Package ‘taxa’

March 11, 2022

Type Package
Title Classes for Storing and Manipulating Taxonomic Data
Description Provides classes for storing and manipulating taxonomic data. Most of the classes can be treated like base R vectors (e.g. can be used in tables as columns and can be named). Vectorized classes can store taxon names and authorities, taxon IDs from databases, taxon ranks, and other types of information. More complex classes are provided to store taxonomic trees and user-defined data associated with them.

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as_data_frame

Convert a taxa object to a data.frame

Description

Convert the information in a taxa object to a data.frame using base R vectors as columns. Use as_tibble to convert to tibbles.

Usage

as_data_frame(
  x, 
  row.names = NULL, 
  optional = FALSE, 
  ..., 
  stringsAsFactors = FALSE 
)

Arguments

x An object defined by taxa, such as taxon or taxon_id
row.names NULL or a character vector giving the row names for the data frame. Missing values are not allowed.
optional logical. If TRUE, setting row names and converting column names (to syntactic names: see make.names) is optional. Note that all of R’s base package as.data.frame() methods use optional only for column names treatment, basically with the meaning of data.frame(*,check.names = !optional). See also the make.names argument of the matrix method.
... additional arguments to be passed to or from methods.
stringsAsFactors logical: should the character vector be converted to a factor?

Examples

x <- taxon(name = c('Homo sapiens', 'Bacillus', 'Ascomycota', 'Ericaceae'),
  rank = c('species', 'genus', 'phylum', 'family'),
  id = taxon_id(c('9606', '1386', '4890', '4345'), db = 'ncbi'),
  auth = c('Linnaeus, 1758', 'Cohn 1872', NA, 'Juss., 1789'))

as_data_frame(x)
**as_taxon**  
*Convert to a taxon vector*

**Description**  
Convert other objects to taxon vectors. Compatible base R vectors can also be converted using the taxon constructor.

**Usage**  
```r  
as_taxon(x, ...)  
```

**Arguments**  
- **x**: An object to be converted to a taxon vector
- **...**: Additional parameters.

**Examples**  
```r  
# Convert a taxonomy object to a taxon vector  
x <- taxonomy(taxon(name = c("Carnivora", "Felidae", "Panthera", "Panthera leo",  
                              "Panthera tigris", "Ursidae", "Ursus", "Ursus arctos"),  
                              rank = c("order", "family", "genus", "species",  
                                      "species", "family", "genus", "species"),  
                              id = taxon_id(c("33554", "9681", "9688", "9689",  
                                             "9694", "9632", "9639", "9644")),  
                              db = "ncbi"),  
                              auth = c("Bowdich, 1821", "Fischer de Waldheim, 1817", "Oken, 1816", "L., 1758",  
                                       "L., 1758", "Fischer de Waldheim, 1817", "L., 1758", "L., 1758"),  
                              supertaxa = c(NA, 1, 2, 3, 3, 1, 6, 7))  
names(x) <- letters[1:8]  
as_taxon(x)  
```

```r  
# Convert base R vectors  
as_taxon(c("Carnivora", "Felidae", "Panthera", "Panthera leo"))  
as_taxon(factor(c("Carnivora", "Felidae", "Panthera", "Panthera leo")))  
```

**classification**  
*Taxon class*

**Description**  
Experimental Used to store classifications in reference to a taxonomic tree.

**Usage**  
```r  
classification(x = NULL, taxonomy = NULL, .names = NULL)  
```
Arguments

x  One of:
   • A list where each item represents a series of nested taxa. The contents of the list can be in any form that can be converted to a taxon vector.
   • The indexes/names of each instance of a taxon in a taxonomy object specified by the taxonomy option. Can be any length, but must consist of valid indexes for taxa in the taxonomy object.

taxonomy  A taxonomy object. Only needed if taxon indexes are supplied as the first argument.
.names  The names of the vector.

Value

An S3 object of class taxa_classification

See Also

Other classes: [.taxa_classification(), taxon_authority(), taxon_db(), taxon_id(), taxon_rank(), taxon()}

Examples

# Create classification vector with a list
x <- classification(list(
   c('Carnivora', 'Felidae', 'Panthera', 'Panthera leo'),
   c('Carnivora', 'Felidae', 'Panthera', 'Panthera tigris'),
   c('Carnivora', 'Ursidae', 'Ursus', 'Ursus arctos'),
   c('Carnivora', 'Ursidae', 'Ursus', 'Ursus arctos'),
   c('Carnivora', 'Felidae', 'Panthera', 'Panthera tigris')
))

# Create classification vector with indexes and a taxonomy
x <- classification(c(3, 4, 4, 5, 5, 6, 8, 8, 2, 5, 6, 2),
   taxonomy(c('Carnivora', 'Felidae', 'Panthera', 'Panthera leo',
              'Panthera tigris', 'Ursidae', 'Ursus', 'Ursus arctos'),
            supertaxa = c(NA, 1, 2, 3, 1, 6, 7)))

x <- classification(c(3, 4, 4, 5, 5, 6, 8, 8, 2, 5, 6, 2),
   taxonomy(taxon(name = c('Carnivora', 'Felidae', 'Panthera', 'Panthera leo',
                           'Panthera tigris', 'Ursidae', 'Ursus', 'Ursus arctos'),
                rank = c('order', 'family', 'genus', 'species',
                         'family', 'genus', 'species'),
                id = taxon_id(c('33554', '9681', '9688', '9689',
                                '9694', '9632', '9639', '9644'),
                               db = 'ncbi'),
                auth = c('Bowdich, 1821', 'Fischer, 1817',
                         'Oken, 1816', 'L., 1758',
                         'L., 1758', 'Fischer, 1817',
                         'L., 1758', 'L., 1758')))
supertaxa = c(NA, 1, 2, 3, 1, 6, 7))

names(x) <- letters[1:12]

# Get parts of the classification vector
tax_name(x)
tax_rank(x)
tax_id(x)
tax_db(x)
tax_auth(x)
tax_author(x)
tax_date(x)
tax_cite(x)

# Manipulate classification vectors
x[1:3]
x[tax_rank(x) > 'family']
# c(x, x)
# x['b'] <- NA
is.na(x)
# as.data.frame(x)
# tibble::as_tibble(x)

# Use as columns in tables
tibble::tibble(x = x, y = 1:12)
data.frame(x = x, y = 1:12)

db_ref

Valid taxonomy databases

Description

This defines the valid taxonomic databases that can be used in taxon_db objects and objects that use taxon_db objects, such as taxon_id and taxon. db_ref$get can be used to see information for the databases. Users can add their own custom databases to the list using db_ref$set. For each database the following information is included:

- The URL for the website associated with the database
- A short description
- The regular expression that defines valid taxon IDs
- The ranks used in the database if specified

Usage

db_ref

Format

An object of class list of length 3.
### internodes

#### Get internodes

**Description**

Get internodes indexes for each taxon or another per-taxon value. An internode is a taxon with exactly one supertaxon and one subtaxon. These taxa can be removed without losing information on the relationships of the remaining taxa.

**Usage**

```r
internodes(x)
```

**Arguments**

- `x` The object to get internodes for, such as a `taxonomy` object.

**See Also**

Other taxonomy functions: `leaves()`, `roots()`, `stems()`, `subtaxa()`, `supertaxa()`

Other internode functions: `is_internode()`
is_internode

Examples
x <- taxonomy(c('Carnivora', 'Felidae', 'Panthera', 'Panthera leo',
                'Panthera tigris', 'Ursidae', 'Ursus', 'Ursus arctos'),
supertaxa = c(NA, 1, 2, 3, 3, 1, 6, 7))
internodes(x)

is_classification  Check if is a classification

Description
Check if an object is the classification class

Usage
is_classification(x)

Arguments
x  An object to test

is_internode  Check if taxa are internodes

Description
Check if each taxon is an internode. An internode is a taxon with exactly one supertaxon and
one subtaxon. These taxa can be removed without losing information on the relationships of the
remaining taxa.

Usage
is_internode(x)

Arguments
x  The object to get internodes for, such as a taxonomy object.

See Also
Other internode functions: internodes()
### is_leaf

**Check if taxa are leaves**

Check if each taxon is a leaf. A leaf is a taxon with no subtaxa.

**Usage**

```r
is_leaf(x)
```

**Arguments**

- `x` The object to get leaves for, such as a `taxonomy` object

**See Also**

Other leaf functions: `leaves()`, `n_leaves()`

**Examples**

```r
x <- taxonomy(c('Carnivora', 'Felidae', 'Panthera', 'Panthera leo',
                 'Panthera tigris', 'Ursidae', 'Ursus', 'Ursus arctos'),
               supertaxa = c(NA, 1, 2, 3, 3, 1, 6, 7))
is_leaf(x)
```

### is_root

**Test if taxa are roots**

Check if each taxon is a root. A root is a taxon with no supertaxon.

**Usage**

```r
is_root(x, subset = NULL)
```

**Examples**

```r
x <- taxonomy(c('Carnivora', 'Felidae', 'Panthera', 'Panthera leo',
                 'Panthera tigris', 'Ursidae', 'Ursus', 'Ursus arctos'),
               supertaxa = c(NA, 1, 2, 3, 3, 1, 6, 7))
is_root(x)
```
Arguments

x An object containing taxonomic relationships, such as taxonomy objects.

subset The subset of the tree to search for roots to that subset. Can be indexes or names.

See Also

Other root functions: roots()

Examples

x <- taxonomy(c("Carnivora", "Felidae", "Panthera", "Panthera leo", "Panthera tigris", "Ursidae", "Ursus", "Ursus arctos"), supertaxa = c(NA, 1, 2, 3, 3, 1, 6, 7))
is_root(x)
is_root(x, subset = 2:8)
is_taxon  
*Check if something is a *taxon* object*

**Description**
Check if an object is of the *taxon* class

**Usage**
```r
is_taxon(x)
```

**Arguments**
- `x` An object to test

**Examples**
```r
x <- taxon(c("A", "B", "C"))
is_taxon(x)
is_taxon(1:2)
```

---

is_taxonomy  
*Check if something is a *taxonomy* *

**Description**
Check if an object is of the *taxonomy* class

**Usage**
```r
is_taxonomy(x)
```

**Arguments**
- `x` An object to test

**Examples**
```r
x <- taxonomy(c("Carnivora", "Felidae", "Panthera", "Panthera leo", "Panthera tigris", "Ursidae", "Ursus", "Ursus arctos"), supertaxa = c(NA, 1, 2, 3, 3, 1, 6, 7))
is_taxonomy(x)
is_taxonomy(1:2)
```
is_taxon_authority  
*Check if is a* taxon_authority

**Description**
Check if an object is of the taxon_authority class

**Usage**

```r
is_taxon_authority(x)
```

**Arguments**

- `x` An object to test

**Examples**

```r
x <- taxon_authority(c('Cham. & Schldl.', 'L.'),
                      date = c('1827', '1753'))
is_taxon_authority(x)
is_taxon_authority(1:3)
```

---

is_taxon_db  
*Check if something is a* taxon_db

**Description**
Check if an object is of the taxon_db class

**Usage**

```r
is_taxon_db(x)
```

**Arguments**

- `x` An object to test

**Examples**

```r
x <- taxon_db(c('ncbi', 'ncbi', 'itis'))
is_taxon_db(x)
is_taxon_db(1:3)
```
is_taxon_id

Check if something is a taxon_id object

Description

Check if an object is of the taxon_id class

Usage

is_taxon_id(x)

Arguments

x An object to test

Examples

x <- taxon_id(c('9606', '1386', '4890', '4345'), db = 'ncbi')
is_taxon_id(x)
is_taxon_id(1:3)

is_taxon_rank

Check if something is a taxon_rank

Description

Check if an object is of the taxon_rank class

Usage

is_taxon_rank(x)

Arguments

x An object to test

Examples

x <- taxon_rank(c('species', 'species', 'phylum', 'family'))
is_taxon_rank(x)
is_taxon_rank(1:3)
leaves

Get leaves

Description

Get leaves indexes for each taxon or another per-taxon value. Leaves are taxa with no subtaxa.

Usage

leaves(x, value = NULL, ...)

Arguments

x  The object to get leaves for, such as a taxonomy object
value  Something to return instead of indexes. Must be the same length as the number of taxa.
...  Additional arguments.

See Also

Other taxonomy functions: internodes(), roots(), stems(), subtaxa(), supertaxa()
Other leaf functions: is_leaf(), n_leaves()

Examples

x <- taxonomy(c("Carnivora", "Felidae", "Panthera", "Panthera leo", "Panthera tigris", "Ursidae", "Ursus", "Ursus arctos"), supertaxa = c(NA, 1, 2, 3, 1, 6, 7))
leaves(x)
leaves(x, value = tax_name(x))

n_leaves

Number of leaves per taxon

Description

Get the number of leaves per taxon. A leaf is a taxon with no subtaxa.

Usage

n_leaves(x)

Arguments

x  The object to get leaves for, such as a taxonomy object
**n_subtaxa**

**See Also**

Other leaf functions: `is_leaf()`, `leaves()`

**Examples**

```r
x <- taxonomy(c("Carnivora", "Felidae", "Panthera", "Panthera leo", "Panthera tigris", "Ursidae", "Ursus", "Ursus arctos"), supertaxa = c(NA, 1, 2, 3, 3, 1, 6, 7))

n_leaves(x)
```

**Description**

Get the number of subtaxa per taxon.

**Usage**

```r
n_subtaxa(x, subset = NULL, max_depth = NULL, include = FALSE)
```

**Arguments**

- `x`: The object to get subtaxa for, such as a `taxonomy` object.
- `subset`: The subset of the tree to search. Can be indexes or names.
- `max_depth`: The number of ranks to traverse. For example, `max_depth = 1` returns only immediate subtaxa. By default (NULL) information for all subtaxa is returned (i.e. subtaxa of subtaxa, etc).
- `include`: If TRUE, include information for each taxon in the output.

**See Also**

Other subtaxa functions: `subtaxa()`

**Examples**

```r
# Generate example data
x <- taxonomy(c("Carnivora", "Felidae", "Panthera", "Panthera leo", "Panthera tigris", "Ursidae", "Ursus", "Ursus arctos"), supertaxa = c(NA, 1, 2, 3, 3, 1, 6, 7))

# Find number of subtaxa (including subtaxa of subtaxa, etc)
n_subtaxa(x)

# Find the number of subtaxa one rank below each taxon
n_subtaxa(x, max_depth = 1)
```
# Only return data for some taxa (faster than subsetting the whole result)
n_supertaxa(x, subset = 1:3)

## n_supertaxa

### Description

Get the number of supertaxa each taxon is contained in.

### Usage

```
n_supertaxa(x, subset = NULL, max_depth = NULL, include = FALSE)
```

### Arguments

- **x**: The object to get supertaxa for, such as a taxonomy object.
- **subset**: The subset of the tree to search for roots to that subset. Can be indexes or names.
- **max_depth**: The number of levels to traverse. For example, `max_depth = 1` returns only immediate supertaxa. By default (NULL) information for all supertaxa is returned.
- **include**: If TRUE, include information for each taxon in the output.

### See Also

Other supertaxa functions: `supertaxa()`

### Examples

```
# Generate example data
x <- taxonomy(c("Carnivora", "Felidae", "Panthera", "Panthera leo", 
                "Panthera tigris", "Ursidae", "Ursus", "Ursus arctos"),
              supertaxa = c(NA, 1, 2, 3, 3, 1, 6, 7))

# Find number of supertaxa each taxon is contained in
n_supertaxa(x)

# Only return data for some taxa (faster than subsetting the whole result)
n_supertaxa(x, subset = 1:3)
```
roots

Get root taxa

Description
Get the indexes of root taxa in a taxonomy.

Usage
roots(x, subset = NULL)

Arguments
x An object containing taxonomic relationships, such as taxonomy objects.
subset The subset of the tree to search for roots to that subset. Can be indexes or names.

See Also
Other taxonomy functions: internodes(), leaves(), stems(), subtaxa(), supertaxa()
Other root functions: is_root()

Examples
x <- taxonomy(c("Carnivora", "Felidae", "Panthera", "Panthera leo", "Panthera tigris", "Ursidae", "Ursus", "Ursus arctos"), supertaxa = c(NA, 1, 2, 3, 3, 1, 6, 7))
roots(x)
roots(x, subset = 2:8)

stems

Get stems

Description
Get stem indexes for each taxon or another per-taxon value.

Usage
stems(x, value = NULL, ...)

Arguments
x An object with taxonomic relationships, like taxonomy objects.
value Something to return instead of indexes. Must be the same length as the number of taxa.
... Additional arguments.
See Also

Other taxonomy functions: `internodes()`, `leaves()`, `roots()`, `subtaxa()`, `supertaxa()`
Other stem functions: `is_stem()`

Examples

```r
x <- taxonomy(c("Carnivora", "Felidae", "Panthera", "Panthera leo", "Panthera tigris"),
               supertaxa = c(NA, 1, 2, 3, 3))
x <- c(x, x)
stems(x)
stems(x, value = tax_name(x))
```

---

**subtaxa**

Get subtaxa

**Description**

Get subtaxa indexes for each taxon or another per-taxon value. Subtaxa are taxa contained within a taxon.

**Usage**

```r
subtaxa(x, subset = NULL, max_depth = NULL, include = FALSE, value = NULL, ...)
```

**Arguments**

- **x**: The object to get subtaxa for, such as a `taxonomy` object.
- **subset**: The subset of the tree to search. Can be indexes or names.
- **max_depth**: The number of ranks to traverse. For example, `max_depth = 1` returns only immediate subtaxa. By default (NULL) information for all subtaxa is returned (i.e. subtaxa of subtaxa, etc).
- **include**: If `TRUE`, include information for each taxon in the output.
- **value**: Something to return instead of indexes. Must be the same length as the number of taxa.
- **...**: Additional arguments.

**See Also**

Other taxonomy functions: `internodes()`, `leaves()`, `roots()`, `stems()`, `supertaxa()`
Other subtaxa functions: `n_subtaxa()`
Examples

# Generate example data
x <- taxonomy(c('Carnivora', 'Felidae', 'Panthera', 'Panthera leo',
                'Panthera tigris', 'Ursidae', 'Ursus', 'Ursus arctos'),
              supertaxa = c(NA, 1, 2, 3, 3, 1, 6, 7))

# The indexes of all subtaxa (with subtaxa of subtaxa, etc) for each taxon
subtaxa(x)

# The indexes of immediate subtaxa (without subtaxa of subtaxa, etc) for each taxon
subtaxa(x, max_depth = 1)

# Return something other than index
subtaxa(x, value = tax_name(x))

# Include each taxon with its subtaxa
subtaxa(x, value = tax_name(x), include = TRUE)

# Only return data for some taxa (faster than subsetting the whole result)
subtaxa(x, subset = 3)

Description

Get supertaxa indexes for each taxon or another per-taxon value. Supertaxa are taxa a taxon is contained in.

Usage

supertaxa(
  x,
  subset = NULL,
  max_depth = NULL,
  include = FALSE,
  value = NULL,
  use_na = FALSE,
  ...
)

Arguments

x The object to get supertaxa for, such as a taxonomy object.
subset The subset of the tree to search for roots to that subset. Can be indexes or names.
max_depth The number of levels to traverse. For example, max_depth = 1 returns only immediate supertaxa. By default (NULL) information for all supertaxa is returned.
include
If TRUE, include information for each taxon in the output.

value
Something to return instead of indexes. Must be the same length as the number
of taxa.

use_na
Add a NA to represent the root of the taxonomy (i.e. no supertaxon)

See Also

Other taxonomy functions: `internodes()`, `leaves()`, `roots()`, `stems()`, `subtaxa()`

Other supertaxa functions: `n_supertaxa()`

Examples

```r
# Generate example data
x <- taxonomy(c('Carnivora', 'Felidae', 'Panthera', 'Panthera leo',
                 'Panthera tigris', 'Ursidae', 'Ursus', 'Ursus arctos'),
               supertaxa = c(NA, 1, 2, 3, 3, 1, 6, 7))

# The indexes of all supertaxa (with supertaxa of supertaxa, etc) for each taxon
supertaxa(x)

# Return something other than index
supertaxa(x, value = tax_name(x))

# Include each taxon with its supertaxa
supertaxa(x, value = tax_name(x), include = TRUE)

# Only return data for some taxa (faster than subsetting the whole result)
supertaxa(x, subset = 3)
```

---

**taxa_taxon-class**

*Taxon class*

**Description**

Taxon class. See `taxon` for more information

---

**taxa_taxonomy-class**

*Taxonomy class*

**Description**

Taxonomy class. See `taxonomy` for more information
<table>
<thead>
<tr>
<th>Class Name</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>taxa_taxon_authority-class</td>
<td>Taxon authority class. See taxon_authority for more information</td>
</tr>
<tr>
<td>taxa_taxon_db-class</td>
<td>Taxon database class. See taxon_db for more information</td>
</tr>
<tr>
<td>taxa_taxon_id-class</td>
<td>Taxon ID class. See taxon_id for more information</td>
</tr>
<tr>
<td>taxa_taxon_rank-class</td>
<td>Taxon rank class. See taxon_rank for more information</td>
</tr>
</tbody>
</table>
**taxon**

*Taxon class*

**Description**

**Maturing** Used to store information about taxa, such as names, ranks, and IDs.

**Usage**

```r
taxon(name = character(0), rank = NA, id = NA, auth = NA, .names = NA, ...)
```

**Arguments**

- `name`: The names of taxa. Inputs with be coerced into a `character` vector if anything else is given.
- `rank`: The ranks of taxa. Inputs with be coerced into a `taxon_rank` vector if anything else is given.
- `id`: The ids of taxa. These should be unique identifier and are usually associated with a database. Inputs with be coerced into a `taxon_id` vector if anything else is given.
- `auth`: The authority of the taxon. Inputs with be coerced into a `taxon_authority` vector if anything else is given.
- `.names`: The names of the vector.
- `...`: Additional arguments.

**Value**

An S3 object of class `taxa_taxon`.

**See Also**

Other classes: `.taxa_classification()`, `classification()`, `taxon_authority()`, `taxon_db()`, `taxon_id()`, `taxon_rank()`

**Examples**

```r
# Create taxon name vector
x <- taxon(c('A', 'B', 'C'))
x <- taxon(name = c('Homo sapiens', 'Bacillus', 'Ascomycota', 'Ericaceae'),
           rank = c('species', 'genus', 'phylum', 'family'),
           id = taxon_id(c('9606', '1386', '4890', '4345'), db = 'ncbi'),
           auth = c('Linnaeus, 1758', 'Cohn 1872', 'Juss., 1789'))
names(x) <- c('a', 'b', 'c', 'd')

# Get parts of the taxon name vector
tax_name(x)
tax_rank(x)
```
taxon_author

# Set parts of the taxon name vector
tax_name(x) <- tolower(tax_name(x))
tax_rank(x)[1] <- NA
tax_name(x)['b'] <- 'Billy'
tax_id(x) <- '9999'
tax_db(x) <- 'itis'
tax_auth(x) <- NA
tax_author(x)[2:3] <- c('Joe', 'Billy')
tax_date(x) <- c('1999', '2013', '1796', '1899')
tax_cite(x)[1] <- 'Linnaeus, C. (1771). Mantissa plantarum altera generum.'

# Manipulate taxon name vectors
x[1:3]
x[tax_rank(x) > 'family']
x['b'] <- NA
x[c('c', 'd')] <- 'unknown'
is.na(x)

# Use as columns in tables
tibble::tibble(x = x, y = 1:4)
data.frame(x = x, y = 1:4)

# Converting to tables
tibble::as_tibble(x)
as_data_frame(x)

taxon_authority  Taxon authority class

**Description**

Maturing  Used to store information on taxon authorities, such as author names, date, and citation.

**Usage**

```r
taxon_authority(
  author = character(),
  date = NA,
  citation = NA,
  .names = NA,
  extract.date = TRUE
)
```
Arguments

- **author**: Zero or more author names.
- **date**: Zero or more dates.
- **citation**: Zero or more literature citations.
- **names**: The names of the vector.
- **extract_date**: If TRUE (the default), then if a date is detected in the author input and no date input is given, then the date is separated from the author input.

Value

An S3 object of class `taxa_taxon_author`

See Also

Other classes: `.taxa_classification`, `classification`, `taxon_db`, `taxon_id`, `taxon_rank`, `taxon`

Examples

```
# Making new objects
x <- taxon_authority(c('A', 'B', 'C'))
x <- taxon_authority(c('Cham. & Schldl.', 'L.'),
                    date = c('1827', '1753'))

# Manipulating objects
as.character(x)
x[2] <- 'ABC'
names(x) <- c('a', 'b')
x['b'] <- 'David Bowie'
tax_author(x)[1] <- tolower(tax_author(x)[1])
tax_author(x)
tax_date(x) <- c('2000', '1234')
tax_date(x)
tax_cite(x)[2] <- c('Linnaeus, C. (1771). Mantissa plantarum altera generum.')
tax_cite(x)

# Using as columns in tables
tibble::tibble(x = x, y = 1:2)
data.frame(x = x, y = 1:2)

# Converting to tables
tibble::as_tibble(x)
as_data_frame(x)
```
Taxon database class

Description

Maturing Used to store the names of taxon databases defined in \texttt{db_ref}. Primarily used in other classes like \texttt{taxon_id} to define databases for each item.

Usage

taxon_db(db = character(), .names = NULL, ...)

Arguments

- \textbf{db}  
  Zero or more taxonomic database names. Should be a name contained in \texttt{db_ref}. Inputs will be transformed to a \texttt{character} vector if possible.

- \textbf{.names}  
  The names of the vector.

- \textbf{...}  
  Additional arguments.

Value

An S3 object of class \texttt{taxa_taxon_db}

See Also

Other classes: \texttt{[.taxa_classification(), classification(), taxon_authority(), taxon_id(), taxon_rank(), taxon()}

Examples

# Making new objects
x <- taxon_db(c('ncbi', 'ncbi', 'itis'))
x

# Manipulating objects
as.character(x)
x[2:3] <- 'nbn'
names(x) <- c('a', 'b', 'c')
x['b']
x['b'] <- 'nbn'
x[3] <- 'gbif'

# Using as columns in tables
tibble::tibble(x = x, y = 1:3)
data.frame(x = x, y = 1:3)

# Converting to tables
tibble::as_tibble(x)
as_data_frame(x)

# Trying to use an invalid database generates an error
# x <- taxon_db(c('ncbi', 'ncbi', 'my_custom_db'))
# x[x == 'itis'] <- 'my_custom_db'

# Listing known databases and their properties
db_ref$get()

# Adding and using a new database
db_ref$set(name = 'my_custom_db', desc = 'I just made this up')
db_ref$get()
x <- taxon_db(c('ncbi', 'ncbi', 'my_custom_db'))

---

taxon_id | Taxon ID class

Description

*Maturing* Used to store the ID corresponding to taxa, either arbitrary or from a particular taxonomy database. This is typically used to store taxon IDs in taxon objects.

Usage

taxon_id(id = character(), db = NA, .names = NULL)

Arguments

- **id**
  Zero or more taxonomic ids. Inputs will be transformed to a character vector if possible.

- **db**
  The name(s) of the database(s) associated with the IDs. If not NA (the default), the input must consist of names of databases in db_ref$get().

- **.names**
  The names that will be applied to the vector.

Value

An S3 object of class taxa_taxon_id

See Also

Other classes: [.taxa_classification(), .classification(), taxon_authority(), taxon_db(), .taxon_rank(), taxon()
Examples

# Making new objects
x <- taxon_id(c('A', 'B', 'C'))
x <- taxon_id(c('9606', '1386', '4890', '4345'), db = 'ncbi')
x <- taxon_id(c('9606', '1386', '4890', '4345'),
    db = c('ncbi', 'ncbi', 'itis', 'itis'))
names(x) <- c('a', 'b', 'c', 'd')

# Manipulating objects
as.character(x)
x[2:3] <- 'ABC'
x[c('a', 'c')] <- '123'
x[[ 'b']] <- taxon_id('123423', db = 'ncbi')
tax_db(x)
tax_db(x) <- 'nbn'
c(x, x)

# Using as columns in tables
tibble::tibble(x = x, y = 1:4)
data.frame(x = x, y = 1:4)

# Convert to tables
tibble::as_tibble(x)
as_data_frame(x)

# Trying to use an invalid ID with a specified database causes an error
#taxon_id('NOLETTERS', db = 'ncbi')

taxon_rank

Description

Maturing Used to store taxon ranks, possibly associated with a taxonomy database. This is typically used to store taxon ranks in taxon objects.

Usage

taxon_rank(
    rank = character(),
    .names = NULL,
    levels = NULL,
    guess_order = TRUE
)

Arguments
rank  Zero or more taxonomic rank names. Inputs will be transformed to a character vector.
.names  The names of the vector
levels  A named numeric vector indicating the names and orders of possible taxonomic ranks. Higher numbers indicate for fine-scale groupings. Ranks of unknown order can be indicated with NA instead of a number.
guess_order  If TRUE and no rank order is given using numbers, try to guess order based on rank names.

Value
An S3 object of class taxa_taxon_rank

See Also
Other classes: [.taxa_classification(), classification(), taxon_authority(), taxon_db(),
taxon_id(), taxon()]

Examples
# Making new objects
x <- taxon_rank(c('species', 'species', 'phylum', 'family'))

# Specifying level order
taxon_rank(c('A', 'B', 'C', 'D', 'A', 'D', 'D'),
  levels = c('D', 'C', 'B', 'A'))
taxon_rank(c('A', 'B', 'C', 'D', 'A', 'D', 'D'),
  levels = c(NA, 10, 20, 30))
names(x) <- c('a', 'b', 'c', 'd')

# Manipulating objects
as.character(x)
as.factor(x)
as.ordered(x)
x[2:3]
x[x > 'family'] <- taxon_rank('unknown')
x[1] <- taxon_rank('order')
x['b']
x['b'] <- 'order'

# Using as columns in tables
tibble::tibble(x = x, y = 1:4)
data.frame(x = x, y = 1:4)

# Converting to tables
tibble::as_tibble(x)
as_data_frame(x)

# Trying to add an unknown level as a character causes an error
tax_auth.taxa_classification

Set and get taxon authorities

Description

Set and get the taxon authorities in objects that have them, such as taxon objects. Note that this sets all the authority information, such as author name, date, and citations. To set or get just one of part of the authorities, use tax_author, tax_date, or tax_cite instead.

Usage

## S3 method for class 'taxa_classification'
tax_auth(x)

## S3 replacement method for class 'taxa_classification'
tax_auth(x) <- value
tax_auth(x)
tax_auth(x) <- value

## S3 method for class 'taxa_taxon'
tax_auth(x)

## S3 replacement method for class 'taxa_taxon'
tax_auth(x) <- value

## S3 method for class 'taxa_taxonomy'
tax_auth(x)

## S3 replacement method for class 'taxa_taxonomy'
tax_auth(x) <- value

Arguments

x       An object with taxon authorities.
value   The taxon IDs to set. Inputs will be coerced into a taxon_id vector.
Examples

```r
x <- taxon(name = c('Homo sapiens', 'Bacillus', 'Ascomycota', 'Ericaceae'),
            rank = c('species', 'genus', 'phylum', 'family'),
            id = taxon_id(c('9606', '1386', '4890', '4345'), db = 'ncbi'),
            auth = c('Linnaeus, 1758', 'Cohn 1872', NA, 'Juss., 1789'))

tax_auth(x)
tax_auth(x) <- tolower(tax_auth(x))
tax_auth(x)[1] <- 'Billy'
```

tax_author.taxa_classification

Set and get taxon authors

Description

Set and get taxon authors in objects that have them, such as taxon_authority objects.

Usage

```r
## S3 method for class 'taxa_classification'
tax_author(x)

## S3 replacement method for class 'taxa_classification'
tax_author(x) <- value

tax_author(x)
tax_author(x) <- value

## S3 method for class 'taxa_taxon'
tax_author(x)

## S3 replacement method for class 'taxa_taxon'
tax_author(x) <- value

## S3 replacement method for class 'taxa_taxon_authority'
tax_author(x) <- value

## S3 method for class 'taxa_taxon_authority'
tax_author(x)

## S3 method for class 'taxa_taxonomy'
tax_author(x)

## S3 replacement method for class 'taxa_taxonomy'
tax_author(x) <- value
```
Arguments

x An object with taxon authors.
value The taxon authors to set. Inputs will be coerced into a character vector.

Examples

```r
x <- taxon_author(c('Cham. & Schdl.', 'L.'),
                  date = c('1827', '1753'))
tax_author(x)
tax_author(x)[1] <- "Billy"
tax_author(x) <- tolower(tax_author(x))
```

Description

Set and get taxon authority citations

Usage

```r
## S3 method for class 'taxa_classification'
tax_cite(x)
## S3 replacement method for class 'taxa_classification'
tax_cite(x) <- value
tax_cite(x)
tax_cite(x) <- value
## S3 method for class 'taxa_taxon'
tax_cite(x)
## S3 replacement method for class 'taxa_taxon'
tax_cite(x) <- value
tax_cite(x)
## S3 method for class 'taxa_taxon_authority'
tax_cite(x)
## S3 replacement method for class 'taxa_taxon_authority'
tax_cite(x) <- value
tax_cite(x)
## S3 method for class 'taxa_taxonomy'
tax_cite(x)
```
## S3 replacement method for class 'taxa_taxonomy'

tax_cite(x) <- value

### Arguments

- **x**
  - An object with taxon authority dates.

- **value**
  - The taxon citations to set. Inputs will be coerced into a `taxon_authority` vector.

### Examples

```r
x <- taxon_authority(c('Cham. & Schltdl.', 'L.'),
  date = c('1827', '1753'),
  citation = c(NA, 'Species Plantarum'))
tax_cite(x)
tax_cite(x)[1] <- "Cham. et al 1984"
```

---

### Description

Set and get taxon authority dates in objects that have them, such as `taxon_authority` objects.

### Usage

```r
## S3 method for class 'taxa_classification'
tax_date(x)

## S3 replacement method for class 'taxa_classification'
tax_date(x) <- value
tax_date(x)
tax_date(x) <- value

## S3 method for class 'taxa_taxon'
tax_date(x)

## S3 replacement method for class 'taxa_taxon'
tax_date(x) <- value
tax_date(x) <- value

## S3 replacement method for class 'taxa_taxon_authority'
tax_date(x) <- value
```
## S3 method for class 'taxa_taxon_authority'
tax_date(x)

## S3 method for class 'taxa_taxonomy'
tax_date(x)

## S3 replacement method for class 'taxa_taxonomy'
tax_date(x) <- value

### Arguments

- **x**
  - An object with taxon authority dates.

- **value**
  - The taxon authority dates to set. Inputs will be coerced into a character vector.

### Examples

```r
x <- taxon_authority(c('Cham. & Schldl.', 'L.'),
                      date = c('1827', '1753'))
tax_date(x)
tax_date(x)[1] <- "1984"
tax_date(x) <- c(NA, '1800')
```

---

tax_db.taxa_classification

### Set and get taxon ID databases

### Description

Set and get the taxon ID databases in objects that have them, such as taxon_id objects.

### Usage

```r
## S3 method for class 'taxa_classification'
tax_db(x)

## S3 replacement method for class 'taxa_classification'
tax_db(x) <- value

tax_db(x)
tax_db(x) <- value

## S3 method for class 'taxa_taxon'
tax_db(x)

## S3 replacement method for class 'taxa_taxon'
```
tax_db(x) <- value

## S3 method for class 'taxa_taxon_id'
tax_db(x)

## S3 replacement method for class 'taxa_taxon_id'
tax_db(x) <- value

## S3 method for class 'taxa_taxonomy'
tax_db(x)

## S3 replacement method for class 'taxa_taxonomy'
tax_db(x) <- value

Arguments

x An object with taxon authority dates.
value The taxon citations to set. Inputs will be coerced into a taxon_db vector.

Examples

x <- taxon_id(c('9606', '1386', '4890', '4345'), db = 'ncbi')
tax_db(x)
tax_db(x) <- 'nbn'
tax_db(x)[2] <- 'itis'

tax_id.taxon_classification

Set and get taxon IDs

description

Set and get the taxon IDs in objects that have them, such as taxon objects.

Usage

## S3 method for class 'taxa_classification'
tax_id(x)

## S3 replacement method for class 'taxa_classification'
tax_id(x) <- value

tax_id(x)
tax_id(x) <- value
tax_name.taxa_classification

## S3 method for class 'taxa_taxon'
tax_id(x)

## S3 replacement method for class 'taxa_taxon'
tax_id(x) <- value

## S3 method for class 'taxa_taxonomy'
tax_id(x)

## S3 replacement method for class 'taxa_taxonomy'
tax_id(x) <- value

**Arguments**

- **x**  
  An object with taxon IDs.

- **value**  
  The taxon IDs to set. Inputs will be coerced into a `taxon_id` vector.

**Examples**

```r
x <- taxon(name = c("Homo sapiens", "Bacillus", "Ascomycota", "Ericaceae"),
rank = c("species", "genus", "phylum", "family"),
id = taxon_id(c("9606", "1386", "4890", "4345"), db = "ncbi"),
auth = c("Linnaeus, 1758", "Cohn 1872", NA, "Juss., 1789"))

tax_id(x)
tax_id(x) <- paste0('00', tax_id(x))
tax_id(x)[1] <- '00000'
```

---

**tax_name.taxa_classification**

*Set and get taxon names*

---

**Description**

Set and get the taxon names in objects that have them, such as `taxon` objects. Note that this is not the same as adding vector names with `names`.

**Usage**

```r
## S3 method for class 'taxa_classification'
tax_name(x)

## S3 replacement method for class 'taxa_classification'
tax_name(x) <- value
```

tax_name(x)
tax_name(x) <- value
## S3 method for class 'taxa_taxon'
tax_name(x)

## S3 replacement method for class 'taxa_taxon'
tax_name(x) <- value

## S3 method for class 'taxa_taxonomy'
tax_name(x)

## S3 replacement method for class 'taxa_taxonomy'
tax_name(x) <- value

**Arguments**

- **x**
  - An object with taxon names.

- **value**
  - The taxon names to set. Inputs will be coerced into a character vector.

**Examples**

```r
x <- taxon(name = c('Homo sapiens', 'Bacillus', 'Ascomycota', 'Ericaceae'),
           rank = c('species', 'genus', 'phylum', 'family'),
           id = taxon_id(c('9606', '1386', '4890', '4345'), db = 'ncbi'),
           auth = c('Linnaeus, 1758', 'Cohn 1872', NA, 'Juss., 1789'))

tax_name(x)
tax_name(x) <- tolower(tax_name(x))
tax_name(x)[1] <- 'Billy'
```

---

**tax_rank.taxa_classification**

*Set and get taxon ranks*

**Description**

Set and get the taxon ranks in objects that have them, such as `taxon` objects.

**Usage**

```r
## S3 method for class 'taxa_classification'
tax_rank(x)

## S3 replacement method for class 'taxa_classification'
tax_rank(x) <- value
```
tax_rank(x) <- value

## S3 method for class 'taxa_taxon'
tax_rank(x)

## S3 replacement method for class 'taxa_taxon'
tax_rank(x) <- value

## S3 method for class 'taxa_taxonomy'
tax_rank(x)

## S3 replacement method for class 'taxa_taxonomy'
tax_rank(x) <- value

### Arguments

- **x**: An object with taxon ranks.
- **value**: The taxon ranks to set. Inputs will be coerced into a `taxon_rank` vector.

### Examples

```r
x <- taxon(name = c('Homo sapiens', 'Bacillus', 'Ascomycota', 'Ericaceae'),
           rank = c('species', 'genus', 'phylum', 'family'),
           id = taxon_id(c('9606', '1386', '4890', '4345'), db = 'ncbi'),
           auth = c('Linnaeus, 1758', 'Cohn 1872', NA, 'Juss., 1789'))

tax_rank(x)
tax_rank(x) <- 'species'
tax_rank(x)[1] <- taxon_rank('family')
```

---

### %in%

**Value matching for taxa package**

### Description

A wrapper for the base value matching `%in%` that is used to take into consideration features of the taxa package.

### Usage

```r
x %in% table
```

### Arguments

- **x**: vector or NULL: the values to be matched. Long vectors are supported.
- **table**: vector or NULL: the values to be matched against. Long vectors are not supported.
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