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://github.com/ropensci/taxlist,
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         'id_generator.R' 'replace_x.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_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'
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R topics documented:

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Description

The class taxlist is defined in this package using the S4 language. The main task of taxlist objects is to keep the taxonomic coherence of information included in taxonomic lists and to implement functions (methods) for a proper data handling. Objects of class taxlist can be included in further objects, for instance in biodiversity records as done in the package vegtable.

Details

The class taxlist is defined in this package using the S4 language. The main task of taxlist objects is to keep the taxonomic coherence of information included in taxonomic lists and to implement functions (methods) for a proper data handling. Objects of class taxlist can be included in further objects, for instance in biodiversity records as done in the package vegtable.

For a more detailed description of this package, see Alvarez & Luebert (2018).

Author(s)

Miguel Alvarez <kamapu78@gmail.com>

References


accepted_name

Manage accepted names, synonyms and basionyms

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, ...)

basionym(taxlist, ...) <- value

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

change_concept(taxlist, ...)

## 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.
**add_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**

```r
## 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
summary(Easplist, 68)

## Display synonyms
head(synonyms(taxlist = Easplist))

## Synonyms for an specific concept
synonyms(taxlist = Easplist, ConceptID = 20)

## Basionym for Cyclosorus interruptus
summary(Easplist, 50074)
basionym(Easplist, 50074) <- 53097
summary(Easplist, 50074)
basionym(Easplist, 50074)

## Move the name Typha aethiopica to concept 573 (T. latifolia)
summary(Easplist, c(50105, 573))
change_concept(Easplist, 53130) <- 573
summary(Easplist, c(50105, 573))
```
**Description**

Alternative methods to add new concepts into existing taxlist objects.

**Usage**

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

```r
## S4 method for signature 'taxlist, data.frame'
add_concept(taxlist, TaxonName, ...)
```

```r
## S4 method for signature 'taxlist, character'
add_concept(taxlist, TaxonName, ...)
```

```r
## S4 method for signature 'taxlist, taxlist'
add_concept(taxlist, TaxonName, insert_view = FALSE, ...)
```

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

**Arguments**

- **taxlist**  
  A taxlist object.

- **TaxonName**  
  Character vector with the accepted name for the new taxon concepts.

- **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**

```r
S4_to_list(x)
```

**Arguments**

- **x**  
  An object of class taxlist or any S4 class.

**Details**

Coerce taxlist objects to lists.
backup_object

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

backup_object(
  ...
  objects = character(),
  file,
  stamp = TRUE,
  overwrite = FALSE
)

load_last(file, fext = ".rda")

Arguments

... Names of the objects to be saved (either symbols or character strings).
objects A character vector indicating the names of objects to be included in the backup file.
**backup_object**

- **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.
- **overwrite**: A logical value indicating whether existing files must be overwritten or not.
- **fext**: A character value indicating the file extension (including the dot symbol).

**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**

An R image with extension `*.rda`.

**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(), "Pseudonaphalium"))

## The same again
backup_object(Pseudognaphalium, file = file.path(tempdir(), "Pseudonaphalium"))

## Delete object
rm(list = "Pseudognaphalium")

## To load the last backup into a session
load_last(file = file.path(tempdir(), "Pseudonaphalium"))

## Load pre-installed backup
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, ...)```

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

**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)
```
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

clean_strings(x, ...)

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

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

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

Arguments

x  Object to be cleaned.
...
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

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

Count taxa within a taxlist object.

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

- `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'
df2taxlist(x, taxonTraits, taxonViews, levels, clean_strings = TRUE, ...)

## 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 mandatorial.

taxonViews  A data frame or lib_df with references of taxonomic views (optional). If provided, the column ViewID is mandatorial 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

```r
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

```r
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.
Easplist-data

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)
### Description

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

### Usage

#### S4 method for signature 'taxlist'

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

#### S4 method for signature 'taxlist'

```r
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

#### Statistics on life forms

```r
summary(as.factor(Easplist$life_form))
```

#### First concepts in this list

```r
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**

```r
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**

```r
## 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
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 `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,
```

---

### 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,
alphabetical = 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 synonyms, independent of the argument applied in parameter 'synonyms'.
keep_children A logical value indicating whether children of matched concept should be included in the result.
keep_parents A logical value indicating whether parents of matched concept should be included 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 accepted 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 synonyms.
levels

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

```r
## Show taxonomy of papyrus
indented_list(Easplist, "papyrus")

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

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)

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

levels(x) <- value

## 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.

Value

A character vector or a `taxlist` object with added or modified taxonomic levels.

Author(s)

Miguel Alvarez <kamapu78@gmail.com>

Examples

```r
## Get levels of species list
levels(Easplist)

## Add aggregate as new taxonomic level
levels(Easplist) <- c("form", "variety", "subspecies", "species", "complex", "aggregate", "genus", "family")
summary(Easplist)
```

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 `stringsim()`.
Usage

match_names(x, object, ...)

## S4 method for signature 'character,character'
match_names(
  x,  
  object,  
  UsageID,  
  best = 1,  
  nomatch = TRUE,  
  method = "lcs",  
  cutlevel = NULL,  
  ...  
)

## 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 stringsim().
merge_taxa

merge_taxa

Merge concepts or move names

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, print_output = FALSE, ...)

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.

Author(s)

Miguel Alvarez <kamapu78@gmail.com>

See Also

stringsim()

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)
Arguments

- object, taxlist: Object of class taxlist.
- ...: Further arguments to be passed to or from other methods.
- concepts: Numeric (integer) vector including taxon concepts to be merged.
- level: Character vector indicating the lowest level for merging.
- print_output: Logical value indicating whether the merged concept should be displayed in the console.

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

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.
print_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"),
  ...
)

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

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.
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
text(x = 0, y = 7, labels = print_name(Easplist, 363, style = "knitr"), pos = 4, cex = 0.7)
**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 and data frames. 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).

The function `insert_rows()` will add rows and columns at the same time. This function will be used when a new table is appended to another but sharing only part of the columns.

**Usage**

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

**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`.
- `y`: A data frame including rows (and columns) to be inserted in `x`.

**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"))
```

```r
## Replace values if they are NAs
```
letters[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))

## 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)

subset  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.
summary

subset Logical vector or logical operation to apply as subset.
slot Character value 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

## 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))

summary

Print overviews for taxlist Objects and their content

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,
  ...
)
```

```r
## S4 method for signature 'taxlist'
show(object)
```

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

## S3 method for class 'taxlist'
tax2traits(object, get_names = FALSE, ...)
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))
```

---

taxlist-class  
An S4 class to represent taxonomic lists.

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

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
taxon_names(taxlist, ...)

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

taxon_names(taxlist, ...) <- value

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

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

update_name(taxlist, ...)

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

delete_name(taxlist, ...)

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

**Arguments**

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

- **...**  
  Further arguments passed among methods. In `update_name` are vectors including the variables to be updated for the respective taxon usage ID.

- **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.

**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)
```
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`

Examples
```r
## Subset for the genus Euclea and display of slot 'taxonNames'
Euclea <- subset(x = Easplist, subset = charmatch("Euclea", TaxonName),
                 slot = "names", keep_children = TRUE)
Euclea
taxon_relations(Euclea)
```

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

taxon_traits(taxlist, ...) <- value

update_trait(taxlist, ...)

## S3 method for class 'taxlist'
update_trait(taxlist, taxonTraits, ...)

**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().

**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)
```
Management of concept views in taxonomic lists.

Description

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

Usage

```r
taxon_views(taxlist, ...)
```

### S3 method for class 'taxlist'

```r
taxon_views(taxlist, ...)
```

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

### S3 replacement method for class 'taxlist'

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

```r
add_view(taxlist, taxonViews, ...)
```

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

```r
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",

taxon_views(sp_list)
```

---

tv2taxlist Import species lists from Turboveg databases

Description

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

Usage

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 `tv.home()` from `vegdata-package` is called.
...

Value

A `taxlist` object.
tv2taxlist

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

See Also
df2taxlist()

Examples

## 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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