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<<https://api.neotomadb.org/api-docs/>>.

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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 collectionunit 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 collectionunit.

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)
```


Arguments

x chronologies object

Value

data.frame with chronologies metadata

as.data.frame,chronology-method

Create a data.frame from a chronology object.

Description

Convert all slots within a chronology to a data.frame.

Usage

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

Arguments

x chronology object

Value

data.frame

as.data.frame,collunit-method

as.data.frame site

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

as.data.frame, collunits-method
as.data.frame collunits

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.

as.data.frame, contact-method
Transform a contacts object to a data.frame()

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

as.data.frame,contacts-method

Transform a contacts object to a data.frame()

Description

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

as.data.frame,dataset-method

as.data.frame dataset

Description

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
as.data.frame datasets

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
as.data.frame sites

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
as.data.frame specimen

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

```
## 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

```
## 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 `authors` object.

Value

object of class `author`

Examples

```
{
  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

```
{
  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	<i>build_chron</i>
-------------	--------------------

Description

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

Usage

```
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	<i>Build a collection unit from the API response</i>
-----------------	--

Description

Build a collection unit from the API response

Usage

```
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	<i>Build a dataset object from a JSON list representation.</i>
---------------	--

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	<i>Build a samples data.frame from Neotoma API JSON</i>
--------------	---

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 <s.dominguez@ht-data.com>

build_sites	<i>Build a site from the Neotoma API response.</i>
-------------	--

Description

Build a site from the Neotoma API response.

Usage

```
build_sites(x)
```

Arguments

x A list returned from the Neotoma API data section.

Value

A simple site object

build_specimen	<i>Build a specimen objects.</i>
----------------	----------------------------------

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

```
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

```
## 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

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

Arguments

x	collunits object 1
y	collunits object 2

Value

concatenated collection units without duplicates

c, contact-method *c Method - Combine contacts objects*

Description

c Method - Combine contacts objects

Usage

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

Arguments

x contacts object 1
y contacts object 2

Value

contacts concatenated object

c, contacts-method *c Method - Combine contacts objects*

Description

c Method - Combine contacts objects

Usage

```
## 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 *c Method - Combine datasets objects*

Description

c Method - Combine datasets objects

Usage

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

Arguments

x	datasets object 1
y	datasets object 2

Value

concatenated datasets object

c,missingOrNULL-method
c Method for NULL values

Description

c Method for NULL values
c Method for NULL values

Usage

```
## S4 method for signature 'missingOrNULL'
c(x = "missingOrNULL", y)
```

```
## S4 method for signature 'missingOrNULL'
c(x = "missingOrNULL", y)
```

Arguments

x	NULL object
y	sites/datasets object

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

```
## 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

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

Arguments

x	sites object 1
y	sites object 2

Value

concatenated and cleaned sites object

c,specimens-method *c Method - Combine specimens objects*

Description

c Method - Combine specimens objects

Usage

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

Arguments

x	specimens object 1
y	specimens object 2

Value

concatenated specimens object

check_args *check_args*

Description

Internal function to check passed arguments.

Usage

```
check_args(c1)
```

Arguments

c1	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

References

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

check_contacts	<i>Check contact information for a record against Neotoma contributors</i>
----------------	--

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	<i>Get contact information for Neotoma contributors</i>
-------------------------	---

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

chroncontrols	<i>chroncontrols</i>
---------------	----------------------

Description

Show the samples table

Usage

```
chroncontrols(x)
```

Arguments

x Sites object to extract chroncontrols table from

Value

data.frame with chroncontrols information

chroncontrols,site-method

Recover information about the chron controls for a collectionunit.

Description

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

chroncontrols,sites-method

Recover information about the chron controls for a collectionunit.

Description

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

Usage

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

Arguments

x sites object

Value

data.frame with chronological controls

chronologies

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

```
## 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

```
## 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

cite_data,site-method *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

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

Arguments

x sites object

Value

data.frame object with citation information.

Examples

```
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

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

Arguments

x sites object

Value

data.frame object with citation information.

Examples

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

collunit-class	<i>S4 class for collection units information.</i>
----------------	---

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	<i>Extract collection units from a sites object</i>
-----------	---

Description

Extract collection units from a sites object

Usage

```
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

```
## 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

```
## 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	<i>Obtain coordinates from a sites object.</i>
-------------	--

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	<i>Return the latitude and longitude of sites</i>
---------------------------	---

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	<i>S4 class for dataset information</i>
---------------	---

Description

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

Value

object of class dataset

datasets	<i>Extract datasets from a sites object.</i>
----------	--

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	<i>Extract datasets from a collunit object.</i>
---------------------------	---

Description

Extract datasets from a collunit object.

Usage

```
## S4 method for signature 'collunit'  
datasets(object)
```

Arguments

object A collunit object

Value

datasets from a collunit object

datasets, collunits-method

Extract datasets from a collunits object.

Description

Extract datasets from a collunits object.

Usage

```
## 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

```
## 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

```
## 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

```
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

```
## 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

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

Arguments

x a Neotoma2 site object

Value

data.frame object with DOIs information.

Examples

```
{
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

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

Arguments

x a Neotoma2 site object

Value

data.frame object with DOIs information.

Examples

```
{
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

<code>x</code>	A site, dataset or download.
<code>...</code>	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

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

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")
```

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

```
## 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

```
{
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

```
## 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

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

getids.site	<i>Get object IDs from a site object.</i>
-------------	---

Description

Get object IDs from a site object.

Usage

```
## 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	<i>Get object IDs from sites</i>
--------------	----------------------------------

Description

Get object IDs from sites

Usage

```
## 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

```
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

get_datasets	<i>get_datasets</i>
--------------	---------------------

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 Paleocological Database. The user may define all or none of the possible fields.

Usage

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

Arguments

<code>x</code>	A single datasetid, or a vector of unique dataset ids.
<code>...</code>	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.
- `gpuid` 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 <s.dominguez@ht-data.com>

Examples

```
# 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)
```

get_datasets.default *Get Dataset Default*

Description

Get Dataset Default

Usage

```
## Default S3 method:
get_datasets(x, ...)
```

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

```
{
# To find all datasets with a min altitude of 12 and a max altitude of 25:
sites_12to25 <- get_datasets(altmin=12, altmax=25, limit=2)
# 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)
}
```

get_datasets.numeric *Get Dataset Numeric*

Description

Get Dataset Numeric

Usage

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

Arguments

x Use a single number to extract site information
... Additional parameters to get_datasets

Value

sites object with full metadata up to the dataset level

Examples

```
allds <- get_datasets(1:3)
```

get_datasets.site *Get Dataset from a site object.*

Description

Get Dataset from a site object.

Usage

```
## S3 method for class 'site'  
get_datasets(x, ...)
```

Arguments

x An object of class site.
... additional arguments accepted by get_datasets()

Value

sites object with full metadata up to the dataset level

Examples

```
random_sites <- get_sites(1)  
alllds <- get_datasets(random_sites, limit=3)
```

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

Description

Get Dataset from a sites object.

Usage

```
## 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

```
random_sites <- get_sites(1)
alllds <- get_datasets(random_sites, limit=3)
```

<code>get_downloads</code>	<i>get_downloads</i>
----------------------------	----------------------

Description

Information for Fossil Datasets

Usage

```
get_downloads(x = NA, verbose = TRUE, ...)
```

Arguments

<code>x</code>	Use a single number to extract site information
<code>verbose</code>	Status bar of items being downloaded
<code>...</code>	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:

<code>siteid</code>	site ID number
<code>sitename</code>	site's name
<code>location</code>	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 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

Author(s)

Socorro Dominguez <s.dominguez@ht-data.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 get_downloads
```

Description

get_downloads

Usage

```
## 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 *get_downloads sites*

Description

get_downloads sites

Usage

```
## 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.

get_manual *get_manual*

Description

Open up the Neotoma manual homepage.

Usage

```
get_manual()
```

Value

NULL side effect for opening browser with the manual

Author(s)

Simon Goring <goring@wisc.edu>

Examples

```
{
# 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 Paleocology Database

Usage

```
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

```
# 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

```
## 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 associ-  
          ated with a publication. familyname The full or partial last name for an individ-  
          ual 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

```
# 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

```
## 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

```
{
# 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

```
## 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

```
# 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

```
## 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

```
# 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 publicaitonid.
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]]
```

get_sites

get_sites

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 Paleocological Database. The user may define all or none of the possible fields.

Usage

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

Arguments

<code>x</code>	Use a single integer or vector of integers representing unique Neotoma site identifiers (siteids) to extract site information.
<code>...</code>	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 datasettypes. This returns a subset of data types. For a complete list of available datasettypes, 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).
- `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 <s.dominguez@ht-data.com>

Examples

```
## 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, -33.137551192346145],
[-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:
lilysites <- c()
for (i in seq(0, 10000, by = 1000)) {
  lily <- get_sites(taxa=c("Liliaceae"),
                   ageyoung = i - 500,
                   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.
- collunits limited information on collunits

Author(s)

Socorro Dominguez <s.dominguez@ht-data.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.
- 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.
- 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)
```

get_specimens	<i>get_specimens</i>
---------------	----------------------

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

Author(s)

Socorro Dominguez <s.dominguez@ht-data.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

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_stats	get_stats
-----------	-----------

Description

Returns a count of sites, datasets, publications and other objects added to Neotoma during the requested time period.

Usage

```
get_stats(start, end)
```

Arguments

start	The starting month (from present == 0) for which to generate the summary.
end	The ending month (from present == 0) for which to generate the summary.

Details

This function returns summaries about the data holdings within Neotoma using the existing Neotoma API's summary endpoint. This can provide information about recent uploads (the number of new sites uploaded within the last month, for example), or can be used to provide information about the overall number of sites/datasets (using an arbitrarily high value for end).

Value

data.frame with summary statistics

Author(s)

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

Simon Goring <goring@wisc.edu>

Examples

```
last_month <- get_stats(start = 0, end = 1)
```

get_table	<i>Get table record from Neotoma</i>
-----------	--------------------------------------

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')
}
```

length.chronologies-method

Length Method chronologies

Description

Length Method chronologies

Usage

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

Arguments

x	chronologies object
---	---------------------

Value

integer describing length

length,collunits-method
Length Method collunits

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

```
## 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

```
## 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

```
## 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

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

Arguments

x sites object

Value

int with the length of sites object

length,specimens-method
Length Method specimens

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 *c Method - Combine objects, including NULL*

Description

c Method - Combine objects, including NULL
 c Method - Combine objects, including NULL

names,collunit-method *Get slot names*

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

```
## 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

```
## 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

```
## 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

```
## 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.

parseURL	<i>parseURL</i>
----------	-----------------

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 <s.dominguez@ht-data.com>
Simon Goring <goring@wisc.edu>

parse_site	<i>parse_site</i>
------------	-------------------

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	<i>pingNeotoma</i>
-------------	--------------------

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

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

plot, sites-method	<i>Plot site coordinates using a basic plot.</i>
--------------------	--

Description

Plot site coordinates using a basic plot.

Usage

```
## S4 method for signature 'sites'  
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 <s.dominguez@ht-data.com>

plotLeaflet,site-method
plotLeaflet

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]])
```

plotLeaflet,sites-method
plotLeaflet

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(modernSites)
```

publication-class *An S4 class for a single Neotoma publication.*

Description

A publication is linked 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	<i>An S4 class for multi-publication information from the Neotoma Paleocology Database. This S4 class allows a single dataset to have one or more publication classes associated with it.</i>
--------------------	---

Description

An S4 class for multi-publication information from the Neotoma Paleocology 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	<i>S4 class for repositories information</i>
--------------------	--

Description

The grouped class for repositories from the Neotoma Paleocology Database.

Value

object of class repositories

repository-class	<i>S4 class for repository information</i>
------------------	--

Description

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

Value

object of class repository

sample-class	<i>S4 class for dataset information</i>
--------------	---

Description

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

Value

object of class sample

samples	<i>Obtain samples from a record or multiple records.</i>
---------	--

Description

Obtain samples from a record or multiple records.

Usage

samples(x)

Arguments

x sites object

Value

data.frame with record information at sample level

samples, collunit-method
samples

Description

Obtain elements from collunit

Usage

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

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 *samples*

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)
```

samples,sites-method *samples*

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	<i>S4 class for the set of samples</i>
---------------	--

Description

The grouped class for samples from the Neotoma Paleoecology Database.

Value

object of class samples

selectMatch	<i>Select the best match for an object.</i>
-------------	---

Description

Select the best match for an object.

Usage

```
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

```
## 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

```
## 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	<i>set chronology information for a new record.</i>
----------------	---

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.

Function to create new chronology objects for personal analysis. The new object will not be uploaded to the database.

Usage

```
set_chronology(
  x = NA,
  chronologyid = NA_integer_,
  notes = NA_character_,
  contact = list(),
  ageomodel = 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	<i>set Site Information for Fossil Sites</i>
--------------	--

Description

Function to create new collection unit objects for personal analysis. The new object will not be uploaded to the database.

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
depositionalenvironment	depositional environment
datasets	datasets that the collection unit has
chronologies	chronologies taken from the collection unit
defaultchronology	best chronology model identifier to be used with this collection unit

Value

collunit object

Examples

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

set_contact	<i>Set contact information for a new record.</i>
-------------	--

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. This is not to be updated to the database.

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_
)

```

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 individuals 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

Function to create new dataset objects for personal analysis. The new object will not be uploaded to the database.

Usage

```
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")
)
```

Arguments

x	object to be set as dataset,
datasetid	dataset identifier
database	dataset where the dataset came from
doi	DOI
datasettype	type the dataset belongs to
age_range_old	age range old
age_range_young	age range young
notes	notes
pi_list	pi list
samples	taxa objects

Value

dataset object

Examples

```
{  
# Create a dataset  
my_dataset <- set_dataset(database = "EPD",  
                           datasettype = "pollen",  
                           notes = "my lake")  
}
```

set_default	<i>Set the default chronology within a collectionunit.</i>
-------------	--

Description

Set the default chronology within a collectionunit.

Usage

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

Arguments

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

Value

sites object with new default chronology

set_default, chronologies-method	<i>Change the default age model for a record.</i>
----------------------------------	---

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	<i>Create a new publication (or publication set)</i>
------------------	--

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_,
  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)
edition	The book edition.
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.
originallanguage	Original language of publication.
notes	Publication notes.
author	name of the author of publication.

Value

publication object

 set_sample

set Sample Information

Description

Function to create new samples objects for analysis. The new object will not be uploaded to the database.

Usage

```
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

sample object

Examples

```
{  
  # 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

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

Arguments

server One of local (when the API is running locally on port 3005), neotoma or dev.

Value

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

Examples

```
# 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 <i>ha</i> . Can be calculated from the polygon.
notes	additional information of the site
description	Function to create new site objects for personal analysis. The new object will not be uploaded to the database.
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)
}

```

show, collunit-method *Show the collection unit information*

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

show, collunits-method *Show the collection unit information*

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

```
## 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

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

Arguments

object datasets object

Value

null - side effect, prints a data.frame with datasets metadata

show,publication-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	<i>Show a site object as a dataframe</i>
------------------	--

Description

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

Usage

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

Arguments

object site object

Value

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

show,sites-method	<i>Show sites objects as a dataframe</i>
-------------------	--

Description

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

Usage

```
## 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	<i>Show matches for objects.</i>
-----------	----------------------------------

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	<i>Show matched publication objects.</i>
------------------------------	--

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	<i>An S4 class for site information</i>
------------	---

Description

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

Value

object of class site

sites-class	<i>An S4 class for multi-site information</i>
-------------	---

Description

The standard object class for multi-sites from the Neotoma Paleoecology Database. from @ returns object of class sites

specimen-class	<i>S4 class for specimen information</i>
----------------	--

Description

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

Value

object of class specimen

specimens	<i>Obtain specimens from a record or multiple records.</i>
-----------	--

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
<i>specimens</i>

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,collunits-method
specimens

Description

Obtain specimen elements from collunits

Usage

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

Arguments

x collunits object

Value

data.frame with specimens summary table

specimens,site-method *specimens*

Description

Obtain elements on the specimens level

Usage

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

Arguments

x site object

Value

data.frame with specimens summary table

specimens,sites-method
specimens

Description

Information table for Specimens

Usage

```
## 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

```
# 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

```
## 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	<i>taxa</i>
------	-------------

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,site-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(datasestype = "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

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

toJSON

toJSON

Description

Export toJSON

Usage

```
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>

toJSON, sites-method *toJSON*

Description

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

Usage

```
## 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 <s.dominguez@ht-data.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)  
}
```

toWide *toWide*

Description

Obtain a wide table with information regarding of samples grouped by variable name 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

```
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')
```

write.csv,chronologies-method
write CSV

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
write CSV

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

```
write.csv,specimens-method  
write CSV
```

Description

write CSV

Usage

```
## 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

```
[,collunits,numeric-method  
Get or remove sites by numeric index
```

Description

Retrieve sites by numeric index

Usage

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

Arguments

x	The collunits object
i	The numeric index

Value

null used for side effects. Printing a data.frame

```
[,datasets,numeric-method
```

Get or remove datasets by numeric index

Description

Get or remove datasets by numeric index

Usage

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

Arguments

x	The datasets object
i	The numeric index

Value

Get or remove datasets by numeric index

```
[,site,character-method
```

Get site field by character index

Description

Get site field by character index

Usage

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

Arguments

x	The site object
i	The column indicator

Value

sliced site object

[,site,numeric-method] *Get site field by numeric index*

Description

Get site field by numeric index

Usage

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

Arguments

x	The site object
i	The column indicator

Value

sliced site object

[,sites,numeric-method] *Get or remove sites by numeric index*

Description

Get or remove sites by numeric index

Usage

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

Arguments

x	The sites object
i	The numeric index

Value

sliced site object

[,specimens,numeric-method

Get or remove specimens by numeric index

Description

Get or remove specimens by numeric index

Usage

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

Arguments

x	The specimens object
i	The numeric index

Value

sliced specimens object

[<- ,collunit,character,ANY,ANY-method

Assign collunit field by numeric index

Description

Assign collunit field by numeric index

Usage

```
## 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

[<- ,dataset,numeric,ANY,ANY-method
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

[<- ,site,character,ANY,ANY-method
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-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'  
x[[i]]
```

Arguments

x	chronologies object
i	iteration in chronologies list

Value

selected chronology object

```
[[,collunits,numeric-method
    Slicer
```

Description

Obtain one of the elements within a collunits list

Usage

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

Arguments

x	collunits object
i	iteration in collunits list

Value

sliced collunits object

```
[[,contacts,numeric-method
    Extract or Replace Parts of an Object
```

Description

Extract or Replace Parts of an Object

Usage

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

Arguments

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

Value

sliced contacts

```
[[,datasets,numeric-method  
    Slicer
```

Description

Obtain one of the elements within a datasets list

Usage

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

Arguments

x	datasets object
i	iteration in datasets list

Value

sliced dataset object

```
[[,publications,numeric-method  
    Obtain one of the elements within a publication list.
```

Description

Obtain one of the elements within a publication list.

Usage

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

Arguments

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

Value

selected publications object from index

```
[[,samples,numeric-method  
    Slicer
```

Description

Obtain one of the elements within a samples list

Usage

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

Arguments

x	samples object
i	iteration in samples list

Value

samples sliced object

```
[[,sites,numeric-method  
    Slicer
```

Description

Obtain one of the elements within a sites list

Usage

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

Arguments

x	sites object
i	iteration in sites list

Value

sliced site object

Examples

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

[[,specimens,numeric-method
Slicer

Description

Obtain one of the elements within a specimens list

Usage

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

Arguments

x	specimens object
i	iteration in specimens list

Value

sliced specimens object

[[<- ,collunits,ANY,ANY,ANY-method
Insert collunit

Description

Obtain one of the elements within a collunits list

Usage

```
## 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

```
## 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

```
## 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

\$,collunit-method *\$*

Description

Obtain slots of a collunit without using at-mark

Usage

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

Arguments

x	collunit object
name	name of the slot

Value

null prints element of a slot

\$,collunits-method *\$ for collunits*

Description

Obtain slots of a collunit without using at-mark

Usage

```
## S4 method for signature 'collunits'  
x$name
```

Arguments

x	collunits object
name	name of the slot

Value

null prints element of a slot

\$.contact-method *Extract or Replace Parts of an Object*

Description

Extract or Replace Parts of an Object

Usage

```
## 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

\$.contacts-method *Extract or Replace Parts of an Object*

Description

Extract or Replace Parts of an Object

Usage

```
## 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

,\$dataset-method \$

Description

Obtain slots of a dataset without using at-mark

Usage

```
## S4 method for signature 'dataset'  
x$name
```

Arguments

x	dataset object
name	name of the slot

Value

Obtain a dataset's slot value using \$

,\$datasets-method *\$ for datasets*

Description

Obtain slots of a dataset without using at-mark

Usage

```
## 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

```
## 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 \$

Description

Obtain slots of a sample without using at-mark

Usage

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

Arguments

x	sample object
name	name of the slot

Value

value at selected slot

\$.samples-method *\$ for samples*

Description

Obtain slots of a site without using at-mark

Usage

```
## 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

```
## 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

\$,sites-method *\$ for sites*

Description

Obtain slots of a site without using at-mark

Usage

```
## 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

\$,specimen-method \$

Description

Obtain slots of a specimen without using at-mark

Usage

```
## 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

\$.specimens-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

```
## 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

```
## 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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