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Author Dominguez Vidana Socorro [aut]
    (<https://orcid.org/0000-0002-7926-4935>),
    Simon Goring [aut, cre] (<https://orcid.org/0000-0002-2700-4605>)
Maintainer Simon Goring <goring@wisc.edu>
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add_chronology

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add_chronology

Add a new chronology to a collection unit.

Description

Add a new chronology to a collection unit.

Usage

add_chronology(object, x, y)

Arguments

object
A collection unit object

x
A chronology object

y
A data.frame of sample ages

Value

chronology object defined by user,

add_chronology, collunit, chronology, data.frame-method

Add a new chronology into an existing collection unit.

Description

Given a collunit, add a new chronology object to the unit with both the chronology metadata and the age information (as y).

Usage

## S4 method for signature 'collunit,chronology,data.frame'
add_chronology(object, x, y)

Arguments

object
A collection unit object

x
A chronology object generated using set_chronology()

y
A data.frame of sample ages, with required columns: "analysisunitid", "age", "agetype", "ageolder", and "ageyounger".
Details

When undertaking analysis we may wish to add a new chronology to existing records within Neotoma. To do this we must first build the chronology, but also link it to existing analysis units within the collection unit. For examples from this function, see the Complex Workflows documentation online.

Value

chronologies with new added chronology

as.data.frame,authors-method

Convert a publication author to a data.frame

Description

Convert a publication author to a data.frame

Usage

## S4 method for signature 'authors'

as.data.frame(x)

Arguments

x An author

Value

data.frame with publications metadata

as.data.frame,chronologies-method

as.data.frame chronologies

Description

Convert all slots within each chronology within a chronologies object to a data.frame.

Usage

## S4 method for signature 'chronologies'

as.data.frame(x)
as.data.frame, chronology-method

Arguments
x chronologies object

Value
data.frame with chronologies metadata

Description
Create a data.frame from a chronology object.

Usage
## S4 method for signature 'chronology'
as.data.frame(x)

Arguments
x chronology object

Value
data.frame

as.data.frame, collunit-method

Description
show as dataframe

Usage
## S4 method for signature 'collunit'
as.data.frame(x)

Arguments
x site object

Value
data.frame object with a collection units metadata
Description
show as dataframe as prep to save as csv

Usage
## S4 method for signature 'collunits'
as.data.frame(x)

Arguments
x collunits object

Value
data.frame of multiple collection units metadata.

Description
Transform a contacts object to a data.frame()

Usage
## S4 method for signature 'contact'
as.data.frame(x)

Arguments
x A contact object.

Value
data.frame object with contact metadata
Transform a contacts object to a data.frame()

Usage

## S4 method for signature 'contacts'
as.data.frame(x)

Arguments

x A contacts object.

Value
data.frame object with multiple contacts metadata

show as dataframe as prep to save as csv

Usage

## S4 method for signature 'dataset'
as.data.frame(x)

Arguments

x dataset object

Value
data.frame with dataset metadata
as.data.frame,datasets-method

Description

show as dataframe as prep to save as csv

Usage

## S4 method for signature 'datasets'
as.data.frame(x)

Arguments

x datasets object

Value

data.frame with datasets metadata

as.data.frame,publication-method

Convert a publication to a data.frame

Description

Convert a publication to a data.frame

Usage

## S4 method for signature 'publication'
as.data.frame(x)

Arguments

x A publication object.

Value

data.frame with publications’ metadata.
as.data.frame,publications-method

Convert publications to a data.frame

Description
Convert publications to a data.frame

Usage

## S4 method for signature 'publications'
as.data.frame(x)

Arguments

x
A publications object.

Value
data.frame with publications’ metadata.

as.data.frame,site-method

as.data.frame site

Description
show as dataframe as prep to save as csv

Usage

## S4 method for signature 'site'
as.data.frame(x)

Arguments

x
site object

Value
data.frame object with site metadata
as.data.frame,sites-method

Description

shows object as data.frame

Usage

## S4 method for signature 'sites'
as.data.frame(x)

Arguments

x sites object

Value

data.frame object with sites metadata

as.data.frame,specimen-method

Description

show as data.frame

Usage

## S4 method for signature 'specimen'
as.data.frame(x)

Arguments

x specimen object

Value

data.frame with specimen metadata
**as.data.frame, specimens-method**

**as.data.frame specimens**

### Description
show as data.frame

### Usage
```r
## S4 method for signature 'specimens'
as.data.frame(x)
```

### Arguments
- **x** specimens object

### Value
data.frame with specimens metadata

---

**as.list, sites-method**

**as.list sites**

### Description
show as dataframe as prep to save as csv

### Usage
```r
## S4 method for signature 'sites'
as.list(x)
```

### Arguments
- **x** sites object

### Value
list object with sites metadata
**author-class**

*An S4 class for the authors of a Neotoma publication.*

**Description**

This class combines the S4 class `contact` with a numeric author order. This allows us to reuse `contact` objects and to assign the authorship order within a publication. The full set of authors for a publication are represented by the `author` object.

**Value**

object of class `author`

**Examples**

```r
{ 
  simon <- new("contact", familyname = "Goring", givennames = "Simon J.")
  firstauthor <- new("author", author = simon, order = 1)
}
```

---

**authors-class**

*An S4 class for a set of Neotoma author objects.*

**Description**

The S4 `authors` are a set of individual `author` objects that are then associated with a single S4 publication class.

**Value**

object of class `authors`

**Examples**

```r
{ 
  simon <- new("contact", familyname = "Goring", givennames = "Simon J.")
  socorro <- new("contact", familyname = "Dominguez", givennames = "Socorro")
  first_author <- new("author", author = simon, order = 1)
  second_author <- new("author", author = socorro, order = 2)
  author_list <- new("authors", authors = list(first_author, second_author))
}
```
**build_chron**

**Description**

A helper function to build a new chronology object from the Neotoma API response.

**Usage**

```r
build_chron(x)
```

**Arguments**

- `x`: A chronology element from the API JSON output.

**Details**

This function is an internal function called from `build_collunit()` to help support the translation between the JSON representation of data in the API and the R implementation.

**Value**

A single chronology object.

**Author(s)**

Socorro Dominguez

---

**build_collunits**

**Build a collection unit from the API response**

**Description**

Build a collection unit from the API response

**Usage**

```r
build_collunits(x)
```

**Arguments**

- `x`: The structured JSON from a Neotoma API v2.0 response that returns a collection unit in any form.

**Value**

An simple `collunit` object
build_dataset | Build a dataset object from a JSON list representation.

Description
Helper function to build a dataset from the API JSON response.

Usage
build_dataset(x)

Arguments
x | a JSON dataset object passed from the Neotoma API.

Value
A simple dataset object.

Author(s)
Socorro Dominguez

build_sample | Build a samples data.frame from Neotoma API JSON

Description
Helper function to build a sample from the API input (list formatted) coming from the Neotoma API.

Usage
build_sample(x)

Arguments
x | sample list

Value
A simple sample object

Author(s)
Socorro Dominguez <sedv8808@gmail.com>
**build_sites**  
*Build a site from the Neotoma API response.*

**Description**

Build a site from the Neotoma API response.

**Usage**

```r
build_sites(x)
```

**Arguments**

- `x` A list returned from the Neotoma API data section.

**Value**

A simple site object

---

**build_specimen**  
*Build a specimen objects.*

**Description**

A helper function to build a specimen object from a list returned by the Neotoma API call. The function is not exported, but called from the get_specimens() call.

**Usage**

```r
build_specimen(x)
```

**Arguments**

- `x` specimen list

**Value**

A simple specimen object
c,chronologies-method  

**c Method - Combine chronologies objects**

**Description**

c Method - Combine chronologies objects

**Usage**

```r
## S4 method for signature 'chronologies'
c(x, y)
```

**Arguments**

- `x`: chronologies object 1
- `y`: chronologies object 2

**Value**

concatenated chronologies

---

c,collunits-method  

**c Method - Combine collunits objects**

**Description**

c Method - Combine collunits objects

**Usage**

```r
## S4 method for signature 'collunits'
c(x, y)
```

**Arguments**

- `x`: collunits object 1
- `y`: collunits object 2

**Value**

concatenated collection units without duplicates
Description

c Method - Combine contacts objects

Usage

```r
## S4 method for signature 'contact'
c(x, y)
```

Arguments

- `x`: contacts object 1
- `y`: contacts object 2

Value

 contacts concatenated object

Description

c Method - Combine contacts objects

Usage

```r
## S4 method for signature 'contacts'
c(x, y)
```

Arguments

- `x`: contacts object 1
- `y`: contacts object 2

Value

 concatenated and clean objects
c,datasets-method

\textit{c Method - Combine datasets objects}

\textbf{Description}

\textit{c Method - Combine datasets objects}

\textbf{Usage}

\texttt{## S4 method for signature 'datasets'
\texttt{c(x, y)}

\textbf{Arguments}

\begin{itemize}
  \item \texttt{x} datasets object 1
  \item \texttt{y} datasets object 2
\end{itemize}

\textbf{Value}

concatenated datasets object

---

c,missingOrNULL-method

\textit{c Method for NULL values}

\textbf{Description}

\textit{c Method for NULL values}

\textbf{Usage}

\texttt{## S4 method for signature 'missingOrNULL'
\texttt{c(x = "missingORNULL", y)}

\texttt{## S4 method for signature 'missingOrNULL'
\texttt{c(x = "missingORNULL", y)}

\textbf{Arguments}

\begin{itemize}
  \item \texttt{x} NULL object
  \item \texttt{y} sites/datasets object
\end{itemize}

\textbf{Value}

concatenated collunits object

list of concatenated items when the first object is NULL
c.publications-method

Combine publication objects.

**Description**
Combine publication objects.

**Usage**

```r
## S4 method for signature 'publications'
c(x, y)
```

**Arguments**

- `x`: A publications object.
- `y`: A publications object

**Value**
concatenated publications object

---

c.sites-method

c Method - Combine sites objects

**Description**

`c` Method - Combine sites objects

**Usage**

```r
## S4 method for signature 'sites'
c(x, y)
```

**Arguments**

- `x`: sites object 1
- `y`: sites object 2

**Value**
concatenated and cleaned sites object
## c Method - Combine specimens objects

### Description

`c Method - Combine specimens objects`

### Usage

```r
## S4 method for signature 'specimens'
c(x, y)
```

### Arguments

- `x`: specimens object 1
- `y`: specimens object 2

### Value

concatenated specimens object

---

## check_args

### Description

Internal function to check passed arguments.

### Usage

```r
check_args(cl)
```

### Arguments

- `cl`: called arguments. Arguments are going to be called by match_call inside:
  - `get_sites`
  - `get_datasets`
  - `get_downloads`

### Value

A list with two components:

- `flag`: Returns a 0 if everything’s fine, a 1 if there’s a problem.
- `message`: A list of error messages.

### Author(s)

Socorro Dominguez
check_contacts

References

Neotoma Project Website: https://www.neotomadb.org/

check_contacts  Check contact information for a record against Neotoma contributors

Description

Uses the Neotoma API to search and access information about individuals who have contributed to the data in the Neotoma Paleoecology Database

Usage

check_contacts(x, ...)

Arguments

x  contacts A contacts object associated with a set of names.
...  Additional parameters associated with the call.

Value

contacts object

check_contacts.contacts  Get contact information for Neotoma contributors

Description

Get contact information for Neotoma contributors

Usage

## S3 method for class 'contacts'
check_contacts(x, similarity = 0.5, ...)

Arguments

x  contacts A contacts object associated with a set of names.
similarity  The similarity score between matched records (from 0 - 1).
...  Additional parameters associated with the call.

Value

contacts object
Description

Show the samples table

Usage

chroncontrols(x)

Arguments

x Sites object to extract chroncontrols table from

Value

data.frame with chroncontrols information

Description

Recover information about the chron controls for a collectionunit.

For a site that includes collection units with chronologies return the chronological controls that are used in building the chronology.

Usage

## S4 method for signature 'site'
chroncontrols(x)

Arguments

x site object

Value

data.frame with chronological controls
Recover information about the chron controls for a collection unit.

Description

For all sites that includes collection units with chronologies return the chronological controls that are used in building the chronology.

Usage

```r
## S4 method for signature 'sites'
chroncontrols(x)
```

Arguments

- `x` sites object

Value

data.frame with chronological controls

Obtain the chronology from a record or multiple records.

Description

Obtain the chronology from a record or multiple records.

Usage

`chronologies(x)`

Arguments

- `x` sites object that contains chronologies

Value

chronologies object with all chronologies used.
chronologies,collunit-method

Extract chronologies from a collunit object.

Description

Extract chronologies from a collunit object.

Usage

```r
## S4 method for signature 'collunit'
chronologies(x)
```

Arguments

x A collunit object

Value

chronologies from a collunit object

chronologies,collunits-method

Extract chronologies from a collunits object.

Description

Extract chronologies from a collunits object.

Usage

```r
## S4 method for signature 'collunits'
chronologies(x)
```

Arguments

x A collunits object

Value

chronologies from a collunits object
chronologies, site-method

Extract chronologies from a site object.

Description

Extract chronologies from a site object.

Usage

## S4 method for signature 'site'
chronologies(x)

Arguments

x A site object

Value

chronologies from a site object

chronologies, sites-method

Extract chronologies from a sites object.

Description

Extract chronologies from a sites object.

Usage

## S4 method for signature 'sites'
chronologies(x)

Arguments

x A sites object

Value

chronologies from a sites object
chronologies-class  
*S4 class for chronologies information*

**Description**

The grouped class for chronologies from the Neotoma Paleoecology Database.

**Value**

object of class chronologies

chronology-class  
*S4 class for chronologies information*

**Description**

The class for chronologies from the Neotoma Paleoecology Database. A single collection unit may have one or more chronology. These individual chronology classes are then grouped into an S4 chronologies class.

**Value**

object of class chronology

cite_data

*Generate a data citation from a Neotoma2 object.*

**Description**

The function, applied to a data object with a valid dataset, will return a properly formatted data citation for the record.

**Usage**

cite_data(x)

**Arguments**

x  
Object with DOIs associated to it.

**Value**

data.frame with citation data
Obtain data citations from a single record.

Description

Given complete dataset objects in Neotoma (must have used `get_datasets()` or `get_downloads()`), return a formatted citation for the record, including the dataset DOI.

Usage

```r
## S4 method for signature 'site'
cite_data(x)
```

Arguments

- `x`: sites object

Value
data.frame object with citation information.

Examples

```r
{
  ds <- get_datasets(1)
cite_data(ds)
}
```

cite_data, sites-method

Obtain data citations from multiple records.

Description

Given complete dataset objects in Neotoma (must have used `get_datasets()` or `get_downloads()`), return a formatted citation for the record, including the dataset DOI.

Usage

```r
## S4 method for signature 'sites'
cite_data(x)
```

Arguments

- `x`: sites object
Value

data.frame object with citation information.

Examples

```r
{ 
  ds <- get_datasets(1)
  cite_data(ds)
}
```

Description

Function that removes duplicate objects such as sites, datasets, or collection units. When we pull in a large number of objects, or overlapping searches, we can run into a problem where we have multiple instances of the same site, but with different datasets. This function attempts to gather all objects together:

- Before: `{site: 1, dataset: 1}, {site: 1, dataset: 2}
- After: `{site: 1, dataset: [1, 2]} So the site is gathered, and the datasets are now part of an array of datasets.

Usage

```r
clean(x = NA, verbose = TRUE, ...)
```

Arguments

- `x` sites, datasets, collunits that may have duplicates.
- `verbose` parameter to prints out progress bar
- `...` Additional parameters associated with the call.

Value

clean Neotoma objects to remove duplicates and empty objects.

Author(s)

Simon Goring <goring@wisc.edu>
**Examples**

```
clean_sites <- get_sites(sitename = "L%", limit = 20)
more_sites <- get_sites(sitename = "La%", limit = 20)
long_set <- c(clean_sites, more_sites)
length(long_set)
# By removing duplicates we get a smaller object.
length(clean(long_set))
# We can do the same thing with collection units:
clean_cols <- get_sites(sitename = "L%", limit = 20) %>%
  collunits()
more_cols <- get_sites(sitename = "La%", limit = 20) %>%
  collunits()
long_set <- c(clean_cols, more_cols)
length(long_set)
# By removing duplicates we get a smaller object.
length(clean(long_set))
# And datasets:
clean_ds <- get_sites(sitename = "L%", limit = 20) %>%
  get_downloads() %>%
  datasets()
more_ds <- get_sites(sitename = "La%", limit = 20) %>%
  get_downloads() %>%
  datasets()
long_set <- c(clean_ds, more_ds)
length(long_set)
# By removing duplicates we get a smaller object.
length(clean(long_set))
```

---

**clean.collunits**

*clean sites objects to remove duplicates.*

**Description**

Function that removes duplicate objects such as sites, datasets, or collection units.

**Usage**

```
## S3 method for class 'collunits'
clean(x, verbose = TRUE, ...)
```

**Arguments**

- `x` sites, datasets, collunits that may have duplicates.
- `verbose` parameter to prints out progress bar
- `...` Additional parameters associated with the call.

**Value**

cleaned collunits
**Author(s)**

Simon Goring <goring@wisc.edu>

**Examples**

```r
clean_cols <- get_sites(sitename = "L\%", limit = 1) %>% collunits()
more_cols <- get_sites(sitename = "La\%", limit = 1) %>% collunits()
long_set <- c(clean_cols, more_cols)
length(long_set)
# By removing duplicates we get a smaller object.
length(clean(long_set))
```

---

**clean.datasets**

*clean sites objects to remove duplicates.*

**Description**

Function that removes duplicate objects such as sites, datasets, or collection units.

**Usage**

```r
## S3 method for class 'datasets'
clean(x, verbose = TRUE, ...)
```

**Arguments**

- `x` sites, datasets, collunits that may have duplicates.
- `verbose` parameter to prints out progress bar
- `...` Additional parameters associated with the call.

**Value**

cleaned datasets after concatenation (no duplicates)

**Author(s)**

Simon Goring <goring@wisc.edu>
clean.sites

Examples

clean_ds <- get_sites(sitename = "L\%", limit = 1) %>%
  get_downloads() %>% datasets()
more_ds <- get_sites(sitename = "La\%", limit = 1) %>%
  get_downloads() %>% datasets()
long_set <- c(clean_ds, more_ds)
length(long_set)
# By removing duplicates we get a smaller object.
length(clean(long_set))

clean.sites

*clean sites objects to remove duplicates.*

Description

Function that removes duplicate objects such as sites, datasets, or collection units.

Usage

## S3 method for class 'sites'
clean(x, verbose = TRUE, ...)

Arguments

x       sites, datasets, collunits that may have duplicates.
verbose parameter to prints out progress bar
...     Additional parameters associated with the call.

Value

sites object

Author(s)

Simon Goring <goring@wisc.edu>

Examples

{
clean_sites <- get_sites(sitename = "L\%", limit = 1)
more_sites <- get_sites(sitename = "La\%", limit = 1)
long_set <- c(clean_sites, more_sites)
length(long_set)
# By removing duplicates we get a smaller object.
length(clean(long_set))
}
cleanNULL  

**Clean NULL values**

**Description**

Pass an object and convert all NULL elements to NA.

**Usage**

```r
cleanNULL(x)
```

**Arguments**

- `x` An element that may or may not have NULL values.

**Value**

parsed list where NULL values are changed to NA

---

**collunit-class**  

**S4 class for collection units information.**

**Description**

A collection unit represents a collection event from within a site. For example, a lake sediment core, or a single dig site within an archaeological site.

**Value**

object of class collunit

---

**collunits**  

*Extract collection units from a sites object*

**Description**

Extract collection units from a sites object

**Usage**

```r
collunits(object)
```

**Arguments**

- `object` A sites object
Value
collunits detail from a sites object

collunits,site-method  
*Extract collunits from a site object.*

Description
Extract collunits from a site object.

Usage
```r
## S4 method for signature 'site'
collunits(object)
```

Arguments
- object: A site object

Value
collunits from a site object

collunits,sites-method
*Extract collunits from a sites object.*

Description
Extract collunits from a sites object.

Usage
```r
## S4 method for signature 'sites'
collunits(object)
```

Arguments
- object: A sites object

Value
collunits from a sites object
collunits-class *An S4 class for Neotoma Collection Units*

**Description**

Holds Collection unit information from the Neotoma Paleoecology Database. Returns object of class collunits

contact-class *An S4 class for Neotoma contacts*

**Description**

The object that contains the contact information for an individual, along with associated metadata.

**Value**

Object of class contact

**Examples**

```
new("contact", familyname = "Goring", givennames = "Simon J.")
```

contacts-class *An S4 class for multi-contact information from the Neotoma Paleoecology Database.*

**Description**

An unordered list of individual S4 contact objects.

**Value**

Object of class contacts

**Examples**

```
{
  # Create two contact objects and associate them within a contacts object.
  simon <- new("contact", familyname = "Goring", givennames = "Simon J.")
  socorro <- new("contact", familyname = "Dominguez", givennames = "Socorro")
  packagers <- new("contacts", contacts = list(simon, socorro))
  packagers
}
```
coordinates

Description
Obtain coordinates from a sites object.

Usage
coordinates(obj, ...)

Arguments
obj A sites object
... Additional parameters associated with the call.

Value
dataframe with coordinate values

coordinates, sites-method

Return the latitude and longitude of sites

Description
Return the latitude and longitude of sites

Usage
## S4 method for signature 'sites'
coordinates(obj, ...)

Arguments
obj A sites object
... Additional parameters associated with the call.

Value
data.frame object with site coordinates.
dataset-class  

*S4 class for dataset information*

**Description**

The standard object class for datasets from the Neotoma Paleoecology Database.

**Value**

object of class dataset

datasets  

*Extract datasets from a sites object.*

**Description**

If the sites object contains datasets, then the datasets will be returned. If the sites object does not contain datasets then the user can apply `get_datasets()` to the object.

**Usage**

datasets(object)

**Arguments**

object  

A sites object

**Value**

datasets object specific to the metadata contained in datasets

datasets, collunit-method  

*Extract datasets from a collunit object.*

**Description**

Extract datasets from a collunit object.

**Usage**

```r
## S4 method for signature 'collunit'
datasets(object)
```
**datasets,collunits-method**

*Extract datasets from a collunits object.*

**Arguments**

- **object**
  - A collunit object

**Value**

- datasets from a collunit object

**Description**

Extract datasets from a collunits object.

**Usage**

```r
## S4 method for signature 'collunits'
datasets(object)
```

**Arguments**

- **object**
  - A collunits object

**Value**

- datasets from a collunits object

*datasets,site-method  Extract datasets from a site object.*

**Description**

Extract datasets from a site object.

**Usage**

```r
## S4 method for signature 'site'
datasets(object)
```

**Arguments**

- **object**
  - A site object

**Value**

- datasets from a site object
datasets/sites-method  

* Extract datasets from a sites object.*

**Description**

Extract datasets from a sites object.

**Usage**

```r
## S4 method for signature 'sites'
datasets(object)
```

**Arguments**

- `object`  A sites object

**Value**

datasets from a sites object

---

**datasets-class**  

*S4 class for datasets information*

**Description**

The grouped class for datasets from the Neotoma Paleoecology Database.

**Value**

- object of class datasets

---

**doi**  

*Obtain the DOI for publications or datasets.*

**Description**

Obtain the DOI for publications or datasets.

**Usage**

```r
doi(x)
```

**Arguments**

- `x`  Object with DOIs associated to it.
Value

doi object with DOI information

---

### doi.publication-method

*Get a publication DOI.*

Description

Get a publication DOI.

Usage

```r
## S4 method for signature 'publication'
doi(x)
```

Arguments

- `x`: A publication object.

Value

DOI from a publication

---

### doi.site-method

*Obtain dataset DOIs from records.*

Description

Given complete dataset objects in Neotoma (must have used `get_datasets()` or `get_downloads()`), return the dataset DOI for the record.

Usage

```r
## S4 method for signature 'site'
doi(x)
```

Arguments

- `x`: a Neotoma2 site object

Value

data.frame object with DOIs information.
Examples

```r
{  
  ds <- get_datasets(1)
  doi(ds)
}
```

---

**doi, sites-method**

*Obtain dataset DOIs from records.*

**Description**

Given complete dataset objects in Neotoma (must have used `get_datasets()` or `get_downloads()`), return the dataset DOI for the record.

**Usage**

```r
## S4 method for signature 'sites'
doi(x)
```

**Arguments**

- `x`: a Neotoma2 site object

**Value**

data.frame object with DOIs information.

**Examples**

```r
{  
  ds <- get_datasets(1)
  doi(ds)
}
```

---

**filter**

*Apply a filter for Neotoma sites objects.*

**Description**

The `filter` function takes a sites object and allows a user to filter on a number of properties. Since a sites object is a nested object (it contains collection units, datasets, samples, etc.) the degree to which filtering occurs depends on the amount of data contained within the sites object. Filtering parameters include:

- "siteid" A numeric site identifier from the Neotoma Database
- "sitename" The character string sitename.
• "lat" A numeric latitude value.
• "long" A numeric longitude value.
• "altitude" The elevation of the site. Note that some sites do not include elevation information. For these an NA value appears, and they would be removed when using an elevation filter.
• "datasetid" A numeric datasetid from Neotoma.
• "database" A character string naming the constituent database from which the dataset is drawn.
• "datasettype" A character string representing one of the many dataset types within Neotoma.
• "age_range_old" A dataset-level parameter indicating the oldest date covered by the dataset chronology.
• "age_range_young" A dataset-level parameter indicating the youngest date covered by the dataset chronology.
• "notes" Free-form dataset notes provided by the dataset PI(s), analysts or data stewards.
• "collectionunitid" A numeric collection unit identifier from Neotoma.
• "handle" A character string identifying the collection unit. These are often shorter form names (originally a default 8 character length).
• "collectionunitname" A character string identifying the collection unit name.
• "colldate" The date on which the collection unit was sampled. Many of these are empty.
• "location" A free-form character string indicating the location of the collection unit within the site.
• "waterdepth" A numeric depth at which the core was obtained.
• "collunittype" A character string for the collection unit type.
• "collectiondevice" A fixed vocabulary term for the collection device.
• "depositionalenvironment" A fixed vocabulary name for the depositional environment.

Usage

filter(x, ...)

Arguments

x

A site, dataset or download.

... arguments to filter by.

Value

filtered sites object
filter.sites  

Apply a filter for Neotoma sites objects.

Description

The `filter` function takes a `sites` object and allows a user to filter on a number of properties. Since a `sites` object is a nested object (it contains collection units, datasets, samples, etc.) the degree to which filtering occurs depends on the amount of data contained within the `sites` object. Filtering parameters include:

- "siteid"A numeric site identifier from the Neotoma Database
- "sitename"The character string sitename.
- "lat"A numeric latitude value.
- "long"A numeric longitude value.
- "altitude"The elevation of the site. Note that some sites do not include elevation information. For these an NA value appears, and they would be removed when using an elevation filter.
- "datasetid"A numeric datasetid from Neotoma.
- "database"A character string naming the constituent database from which the dataset is drawn.
- "datasettype"A character string representing one of the many dataset types within Neotoma.
- "age_range_old"A dataset-level parameter indicating the oldest date covered by the dataset chronology.
- "age_range_young"A dataset-level parameter indicating the youngest date covered by the dataset chronology.
- "notes"Free-form dataset notes provided by the dataset PI(s), analysts or data stewards.
- "collectionunitid"A numeric collection unit identifier from Neotoma.
- "handle"A character string identifying the collection unit. These are often shorter form names (originally a default 8 character length).
- "collectionunitname"A character string identifying the collection unit name.
- "colldate"The date on which the collection unit was sampled. Many of these are empty.
- "location"A free-form character string indicating the location of the collection unit within the site.
- "waterdepth"A numeric depth at which the core was obtained.
- "collunittype"A character string for the collection unit type.
- "collectiondevice"A fixed vocabulary term for the collection device.
- "depositionalenvironment"A fixed vocabulary name for the depositional environment.

Usage

```r
## S3 method for class 'sites'
filter(x, ...)
```
fix_null

Arguments

  x A sites object.
  ... arguments to filter by.

Value

filtered sites object

Examples

# Download 100 sites, but only keep the sites that are close to sea level.
some_sites <- get_sites(sitename = "Lake%", limit = 3)
site_subset <- some_sites %>% filter(altitude < 100)
# Download 100 sites, get all associated datasets, but keep only
# sites/datasets that are of datasettype "pollen":
sites <- get_sites(limit = 1) %>%
  get_datasets(all_data = TRUE)
pollen_subset <- sites %>% filter(datasettype == "pollen")

---

fix_null  Fix null values from API responses

Description

API responses from the Neotoma API return many fields as NULL values. This function turns the
NULL values into logical NAs.

Usage

fix_null(x)

Arguments

  x item that has null objects.

Value

list with NAs instead of null objects
getids **Get object IDs**

Description

This function parses a site object, from site to dataset level and returns a data.frame that contains the site, collectionunit and dataset IDs for each element within the site.

Usage

getids(x, order = TRUE)

Arguments

- x: A Neotoma2 sites object.
- order: sort items by siteid, collunitid, datasetid

Value

data.frame containing siteid, datasetid, and collunitid

getids.collunit **Get object IDs from a single collectionunit.**

Description

From a collectionunit object, return the collectionunit and dataset ids.

Usage

```r
## S3 method for class 'collunit'
getids(x, order = TRUE)
```

Arguments

- x: A Neotoma2 collunit object.
- order: sort items by siteid, collunitid, datasetid

Value

data.frame containing siteid, datasetid, and collunitid

Examples

```r
marion <- get_sites(sitename = "Marion Lake")
collunitids <- getids(collunits(marion)[[1]])
```
getids.collunits  Get object IDs from collectionunits.

Description
From a set of collectionunit objects, return the collectionunit and dataset ids.

Usage
```r
## S3 method for class 'collunits'
getids(x, order = TRUE)
```

Arguments
- `x`: A Neotoma2 collunits object.
- `order`: sort items by siteid, collunitid, datasetid

Value
data.frame containing siteid, datasetid, and collunitid

Examples
```r
{  
  marion <- get_sites(sitename = "Marion Lake")  
  collunitids <- getids(collunits(marion))  
  }
```

getids.site  Get object IDs from a site object.

Description
Get object IDs from a site object.

Usage
```r
## S3 method for class 'site'
getids(x, order = TRUE)
```

Arguments
- `x`: A Neotoma2 site object.
- `order`: sort items by siteid, collunitid, datasetid

Value
data.frame containing siteid, datasetid, and collunitid
getids.sites  
*Get object IDs from sites*

**Description**

Get object IDs from sites

**Usage**

```r
## S3 method for class 'sites'
getids(x, order = TRUE)
```

**Arguments**

- `x` A Neotoma2 sites object.
- `order` sort items by siteid, collunitid, datasetid

**Value**

data.frame containing siteid, datasetid, and collunitid

---

get_contacts  
*Get contact information for Neotoma contributors*

**Description**

Uses the Neotoma API to search and access information about individuals who have contributed to the data in the Neotoma Paleoecology Database

**Usage**

```r
get_contacts(x = NA, ...)
```

**Arguments**

- `x` integer A contact ID
- `...` (contactname) A full or partial name for an individual contributor to the database. (familyname) The full or partial last name for an individual contributor to the database. (status) The current status of the contributor (active or retired)

**Value**

contacts object
get_contacts.default  Get contact information for Neotoma contributors

Description
Uses the Neotoma API to search and access information about individuals who have contributed to the data in the Neotoma Paleoecology Database

Usage
## Default S3 method:
get_contacts(x, ...)

Arguments

- `x` integer A contact ID
- `...` (contactname) A full or partial name for an individual contributor to the database.
  (familyname) The full or partial last name for an individual contributor to the database. (status) The current status of the contributor (active or retired)

Value
contacts object

get_contacts.numeric  Get contact information for Neotoma contributors

Description
Uses the Neotoma API to search and access information about individuals who have contributed to the data in the Neotoma Paleoecology Database

Usage
## S3 method for class 'numeric'
get_contacts(x, ...)

Arguments

- `x` integer A contact ID
- `...` (contactname) A full or partial name for an individual contributor to the database.
  (familyname) The full or partial last name for an individual contributor to the database. (status) The current status of the contributor (active or retired)

Value
contacts object
Description

The `get_datasets()` function is a wrapper for the Neotoma datasets API endpoint. The function takes parameters defined by the user and returns dataset information supplied by the Neotoma Paleoecological Database. The user may define all or none of the possible fields.

Usage

`get_datasets(x = NA, ...)`

Arguments

- `x` A single datasetid, or a vector of unique dataset ids.
- `...` accepted arguments, see details for more information.

Details

A dataset is an element nested within `neotoma2` site objects. The `get_datasets()` call returns a list of individual site objects with `collunits` (collection units) that contain valid, matching dataset elements. So, `get_sites()` returns only site metadata. `get_datasets()` returns site metadata, plus metadata about the individual datasets present at that site. The `get_datasets()` function searches for each site within Neotoma that matches the query parameters, and returns them as a `sites` object, a list of `site` objects, plus returns all the additional metadata for the datasets at that site. The `get_datasets()` command wraps the Neotoma API (api.neotomadb.org) call for datasets. The call itself uses a SQL query which accepts any one of the following parameters:

- `siteid` The unique site ID (integer) in Neotoma. Can be passed as a vector of site IDs.
- `sitename` The site name, or approximate match using the `%` wildcard.
- `database` The constituent database for the record. See `get_table("constituentdatabases")`
- `datasettype` Neotoma contains data for a number of dataset types. This returns a subset of data types. For a complete list of available dataset types, run `neotoma2::get_table('datasettypes')`
- `altmin` The minimum altitude range for site elevation (in meters).
- `altmax` The maximum altitude range for site elevation (in meters).
- `datasetid` The unique dataset ID (integer) in Neotoma. Can be passed as a vector of dataset IDs.
- `doi` The dataset DOI for a dataset contained within a site. Can be passed as a vector of DOIs.
- `gpid` The geopolitical name or identifier containing a site. Can be passed as a vector of names.
- `keywords` Keywords for samples within a set of sites. For example "modern" indicates a sample within the record uses the keyword "modern".
- `contacts` Contact names or IDs associated with a site.
- `ageyoung` A minimum spanning age for the record, in years before radiocarbon present (1950).
• ageold A maximum spanning age for the record, in years before radiocarbon present (1950).
• ageof An age which must be contained within the range of sample ages for a site.
• taxa The names of taxa which must be present within samples in a record.
• all_data The API only downloads the first 25 records of the query. For the complete records, use all_data=TRUE

Value

The function returns either a single item of class "try-error" describing the reason for failure (either misdefined parameters or an error from the Neotoma API), or list of site objects, each containing one or more collunit objects, with fully populated datasets elements.

Author(s)

Socorro Dominguez <sedv8808@gmail.com>

Examples

```r
# To find all datasets with a min altitude of 12 and a max altitude of 25:
sites_12to25 <- get_datasets(altmin=12, altmax=25)
# To find all datasets in Brazil
brazil <- '{"type": "Polygon",
"coordinates": [[
[-73.125, -9.102096738726443],
[-56.953125,-33.137551192346145],
[-36.5625,-7.710991655433217],
[-68.203125,13.923403897723347],
[-73.125,-9.102096738726443]]])

brazil_datasets <- get_datasets(loc = brazil[[1]], limit=2)
# To obtain the dataset metadata:
datasets(brazil_datasets)
# There is insufficient metadata at this point to obtain information
# about taxa present at the site. We must use get_downloads() to
# obtain the full set of sample information:
# This fails: taxa(brazil_datasets)
```
Arguments

x Use a single number to extract site information

... accepted arguments, see details for more information.

Value

sites object with full metadata up to the dataset level

Examples

```r
allds <- get_datasets(1:3)
```
**get_datasets.sites**  

Get Dataset from a sites object.

**Description**  
Get Dataset from a sites object.

**Usage**  
```r  
## S3 method for class 'sites'  
get_datasets(x, ...)  
```

**Arguments**  
- `x`  
  An object of class sites.
- `...`  
  additional arguments accepted by get_datasets()

**Value**  
sites object with full metadata up to the dataset level

**Examples**  
```r  
random_sites <- get_sites(1)  
allds <- get_datasets(random_sites, limit=3)  
```

---

**get_downloads**  

**Description**  
Information for Fossil Datasets

**Usage**  
```r  
get_downloads(x = NA, verbose = TRUE, ...)  
```

**Arguments**  
- `x`  
  Use a single number to extract site information
- `verbose`  
  Status bar of items being downloaded
- `...`  
  accepted arguments: sites, datasets
Details

The `get_downloads()` command wraps the Neotoma API (api.neotomadb.org) call for downloads. The call itself uses a SQL query which accepts any one of the following parameters:

- `datasetid` The unique dataset ID (integer) in Neotoma. Can be passed as a vector of dataset IDs.
- `all_data` The API only downloads the first 25 records of the query. For the complete records, use `all_data=TRUE`.

Value

The function returns either a single item of class "try-error" describing the reason for failure (either misdefined parameters or an error from the Neotoma API), or a table of sites, with rows corresponding to the number of individual sites and datasets returned by the Neotoma API. Each "site" object contains 6 parameters that can be accessed as well:

- `siteid` site ID number
- `sitename` site's name
- `location` sf object that describes site's location
- `description` 
- `collunits` limited information on collunits

Each 'collection unit' embedded in the "sites" object contains 6 parameters that can be accessed as well:

- `collunitid` collection unit ID number
- `handle` collection unit's handle
- `collunitname` collection unit's name
- `colldate` date in collection unit
- `substrate` 
- `location` sf object that describes site's location
- `datasets` detailed information regarding dataset

Each 'dataset' nested in the "collection unit" contains the following detail of information:

- `datasetid` dataset ID number
- `datasetname` site's name
- `datasettype` type of data found
- `location` sf object that describes site's location
- `notes` notes on the dataset
- `taxa table` taxa table
- `pi list` P.I. info
- `analyst` analyst info
- `metadata` dataset metadata
get_downloads.character

Author(s)
Socorro Dominguez <sedv8808@gmail.com>

Examples

# To find the downloads object of dataset 24:
downloads24 <- get_downloads(24)

# To find all downloads in Brazil
brazil <- '{"type": "Polygon",
"coordinates": [[
[-73.125, -9.102096738726443],
[-56.953125,-33.137551192346145],
[-36.5625,-7.710991655433217],
[-68.203125,13.923403897723347],
[-73.125,-9.102096738726443]]
}'}
brazil_datasets <- get_datasets(loc = brazil[1])
brazil_downloads <- get_downloads(brazil_datasets)

get_downloads.character

get_downloads JSON

Description
get_downloads JSON

Usage

## S3 method for class 'character'
get_downloads(x, verbose = TRUE, ...)

Arguments

x sites object
verbose Should text be printed during the download process?
... arguments in ellipse form

Value

The function returns either a single item of class "try-error" describing the reason for failure (either misdefined parameters or an error from the Neotoma API), or a table of sites, with rows corresponding to the number of individual sites and datasets returned by the Neotoma API.
### get_downloads numeric

#### Description

get_downloads numeric

#### Usage

```r
## S3 method for class 'numeric'
get_downloads(x, verbose = TRUE, ...)
```

#### Arguments

- `x`: Use a single number to extract site information
- `verbose`: Should text be printed during the download process?
- `...`: arguments in ellipse form

#### Value

The function returns either a single item of class "try-error" describing the reason for failure (either misdefined parameters or an error from the Neotoma API), or a table of sites, with rows corresponding to the number of individual sites and datasets returned by the Neotoma API.

---

### get_downloads sites

#### Description

get_downloads sites

#### Usage

```r
## S3 method for class 'sites'
get_downloads(x, verbose = TRUE, ...)
```

#### Arguments

- `x`: sites object
- `verbose`: Should text be printed during the download process?
- `...`: arguments in ellipse form

#### Value

The function returns either a single item of class "try-error" describing the reason for failure (either misdefined parameters or an error from the Neotoma API), or a table of sites, with rows corresponding to the number of individual sites and datasets returned by the Neotoma API.
**Description**

Open up the Neotoma manual homepage.

**Usage**

```r
get_manual()
```

**Value**

NULL side effect for opening browser with the manual

**Author(s)**

Simon Goring <goring@wisc.edu>

**Examples**

```r
{
  # This call does not work from `source()` calls or in testing.
  # interactive() just lets us know you are interacting with the console:
  if (interactive()) {
    get_manual()
  }
}
```

---

**get_publications**

*Get publication information for Neotoma records*

**Description**

Uses the Neotoma API to search and access information about publications associated with data in the Neotoma Paleoecology Database

**Usage**

```r
get_publications(x = NA, ...)
```
**Arguments**

- `x` integer A contact ID
- `...`
  - `publicationid` The unique numeric identifier associated with a publication in Neotoma.
  - `datasetid` A unique identifier for a Neotoma dataset that is associated with a publication.
  - `familyname` The full or partial last name for an individual author.
  - `pubtype` The publication type, from `get_tables("publicationtypes")`.
  - `year` The year the publication was released.
  - `search` A plain text search string used to search the citation.

**Value**

- `publications` object

**Examples**

```r
# How old are the papers in Neotoma that include the term "mammut"?
mammoth_papers <- get_publications(search="mammut") %>%
  as.data.frame()
hist(as.numeric(mammoth_papers$year))
```

---

**get_publications.default**

*Get publication information from Neotoma*

**Description**

Get publication information from Neotoma

**Usage**

```r
## Default S3 method:
get_publications(...)
```

**Arguments**

- `...`
  - `publicationid` The unique numeric identifier associated with a publication in Neotoma.
  - `datasetid` A unique identifier for a Neotoma dataset that is associated with a publication.
  - `familyname` The full or partial last name for an individual author.
  - `pubtype` The publication type, from `get_tables("publicationtypes")`.
  - `year` The year the publication was released.
  - `search` A plain text search string used to search the citation.

**Value**

- `publications` object
Examples

```r
# How old are the papers in Neotoma that include the term "mammut"?
mammoth_papers <- get_publications(search="mammut") %>%
  as.data.frame()
hist(as.numeric(mammoth_papers$year))
```

**get_publications.numeric**

*Get publications using their unique identifier.*

**Description**

Get publications using their unique identifier.

**Usage**

```r
## S3 method for class 'numeric'
get_publications(x, ...)
```

**Arguments**

- `x` integer A contact ID
- `...` publicationid The unique numeric identifier associated with a publication in Neotoma. datasetid A unique identifier for a Neotoma dataset that is associated with a publication. familyname The full or partial last name for an individual author. pubtype The publication type, from `get_tables("publicationtypes")`. year The year the publication was released. search A plain text search string used to search the citation.

**Value**

publications object

**Examples**

```r
{
# We want the paper identified in Neotoma as 666:
get_publications(666)
}
```
get_publications.publication

Update information for a publications object.

Description

This works for records without publicationids. We assume that data with publicationids is correct.

Usage

```r
## S3 method for class 'publication'
get_publications(x, ...)
```

Arguments

- `x` integer A publication
- `...` publicationid The unique numeric identifier associated with a publication in Neotoma. datasetid A unique identifier for a Neotoma dataset that is associated with a publication. familyname The full or partial last name for an individual author. pubtype The publication type, from `get_tables("publicationtypes")`. year The year the publication was released. search A plain text search string used to search the citation.

Value

updated publication object

Examples

```r
# Take a publication object and purposely degrade the metadata:
bad_pub <- get_publications(666)
# Note this only changes the reported year, not the citation string.
bad_pub[[1]]@year <- "1923"
bad_pub[[1]]@publicationid <- as.character(NA)
updated_pubs <- get_publications(bad_pub[[1]])
attr(updated_pubs, "matches")
# we see the proper citation in the record:
updated_pubs <- attr(updated_pubs, "matches")[[3]]
```
get_publications.publications

Update metadata for a set of publication objects.

Description

Update metadata for a set of publication objects.

Usage

```r
## S3 method for class 'publications'
get_publications(x, ...)
```

Arguments

- `x`: integer A publication
- `...`: publicationid The unique numeric identifier associated with a publication in Neotoma. datasetid A unique identifier for a Neotoma dataset that is associated with a publication. familyname The full or partial last name for an individual author. pubtype The publication type, from `get_tables("publicationtypes")`. year The year the publication was released. search A plain text search string used to search the citation.

Value

publications object

Examples

```r
# Take a publication object and purposely degrade the metadata:
bad_pub <- get_publications(c(666, 667, 668))
# Note this only changes the reported year, not the citation string.
bad_pub[[1]]@year <- "1923"
bad_pub[[1]]@publicationid <- as.character(NA)
updated_pubs <- get_publications(bad_pub)
# Only the first publication object has any matches. It's the only one
# that is missing its publicationid.
attr(updated_pubs[[1]], "matches")
attr(updated_pubs[[2]], "matches")
# we see the proper citation in the record:
updated_pubs[[1]] <- attr(updated_pubs[[1]], "matches")[[1]]
```
Description

The `get_sites()` function is a wrapper for the Neotoma sites API endpoint. The function takes parameters defined by the user and returns a list of site information supplied by the Neotoma Pale-oecological Database. The user may define all or none of the possible fields.

Usage

```r
get_sites(x = NA, ...)
```

Arguments

- `x` Use a single integer or vector of integers representing unique Neotoma site identifiers (siteids) to extract site information.
- `...` accepted arguments, see details for more information.

Details

A site object in Neotoma is a physical location at which one or more collection units are located. Each collection unit may have one or more datasets within it, defined by the dataset type. The `get_sites()` function searches for each site within Neotoma that matches the query parameters, and returns them as a `sites` object, a list of site objects. The `get_sites()` command wraps the Neotoma API (api.neotomadb.org) call for sites. The call itself uses a SQL query which accepts any one of the following parameters:

- `siteid` The unique site ID (integer) in Neotoma. Can be passed as a vector of site IDs.
- `sitename` The site name, or approximate match using the `%` wildcard.
- `database` The constituent database for the record. See `get_table("constituentdatabases")`
- `altmin` The minimum altitude range for site elevation (in meters).
- `altmax` The maximum altitude range for site elevation (in meters).
- `datasetid` The unique dataset ID (integer) in Neotoma. Can be passed as a vector of dataset IDs.
- `datasettype` Neotoma contains data for a number of dataset types. This returns a subset of data types. For a complete list of available dataset types, run `neotoma2::get_table('datasettypes')`
- `doi` The dataset DOI for a dataset contained within a site. Can be passed as a vector of DOIs.
- `gpid` The geopolitical name or identifier containing a site. Can be passed as a vector of names.
- `keywords` Keywords for samples within a set of sites. For example "modern" indicates a sample within the record uses the keyword "modern".
- `contacts` Contact names or IDs associated with a site.
- `ageyoung` A minimum spanning age for the record, in years before radiocarbon present (1950).
get_sites

• ageold A maximum spanning age for the record, in years before radiocarbon present (1950).
• ageof An age which must be contained within the range of sample ages for a site.
• taxa The names of taxa which must be present within samples in a record.
• all_data The API only downloads the first 25 records of the query. For the complete records, use all_data=TRUE This call will then return a data object that contains site metadata for one or more sites, along with limited metadata describing the collection units and datasets located at that site.

Value

The function returns either a single item of class "try-error" describing the reason for failure (either misdefined parameters or an error from the Neotoma API), or a table of sites, with rows corresponding to the number of individual sites returned by the Neotoma API. Each "site" object contains 6 parameters that can be accessed as well: siteid, sitename, location, altitude, description, limited collection units information.

• loc An sf object that describes site's location.
• description
• collunits limited information on collunits

Author(s)

Socorro Dominguez <sedv8808@gmail.com>

Examples

```r
## Find all sites with a min altitude of 12m and a max altitude of 25m
## By default returns only 25 sites (default limit is 25):
sites_12to25 <- get_sites(altmin=12, altmax=25)
## Return all sites, using a minimum altitude of 2500m (returns >500 sites):
sites_2500 <- get_sites(altmin=2500, all_data = TRUE)
## To find all sites that contain the string "Alex%"
alex_sites <- get_sites(sitename="Alex%")

## To find sites in Brazil (again with default 25 records)
brazil <- '\"type\": "Polygon",
coordinates': [[[
[-73.125, -9.102096738726443],
[-56.953125,-33.13755192346145],
[-36.5625,-7.710991655433217],
[-68.203125,13.923403897723347],
[-73.125, -9.102096738726443]]]
'brazil_sites <- get_sites(loc = brazil[1])

# Finding all sites with Liliaceae pollen in 1000 year bins:
liysites <- c()
for (i in seq(0, 10000, by = 1000)) {
  lily <- get_sites(taxa=c("Liliaceae"),
                 ageyoung = i - 500,}
get_sites.default

ageold = i + 500,
all_data = TRUE)
lilysites <- c(lilysites, length(lily))
}
plot(x = seq(0, 10000, by = 1000), y = lilysites, type = 'b')

get_sites.default  get_sites

Description

get_sites

Usage

## Default S3 method:
get_sites(...)

Arguments

...

One of a set of possible query parameters discussed in details.

Value

The function returns either a single item of class "try-error" describing the reason for failure (either misdefined parameters or an error from the Neotoma API), or a table of sites, with rows corresponding to the number of individual sites returned by the Neotoma API. Each "site" object contains 6 parameters that can be accessed as well: siteid, sitename, location, altitude, description, limited collection units information.

- loc An sf object that describes site's location.
- description
- collunits limited information on collunits

Author(s)

Socorro Dominguez <sedv8808@gmail.com>
get_sites.numeric  Get Site Information for Fossil Sites

Description
Get Site Information for Fossil Sites

Usage

## S3 method for class 'numeric'
get_sites(x, ...)

Arguments

x  The numeric site ID from Neotoma
...
accepted arguments if numeric all_data

Value
The function returns either a single item of class "try-error" describing the reason for failure (either misdefined parameters or an error from the Neotoma API), or a table of sites, with rows corresponding to the number of individual sites returned by the Neotoma API. Each "site" object contains 6 parameters that can be accessed as well: siteid, sitename, location, altitude, description, limited collection units information.

- loc  An sf object that describes site's location.
- description
- collunits limited information on collunits

Examples

{
  ## Find all sites by numeric siteid:
  sites <- get_sites(seq(1,3))
}

get_sites.sites  Get Site Information for Fossil Sites from a Set of Sites

Description
Get Site Information for Fossil Sites from a Set of Sites

Usage

## S3 method for class 'sites'
get_sites(x, ...)

Arguments

x The numeric site ID from Neotoma
...

accepted arguments if numeric all_data

Value

The function returns either a single item of class "try-error" describing the reason for failure (either misdefined parameters or an error from the Neotoma API), or a table of sites, with rows corresponding to the number of individual sites returned by the Neotoma API. Each "site" object contains 6 parameters that can be accessed as well: siteid, sitename, location, altitude, description, limited collection units information.

• loc An sf object that describes site's location.
• description
• collunits limited information on collunits

Examples

## Find all sites using a set of prior sites:
char_sites <- get_sites(taxa = "charcoal")
pollen_coloc <- get_sites(char_sites, datasettype = "pollen")
char_coloc <- char_sites %>% filter(siteid %in% getids(pollen_coloc)$siteid)
pol_char <- c(pollen_coloc, char_coloc) %>% clean()

get_specimens

Description

Information for Specimens

Usage

get_specimens(x = NA, ...)

Arguments

x Use a single specimenid
...

Additional terms passed to get_specimens, most common datasetid

Value

The function returns a specimens list
get_specimens.default

Author(s)

Socorro Dominguez <sedv8808@gmail.com>

Examples

# To find specimen with ID 7:
my_specimens <- get_specimens(7)
# To find specimens in datasetid 41610
my_specimens2 <- get_specimens(datasetid = 41610)

get_specimens.default  Get Specimen datasetid

Description

Get Specimen datasetid

Usage

## Default S3 method:
get_specimens(...)  

Arguments

...  

Pass argument datasetid and the corresponding datasetid

Value

The function returns a specimens list

Examples

{
# To find specimens in datasetid 41610
my_specimens <- get_specimens(datasetid = 41610)
}

get_specimens.numeric  Get Specimen Numeric

Description

Get Specimen Numeric

Usage

## S3 method for class 'numeric'
get_specimens(x, ...)

Arguments

x  Use a single number to extract site information
...
    Additional terms passed to get_specimens.

Value

The function returns a specimens list

Examples

{
  ## To find specimen with ID 7
  my_specimens <- get_specimens(7)
}

get_specimens.sites  Get Specimen Sites

Description

Get Specimen Sites

Usage

## S3 method for class 'sites'
get_specimens(x, ...)

Arguments

x  Use a single number to extract site information
...
    Other possible parameters such as datasetid
get_table

Value

The function returns a specimens list

Examples

# To find specimen with ID 7:
my_site <- get_sites(13296)
# To find specimens in `my_site`
my_specimens <- get_specimens(my_site)

get_table

Get table record from Neotoma

Description

Call Neotoma and return a table (with limits & offsets for large tables)

Usage

get_table(x, limit = 25, offset = 0)

Arguments

x Table name (consult https://open.neotomadb.org/dbschema/ for a complete list of table names.

limit Default 25 records

offset Default 0.

Value

selected table values from the Database

Examples

{
  # Returns only the first 25 specimen records.
  someSpec <- get_table('specimens')
}
Description

Length Method chronologies

Usage

## S4 method for signature 'chronologies'
length(x)

Arguments

x chronologies object

Value

integer describing length

Description

Length Method collunits

Usage

## S4 method for signature 'collunits'
length(x)

Arguments

x collunits object

Value

length of a collunits object
## length.datasets-method

**Length Method datasets**

### Description

Length Method datasets

### Usage

```r
## S4 method for signature 'datasets'
length(x)
```

### Arguments

- `x`: datasets object

### Value

`int` that showcases the length of a datasets object

## length.publications-method

**Get the number of publications in a publications object.**

### Description

Get the number of publications in a publications object.

### Usage

```r
## S4 method for signature 'publications'
length(x)
```

### Arguments

- `x`: A publications object.

### Value

`int` of the length of the publications object
### length.samples-method

**Length Method samples**

**Description**
Length Method samples

**Usage**
```r
## S4 method for signature 'samples'
length(x)
```

**Arguments**
- `x` samples object

**Value**
- int representing the length of samples object

### length.sites-method

**Length Method Sites**

**Description**
Length Method Sites

**Usage**
```r
## S4 method for signature 'sites'
length(x)
```

**Arguments**
- `x` sites object

**Value**
- int with the length of sites object
length.specimens-method

Description
Length Method specimens

Usage
## S4 method for signature 'specimens'
length(x)

Arguments
x specimens object

Value
int with length of specimens object

missingOrNULL-class

Description

 c Method - Combine objects, including NULL  

names,collunit-method

Description

Get all names for named elements within a collunit object.

Usage
## S4 method for signature 'collunit'
names(x)

Arguments
x A collection unit object.
**Value**

NULL. Shows the names of the slots

---

**names, contact-method**  
*Get names of contacts slots*

**Description**

Get names of contacts slots

**Usage**

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

**Arguments**

- `x`  
  A contact object.

**Value**

Names of slots

---

**names, dataset-method**  
*Get slot names*

**Description**

Get all names for named elements within a dataset object.

**Usage**

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

**Arguments**

- `x`  
  A dataset object.

**Value**

List with all names of dataset slots
names,publication-method

*Get slot names for a publication object.*

**Description**

Get slot names for a publication object.

**Usage**

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

**Arguments**

- `x`: A publication object.

**Value**

String with publication slots' names

---

names.publications-method

*Get slot names for a publication object.*

**Description**

Get slot names for a publication object.

**Usage**

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

**Arguments**

- `x`: A publications object.

**Value**

String with publications slots' names
names, site-method

Get slot names

Description

Get all names for named elements within a site object.

Usage

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

Arguments

x A site object.

Value

names of the slots of a site object

names, specimen-method

Get slot names

Description

Get all names for named elements within a specimen object.

Usage

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

Arguments

x A specimen object.

Value

names of the slots of a site object
newURL

Format API call to Neotoma from call arguments

Description
Take a set of arguments from the Neotoma2 package and produce the appropriate URL to the Neotoma v2.0 API. This is an internal function used by parseURL().

Usage
newURL(baseurl, args, ...)

Arguments
baseurl The base URL for the Neotoma API
args The set of query arguments to be passed to the API
... Any additional arguments to be passed to the function.

Value
A properly formatted URL.

parsebody

parse_body

Description
An internal helper function to parse the body of POST API requests

Usage
parsebody(x, all_data, ...)

Arguments
x The HTTP path for the particular API call.
all_data recovers all_data parameter to decide how to handle downloads lists that would result in a 414 error.
... Any query parameters passed from the function calling

Value
JSON object to parse as a body in a HTTP request

Author(s)
Socorro Dominguez
parseURL

Description
An internal helper function used to connect to the Neotoma API in a standard manner, and to provide basic validation of any response.

Usage
parseURL(x, use = "neotoma", all_data = FALSE, ...)

Arguments
- **x**: The HTTP/S path for the particular API call.
- **use**: Uses the Neotoma server by default ("neotoma"), but supports either the development API server ("dev") or a local server ("local").
- **all_data**: If TRUE return all possible API calls
- **...**: Any query parameters passed from the calling function.

Value
list with cleaned and parsed data from HTTP request

Author(s)
- Socorro Dominguez <sedv8808@gmail.com>
- Simon Goring <goring@wisc.edu>

parse_location

Description
Retrieve location from datasets WTK, GeoJson, bounding box

Usage
parse_location(x)

Arguments
- **x**: location object
parse_site

Value

sf object to parse as location.

Author(s)

Socorro Dominguez <sedv8808@gmail.com>

Description

An internal helper function to parse the API result into a site object.

Usage

parse_site(result)

Arguments

result A JSON object from the API.

Value

A Neotoma2 site object.

pingNeotoma

Description

A quick function to test whether or not the Neotoma Database API is currently running.

Usage

pingNeotoma(server = "neotoma")

Arguments

server One of localhost:PORT (where PORT is a valid numeric port), neotoma or dev.

Value

A valid HTTP status code or returns an error if a connection is refused.
Examples

```r
{ 
  test_connection <- pingNeotoma("neotoma")
}
```

**plot, sites, ANY-method**  
Plot site coordinates using a basic plot.

---

**plotLeaflet**  
Plot sites on a leaflet map

---

**Description**  
Plot site coordinates using a basic plot.

**Usage**  
```
## S4 method for signature 'sites,ANY'
plot(x, y, ...)
```

**Arguments**

- `x` sites object
- `y` ANY
- `...` Additional parameters associated with the call.

**Value**  
plot object with site coordinates.

---

**plotLeaflet**  
plotLeaflet

---

**Description**  
Plot sites on a leaflet map

**Usage**  
```
plotLeaflet(object)
```

**Arguments**

- `object` Sites object to plot

**Value**  
leaflet map with site markers
Author(s)

Socorro Dominguez <sedv8808@gmail.com>

Description

Plot a site on a leaflet map

Usage

## S4 method for signature 'site'
plotLeaflet(object)

Arguments

object Site object to plot

Value

leaflet map

Examples

modernSites <- get_sites(keyword = "Modern")
plotLeaflet(modernSites[[1]])

Description

Plot sites on a leaflet map

Usage

## S4 method for signature 'sites'
plotLeaflet(object)
Arguments

object Sites object to plot

Value

leaflet map

Examples

# Note that by default the limit for queries is 25 records:
modernSites <- get_sites(keyword = "Modern")
plotLeaflet(mordenSites)

description

A publication is liked to an individual Neotoma dataset object They are grouped using an S4 publications class.

Value

object of class publication

Examples

{  simon <- new("contact", familyname = "Goring", givennames = "Simon J.")
socorro <- new("contact", familyname = "Dominguez", givennames = "Socorro")
first_author <- new("author", author = simon, order = 1)
second_author <- new("author", author = socorro, order = 2)
author_list <- new("authors", authors = list(first_author, second_author))
pub <- new("publication",
  articletitle = "Top or bottom: Best toast spreading surfaces.",
  journal = "Peanut Butter Science",
  year = "2022",
  volume = "2",
  author = author_list)
}
publications-class

An S4 class for multi-publication information from the Neotoma Paleoecology Database. This S4 class allows a single dataset to have one or more publication classes associated with it.

Value

object of class publications

repositories-class

S4 class for repositories information

Description

The grouped class for repositories from the Neotoma Paleoecology Database.

Value

object of class repositories

repository-class

S4 class for repository information

Description

The standard object class for repository from the Neotoma Paleoecology Database.

Value

object of class repository
**sample-class**

*S4 class for dataset information*

**Description**

The standard object class for samples from the Neotoma Paleoecology Database.

**Value**

object of class sample

**samples**

*Obtain samples from a record or multiple records.*

**Description**

Obtain samples from a record or multiple records.

**Usage**

```r
samples(x)
```

**Arguments**

- `x` sites object

**Value**

data.frame with record information at sample level

---

**samples, collunit-method**

**Description**

Obtain elements from collunit

**Usage**

```r
## S4 method for signature 'collunit'
samples(x)
```
samples,collunits-method

Arguments

x       collunit object

Value

data.frame with sample records

samples,collunits-method

Get samples from a collectionunit or set of collection units:

Description

Obtain elements from collunits

Usage

## S4 method for signature 'collunits'
samples(x)

Arguments

x       collunits object

Value

data.frame with sample records

samples,site-method

Description

Obtain elements on the samples level

Usage

## S4 method for signature 'site'
samples(x)

Arguments

x       site object
Value

data.frame with sample records

Examples

```
marion <- get_sites(sitename = "Marion Lake") %>%
  get_datasets() %>%
  filter(datasettype == "pollen") %>%
  get_downloads()
pollen <- samples(marion)
```

Description

Obtain all samples within a sites object

Usage

```
## S4 method for signature 'sites'
samples(x)
```

Arguments

- `x` - sites object

Value

data.frame with sample records

Examples

```
{
dw <- get_downloads(1)
pollen <- samples(dw)
}
```
### samples-class

**S4 class for the set of samples**

**Description**

The grouped class for samples from the Neotoma Paleoecology Database.

**Value**

object of class `samples`

### selectMatch

**Select the best match for an object.**

**Description**

Select the best match for an object.

**Usage**

```r
selectMatch(x, n)
```

**Arguments**

- `x` object
- `n` n elements that are a best match

**Value**

attr Select the match between a local record and a Neotoma match

### selectMatch,publication,logical-method

**Select the best match (between a local record and a Neotoma match)**

**Description**

Select the best match (between a local record and a Neotoma match)

**Usage**

```r
## S4 method for signature 'publication,logical'
selectMatch(x, n)
```
Arguments

- `x`: A publication object
- `n`: The match number (in the case an NA is returned).

Value

the best match to the selected publication.

---

**selectMatch, publication, numeric-method**

*Select the best match (between a local record and a Neotoma match)*

---

**Description**

Select the best match (between a local record and a Neotoma match)

**Usage**

```r
## S4 method for signature 'publication,numeric'
selectMatch(x, n)
```

**Arguments**

- `x`: A publication object
- `n`: The match number.

**Value**

the best match to the selected publication.

---

**set_chronology**

*set chronology information for a new record.*

---

**Description**

Create a new chronology for a record. Within Neotoma all chronologies have unique numeric identifiers. Within R, because of the need to use the identifiers across objects, and because we want to avoid conflicts between naming systems, a universally unique identifier (UUID) is created for the object ID.
**set_chronology**

**Usage**

```r
set_chronology(
  x = NA,
  chronologyid = NA_integer_,
  notes = NA_character_,
  contact = list(),
  agemodel = NA_character_,
  ageboundolder = NA_integer_,
  ageboundyounger = NA_integer_,
  isdefault = NA_integer_,
  dateprepared = as.Date(character(0)),
  modelagetype = NA_character_,
  chronologyname = NA_character_,
  chroncontrols = data.frame(0)
)
```

**Arguments**

- **x** Object to be set as a chronology
- **chronologyid** An optional value. Will be assigned a unique identifier if not provided.
- **notes** Additional notes about the chronology. For more modern models, often the function call to Bacon or Bchron is added here.
- **contact** A contacts object, identifying the individual(s) who created the chronology
- **agemodel** A string representing the age model name, for example "Crummy linear interpolation".
- **ageboundolder** The `ageboundolder` is assigned the oldest sample age rounded up to the nearest 10
- **ageboundyounger** The `ageboundyounger` is assigned the oldest sample age rounded up to the nearest 10
- **isdefault** Defines whether the model is the default for the collection unit for a particular model age type.
- **dateprepared** The date at which the age model was prepared.
- **modelagetype** The age type for the model. For validation, the models should be one of the valid Neotoma agetypes: `https://api.neotomadb.org/v2.0/data/dbtables?table=agetypes`
- **chronologyname** A valid name for the chronology.
- **chroncontrols** A data.frame containing the chronological controls for the age model.

**Value**

- chronology object
set_collunit

set Site Information for Fossil Sites

Description
set Site Information for Fossil Sites

Usage
set_collunit(
  x = NA,
  collectionunitid = NA_integer_,
  notes = NA_character_,
  handle = NA_character_,
  colldate = as.Date(character(1)),
  location = NA_character_,
  waterdepth = NA_integer_,
  gpslocation = st_as_sf(st_sfc()),
  collunittype = NA_character_,
  collectiondevice = NA_character_,
  collectionunitname = NA_character_,
  depositionalenvironment = NA_character_,
  datasets = new("datasets"),
  chronologies = new("chronologies"),
  defaultchronology = NA_integer_,
)

Arguments
  x          object to be set as collunit
  collectionunitid  collection unit identifier
  notes      notes
  handle     handle
  colldate   collection date
  location   location of the collection unit
  waterdepth depth at where the sample is taken
  gpslocation location with GPS
  collunittype type of collection unit
  collectiondevice device used to collect the sample
  collectionunitname name of the collection unit
set_contact

Description
Create a new contact for a record. Within Neotoma all chronologies have unique numeric identifiers. Within R, because of the need to use the identifiers across objects, and because we want to avoid conflicts between naming systems, a universally unique identifier (UUID) is created for the object ID.

Usage

set_contact(
  x = NA,
  contactid = NA_integer_,
  familyname = NA_character_,
  leadinginitials = NA_character_,
  givennames = NA_character_,
  suffix = NA_character_,
  ORCID = NA_character_,
  title = NA_character_,
  institution = NA_character_,
  email = NA_character_,
  phone = NA_character_,
  contactstatus = NA_character_,
  fax = NA_character_,
  url = NA_character_,
  address = NA_character_,
  notes = NA_character_
)

Value
collunit object

Examples

{
  # Create a collunit
  my_collunit <- set_collunit(notes = "my lake")
}
Arguments

- **x**: Object to be set as a contact
- **contactid**: An arbitrary Contact identification number.
- **familyname**: Family or surname name of a person.
- **leadinginitials**: Leading initials for given or forenames without spaces (e.g. G.G.).
- **givennames**: Given or forenames of a person (e.g. George Gaylord). Initials with spaces are used if full given names are not known (e.g. G. G.).
- **suffix**: Suffix of a person’s name (e.g. Jr., III).
- **ORCID**: A unique ORCID (see https://orcid.org).
- **title**: A person’s title (e.g. Dr., Prof., Prof. Dr.).
- **institution**: The institution where an individual works.
- **email**: An individual’s email address
- **phone**: Their phone number
- **contactstatus**: Are they "active" or "retired"?
- **fax**: Do people still use fax machines?
- **url**: Their homepage
- **address**: A physical address
- **notes**: Notes about the individual

Value

- contact object

---

**set_dataset**

*set Site Information for Fossil Sites*

Description

set Site Information for Fossil Sites

Usage

```r
set_dataset(
  x = NA,
  datasetid = NA_integer_,
  database = NA_character_,
  doi = NA,
  datasettype = NA_character_,
  age_range_old = NA_integer_,
  age_range_young = NA_integer_,
  notes = NA_character_,
  pi_list = NA,
  samples = new("samples")
)
```
**set_default**

Set the default chronology within a collectionunit.

### Description

Set the default chronology within a collectionunit.

### Usage

```r
set_default(x, n)
```

### Arguments

- **x**: A chronologies object.
- **n**: The particular chronology to be used as the default.

### Value

A sites object with new default chronology.
set_default, chronologies-method

Change the default age model for a record.

Description
Change the default age model for a record.

Usage

## S4 method for signature 'chronologies'
set_default(x, n)

Arguments

x A chronologies object.

n The particular chronology to be used as the default.

Value

chronologies object with a new defaulted chronology

set_publications Create a new publication (or publication set)

Description
A function to create new publication objects by hand.

Usage

set_publications(
  publicationid = NA_integer_,
  publicationtypeid = NA_integer_,
  publicationtype = NA_character_,
  year = NA_character_,
  citation = NA_character_,
  articletitle = NA_character_,
  journal = NA_character_,
  volume = NA_character_,
  issue = NA_character_,
  pages = NA_character_,
  citationnumber = NA_character_,
  doi = NA_character_,
  booktitle = NA_character_,
)
set_publications

numvolumes = NA_character_,
edition = NA_character_,
volumetitle = NA_character_,
seriestitle = NA_character_,
seriesvolume = NA_character_,
publisher = NA_character_,
url = NA_character_,
city = NA_character_,
state = NA_character_,
country = NA_character_,
originallanguage = NA_character_,
notes = NA_character_,
author = NULL
)

Arguments

publicationid  ID of publication
publicationtypeid  ID of kind of publication
publicationtype  A text string identifying the publication type within the Neotoma database.
year  The year of publication.
citation  A full text citation for the article.
articletitle  The title of the article.
journal  The journal in which the article was published.
volume  The journal volume.
issue  The journal issue.
pages  The pages of the journal.
citationnumber  How many times has the paper been cited?
doi  A DOI for the record.
booktitle  The title of the book (if the publication is a book)
numvolumes  The number of book volumes (if a series)
volumetitle  The title of the volume (in a published series)
seriestitle  The title of the series.
seriesvolume  The series volume.
publisher  The publisher.
url  Publication URL.
city  City of publication.
state  State of publication.
country  Country of publication.
set_sample

Description

set Sample Information

Usage

```r
set_sample(
  x = NA,
  ages = list(),
  igsn = NA_character_,
  datum = data.frame(),
  depth = NA_integer_,
  sampleid = NA_integer_,
  thickness = NA_integer_,
  samplename = NA_character_,
  sampleanalyst = list(),
  analysisunitid = NA_integer_,
  analysisunitname = NA_character_
)
```

Arguments

- **x**: Object to be set as a sample
- **ages**: ages
- **igsn**: IGSN character
- **datum**: dataframe of datum
- **depth**: integer representing depth
- **sampleid**: ID for sample
- **thickness**: thickness of core
- **samplename**: sample’s name
- **sampleanalyst**: Analyst’s contact name
- **analysisunitid**: Which analysis unit it is
- **analysisunitname**: Analysis Unit’s name

Value

publication object
**set_server**

**Value**

sample object

**Examples**

```r
{
  # Set an empty sample
  my_sample <- set_sample()
}
```

---

**set_server**  
*Set Neotoma API Source or Server*

**Description**

Choose to pull Neotoma data from the main Neotoma server, the development server or from a local instance of the API.

**Usage**

```r
set_server(server = "neotoma")
```

**Arguments**

<table>
<thead>
<tr>
<th>server</th>
</tr>
</thead>
<tbody>
<tr>
<td>One of local (when the API is running locally on port 3005), neotoma or dev.</td>
</tr>
</tbody>
</table>

**Value**

NULL modifies how to talk to the API (local, dev, server)

**Examples**

```r
# The user is running the API locally using the node/express API
# cloned from github: https://github.com/NeotomaDB/api_nodetest
set_server(server = "local")

# The user switches back to the remote api server.
set_server(server = "neotoma")
```
set_site

set Site Information for Fossil Sites

Description

set Site Information for Fossil Sites

Usage

set_site(
  x = NA,
  siteid = NA_integer_,
  sitename = NA_character_,
  geography = st_as_sf(st_sfc()),
  altitude = NA_integer_,
  geopolitical = list(),
  area = NA_integer_,
  notes = NA_character_,
  description = NA_character_,
  collunits = new("collunits")
)

Arguments

x Object to be set as a site

siteid The unique site id for a site. If this site is new to Neotoma then leave the ID as NA (the default).

sitename Actual site name as a character string.

geography An sf object representing the site location, either as a polygon or point.

altitude altitude/elevation of the site.

geopolitical The geopolitical unit in which the site is located.

area The area of the site or depositional basin in ha. Can be calculated from the polygon.

notes additional information of the site

description A character description of site.

collunits Collection units in the site

Value

site object
Examples

{  
  # Create a site called "My Lake", to  
  x = sf::st_as_sf(sf::st_sfc(sf::st_point(c(5,5))))  
  my_site <- set_site(sitename = "My Lake",  
                      geography = x,  
                      description = "my lake",  
                      altitude = 30)  
}

Description
Show the collection unit information

Usage

## S4 method for signature 'collunit'
show(object)

Arguments

object collunit object

Value

null used for side effects. Printing a data.frame

Description
Show the collection unit information

Usage

## S4 method for signature 'collunits'
show(object)

Arguments

object collunits object

Value

null used for side effects. Printing a data.frame
show,contact-method  Show contact object

Description
Show contact object
Show a contact object

Usage
## S4 method for signature 'contact'
show(object)

## S4 method for signature 'contact'
show(object)

Arguments
object  a contact object

Value
null - side effect for printing contact object
Null - prints a data.frame

show,contacts-method  Show a contacts object.

Description
Show a contacts object.

Usage
## S4 method for signature 'contacts'
show(object)

Arguments
object  A contacts object.

Value
null - side effect for printing contacts object
**show,dataset-method**  
*Show Dataset Method*

**Description**  
Show Dataset Method

**Usage**  
```r  
## S4 method for signature 'dataset'  
show(object)  
```

**Arguments**  
- `object`: dataset object

**Value**  
- null - side effect, prints a `data.frame` with dataset metadata

**show,datasets-method**  
*Show Datasets object as a dataframe*

**Description**  
Show Datasets object as a dataframe

**Usage**  
```r  
## S4 method for signature 'datasets'  
show(object)  
```

**Arguments**  
- `object`: datasets object

**Value**  
- null - side effect, prints a `data.frame` with datasets metadata
show.publications-method

Print publications to screen.

Description
Print publications to screen.

Usage
## S4 method for signature 'publication'
show(object)

Arguments
object A publication object.

Value
NULL - side effect function of printing a data.frame

show.publications-method
Show the contents of a publication object.

Description
Show the contents of a publication object.

Usage
## S4 method for signature 'publications'
show(object)

Arguments
object A publications object

Value
NULL - side effect function of printing a data.frame
show,site-method

Show a site object as a dataframe

Description
Convert a Neotoma package site object into a data.frame() returning the siteid, sitename, latitude, longitude and altitude of the site.

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

Arguments
- `object` site object

Value
NULL - side effect for printing a data.frame object

show,sites-method

Show sites objects as a dataframe

Description
Return a set of site objects as a single data.frame().

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

Arguments
- `object` sites object

Value
NULL - side effect for printing a data.frame object
show,specimen-method  Show Specimen Method

Description
Show Specimen Method

Usage
## S4 method for signature 'specimen'
show(object)

Arguments
object specimen object

Value
NULL - side effect for printing a data.frame object

show,specimens-method  Show Specimens object as a dataframe

Description
Show Specimens object as a dataframe

Usage
## S4 method for signature 'specimens'
show(object)

Arguments
object specimens object

Value
NULL - side effect for printing a data.frame object
showMatch

Show matches for objects.

Description
Show matches for objects.

Usage
showMatch(x)

Arguments
x object to show matches for

Value
data.frame that marks if a site exists in another sites object

showMatch,publication-method
Show matched publication objects.

Description
Show matched publication objects.

Usage
## S4 method for signature 'publication'
showMatch(x)

Arguments
x A publication object.

Value
NULL printed matches with other publications
site-class

An S4 class for site information

Description
The standard object class for sites from the Neotoma Paleoecology Database.

Value
object of class site

sites-class

An S4 class for multi-site information

Description
The standard object class for multi-sites from the Neotoma Paleoecology Database.

Value
object of class sites

specimen-class

S4 class for specimen information

Description
The standard object class for specimen from the Neotoma Paleoecology Database.

Value
object of class specimen
specimens

Obtain specimens from a record or multiple records.

Description
Obtain specimens from a record or multiple records.

Usage
specimens(x)

Arguments
x sites object

Value
data.frame with record information regarding specimens

specimens,collunit-method

Description
Obtain specimen elements from a collunit

Usage
## S4 method for signature 'collunit'
specimens(x)

Arguments
x collunit object

Value
data.frame with specimens summary table
specimens, site-method

Description

Obtain elements on the specimens level

Usage

```r
## S4 method for signature 'site'
specimens(x)
```

Arguments

- `x`: site object

Value

data.frame with specimens summary table

---

specimens, collunits-method

Description

Obtain specimen elements from collunits

Usage

```r
## S4 method for signature 'collunits'
specimens(x)
```

Arguments

- `x`: collunits object

Value

data.frame with specimens summary table
specimens,sites-method

specimens

Description

Information table for Specimens

Usage

```r
## S4 method for signature 'sites'
specimens(x)
```

Arguments

- `x` Use a `sites` object that has specimens added.

Value

data.frame with specimens summary table

Author(s)

Socorro Dominguez <s.dominguez@ht-data.com>

Examples

```r
# To return a specimens table do:
my_specimens <- get_specimens(7)
my_tbl <- specimens(my_specimens)
```

specimens-class

*S4 class for specimens information*

Description

The grouped class for specimens from the Neotoma Paleoecology Database.

Value

object of class specimens
### summary.sites-method

**Summary of objects within a sites object.**

**Description**

This function summarizes a sites object, from site level and returns a data.frame that contains the site ID, sitename, collectionunit ID, count of chronologies, count of datasets and types of datasets within the site.

**Usage**

```r
## S4 method for signature 'sites'
summary(object, ...)
```

**Arguments**

- **object**
  - sites object
- **...**
  - additional properties passed to summary

**Value**

data.frame object with site summary information

---

### taxa

**Description**

Show the samples table

**Usage**

taxa(object)

**Arguments**

- **object**
  - Sites object to extract taxa table from

**Value**

data.frame with taxa records
taxa.collunit-method

Extract taxonomic data from a set of sites.

Description

Extract taxonomic data from a set of sites.

Usage

## S4 method for signature 'collunit'
taxa(object)

Arguments

object A collunit object.

Value

A data.frame reporting the taxa/data objects, units, elements and other features within a set of records.

taxa.collunits-method

Extract taxonomic data from a set of sites.

Description

Extract taxonomic data from a set of sites.

Usage

## S4 method for signature 'collunits'
taxa(object)

Arguments

object A collunits object.

Value

A data.frame reporting the taxa/data objects, units, elements and other features within a set of records.
taxa,sites-method

Extract taxonomic data from a single site.

Description

Extract taxonomic data from a single site.

Usage

## S4 method for signature 'site'
taxa(object)

Arguments

object A site object.

Value

A data.frame reporting the taxa/data objects, units, elements and other features within a set of records.

Examples

somesites <- get_sites(datasettype = "pollen", limit = 3) %>%
  get_downloads()
diatomtaxa <- taxa(somesites[[1]])

taxa,sites-method

Extract taxonomic data from a set of sites.

Description

From a sites object.

Usage

## S4 method for signature 'sites'
taxa(object)

Arguments

object A sites object.
Value

A data.frame reporting the taxa/data objects, units, elements and other features within a set of records.

Examples

```r
somesites <- get_sites(datasettype = "diatom", limit = 3) %>%
  get_downloads()
diatomtaxa <- taxa(somesites)
common_taxa <- diatomtaxa %>%
dplyr::filter(sites == 3)
```

---

**testNull**

Clear NULL values and replace with value predefined value.

Description

Similar to concatenate, checks to see if a value is NULL and replace it with a known value provided in `out`.

Usage

```r
testNull(val, out = NA)
```

Arguments

- `val` The value to be checked.
- `out` A default value to be returned if `val` is NULL.

Value

The values passed in `val` or `out` if `val` is NULL.

Examples

```r
{
  # Passing a null value into the function returns 12:
  a <- testNull(val = NULL, out = 12)
  # Passing a non-NULL value returns that value:
  b <- testNull(val = 11, out = 12)
}
```
### Description

Export toJSON

#### Usage

```r
toJSON(x)
```  

#### Arguments

- `x`: Sites object to extract taxa table from

#### Value

JSON translation of sites object to JSON

#### Author(s)

Socorro Dominguez <sedv8808@gmail.com>

---

### Description

Convert a Neotoma2 sites object into a standardized JSON file for API management.

#### Usage

```r
## S4 method for signature 'sites'
toJSON(x = NA)
```  

#### Arguments

- `x`: sites R object to be converted

#### Value

The function returns a character string in JSON format

#### Author(s)

Socorro Dominguez <sedv8808@gmail.com>
Examples

{
  # To find all sites that contain the string "Alexander%"
  alex.sites <- get_sites(sitename="Alexander%")
  # Convert the object to json
  toJSON(alex.sites)
}

Description

Obtain a wide table with information regarding of samples grouped by variablename and depth/age.

Usage

toWide(
  x,
  variablenames = c(),
  ecologicalgroups = c(),
  elementtypes = c(),
  unit = c(),
  groupby = "age",
  operation = "prop"
)

Arguments

x dataframe object with samples
variablenames Optional vector to filter by specific variable names.
ecologicalgroups Vector stating the ecological groups to be filtered by, e.g. "DIAT", "TRSH"
elementtypes Label of element type to filter by, e.g. "pollen", "valve"
unit Label stating which units to filter by, e.g. "NISP"
groupby Group by 'age' or 'depth'
operation label or vector of operations to be chosen from: 'prop', 'sum', 'presence'.

Value

wide data.frame obtained from long samples data.frame
Examples

```r
fourcorners <- '{"type": "Polygon", "coordinates": [[[-109.36060497194846, 37.69552879956651], [-107.813845732192, 37.69552879956651], [-107.813845732192, 36.80303716260222], [-109.36060497194846, 36.80303716260222], [-109.36060497194846, 37.69552879956651]]]'

# Download all vertebrate localities within a bounding box.
fc_sites <- neotoma2::get_sites(loc = fourcorners[1])
fc_ds <- neotoma2::get_datasets(fc_sites) %>%
  neotoma2::filter(datasettype="vertebrate fauna")
fc_dl <- neotoma2::get_downloads(fc_ds)
fc_dl1 <- fc_dl[[1]]
fc_smp <- samples(fc_dl1)
toWide(fc_smp, ecologicalgroups=c('AVES', 'RODE'),
  elementtypes='bone/tooth', unit='present/absent')
```

---

**use_na**  
*Change NA values from logic to a prescribed type.*

**Description**

Pass an object and convert all NA elements to particular NA types.

**Usage**

```r
use_na(x, type)
```

**Arguments**

- **x** An element that may or may not have NA values.
- **type** A character string with values either char or int.

**Value**

object converted to NA_character or NA_integer
write.csv,chronologies-method

Description
write CSV

Usage
## S4 method for signature 'chronologies'
write.csv(x, ...)

Arguments
x chronologies object
... Additional parameters associated with the call.

Value
null, called for side effects

write.csv,collunits-method

Description
write CSV

Usage
## S4 method for signature 'collunits'
write.csv(x, ...)

Arguments
x collunits object
... Additional parameters associated with the call.

Value
null side effect for saving a CSV file.
write.csv,datasets-method

write CSV

Description
write CSV

Usage
## S4 method for signature 'datasets'
write.csv(x, ...)

Arguments
x         datasets object
...       Additional parameters associated with the call.

Value
null -side effect for printing a CSV file

write.csv,sites-method

write CSV

Description
write CSV

Usage
## S4 method for signature 'sites'
write.csv(x, ...)

Arguments
x         A sites object
...       Other options to pass to write.csv().

Value
NULL side effect from saving a csv file
### Description
write CSV

### Usage
```r
## S4 method for signature 'specimens'
write.csv(x, ...)
```

### Arguments
- `x`: specimens object
- `...`: Additional parameters associated with the call.

### Value
NULL - side effect of saving CSV file

### Description
Get or remove sites by numeric index

### Usage
```r
## S4 method for signature 'collunits,numeric,ANY'
x[i]
```

### Arguments
- `x`: The collunits object
- `i`: The numeric index

### Value
null used for side effects. Printing a data.frame
### [,datasets,numeric,ANY-method

*Get or remove datasets by numeric index*

**Description**

Get or remove datasets by numeric index

**Usage**

```r
## S4 method for signature 'datasets,numeric,ANY'
x[i]
```

**Arguments**

- `x` The datasets object
- `i` The numeric index

**Value**

Get or remove datasets by numeric index

### [,site,character,ANY-method

*Get site field by character index*

**Description**

Get site field by character index

**Usage**

```r
## S4 method for signature 'site,character,ANY'
x[i]
```

**Arguments**

- `x` The site object
- `i` The column indicator

**Value**

sliced site object
[.site, numeric, ANY-method

*Get site field by numeric index*

---

**Description**

Get site field by numeric index

**Usage**

```r
## S4 method for signature 'site, numeric, ANY'
x[i]
```

**Arguments**

- `x`  
  The site object
- `i`  
  The column indicator

**Value**

sliced site object

---

[.sites, numeric, ANY-method

*Get or remove sites by numeric index*

---

**Description**

Get or remove sites by numeric index

**Usage**

```r
## S4 method for signature 'sites, numeric, ANY'
x[i]
```

**Arguments**

- `x`  
  The sites object
- `i`  
  The numeric index

**Value**

sliced site object
### Description

Get or remove specimens by numeric index

### Usage

```r
## S4 method for signature 'specimens,numeric,ANY'
x[i]
```

### Arguments

- `x`: The specimens object
- `i`: The numeric index

### Value

sliced specimens object

### Description

Assign collunit field by numeric index

### Usage

```r
## S4 replacement method for signature 'collunit,character,ANY,ANY'
x[i] <- value
```

### Arguments

- `x`: The collunit object.
- `i`: The column indicator.
- `value`: The value to be used.

### Value

sliced element
[<-,collunit,numeric,ANY,ANY-method

Assign collunit field by numeric index

Description
Assign collunit field by numeric index

Usage
## S4 replacement method for signature 'collunit,numeric,ANY,ANY'
x[i] <- value

Arguments
x    The collunit object.
i    The column indicator.
value The value to be used.

Value
sliced value

[<-,dataset,character,ANY,ANY-method

Assign dataset field by numeric index

Description
Assign dataset field by numeric index

Usage
## S4 replacement method for signature 'dataset,character,ANY,ANY'
x[i] <- value

Arguments
x    The dataset object.
i    The column indicator.
value The value to be used.

Value
dataset slot with new assigned character value
Assign dataset field by numeric index

Description
Assign dataset field by numeric index

Usage
## S4 replacement method for signature 'dataset,numeric,ANY,ANY'
x[i] <- value

Arguments

- **x**
  - The dataset object.
- **i**
  - The column indicator.
- **value**
  - The value to be used.

Value
dataset slot with new assigned numeric value

Assign site field by numeric index

Description
Assign site field by numeric index

Usage
## S4 replacement method for signature 'site,character,ANY,ANY'
x[i] <- value

Arguments

- **x**
  - The site object.
- **i**
  - The column indicator.
- **value**
  - The value to be used.

Value
site object with reassigned character values
[<-site, numeric, ANY, ANY-method

Assign site field by numeric index

Description

Assign site field by numeric index

Usage

## S4 replacement method for signature 'site, numeric, ANY, ANY'
x[i] <- value

Arguments

x The site object.
i The column indicator.
value The value to be used.

Value

sites object with reassigned numeric values

[<-specimen, character, ANY, ANY-method

Assign specimen field by numeric index

Description

Assign specimen field by numeric index

Usage

## S4 replacement method for signature 'specimen, character, ANY, ANY'
x[i] <- value

Arguments

x The specimen object.
i The column indicator.
value The value to be used.

Value

specimen object with reassigned character values
[<-, specimen, numeric, ANY, ANY-method

Assign specimen field by numeric index

Description
Assign specimen field by numeric index

Usage
## S4 replacement method for signature 'specimen, numeric, ANY, ANY'
x[i] <- value

Arguments
x The specimen object.
i The column indicator.
value The value to be used.

Value
sites object with reassigned numeric values

[[, chronologies, numeric, ANY-method

Extract

Description
Obtain one of the elements within a chronologies list either by element order or by element name.

Usage
## S4 method for signature 'chronologies, numeric, ANY'
x[[i]]

Arguments
x chronologies object
i iteration in chronologies list

Value
selected chronology object
Description

Obtain one of the elements within a collunits list

Usage

```r
## S4 method for signature 'collunits,numeric,ANY'
x[[i]]
```

Arguments

- `x`: collunits object
- `i`: iteration in collunits list

Value

sliced collunits object

Extract or Replace Parts of an Object

Description

Extract or Replace Parts of an Object

Usage

```r
## S4 method for signature 'contacts,numeric,ANY'
x[[i]]
```

Arguments

- `x`: A contact object.
- `i`: The numeric index of a contact slot.

Value

sliced contacts
**Description**

Obtain one of the elements within a datasets list.

**Usage**

```r
## S4 method for signature 'datasets,numeric,ANY'
x[[i]]
```

**Arguments**

- `x` datasets object
- `i` iteration in datasets list

**Value**

sliced dataset object

---

**Description**

Obtain one of the elements within a publication list.

**Usage**

```r
## S4 method for signature 'publications,numeric,ANY'
x[[i]]
```

**Arguments**

- `x` A publications object.
- `i` A numeric index for the requested publication

**Value**

selected publications object from index
Description

Obtain one of the elements within a samples list

Usage

```r
## S4 method for signature 'samples,numeric,ANY'
x[[i]]
```

Arguments

- `x` samples object
- `i` iteration in samples list

Value

samples sliced object

Description

Obtain one of the elements within a sites list

Usage

```r
## S4 method for signature 'sites,numeric,ANY'
x[[i]]
```

Arguments

- `x` sites object
- `i` iteration in sites list

Value

sliced site object
Examples

```r
{  
some_site <- get_sites(sitename = "Site%", limit=3)  
some_site[[2]]
}
```

**Slicer**

Description

Obtain one of the elements within a specimens list

Usage

```r
## S4 method for signature 'specimens,numeric,ANY'

x[[i]]
```

Arguments

- `x` : specimens object
- `i` : iteration in specimens list

Value

sliced specimens object

**Insert collunit**

Description

Obtain one of the elements within a collunits list

Usage

```r
## S4 replacement method for signature 'collunits,ANY,ANY,ANY'

x[[i]] <- value
```

Arguments

- `x` : collunits object
- `i` : iteration in collunits list
- `value` : The value to be used
Value

Modified collunits

[[<-,datasets,ANY,ANY,ANY-method

Insert dataset

Description

Obtain one of the elements within a datasets list

Usage

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

Arguments

- `x` datasets object
- `i` iteration in datasets list
- `value` The value to be used

Value

One dataset slot’s value

[[<-,publications,ANY,ANY,ANY-method

Assign value to an element in a publication list.

Description

Assign value to an element in a publication list.

Usage

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

Arguments

- `x` A publications object.
- `i` A numeric index for the requested publication
- `value` The value to be used
Value
publications with new assigned value.

[[<-, sites, ANY, ANY, ANY-method

Insert site

Description
Obtain one of the elements within a sites list

Usage
## S4 replacement method for signature 'sites,ANY,ANY,ANY'
x[[i]] <- value

Arguments
x sites object
i iteration in sites list
value The value to be used

Value
sites object with reassigned values

[[<-, specimens, ANY, ANY, ANY-method

Insert specimen

Description
Obtain one of the elements within a specimens list

Usage
## S4 replacement method for signature 'specimens,ANY,ANY,ANY'
x[[i]] <- value

Arguments
x specimens object
i iteration in specimens list
value The value to be used
Value

 specimens object with reassigned values

$ chronologies-method Extract

Description

Obtain chronology slots across all chronology elements within a chronologies object.

Usage

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

Arguments

x chronologies object
name name of the slot

Value

A multiple chronologies

$ chronology-method Extract

Description

Extract chronology metadata by slot name.

Usage

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

Arguments

x chronology object
name name of the slot

Value

value of the slot name
Description

Obtain slots of a collunit without using at-mark

Usage

```r
## S4 method for signature 'collunit'
x$name
```

Arguments

- `x`: collunit object
- `name`: name of the slot

Value

null prints element of a slot
## S4 method for signature 'contact'
x$name

### Arguments

- **x**: A contact object.
- **name**: The name of a contact slot.

### Value

value in the selected slot

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

### Arguments

- **x**: A contacts object.
- **name**: The name of a contacts slot.

### Value

object value from the slot
Description

Obtain slots of a dataset without using at-mark

Usage

```r
## S4 method for signature 'dataset'

x$name
```

Arguments

- `x`: dataset object
- `name`: name of the slot

Value

Obtain a dataset's slot value using $

---

Description

Obtain slots of a dataset without using at-mark

Usage

```r
## S4 method for signature 'datasets'

x$name
```

Arguments

- `x`: datasets object
- `name`: name of the slot.

Value

Obtain a datasets' slot value using $

---
**Publication Method**

*Extract an element from a publication*

### Description

Extract an element from a publication

### Usage

```r
## S4 method for signature 'publication'
x$name
```

### Arguments

- **x**: A publication object.
- **name**: The slot to obtain (e.g., `articletitle`)

### Value

value in the selected slot

---

**Sample Method**

*Obtain slots of a sample without using at-mark*

### Usage

```r
## S4 method for signature 'sample'
x$name
```

### Arguments

- **x**: Sample object
- **name**: Name of the slot

### Value

value at selected slot
### $\$,samples-method

#### Description
Obtain slots of a site without using at-mark

#### Usage

```r
## S4 method for signature 'samples'
x$name
```

#### Arguments
- `x` samples object
- `name` name of the slot

#### Value
value at selected slot

### $\$,site-method

#### Description
Obtain slots of a site without using at-mark

#### Usage

```r
## S4 method for signature 'site'
x$name
```

#### Arguments
- `x` site object
- `name` name of the slot

#### Value
value at chosen slot in the site object
Description
Obtain slots of a site without using at-mark

Usage
```r
## S4 method for signature 'sites'
x$name
```

Arguments
- `x` sites object
- `name` name of the slot

Value
value at chosen slot in the site object

Description
Obtain slots of a specimen without using at-mark

Usage
```r
## S4 method for signature 'specimen'
x$name
```

Arguments
- `x` specimen object
- `name` name of the slot

Value
value at chosen slot in the specimen object
$<-,chronology-method

$ for specimens

Description
Obtain slots of a specimen without using at-mark

Usage
## S4 method for signature 'specimens'
  x$name

Arguments
  x specimens object
  name name of the slot.

Value
value at chosen slot in the site object

$<-,chronology-method Replace part of an object

Description
Assign values to slots within a chronology object.

Usage
## S4 replacement method for signature 'chronology'
  x$name <- value

Arguments
  x A chronology object
  name The name of the chronology slot.
  value A value to be assigned to the chronology slot.

Value
reassigned chronology object
### $<-, collunit-method

**Assign collunit field by numeric index**

**Description**

Assign collunit field by numeric index

**Usage**

```r
## S4 replacement method for signature 'collunit'
x$name <- value
```

**Arguments**

- `x`: The collunit object.
- `name`: name of the slot.
- `value`: The value to be used.

**Value**

assign a new value to a slot

### $<-, dataset-method

**Assign dataset field by numeric index**

**Description**

Assign dataset field by numeric index

**Usage**

```r
## S4 replacement method for signature 'dataset'
x$name <- value
```

**Arguments**

- `x`: The dataset object.
- `name`: name of the slot.
- `value`: The value to be used.

**Value**

Assign new dataset by numeric index
$<$-,site-method  
Assign site field by numeric index

Description

Assign site field by numeric index

Usage

## S4 replacement method for signature 'site'
x$name <- value

Arguments

x The site object.
name name of the slot
value The value to be used.

Value

site object with reassigned values

$<$-,specimen-method  
Assign specimen field by numeric index

Description

Assign specimen field by numeric index

Usage

## S4 replacement method for signature 'specimen'
x$name <- value

Arguments

x The specimen object.
name name of the slot.
value The value to be used.

Value

specimen object with reassigned values
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