_concept(taxlist, TaxonName, insert_view = FALSE, ...)
```

```r
update_concept(taxlist, ConceptID, ...)
```

#### Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>taxlist</td>
<td>A <code>taxlist</code> object.</td>
</tr>
<tr>
<td>TaxonName</td>
<td>Character vector with the accepted name for the new taxon concepts.</td>
</tr>
<tr>
<td>...</td>
<td>Further arguments passed among methods.</td>
</tr>
</tbody>
</table>
insert_view  A numeric (integer) vector, indicating the views to be inserted in taxlist or the value TRUE (see details).

ConceptID  Concept IDs to be updated.

as  Coerce taxlist objects to lists.

Description
Coercion of S4 objects to lists can be applied to explore their content, avoiding errors caused by their validation.

Usage
S4_to_list(x)

Arguments
x  An object of class taxlist or any S4 class.

Details
Coerce taxlist objects to lists.

Value
An object of class list.

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

Examples
## Coerce taxlist to list
tax_list <- as(Easplist, "list")

## Coerce data frame to taxlist
Cyperus <- read.csv(file = file.path(path.package("taxlist"), "cyperus", "names.csv"))
Cyperus$AcceptedName <- !Cyperus$SYNONYM
head(Cyperus)
as(Cyperus, "taxlist")
backup_object Make and load backups of R objects

Description

When work with data becomes risky, the best practice is to produce backup files. The function of `backup_object` is a wrapper of `save()`, adding a time stamp and a suffix to the name of the resulting file (an R image file with extension `.rda`). The function `load_last` is adapted to this style, loading the newest version to the session.

Usage

```r
backup_object(
  ..., 
  objects = character(), 
  file, 
  stamp = TRUE, 
  sep = "_", 
  date_format = "%Y-%m-%d", 
  time_format = "%H:%M:%S", 
  overwrite = FALSE 
)

sort_backups(
  name, 
  path = ".", 
  date_format = "%Y-%m-%d", 
  fext = ".rda", 
  sep = "_" 
)

load_last(file, path, ..., choice)
```

Arguments

- `...`: Names of the objects to be saved (either symbols or character strings) in `backup_object()`. In `load_last()`, arguments passed to `sort_backups()`.
- `objects`: A character vector indicating the names of objects to be included in the backup file.
- `file`: A character value indicating the name of the backup file, without the extension.
- `stamp`: A logical value indicating whether time should be stamped in the backup name or not.
- `sep`: A character value used to separate backup's name from stamp and from the suffix.
- `date_format`: A character value indicating the format used for the file stamp. See `strptime()`.
backup_object

- **time_format**: A character value indicating the format used for the time (not including the date), which will be used for the invisible report in backup_object(). See strptime().
- **overwrite**: A logical value indicating whether existing files must be overwritten or not.
- **name**: A character value indicating the root of the backup’s name.
- **path**: A character value indicating the path to the folder containing the backup files.
- **fext**: A character value indicating the file extension (including the dot symbol).
- **choice**: An integer value indicating the backup file to be used for recovery. This value refers to the row in the output of sort_backups(). If not provided, load_last() will select the newest backup.

**Details**

In both functions the argument file may include either the path relative to the working directory or the absolute path to the file, excluding stamps and extension. For overwrite=FALSE (the default), a numeric suffix will be added to the backup’s name, if another backup was produced at the same day. For overwrite=TRUE no suffix will be included in the file and existing files will be overwritten.

The function load_last() will load the newest version among backups stored in the same folder, provided that the backup name includes a time stamp.

**Value**

The function backup_object() writes an R-image with extension *.rda* and an invisible vector with the name of the backup, its absolute path and a time stamp.

The function sort_backups() returns a data frame including the sorted names of backup files from the oldest to the newest.

**Author(s)**

Miguel Alvarez <kamapu78@gmail.com>

**See Also**

save(), load().

**Examples**

```r
## A subset with Pseudognaphalium and relatives
Pseudognaphalium <- subset(x = Easplist, subset = grepl("Pseudognaphalium", TaxonName), slot = "names", keep_parents = TRUE)

## Create a backup with date stamp in tempdir
backup_object(Pseudognaphalium, file = file.path(tempdir(), "Pseudognaphalium"))

## Retrieve paths of backup
info_back <- backup_object(Pseudognaphalium, file = file.path(tempdir(), "Pseudognaphalium"))
info_back
```
## Display all backups

```r
sort_backups("Pseudognaphalium", tempdir())
```

## Delete object

```r
rm(list = "Pseudognaphalium")
```

## To load the last backup into a session

```r
load_last("Pseudognaphalium", path = tempdir())
```

## Load pre-installed backup

```r
load_last(file.path(path.package("taxlist"), "extdata", "Podocarpus"))
```

---

### clean

**Delete orphaned records**

**Description**

Manipulation of slots may generate orphaned entries in `taxlist` objects. The function `clean` deletes such entries and restores the consistency of the objects.

**Usage**

```r
clean(object, ...)
```

**Arguments**

- `object` A `taxlist` object.
- `...` Further arguments passed from or to other methods.
- `times` An integer indicating how many times the cleaning should be repeated.

**Details**

Cleaning of objects will follow the deletion of orphaned names, orphaned taxon trait entries, and orphaned parent entries.

**Value**

A clean `taxlist` object.

**Author(s)**

Miguel Alvarez.
Examples

```r
## Direct manipulation of slot taxonRelations generates an invalid object
Easplist@taxonRelations <- Easplist@taxonRelations[1:5,]

## Now apply cleaning
Easplist <- clean(Easplist)
summary(Easplist)
```

clean_strings

Cleaning character strings.

Description

Multiple, leading and trailing white spaces as well as wrong encodings may cause serious problems in information dealing with taxonomic names. The function `clean_strings` get rid of them.

Usage

```r
clean_strings(x, ...)
```

```r
## S4 method for signature 'character'
clean_strings(x, from = "utf8", to = "utf8", ...)
```

```r
## S4 method for signature 'factor'
clean_strings(x, from = "utf8", to = "utf8", ...)
```

```r
## S4 method for signature 'data.frame'
clean_strings(x, from = "utf8", to = "utf8", ...)
```

Arguments

- `x` Object to be cleaned.
- `...` Further arguments passed among methods (not yet in use).
- `from, to` Arguments passed to `iconv()`.

Details

This function automatically deletes leading, trailing and multiple white spaces, either in strings (method character), levels (method factor) or in single columns (method data.frame).

Value

The same as input `x`.

Author(s)

Miguel Alvarez.
Examples

```r
## Leading, trailing and multiple spaces
clean_strings(" Cyperus papyrus L. ")
```

Description

Counting number of taxa within `taxlist` objects or character vectors containing taxon names.

Usage

```r
count_taxa(object, data, ...)  
## S4 method for signature 'character,missing'
count_taxa(object, na.rm = TRUE, ...)
## S4 method for signature 'factor,missing'
count_taxa(object, na.rm = TRUE, ...)
## S4 method for signature 'taxlist,missing'
count_taxa(object, level, ...)
## S4 method for signature 'formula,taxlist'
count_taxa(object, data, include_na = FALSE, suffix = "_count", ...)
```

Arguments

- `object` An object containing a taxonomic list or a formula.
- `data` An object of class `taxlist` in the `formula` method.
- `...` Further arguments passed among methods.
- `na.rm` Logical value, whether NAs have to be removed from the input vector or not.
- `level` Character value indicating the taxonomic rank of counted taxa.
- `include_na` Logical value indicating whether NA values in a taxon trait should be considered for counting taxa or just ignored (only used in `formula` method).
- `suffix` Character value used as suffix for the counted rank in the output data frame (only used in `formula` method).

Details

This function is written by convenience in order to reduce code for counting taxa within `taxlist` objects and it is just a wrapper of `length()`.
Value

An integer with the number of taxa.

Author(s)

Miguel Alvarez <kamapu78@gmail.com>

Examples

```r
## factor method
count_taxa(iris$Species)

## taxlist method
count_taxa(Easplist)

## count only species
count_taxa(Easplist, level = "species")

## using a formula
count_taxa(~life_form, Easplist, include_na = TRUE)
```

---

Description

Most of those functions have been replaced by alternative 'update' ones.

Usage

```r
add_parent()
add_trait()
add_level()
replace_view()
taxlist2taxmap()
taxmap2taxlist()
taxmap2taxlist()
tnrs()
```
df2taxlist

Convert data frames and strings into taxlist objects

Description

Function converting template data frame into taxlist object. Also character vectors including taxonomic names will be converted but without any information on taxonomic ranks and parental taxa.

Usage

df2taxlist(x, ...)

## S3 method for class 'data.frame'

\[
\text{df2taxlist}(x, \text{taxonTraits}, \text{taxonViews}, \text{levels}, \text{clean_strings} = \text{TRUE}, \ldots)
\]

## S3 method for class 'character'

df2taxlist(x, ...)

Arguments

- **x**: A data frame or a character vector with taxonomic names. If x is a data frame, the columns TaxonUsageID (integer with IDs for each name), TaxonConceptID (integer with IDs for the respective taxon concepts), and TaxonName (character) are mandatory. Other optional columns are AuthorName (character with names’ authorities), AcceptedName (logical indicating whether the name is an accepted name or a synonym and will be set as TRUE by default), Level (factor sorting taxonomic ranks in the bottom-up direction), Parent (integer, the taxon concept ID of the parental taxon), and ViewID (integer pointing to the ID of taxonomic view, usually a bibliographic reference, and will be used only if 'taxonViews' is provided. Any further column not included in the prototype of taxlist will be considered as names’ attributes and inserted in slot taxonNames.

- **...**: Further arguments passed among methods. For the 'character-method', arguments will be passed to the 'data.frame-method'.

- **taxonTraits**: A data frame with attributes of taxonomic concepts (optional). If provided, the column TaxonConceptID is mandatory.

- **taxonViews**: A data frame or biblio::lib_df with references of taxonomic views (optional). If provided, the column ViewID is mandatory and have to match the homonymous column at 'x'.

- **levels**: A character vector setting the levels or taxonomic ranks from the bottom to the top. This argument is optional and if missing, the column Level will be preserved (if factor) or coerced to factor, except in the case that no column Level is provided.

- **clean_strings**: Logical value, whether function clean_strings() should be applied to 'x' or not.
Value
A taxlist object.

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

Examples
Cyperus <- read.csv(file = file.path(path.package("taxlist"), "cyperus", "names.csv"))
head(Cyperus)

## Convert to 'taxlist' object
Cyperus$AcceptedName <- !Cyperus$SYNONYM
df2taxlist(Cyperus)

## Create a 'taxlist' object from character vectors
Plants <- df2taxlist(c("Triticum aestivum", "Zea mays"), AuthorName = "L.")
summary(Plants, "all")

---

dissect_name Dissect Scientific Names into their Elements

Description
Depending the degree of resolution and specific roles of nomenclature, strings containing taxon usage names (scientific names) are constructed with different parts. A string with names can be consequently split into those elements, meanwhile the number of elements may suggest the taxonomic ranks.

This function is a wrapper of `strsplit()`, while name element can be re-pasted if indicated in argument `repaste`.

Usage
dissect_name(x, split = " ", fixed = TRUE, repaste, ...)

Arguments

x A character vector containing taxon names.
split, fixed, ...
Arguments passed to `strsplit()`.
repaste An integer vector indicating the elements of the name selected for the output.

Value
A character matrix with as many rows as names in the input vector. If `repaste` is indicated, then the output will be a character vector.
Author(s)

Miguel Alvarez <kamapu78@gmail.com>

See Also

strsplit()

Examples

# A list of variety names
sp_list <- subset(x = Easplist, subset = Level == "variety", slot = "relations")
sp_list <- accepted_name(sp_list)[c(1:10), "TaxonName"]

# split name
dissect_name(sp_list)

# re-paste the two first words (species name)
  dissect_name(sp_list, repaste = c(1:2))

Easplist-data

List of vascular plants from East Africa

Description

Example of an incomplete taxonomic list including taxa recorded in East Africa.

Usage

Easplist

Format

An object of class taxlist.

Details

This list is a subset of the taxonomic list implemented in the database SWEA-Dataveg. Since this list is being complemented regarding stored vegetation plots, it is an incomplete list.

Source

African Plant Database, SWEA-Dataveg.

Examples

summary(Easplist)
Extract or Replace Parts of taxlist Objects

Description
Quick access to slots `taxonTraits` and `taxonRelations` within `taxlist` objects.

Usage

```r
## S4 method for signature 'taxlist'
x[i, j, drop = FALSE]
## S4 method for signature 'taxlist'
x$name
```

Arguments

- `x`: Object of class `taxlist`.
- `i`: Integer or logical vector used as index for access to taxon concepts, referring to the rows in slot `taxonRelations`. These indices can be used to produce a object with a subset of taxon concepts. It is not recommended to use character values for this index.
- `j`: Integer, logical or character vector used as index for access to variables in slot `taxonTraits`. These indices can be used to reduce the number of variables in the mentioned slot.
- `drop`: A logical value passed to `Extract`.
- `name`: A symbol or character value for the method `$`, corresponding to a variable either at slot `taxonTraits` or slot `taxonRelations`.

Value
The method `$` retrieves a vector, while `[` retrieves a subset of the input `taxlist` object.

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

See Also
- `taxlist`
- `subset`

Examples

```r
## Statistics on life forms
summary(as.factor(Easplist$life_form))

## First concepts in this list
summary(Easplist[1:5, ], "all")
```
get_children

Retrieve children or parents of taxon concepts

Description

Retrieve all children or all parents of a queried taxon concept.

Usage

get_children(taxlist, ...)

## S3 method for class 'taxlist'
get_children(taxlist, ConceptID, ...)

get_parents(taxlist, ...)

## S3 method for class 'taxlist'
get_parents(taxlist, ConceptID, ...)

Arguments

taxlist A taxlist object.
...
Further arguments passed among methods.
ConceptID Concept IDs for selecting parents or children or a subset of taxlist.

Details

This function produces subsets of taxlist objects including all children or parents of queried taxon concepts. Multiple concepts can be queried in these function. The argument ConceptID can be a vector of concept IDs or a subset of the input taxlist object.

Value

A taxlist object with a subset including requested concepts with children or parents.

Author(s)

Miguel Alvarez <kamapu78@gmail.com>

Examples

## Subset with family Ebenaceae and children
Ebenaceae <- subset(x = Easplist, subset = TaxonName == "Ebenaceae")
Ebenaceae

Ebenaceae <- get_children(Easplist, Ebenaceae)
Ebenaceae
## Get parents of *Diospyros tricolor*

```r
Diostri <- subset(x = Easplist, subset = TaxonConceptID == 52403,
                  slot = "relations")
Diostri

Diostri <- get_parents(Easplist, Diostri)
Diostri
```

---

### `id_generator`

**Generate Identifiers**

**Description**

Creating identifiers for new elements in a database.

The function `id_solver()` will compare to set of identifiers and modify the second to avoid duplicated IDs.

**Usage**

```r
id_generator(
    len,
    minvalue = 1,
    nchar = 10,
    mode = c("numeric", "character"),
    ...
)

id_solver(insert, to, suffix = c("numeric", "character"), sep = "")
```

**Arguments**

- `len` Numeric value indicating the length of the retrieved vector with identifiers.
- `minvalue` Numeric value indicating the minimum value in the vector of identifiers. Used only for `mode = "numeric"`.
- `nchar` Numeric value indicating the number of characters included in the retrieved identifiers. Used only for `mode = "character"`.
- `mode` Character value indicating the type of identifier created, which is either numeric (the default) or character.
- `...` Further parameters passed to `stringi::stri_rand_strings()`, actually to the argument `pattern`.
- `insert` A vector (either numeric or character) containing IDs of elements that will be inserted in a database.
- `to` A vector (either numeric or character) containing IDs of elements that already exist in target database.
suffix A character vector indicating the mode used for the suffix. Only 'numeric' or 'character' and partial matchings are accepted here. This argument is only used for character IDs. If 'suffix = "character"', a letter of the alphabet (vector 'letters') will be appended to duplicated IDs.

sep A character value used as separator between original character ID and the appended suffix.

Value
A vector with IDs created by id_generator(), either as numeric or character. In the case of id_solver(), a vector, which is either identical to 'insert' (if no conflicts) or a vector with the same properties but with resolved IDs.

Examples
```r
## Creating numeric IDs
id_generator(len = 10, minvalue = 5)

## Creating character IDs
id_generator(len = 10, mode = "character")

## Solving duplicates in numeric identifiers
id_solver(insert = c(3, 7, 5, 10), to = c(1:5))

## Solving duplicates in bibtexkeys
db.refs <- c("Alvarez2003", "Schmitz1988", "Li2023")
any(duplicated(c(db.refs, new.refs)))

solved.refs <- id_solver(insert = new.refs, to = db.refs, suffix = "character")
solved.refs
any(duplicated(c(db.refs, solved.refs)))
```

### indented_list

Print hierarchical structure in indented lists

**Description**
Print taxonomic hierarchies (ranks and parent-child relationships) from taxlist objects in an indented list.

**Usage**

```r
indented_list(object, ...)
```

```r
## S4 method for signature 'taxlist'
indented_list(
  object,
  filter,
)```
keep_children = TRUE,
keep_parents = TRUE,
rankless_as,
indent = " ",
lead_br = " ",
print = TRUE,
author = TRUE,
level = FALSE,
synonyms = FALSE,
syn_encl = c("= ", ""),
secundum,
apphabetical = FALSE,
...
)

Arguments

 object A taxlist object containing taxonomic concepts.
...

 Further arguments (not used yet).

 filter A character value (optional) that will be matched with the taxon usage names
to produce a subset of 'object'. Note that this filter will be also applied to syn-
onyms, independent of the argument applied in parameter 'synonyms'.

 keep_children A logical value indicating whether children of matched concept should be in-
cluded in the result.

 keep_parents A logical value indicating whether parents of matched concept should be in-
cluded in the result.

 rankless_as A character vector indicating a level (taxonomic rank) to which rankless taxa
may be set before doing the list.

 indent Symbol used for indentation. This symbol will be multiplied by the depth of the
 taxonomic rank. The default is a blank space. This can be also provided as a
named vector, with a different indentation symbol for the respective taxonomic
ranks.

 lead_br Optional line break symbol leading before the indentation. It may be required
for r-markdown documents.

 print A logical value indicating whether the indented list should be printed in the
console or not (default = TRUE).

 author A logical value indicating whether the author should be printed with the name
(default = TRUE).

 level A logical value indicating whether the name of the level (taxonomic rank) should
be included before the name or not (default = FALSE).

 synonyms A logical value indicating whether the synonyms should be included after ac-
cepted names or not (default = FALSE).

 syn_encl A character vector of length 2 including the symbols used to enclose synonyms.
First value will be set before the synonyms and second value, after the syn-
onyms.
secundum A character value matching a name in slot 'taxonViews', which will be printed as secundum (taxon view). It is not printed by default.

alphabetical A logical value indicating whether taxa may be sorted by names or by IDs. The default is FALSE, thus taxa are sorted by IDs. Note that argument TRUE may not work properly if the object contains homonymous taxa.

Value
If 'print = TRUE', the indented list is printed in the console. The result, which is a data frame with the elements used to format the names, can be also assigned to an object.

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

Examples
## Show taxonomy of papyrus
indented_list(Easplist, "papyrus")

## Include synonyms and taxon views
indented_list(Easplist, "papyrus", level = TRUE, synonyms = TRUE, secundum = "secundum")

Description
Adding new rows from data frame sharing some columns. Data contained in y is assumed to be additional data and will be appended.

Columns occurring in only one of the data frames will be added to the output.

Usage
insert_rows(x, y, ...)

## S4 method for signature 'data.frame,data.frame'
insert_rows(x, y, ...)

Arguments
x A data frame.
y A data frame including rows (and columns) to be inserted in x.
... Additional arguments passed among methods.
Value

A data frame.

Examples

```r
## Merge data frames including new columns
data(iris)
iris$Species <- paste(iris$Species)
new_iris <- data.frame(Species = rep("humilis", 2), Height = c(15, 20),
stringsAsFactors = FALSE)
insert_rows(iris, new_iris)
```

## Set and retrieves hierarchical levels

### Description

Taxonomic hierarchies can be set as levels in `taxlist` objects, ordered from lower to higher levels. Add taxonomic levels for specific taxon concepts in a `taxlist` object. Also changes in concept circumscription may implicate changes in its taxonomic hierarchy.

### Usage

```r
levels(x)
```

```r
## S3 method for class 'taxlist'
levels(x)
```

```r
levels(x) <- value
```

```r
## S3 replacement method for class 'taxlist'
levels(x) <- value
```

### Arguments

- `x` A `taxlist` object.
- `value` A character vector with replacement values for levels of `x`.

### Details

Taxonomic levels will be handled as factors in the `taxlist` objects. Those levels are useful for creating subsets of related groups (e.g. by functions `get_children()` or `get_parents()`).

Levels in combination to parent-child relationships will be further used for checking consistency of taxonomic lists.

A replacement method of the form `levels(x) <- value` it is also implemented.
matched_names-class

Names matched with a reference taxonomic list

Description

An S3 class containing results of names compared with a reference list. This class enables further methods applied to these outputs, for instance an interactive selection of multiple choices.

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 within an object of class taxlist by using the function stringdist::stringsim().

Usage

match_names(x, object, ...)

## S4 method for signature 'character,character'
match_names(
  x,
  object,
  UsageID,
match_names

```r
best = 1,
nomatch = TRUE,
method = "lcs",
cutlevel = NULL,
...
```

```r
## S4 method for signature 'character,missing'
match_names(x, best, cutlevel, nomatch = TRUE, ...)

## S4 method for signature 'character,taxlist'
match_names(
  x,
  object,
  show_concepts = FALSE,
  accepted_only = FALSE,
  include_author = FALSE,
  ...
)
```

### Arguments

- **x** A character vector with names to be compared.
- **object** Either a character vector or a taxlist object containing the taxonomic list for comparison. If missing, the similarity of each name in 'x' will be compared with the rest of the names in the same vector.
- **...** Further arguments passed among methods.
- **UsageId** A vector with IDs for single usage names in the compared list. If the IDs are duplicated or not as much as names in 'object', the function retrieves an error message. If missing, this function will number every name anew (see column 'TaxonUsageID' in the output object).
- **best** Integer value indicating how many matches should be displayed in the output. Matches with the same value of similarity will be considered as one. Note that this argument will be overrode by 'cutlevel'.
- **nomatch** A logical value indicating wheter names without matches should be included in the output ('nomatch = TRUE') or not ('nomatch = FALSE').
- **method** Further arguments passed to `stringdist::stringsim()`.
- **cutlevel** A numeric value indicating a cut level of similarity, considering as match names with similarities equal or bigger than the cut value. This argument overrides 'best'.
- **show_concepts** Logical value indicating whether the respective taxon concepts should be displayed in output or not.
- **accepted_only** Logical value indicating whether only accepted names should be matched or all usage names (including synonyms).
- **include_author** A logical value indicating whether the author name in object (method for taxlist) should be included in the matching list or not.
merge_taxa

Description

Merge taxon concepts form a taxlist object into single ones.

Usage

merge_taxa(object, ...)

## S3 method for class 'taxlist'
merge_taxa(
  object,
  concepts,
  level = NULL,
  delete_nomatch = FALSE,
  print_output = FALSE,
  ...
)

Examples

## Names to be compared
species <- c("Cyperus papyrus", "Typha australis", "Luke Skywalker")

## Comparing character vectors
match_names(c("Cyperus paper", "TIE fighter"), species)

## Retrieve taxon usage names
match_names(species, Easplist)

## Display accepted names in output
match_names(x = species, object = Easplist, show_concepts = TRUE)

# Using cut value for similarity
match_names(x = species, object = Easplist, cutlevel = 0.8)
merge_taxa

Arguments

- `object`, `taxlist` Object of class `taxlist`.
- `concepts` Numeric (integer) vector including taxon concepts to be merged.
- `level` Character vector with queried taxonomic ranks. This setting works only if concepts are missing. Ranks in between will be merged to their respective parents by `merge_to_parent()`. Non queried ranks as well as rankless concepts will be deleted from the output.
- `delete_nomatch` A logical value indicating whether no matched ranks (i.e. top rank and rankless concepts) should be deleted from the output or not.
- `print_output` Logical value indicating whether the merged concept should be displayed in the console. This works only if a vector is provided at `concepts`.

Details

Taxon concepts indicated in argument `concepts` will be merged into a single concept. The new concept inherits the ID and respective attributes from slots `taxonRelations` and `taxonTraits` from the first taxon concept indicated in argument `concepts`.

For convenience the resulting concept can be displayed by setting `print_output=TRUE` but only when using argument `concepts`.

An alternative application of this function is implemented through the argument `level`, where all lower rank taxa will be merged to the indicated level or higher (if parent of merged taxa are at a higher rank).

Value

An object of class `taxlist`.

Author(s)

Miguel Alvarez <kamapu78@gmail.com>

Examples

```r
## Merge Cyperus papyrus and Cyperus dives
summary(Easplist, c(206, 197))

merged_cyperus <- merge_taxa(object = Easplist, concepts = c(206, 197),
                              print_output = TRUE)

## Subset with Kyllinga species
ky <- subset(Easplist, TaxonName == "Kyllinga", keep_children = TRUE,
             keep_parents = TRUE)
ky
indented_list(ky)

## Merge to species and family
merge_taxa(ky, level = c("species", "family"))
```
## Merge to variety and genus

```
merge_taxa(ky, level = c("variety", "genus"))
```

### Description

Aggregation of taxon concepts to their respective parents. All names of aggregated concepts will become synonyms in the target parent.

### Usage

```
merge_to_parent(object, ...)
```

#### S3 method for class 'taxlist'

```
merge_to_parent(object, concept_id, ...)
```

### Arguments

- **object**: An object of class `taxlist`.
- **...**: Further arguments passed among methods.
- **concept_id**: A vector of IDs (TaxonConceptID) of taxa that will be aggregated into their respective parents. Note that if one of the IDs is simultaneously the parent of another ID in the vector, this function will retrieve an error message.

### Value

An object of class `taxlist` with merged taxa.

### See Also

- `merge_taxa()`

### Examples

```
## Subset with Kyllinga species
ky <- subset(Easplist, TaxonName == "Kyllinga", keep_children = TRUE, keep_parents = TRUE)
ky
indented_list(ky)

## Merge two species with the genus
summary(ky, c(346, 50400))
summary(ky, "Kyllinga", exact = TRUE)
ky <- merge_to_parent(ky, c(346, 50400))
summary(ky, "Kyllinga", exact = TRUE)
```
parents

Retrieve parents for specific concepts

Description

Retrieve IDs of parents for selected taxa in a taxonomic list.

Usage

parents(taxlist, level, ...)

## S4 method for signature 'taxlist, character'
parents(taxlist, level, concept, ...)

Arguments

- **taxlist**: An object of class taxlist containing a taxonomic list.
- **level**: A character value indicating the level at which the parents will be extracted (upwards in the taxonomic ranks).
- **concept**: A vector containing concept IDs. The taxa for which the parents will be retrieved. If not provided, parents for every single taxon concept in 'taxlist' will be retrieved.
- **...**: Further arguments passed among methods.

Examples

# Random selection of 5 taxa
IDs <- sample(Easplist@taxonRelations$TaxonConceptID, 5)

# Print names and names of parents
print_name(Easplist, IDs)
print_name(Easplist, parents(Easplist, "genus", IDs))
print_name(Easplist, parents(Easplist, "family", IDs))

print_name

Format usage names for publications

Description

When writing on bio-diversity, usage names could be automatically inserted in documents including the typical italic format for different elements of a scientific name. The function print_name can be applied either in markdown documents or for graphics.

In Rmarkdown documents use *Cyperus papyrus* L. for inserting a formatted a species name.
Usage

print_name(object, ...)

## S3 method for class 'character'
print_name(
  object,
  second_mention = FALSE,
  style = "markdown",
  isolate = c("var.", "ssp.", "subsp.", "f.", "fma."),
  trim = c("spp.", "sp.", "species"),
  italics = TRUE,
  collapse,
  ...
)

## S3 method for class 'taxlist'
print_name(
  object,
  id,
  concept = TRUE,
  include_author = TRUE,
  secundum,
  style = "markdown",
  italics = TRUE,
  collapse,
  ...
)

Arguments

object An object of class taxlist.
...
Further arguments passed among methods.
second_mention Logical value, whether the genus name should be abbreviated or not.
style Character value indicating the alternative format for italics. The available options are "markdown" (called within Rmarkdown documents), "html" (for documents rendered into html files), "expression" (used for labels in graphics), and "knitr" (format in LaTeX code).

isolate A character vector with words (usually abbreviations) appearing in the middle of scientific names, which are not formatted in italics.

trim A character vectors with words appearing at the end of scientific names that are not formatted in italics, either.

italics A logical value indicating whether the names should be italized or not.

collapse A character value or vector used to collapse the names and passed to paste0(). If its length is 2, the second value will be used to connect the two last names. Note that collapse is not yet implemented for style = "expression".

id Integer containing either a concept or a name ID.
concept Logical value, whether id corresponds to a concept ID or a taxon usage name ID.
include_author Logical value, whether authors of the name should be mentioned or not.
secundum Character value indicating the column in slot taxonViews that will be mentioned as secundum (according to).

Value
A character value including format to italic font.

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

See Also
ape::mixedFontLabel().

Examples

## Example subspecies
summary(Easplist, 363, secundum = "secundum")

## Empty plot
plot(x = NA, xlim = c(0, 5), ylim = c(7, 1), bty = "n", xaxt = "n", xlab = "",
ylab = "options")

## Accepted name with author
text(x = 0, y = 1, labels = print_name(Easplist, 363, style = "expression"),
pos = 4)

## Including taxon view
text(x = 0, y = 2, labels = print_name(Easplist, 363, style = "expression",
secundum = "secundum"), pos = 4, cex = 0.7)

## Second mention in text
text(x = 0, y = 3, labels = print_name(Easplist, 363, style = "expression",
second_mention = TRUE), pos = 4)

## Using synonym
text(x = 0, y = 4, labels = print_name(Easplist, 50037, style = "expression",
concept = FALSE), pos = 4)

## Markdown style
text(0, 5, labels = print_name(Easplist, 363, style = "markdown"), pos = 4)

## HTML style
text(0, 6, labels = print_name(Easplist, 363, style = "html"), pos = 4,
cex = 0.7)

## LaTeX style for knitr
Description

Taxonomic ranks without taxon concepts will be pruned in taxlist objects.

Usage

prune_levels(object, ...)

## S3 method for class 'taxlist'
prune_levels(object, ...)

Arguments

object An object of class taxlist.

... Further arguments passed among methods (not yet in use).

Value

An object of class taxlist with pruned taxonomic ranks.

See Also

levels()

Examples

## Subset species belonging to Cyperus
Cyperus <- subset(Easplist, TaxonName == "Cyperus", slot = "taxonNames",
                  keep_children = TRUE, keep_parents = TRUE)
Cyperus

## Prune not used ranks
prune_levels(Cyperus)
**Data manipulation.**

**Description**

This is a series of functions designed for a fast coding of replacements both, as internal functions and in workflows dealing with information stored in vectors. Such functions are especially useful when handling with functional traits stored in taxlist objects.

`replace_x()` is used to exchange values in vectors. `replace_idx()` changes values in vectors by matching indices or conditions. The function `replace_na()` works in the same way as `replace_idx()` but will only insert values in empty elements (NAs).

**Usage**

```r
replace_x(x, old, new)
replace_idx(x, idx1 = x, idx2 = idx1, new)
replace_na(x, idx1, idx2 = idx1, new)
```

**Arguments**

- **x** A vector to be modified. In the case of `insert_rows()`, `x` is a data frame.
- **old** A vector with values to be replaced by `replace_x()` in a vector.
- **new** A vector containing values to be inserted, either comparing values or using indices.
- **idx1, idx2** Indices applied for value replacements to match `x` with `new`, respectively. If `idx2` is not provided, it will be assumed as equivalent to `idx1`.

**Value**

A vector or data frame with the modified values.

**Author(s)**

Miguel Alvarez.

**Examples**

```r
## Replace values in vector
replace_x(x = letters, old = c("b", "p", "f"), new = c("bee", "pork", "fungus"))

## Replace values using indices
replace_idx(x = letters, idx1 = 1:length(letters), idx2 = c(2, 7, 17),
            new = c("second", "seventh", "seventeenth"))

## Replace values if they are NAs
```
subset[2] <- NA
replace_na(x = letters, idx1 = 1:length(letters), idx2 = c(1:3),
new = c("alpha", "beta", "zeta"))

## The same applications but this time for functional traits
summary(as.factor(Easplist$life_form))

# Merge annuals
Easplist@taxonTraits$lifeform <- replace_x(x = Easplist@taxonTraits$life_form,
old = c("obligate_annual", "facultative_annual"), new = c("annual", "annual"))
summary(as.factor(Easplist$lifeform))

# The same effect
Easplist@taxonTraits$lifeform <- replace_idx(x = Easplist@taxonTraits$life_form,
idx1 = grepl("annual", Easplist@taxonTraits$life_form), idx2 = TRUE,
new = "annual")
summary(as.factor(Easplist$lifeform))

---

Subset method for taxlist objects

Description

Subset of taxlist objects will be done applying either logical operations or pattern matchings. Subsets can be referred to information contained either in the slot taxonNames, taxonRelations or taxonTraits.

Usage

## S4 method for signature 'taxlist'
subset(
x,
subset,
slot = "names",
keep_children = FALSE,
keep_parents = FALSE,
...
)

Arguments

x Object of class taxlist.
subset Logical vector or logical operation to apply as subset.
slot Character vector indicating the slot to be used for the subset.
keep_children Logical value applied to hierarchical structures.
keep_parents Logical value applied to hierarchical structures.
... Further arguments to be passed to or from other methods.
Details

The argument subset will be applied to the slot specified in argument slot. This argument also allows partial matchings.

Arguments keep_children and keep_parents are applied to objects including parent-child relationships. When those arguments are set as FALSE (the default), children or parents of selected taxon concepts will not be included in the subset.

Be aware that subset() won’t work properly inside of function definitions.

Value

An object of class taxlist.

Author(s)

Miguel Alvarez <kamapu78@gmail.com>

Examples

```r
## Produce a data set with only reed plants
sp_list <- subset(x = Easplist, subset = life_form == "reed_plant",
    slot = "taxonTraits", keep_parents = TRUE)
sp_list

summary(as.factor(sp_list$life_form))
```

Description

A method to display either an overview of the content of taxlist objects or an overview of selected taxa.

Usage

```r
## S4 method for signature 'taxlist'
summary(
    object,
    ConceptID,
    units = "Kb",
    check_validity = TRUE,
    display = "both",
    maxsum = 5,
    secundum = NULL,
    exact = FALSE,
    ...
)
```
## S4 method for signature 'taxlist'
show(object)

## S4 method for signature 'taxlist'
print(x, ...)

Arguments

object, x  A taxlist object.

ConceptID  IDs of concepts to be displayed in the summary.

units  Character value indicating the units shown in the object’s allocated space.

check_validity  Logical value indicating whether the validity of object should be checked or not.

display  Character value indicating the field to be displayed (see details).

maxsum  Integer indicating the maximum number of displayed taxa.

secundum  A character value indicating the column from slot taxonViews to be displayed in the summary.

exact  A logical value indicating whether taxon names should match the exact argument in parameter 'ConceptID'. It works only if 'ConceptID' is provided as character value and is not the keyword 'all'.

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

Details

A general overview indicating number of names, concepts and taxon views included in taxlist objects. If argument ConceptID is a vector with concept IDs or names to be matched by grepl(), then a display of all names included in each concept will be produced. Alternative you can use taxon="all" in order to get the listing of names for all concepts included in the object (truncated to the input number of maxsum).

For summaries applied to concepts, there are three alternative displays of names using the argument display. Use display="name" to show the value TaxonName, display="author" to show the value AuthorName or display="both" to show both values. Such values are taken from slot taxonNames.

For big objects it will be recommended to set units="Mb" (see also object.size() for further alternatives).

Author(s)

Miguel Alvarez <kamapu78@gmail.com>

See Also
taxlist
Examples

```r
## summary of the object
summary(Easplist, units = "Mb")

## the same output
summary(Easplist)
show(Easplist)
print(Easplist)
Easplist

## summary for two taxa
summary(Easplist, c(51128, 51140))

## summary by matching a name
summary(Easplist, "Acmella")

## summary for the first 10 taxa
summary(object = Easplist, ConceptID = "all", maxsum = 10)
```

---

**tax2traits**  
*Set taxonomic information as taxon traits*

### Description

Taxonomic classification can be included in `taxlist` objects within the information provided at slot `taxonRelations`. Nevertheless, for statistical analyses it may be more convenient to insert such information in the slot `taxonTraits`.

### Usage

```r
tax2traits(object, ...)
```

### Arguments

- **object**: An object of class `taxlist`.
- **...**: Further arguments to be passed among methods.
- **get_names**: Logical value indicating whether taxon names should be retrieved instead of taxon IDs.

### Details

This function can only be applied to objects containing parent-child relationships and information on taxonomic levels.
Value

An object of class `taxlist` with taxonomy added as traits.

Author(s)

Miguel Alvarez <kamapu78@gmail.com>.

Examples

```r
## Family Acanthaceae with children
Acanthaceae <- subset(x = Easplist, subset = TaxonName == "Acanthaceae",
                        slot = "names", keep_children = TRUE)
summary(Acanthaceae)

## Insert taxonomy to taxon traits
Acanthaceae <- tax2traits(Acanthaceae, get_names = TRUE)
head(taxon_traits(Acanthaceae))
```

Description

Class for taxonomic lists including synonyms, hierarchical ranks, parent-child relationships, taxon views and taxon traits.

Note that each taxon becomes an identifier, represented by the column `TaxonConceptID` in the slot `taxonRelations`, analogous to a primary key in a relational database. This identifier is restricted to an integer in taxlist and is specific for the object.

In the same way, each taxon usage name has an identifier in the column `TaxonUsageID`, slot `taxonNames`. The column `ViewID` in slot `taxonViews` is the identifier of the taxon view.

Slots

- `taxonNames` (data.frame) Table of taxon usage names (accepted names and synonyms).
- `taxonRelations` (data.frame) Relations between concepts, accepted names, basionyms, parents and hierarchical level.
- `taxonTraits` Table of taxon traits.
- `taxonViews` References used to determine the respective concept circumscription.

Author(s)

Miguel Alvarez

References

Examples

```r
## Class 'taxlist'
showClass("taxlist")

## Create an empty object
sp_list <- new("taxlist")
sp_list
```

---

taxlist2df  

**Coerce taxlist objects to data frames**

Description

Transform taxlist objects into data frames.

Usage

```r
taxlist2df(x, ...)

## S3 method for class 'taxlist'
taxlist2df(
  x,
  include_traits = FALSE,
  include_views = FALSE,
  standard = c("taxlist", "dwc"),
  ...
)
```

Arguments

- `x` A taxlist object to be coerced.
- `...` Further arguments passed among methods.
- `include_traits` A logical value indicating whether taxon concept attributes have to be included in the output or not.
- `include_views` A logical value indicating whether taxon views have to be included in the output or not.
- `standard` A character value indicating the standard used to name columns in the output data frame. Per default taxlist names are used but it can be set to dwc for renaming some columns according to Darwin Core.
**taxon_names**

Handle information on taxon usage names.

**Description**

The slot `taxonNames` in `taxlist` objects contains taxon usage names for the respective taxon. These functions assist on the access and modification of entries for names.

**Usage**

```r
 taxation_names(taxlist, ...)  
```

```r
## S3 method for class 'taxlist'
taxation_names(taxlist, ...)
```

```r
taxon_names(taxlist, ...) <- value  
```

```r
## S3 replacement method for class 'taxlist'
taxon_names(taxlist, ...) <- value
```

```r
add_synonym(taxlist, ...)
```

```r
## S3 method for class 'taxlist'
add_synonym(taxlist, ConceptID, TaxonName, AuthorName, ...)
```

```r
update_name(taxlist, ...)
```

```r
## S3 method for class 'taxlist'
update_name(taxlist, UsageID, ...)
```

```r
delete_name(taxlist, ...)
```

```r
## S3 method for class 'taxlist'
delete_name(taxlist, UsageID, ...)
```

**Arguments**

- **taxlist**
  A `taxlist` object to be modified.

- **value**
  A data frame used as new slot `taxonNames` in `taxlist`.

- **ConceptID**
  Numeric vector indicating the concept ID to which the synonyms will be added.

- **TaxonName, AuthorName**
  Character values used for the new names (synonyms).

- **UsageID**
  Numeric vector indicating the taxon usage IDs to be updated.
taxon_relations

Details

The replacement method `taxon_names<-` is a quick alternative to include names in empty `taxlist` objects.

The function `add_synonym()` works only for adding names to existing taxon concepts. For adding new taxon concepts as well you should use `add_concept()`.

Value

A data frame or, in the case of the replacement method, a `taxlist` object with modified slot `taxonNames`.

Author(s)

Miguel Alvarez <kamapu78@gmail.com>

See Also

taxlist

Examples

```r
## Display of slot 'taxonNames'
Euclea <- subset(x = Easplist, subset = charmatch("Euclea", TaxonName),
    slot = "names", keep_children = TRUE)
Euclea
taxon_names(Euclea)

## Insert a synonym to Diospyros scabra
summary(Easplist, "Diospyros scabra")
sp_list <- add_synonym(taxlist = Easplist, ConceptID = 51793,
    TaxonName = "Maba scabra", AuthorName = "Chiov.")
summary(sp_list, "Diospyros scabra")

## Delete a synonym of Launaea cornuta
summary(sp_list, "Launaea cornuta")
sp_list <- delete_name(sp_list, 53821)
summary(sp_list, "Launaea cornuta")

## Hypothetical correction in author name in Launaea cornuta
sp_list <- update_name(taxlist = sp_list, UsageID = 355, AuthorName = "L.")
summary(sp_list, "Launaea cornuta")
```

taxon_relations

Retrieve or replace slot taxonRelations in taxlist objects

Description

Retrieve the content of slot `taxonRelations` from a `taxlist` object or replace it by a new data frame.
Usage

taxon_relations(taxlist, ...)

## S3 method for class 'taxlist'
taxon_relations(taxlist, ...)

taxon_relations(taxlist, ...) <- value

## S3 replacement method for class 'taxlist'
taxon_relations(taxlist, ...) <- value

## S4 method for signature 'taxlist,numeric'
update_concept(taxlist, ConceptID, ...)

Arguments

taxlist A taxlist object.
...
Further arguments passed among methods.
value A data.frame object to be set as slot taxonRelations.
ConceptID Concept IDs to be updated.

Details

The replacement method taxon_relations<- should be only used when constructing taxlist objects from an empty one (prototype).

New concepts should be first added to a taxlist object using their respective accepted names. Synonyms can be further provided using the function add_synonym().

Additional named vectors can be provided to be included in slot taxonNames, in the cases where those variables already exist, otherwise they will be ignored.

It is recommended also to provide a concept view as ViewID (see taxon_views()). For adding a new view, use add_view().

Value

An object of class taxlist with added names and concepts.

Author(s)

Miguel Alvarez <kamapu78@gmail.com>

See Also
taxlist
## Subset for the genus Euclea and display of slot ‘taxonNames’

```r
Euclea <- subset(x = Easplist, subset = charmatch("Euclea", TaxonName),
                 slot = "names", keep_children = TRUE)
Euclea
taxon_relations(Euclea)
```

### taxon_traits

**Manipulation of taxon traits in taxlist objects.**

**Description**

The slot `taxonTraits` in taxlist objects contains attributes of taxon concepts (e.g. functional traits). These functions are suitable for replacing, retrieving and appending trait information in taxonomic lists.

**Usage**

```r
taxon_traits(taxlist, ...)
```

**S3 method for class 'taxlist'**

```r
taxon_traits(taxlist, ...)
taxon_traits(taxlist, ...) <- value
```

**S3 replacement method for class 'taxlist'**

```r
taxon_traits(taxlist, ...) <- value
```

**S3 method for class 'taxlist'**

```r
update_trait(taxlist, ...)
```

**Arguments**

- `taxlist`: A taxlist object.
- `...`: Further arguments to be passed among methods.
- `value`: Data frame to be set as slot `taxonTraits`.
- `taxonTraits`: a data frame with taxon traits to be inserted in 'taxlist'. A column 'TaxonConceptID' is mandatory in this table. If some taxon concept IDs are not occurring in 'taxlist', an error message is retrieved by `update_trait()`. 

Text of the document:

**taxon_views**

*Management of concept views in taxonomic lists.*

**Details**

Taxon traits are contained in a data frame at the slot `taxonTraits` in `taxlist` objects. To optimise space, this data frame contain only entries for those concepts with information, while taxa with no information are skipped from this table. Thus appending new variables may also have to include new rows in this slot, which is automatically carried out by this function.

The replacement method `taxon_traits<-` should be only used when constructing `taxlist` objects from an empty one.

**Author(s)**

Miguel Alvarez <kamapu78@gmail.com>

**See Also**

taxlist.

**Examples**

```r
## Displaying taxon traits
head(taxon_traits(Easplist))

## Updating traits for Launaea cornuta
summary(Easplist, "Launaea cornuta")
accepted_name(taxlist = Easplist, ConceptID = 355, show_traits = TRUE)

sp_list <- update_trait(taxlist = Easplist, taxonTraits = data.frame(  
  TaxonConceptID = 355,  
  life_form = "annual"))
accepted_name(taxlist = sp_list, ConceptID = 355, show_traits = TRUE)
```

**taxon_views**

Retrieve or replace slot `taxonViews` in an object of class `taxlist`.

**Usage**

taxon_views(taxlist, ...)

## S3 method for class 'taxlist'
taxon_views(taxlist, ...)

taxon_views(taxlist, ...) <- value

## S3 replacement method for class 'taxlist'
taxon_views(taxlist, ...) <- value
add_view(taxlist, taxonViews, ...) 

## S4 method for signature 'taxlist,data.frame'
add_view(taxlist, taxonViews, ...)

**Arguments**

- **taxlist**
  A *taxlist* object.

- **...**
  Further arguments to be passed among methods.

- **value**
  An object of class *data.frame* containing the references used to define the circumscription of taxon concepts included in *taxlist*.

- **taxonViews**
  A data frame with taxon views to be inserted in 'taxlist'.

**Details**

Taxon views indicate in *taxlist* objects the references determining the circumscription of the respective taxon concepts. When adding a new concept (see *add_concept()*), the respective reference may not yet occur in the input *taxlist* object.

The term taxon view was introduced by Zhong et al. (1996) and corresponds to the reference used for the definition of a concept.

This function retrieves the slot *taxonViews* from objects of the class *taxlist*.

The replacement method *taxon_views<-* replaces the whole content of slot *taxonViews* and it is only recommended to use when constructing a new *taxlist* object from an empty prototype.

**Value**

An object of class *taxlist* with added views.

**Author(s)**

Miguel Alvarez <kamapu78@gmail.com>

**References**


**See Also**

taxlist
Examples

```r
## See existing views
taxon_views(Easplist)

## Add a new view
sp_list <- add_view(taxlist = Easplist, taxonViews = data.frame(
  secundum = "Beentje et al. (1952)",
  Title = "Flora of Tropical East Africa",
  URL = "http://www.kew.org/science/directory/projects/FloraTropEAfrica.html")

taxon_views(sp_list)
```

Description

Importing species lists from Turboveg 2 databases into a taxlist object. Internally the functions `foreign::read.dbf()` and `df2taxlist()` are called.

Usage

```r
tv2taxlist(taxlist, tv_home = tv.home(), ...)
```

Arguments

- `taxlist`: Character value indicating the name of a species list in Turboveg.
- `tv_home`: Character value indicating the path to the main Turboveg folder. By default the function `vegdata::tv.home()` is called.
- `...`: Further arguments passed to `df2taxlist()`.

Value

A `taxlist` object.

Author(s)

Miguel Alvarez <kamapu78@gmail.com>

See Also

`df2taxlist()`

Examples

```r
## Cyperus data set installed as Turboveg species list
Cyperus <- tv2taxlist(taxlist = "cyperus",
  tv_home = file.path(path.package("taxlist"), "tv_data"))
Cyperus
```
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