

Package ‘neotoma2’

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add_chronology	<i>Add a new chronology to a collection unit.</i>
----------------	---------------------------------------------------

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

 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.

 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
---	-----------

```
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

```
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

```
as.data.frame,collunit-method
      as.data.frame site
```

Description

show as dataframe as prep to save as csv

Usage

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

Arguments

x site object

```
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
---	------------------

```
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.
---	-------------------

```
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.
---	--------------------

```
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

```
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

```
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.

```
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.

```
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

```
as.data.frame,sites-method
```

as.data.frame sites

Description

show as dataframe as prep to save as csv

Usage

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

Arguments

x sites object

```
as.data.frame,specimen-method
      as.data.frame specimen
```

Description

show as dataframe as prep to save as csv

Usage

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

Arguments

x specimen object

```
as.data.frame,specimens-method
      as.data.frame specimens
```

Description

show as dataframe as prep to save as csv

Usage

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

Arguments

x specimens object

```
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

author-class	<i>An S4 class for the authors of a Neotoma publication.</i>
--------------	--------------------------------------------------------------

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.

Examples

```
## Not run:
simon <- new("contact", familyname = "Goring", givennames = "Simon J.")
firstauthor <- new("author", author = simon, order = 1)

## End(Not run)
```

authors-class	<i>An S4 class for a set of Neotoma author objects.</i>
---------------	---------------------------------------------------------

Description

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

Examples

```
## Not run:
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))

## End(Not run)
```

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 <sedv8808@gmail.com>

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

Description

Build a collection unit from the API response

Usage

```
build_collunits(x)
```

Arguments

<code>x</code>	The structured JSON from a Neotoma API v2.0 response that returns a collection unit in any form.
----------------	--------------------------------------------------------------------------------------------------

Value

An object of class `collunit`

<code>build_dataset</code>	<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

<code>x</code>	a JSON dataset object passed from the Neotoma API.
----------------	----------------------------------------------------

Value

A dataset object.

Author(s)

Socorro Dominguez <sedv8808@gmail.com>

Examples

```
## Not run:  
# To build dataset from API call:  
build_dataset(x)  
  
## End(Not run)
```

build_sample

Build a samples data.frame from Neotoma API JSON

Description

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

Usage

```
build_sample(x)
```

Arguments

x sample list

Value

list parsed into samples

Author(s)

Socorro Dominguez <sedv8808@gmail.com>

Examples

```
## Not run:  
# To build sample from API call:  
build_sample(x)  
  
## End(Not run)
```

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's data slot.
---	---------------------------------------------------

Examples

```
## Not run:
response <- jsonlite::fromJSON(
  "https://api.neotomadb.org/v2.0/data/datasets/100,101",
  flatten = FALSE, simplifyVector = FALSE)
response <- cleanNULL(response)
newSites <- build_sites(response$data)
newSites

## End(Not run)
```

build_specimen	<i>Build 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_speciments()` call.

Usage

```
build_specimen(x)
```

Arguments

x	specimen list
---	---------------

Value

A list (from JSON) parsed into specimen

Author(s)

Socorro Dominguez <sedv8808@gmail.com>

Examples

```
## Not run:  
build_specimen(x)  
  
## End(Not run)
```

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

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

c,contact-method	<i>c Method - Combine contacts objects</i>
------------------	--------------------------------------------

Description

c Method - Combine contacts objects

Usage

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

Arguments

x	contacts object 1
y	contacts object 2

c,contacts-method	<i>c Method - Combine contacts objects</i>
-------------------	--------------------------------------------

Description

c Method - Combine contacts objects

Usage

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

Arguments

x	contacts object 1
y	contacts object 2

c,datasets-method	<i>c Method - Combine datasets objects</i>
-------------------	--------------------------------------------

Description

c Method - Combine datasets objects

Usage

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

Arguments

x	datasets object 1
y	datasets object 2

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

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

c, sites-method	<i>c Method - Combine sites objects</i>
-----------------	-----------------------------------------

Description

c Method - Combine sites objects

Usage

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

Arguments

x	sites object 1
y	sites object 2

c, specimens-method	<i>c Method - Combine specimens objects</i>
---------------------	---------------------------------------------

Description

c Method - Combine specimens objects

Usage

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

Arguments

x	specimens object 1
y	specimens object 2

check_args	<i>check_args</i>
------------	-------------------

Description

Internal function to check passed arguments.

Usage

```
check_args(c1)
```

Arguments

cl called arguments. Arguments are going to be called by match_call inside: [get_sites](#)
[get_datasets](#) [get_downloads](#)

Value

A list with two components:

flag Returns a 0 if everything's fine, a 1 if there's a problem.
 message A list of error messages.

Author(s)

Socorro Dominguez <sedv8808@gmail.com>

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.

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.

chroncontrols

chroncontrols

Description

Show the samples table

Usage

```
chroncontrols(x)
```

Arguments

x	Sites object to extract chroncontrols table from
---	--------------------------------------------------

Author(s)

Socorro Dominguez <sedv8808@gmail.com>

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
---	-------------

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

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

chronologies,collunit-method

Extract chronologies from a sites object.

Description

Extract chronologies from a sites object.

Usage

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

Arguments

x A collunit object

chronologies,collunits-method

Extract chronologies from a sites object.

Description

Extract chronologies from a sites object.

Usage

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

Arguments

x A collunit object

chronologies,site-method

Extract chronologies from a sites object.

Description

Extract chronologies from a sites object.

Usage

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

Arguments

x 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

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

Description

The grouped class for chronologies from the Neotoma Paleoecology Database.

chronology-class	<i>S4 class for chronologies information</i>
------------------	----------------------------------------------

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.

cite_data	<i>Generate a data citation from a Neotoma2 object.</i>
-----------	---------------------------------------------------------

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.
---	------------------------------------

`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

Examples

```
## Not run:  
mb <- get_sites(gpid = "Manitoba", datasettype = "pollen")  
mb_ds <- get_datasets(mb)  
cite_data(mb_ds)  
  
## End(Not run)
```

`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

Examples

```
## Not run:  
mb <- get_sites(gpid = "Manitoba", datasettype = "pollen")  
mb_ds <- get_datasets(mb)  
cite_data(mb_ds)  
  
## End(Not run)
```

clean	<i>clean Neotoma objects to remove duplicates and empty objects.</i>
-------	----------------------------------------------------------------------

Description

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

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

Usage

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

Arguments

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

Author(s)

Simon Goring <goring@wisc.edu>

Examples

```
## Not run:
clean_sites <- get_sites(sitename = "L%", limit = 20)
more_sites <- get_sites(sitename = "La%", limit = 20)
long_set <- c(clean_sites, more_sites)
length(long_set)
# By removing duplicates we get a smaller object.
length(clean(long_set))
# We can do the same thing with collection units:
clean_cols <- get_sites(sitename = "L%", limit = 20) %>%
  collunits()
more_cols <- get_sites(sitename = "La%", limit = 20) %>%
  collunits()
long_set <- c(clean_cols, more_cols)
length(long_set)
# By removing duplicates we get a smaller object.
length(clean(long_set))
# And datasets:
clean_ds <- get_sites(sitename = "L%", limit = 20) %>%
  get_downloads() %>% datasets()
more_ds <- get_sites(sitename = "La%", limit = 20) %>%
  get_downloads() %>% datasets()
long_set <- c(clean_ds, more_ds)
length(long_set)
```

```
# By removing duplicates we get a smaller object.
length(clean(long_set))

## End(Not run)
```

clean.collunits	<i>clean sites objects to remove duplicates.</i>
-----------------	--------------------------------------------------

Description

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

Usage

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

Arguments

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

Author(s)

Simon Goring <goring@wisc.edu>

Examples

```
## Not run:
clean_cols <- get_sites(sitename = "L%", limit = 20) %>%
  collunits()
more_cols <- get_sites(sitename = "La%", limit = 20) %>%
  collunits()
long_set <- c(clean_cols, more_cols)
length(long_set)
# By removing duplicates we get a smaller object.
length(clean(long_set))

## End(Not run)
```

clean.datasets	<i>clean sites objects to remove duplicates.</i>
----------------	--------------------------------------------------

Description

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

Usage

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

Arguments

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

Author(s)

Simon Goring <goring@wisc.edu>

Examples

```
## Not run:
clean_ds <- get_sites(sitename = "L%", limit = 20) %>%
  get_downloads() %>% datasets()
more_ds <- get_sites(sitename = "La%", limit = 20) %>%
  get_downloads() %>% datasets()
long_set <- c(clean_ds, more_ds)
length(long_set)
# By removing duplicates we get a smaller object.
length(clean(long_set))

## End(Not run)
```

clean.sites	<i>clean sites objects to remove duplicates.</i>
-------------	--------------------------------------------------

Description

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

Usage

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

Arguments

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

Author(s)

Simon Goring <goring@wisc.edu>

Examples

```
## Not run:
clean_sites <- get_sites(sitename = "L%", limit = 20)
more_sites <- get_sites(sitename = "La%", limit = 20)
long_set <- c(clean_sites, more_sites)
length(long_set)
# By removing duplicates we get a smaller object.
length(clean(long_set))

## End(Not run)
```

cleanNULL	<i>Clean NULL values</i>
-----------	--------------------------

Description

Pass an object and convert all NULL elements to NA.

Usage

```
cleanNULL(x)
```

Arguments

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

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.

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
--------	----------------

collunits,site-method	<i>Extract datasets from a sites object.</i>
-----------------------	----------------------------------------------

Description

Extract datasets from a sites object.

Usage

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

Arguments

object	A sites object
--------	----------------

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

Description

Extract datasets from a sites object.

Usage

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

Arguments

object	A sites object
--------	----------------

collunits-class	<i>An S4 class for Neotoma Collection Units</i>
-----------------	-------------------------------------------------

Description

Holds Collection unit information from the Neotoma Paleoecology Database.

contact-class	<i>An S4 class for Neotoma contacts</i>
---------------	-----------------------------------------

Description

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

Examples

```
## Not run:
new("contact", familyname = "Goring", givennames = "Simon J.")
## End(Not run)
```

contacts-class	<i>An S4 class for multi-contact information from the Neotoma Paleoe-cology Database.</i>
----------------	-------------------------------------------------------------------------------------------

Description

An unordered list of individual S4 contact objects.

Examples

```
### Not run:
# 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

## End(Not run)
```

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.

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.

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

Description

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

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
--------	----------------

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 collunits object
--------	--------------------

datasets,collunits-method	<i>Extract datasets from a collunits object.</i>
---------------------------	--------------------------------------------------

Description

Extract datasets from a collunits object.

Usage

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

Arguments

object	A collunits object
--------	--------------------

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

Description

Extract datasets from a sites object.

Usage

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

Arguments

object A sites 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

datasets-class *S4 class for datasets information*

Description

The grouped class for datasets from the Neotoma Paleoecology Database.

doi	<i>Obtain the DOI for publications or datasets.</i>
-----	-----------------------------------------------------

Description

Obtain the DOI for publications or datasets.

Usage

```
doi(x)
```

Arguments

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

doi,publication-method	<i>Get a publication DOI.</i>
------------------------	-------------------------------

Description

Get a publication DOI.

Usage

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

Arguments

x	A publication object.
---	-----------------------

doi,site-method	<i>Obtain dataset DOIs from records.</i>
-----------------	------------------------------------------

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
---	------------------------

Examples

```
## Not run:
mb <- get_sites(gpid = "Manitoba", datasettype = "pollen")
mb_ds <- get_datasets(mb)
doi(mb_ds)

## End(Not run)
```

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

Examples

```
## Not run:
mb <- get_sites(gpid = "Manitoba", datasettype = "pollen")
mb_ds <- get_datasets(mb)
doi(mb_ds)

## End(Not run)
```

filter

*Apply a filter for Neotoma sites objects.***Description**

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

- "siteid" A numeric site identifier from the Neotoma Database
- "sitename" The character string sitename.
- "lat" A numeric latitude value.
- "long" A numeric longitude value.

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

Usage

```
filter(x, ...)
```

Arguments

x	A site, dataset or download.
...	arguments to filter by.

filter.sites	<i>Apply a filter for Neotoma sites objects.</i>
--------------	--------------------------------------------------

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.

Examples

```
## Not run:
# Download 100 sites, but only keep the sites that are close to sea level.
some_sites <- get_sites(sitename = "Lake%", limit = 100)
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 = 100) %>%
  get_datasets(all_data = TRUE)
pollen_subset <- sites %>% filter(datasettype == "pollen")

## End(Not run)
```

fix_null	<i>Fix null values from API responses</i>
----------	-------------------------------------------

Description

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

Usage

```
fix_null(x)
```

Arguments

x	item that has null objects.
---	-----------------------------

getids	<i>Get object IDs</i>
--------	-----------------------

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

getids.collunit	<i>Get object IDs from a single collectionunit.</i>
-----------------	-----------------------------------------------------

Description

From a collecitonunit 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

Examples

```
## Not run:
marion <- get_sites(sitename = "Marion Lake") %>%
  get_datasets() %>%
  filter(datasettype == "pollen") %>%
  get_downloads()
collunitids <- getids(collunits(marion)[[1]])

## End(Not run)
```

getids.collunits	<i>Get object IDs from collectionunits.</i>
------------------	---------------------------------------------

Description

From a set of collecitonunitobjects, 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

Examples

```
## Not run:
marion <- get_sites(sitename = "Marion Lake") %>%
  get_datasets() %>%
  filter(datasettype == "pollen") %>%
  get_downloads()
collunitids <- getids(collunits(marion))

## End(Not run)
```

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

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

get_contacts	<i>Get contact information for 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

```
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)

get_contacts.default	<i>Get contact information for 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

```
## 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)

get_contacts.numeric	<i>Get contact information for 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

```
## 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)

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.
- `gpid` The geopolitical name or identifier containing a site. Can be passed as a vector of names.
- `keywords` Keywords for samples within a set of sites. For example "modern" indicates a sample within the record uses the keyword "modern".
- `contacts` Contact names or IDs associated with a site.
- `ageyoung` A minimum spanning age for the record, in years before radiocarbon present (1950).
- `ageold` A maximum spanning age for the record, in years before radiocarbon present (1950).
- `ageof` An age which must be contained within the range of sample ages for a site.
- `taxa` The names of taxa which must be present within samples in a record.
- `all_data` The API only downloads the first 25 records of the query. For the complete records, use `all_data=TRUE`

Value

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

Author(s)

Socorro Dominguez <sedv8808@gmail.com>

Examples

```
## Not run:
# 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])
# 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)

## End(Not run)
```

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
...	contactid, datasettype, altmin, altmax, loc, ageyoung, ageold, ageof

Examples

```
## Not run:
# 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])

## End(Not run)
```

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

Examples

```
## Not run:
allds <- get_datasets(1:29)
plotLeaflet(allds)

## End(Not run)
```

get_datasets.sites	<i>Get Dataset from a sites object.</i>
--------------------	-----------------------------------------

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()

Examples

```
## Not run:
random_sites <- get_sites(1:100)
allds <- get_datasets(random_sites)
plotLeaflet(allds)

## End(Not run)
```

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

Description

Information for Fossil Datasets

Usage

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

Arguments

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

Details

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

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

Value

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

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

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

collunitid	collection unit ID number
handle	collection unit's handle
collunitname	collection unit's name
colldate	date in collection unit
substrate	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 <sedv8808@gmail.com>

Examples

```
## Not run:
# 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)

## End(Not run)

```

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

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

get_downloads.sites	<i>get_downloads sites</i>
---------------------	----------------------------

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

get_manual	<i>get_manual</i>
------------	-------------------

Description

Open up the Neotoma manual homepage.

Usage

```
get_manual()
```

Author(s)

Simon Goring <goring@wisc.edu>

Examples

```
## Not run:  
# 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()  
}  
  
## End(Not run)
```

get_publications	<i>Get publication information for Neotoma records</i>
------------------	--------------------------------------------------------

Description

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

Examples

```
## Not run:
# 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))

## End(Not run)
```

get_publications.default	<i>Get publication information from Neotoma</i>
--------------------------	-------------------------------------------------

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 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.

Examples

```
## Not run:
# 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))

## End(Not run)
```

```
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.

Examples

```
## Not run:
# We want the paper identified in Neotoma as 666:
get_publications(666)

## End(Not run)
```

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.

Examples

```
## Not run:
# 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]]

## End(Not run)
```

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.

Examples

```
## Not run:
# 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]]

## End(Not run)
```

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

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

Details

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

- `siteid` The unique site ID (integer) in Neotoma. Can be passed as a vector of site IDs.
- `sitename` The site name, or approximate match using the `%` wildcard.
- `database` The constituent database for the record. See `get_table("constituentdatabases")`
- `altmin` The minimum altitude range for site elevation (in meters).
- `altmax` The maximum altitude range for site elevation (in meters).
- `datasetid` The unique dataset ID (integer) in Neotoma. Can be passed as a vector of dataset IDs.
- `datasettype` Neotoma contains data for a number of 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 <sedv8808@gmail.com>

Examples

```
## Not run:
## 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')

## End(Not run)
```

get_sites.default	<i>get_sites</i>
-------------------	------------------

Description

get_sites

Usage

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

Arguments

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

Author(s)

Socorro Dominguez <sedv8808@gmail.com>

get_sites.numeric	<i>Get Site Information for Fossil Sites</i>
-------------------	----------------------------------------------

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

Examples

```
## Not run:
## Find all sites by numeric siteid:
sites <- get_sites(seq(1,100))

## End(Not run)
```

get_sites.sites	<i>Get Site Information for Fossil Sites from a Set of Sites</i>
-----------------	------------------------------------------------------------------

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

Examples

```
## Not run:
## Find all sites using a set of prior sites:
char_sites <- get_sites(taxa = "charcoal")
pollen_coloc <- get_sites(char_sites, datasettype = "pollen")
char_coloc <- char_sites %>% filter(siteid %in% getids(pollen_coloc)$siteid)
pol_char <- c(pollen_coloc, char_coloc) %>% clean()

## End(Not run)
```

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 <sedv8808@gmail.com>

Examples

```
## Not run:
# To find specimen with ID 19832:
my_specimens <- get_specimens(19832)

## End(Not run)
# To find specimens in datasetid 41610
my_specimens2 <- get_specimens(datasetid = 41610)
```

get_specimens.default	<i>Get Specimen datasetid</i>
-----------------------	-------------------------------

Description

Get Specimen datasetid

Usage

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

Arguments

...	Pass argument datasetid and the corresponding datasetid
-----	---------------------------------------------------------

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.

get_specimens.sites *Get Specimen Sites*

Description

Get Specimen Sites

Usage

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

Arguments

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

get_table *Get table record from Neotoma*

Description

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

Usage

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

Arguments

x	Table name (consult https://open.neotomadb.org/dbschema/ for a complete list of table names).
limit	Default 25 records
offset	Default 0.

Examples

```
## Not run:
# Returns only the first 25 specimen records.
someSpec <- get_table('specimens')
# Loop with the offset to get all specimens:
okay <- TRUE
counter <- 1
specimens <- list()
while(okay) {
  specimens[[counter]] <- get_table('specimens', offset = (counter - 1) * 25)
  if(nrow(specimens[[counter]]) < 25) {
    okay <- FALSE
  } else {
    counter <- counter + 1
  }
}
specimens <- specimens %>% dplyr::bind_rows()

## End(Not run)
```

length,chronologies-method

Length Method chronologies

Description

Length Method chronologies

Usage

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

Arguments

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

length,collunits-method

Length Method collunits

Description

Length Method collunits

Usage

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

Arguments

x collunits object

length,datasets-method

Length Method datasets

Description

Length Method datasets

Usage

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

Arguments

x 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.

length,samples-method *Length Method samples*

Description

Length Method samples

Usage

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

Arguments

x samples object

length,sites-method *Length Method Sites*

Description

Length Method Sites

Usage

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

Arguments

x sites object

length,specimens-method
 Length Method specimens

Description

Length Method specimens

Usage

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

Arguments

x 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.

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.

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.

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.

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.

names,site-method	<i>Get slot names</i>
-------------------	-----------------------

Description

Get all names for named elements within a site object.

Usage

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

Arguments

x	A site object.
---	----------------

names,specimen-method	<i>Get slot names</i>
-----------------------	-----------------------

Description

Get all names for named elements within a specimen object.

Usage

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

Arguments

x	A specimen object.
---	--------------------

newURL	<i>Format API call to Neotoma from call arguments</i>
--------	-------------------------------------------------------

Description

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

Usage

```
newURL(baseUrl, args, ...)
```

Arguments

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

Value

A properly formatted URL.

parsebody	<i>parse_body</i>
-----------	-------------------

Description

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

Usage

```
parsebody(x, ...)
```

Arguments

x	The HTTP path for the particular API call.
...	Any query parameters passed from the function calling

Author(s)

Socorro Dominguez <sedv8808@gmail.com>

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.

Author(s)

Socorro Dominguez <sedv8808@gmail.com>

Simon Goring <goring@wisc.edu>

<code>parse_location</code>	<i>parse_location</i>
-----------------------------	-----------------------

Description

Retrieve location from datasets WTK, GeoJson, bounding box

Usage

```
parse_location(x)
```

Arguments

<code>x</code>	location object
----------------	-----------------

Author(s)

Socorro Dominguez <sedv8808@gmail.com>

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

Description

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

Usage

```
parse_site(result)
```

Arguments

<code>result</code>	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

```
## Not run:
test_connection <- pingNeotoma("neotoma")

## End(Not run)
```

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

Description

Plot site coordinates using a basic plot.

Usage

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

Arguments

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

plotLeaflet	<i>plotLeaflet</i>
-------------	--------------------

Description

Plot sites on a leaflet map

Usage

```
plotLeaflet(object, save_im = FALSE, path = "")
```

Arguments

object	Sites object to plot
save_im	save output
path	location where output should be saved in. save_im must be TRUE

Author(s)

Socorro Dominguez <sedv8808@gmail.com>

plotLeaflet,site-method	<i>plotLeaflet</i>
-------------------------	--------------------

Description

Plot a site on a leaflet map

Usage

```
## S4 method for signature 'site'
plotLeaflet(object, save_im = FALSE, path = "")
```

Arguments

object	Site object to plot
save_im	save output
path	location where output should be saved in. save_im must be TRUE

Examples

```
## Not run:
modernSites <- get_sites(keyword = "Modern")
plotLeaflet(modernSites[[1]])

## End(Not run)
```

```
plotLeaflet,sites-method
      plotLeaflet
```

Description

Plot sites on a leaflet map

Usage

```
## S4 method for signature 'sites'
plotLeaflet(object, save_im = FALSE, path = "")
```

Arguments

object	Sites object to plot
save_im	save output
path	location where output should be saved in. save_im must be TRUE

Examples

```
## Not run:
# Note that by default the limit for queries is 25 records:
modernSites <- get_sites(keyword = "Modern")
plotLeaflet(modernSites)
# Save map to file:
plotLeaflet(modernSites, save_im = '/tmp/myMap.png')

## End(Not run)
```

publication-class	<i>An S4 class for a single Neotoma publication.</i>
-------------------	------------------------------------------------------

Description

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

Examples

```
## Not run:
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)

## End(Not run)

```

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

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

Description

The grouped class for repositories from the Neotoma Paleoeecology Database.

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

Description

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

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

Description

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

`samples`

Obtain samples from a record or multiple records.

Description

Obtain samples from a record or multiple records.

Usage

```
samples(x)
```

Arguments

`x` sites object

`samples, collunit-method`

samples

Description

Obtain elements from collunit

Usage

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

Arguments

`x` collunit object

Examples

```
## Not run:
marion <- get_sites(sitename = "Marion Lake") %>%
  get_datasets() %>%
  filter(datasettype == "pollen") %>%
  get_downloads()
pollen <- samples(collunits(marion)[[1]])
plot(value ~ I(-1 * age),
      data = pollen[pollen$variablename == "Cupressaceae",],
      xlab = "Years before present",
      ylab = "Cupressaceae pollen count")

## End(Not run)
```

`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

Examples

```
## Not run:
marion <- get_sites(sitename = "Marion Lake") %>%
  get_datasets() %>%
  filter(datasettype == "pollen") %>%
  get_downloads()
pollen <- samples(collunits(marion))
plot(value ~ I(-1 * age),
      data = pollen[pollen$variablename == "Cupressaceae",],
      xlab = "Years before present",
      ylab = "Cupressaceae pollen count")

## End(Not run)
```

`samples, site-method` *samples*

Description

Obtain elements on the samples level

Usage

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

Arguments

`x` site object

Examples

```
## Not run:
marion <- get_sites(sitename = "Marion Lake") %>%
  get_datasets() %>%
  filter(datasettype == "pollen") %>%
  get_downloads()
pollen <- samples(marion)
plot(value ~ I(-1 * age),
      data = pollen[pollen$variablename == "Cupressaceae",],
      xlab = "Years before present",
      ylab = "Cupressaceae pollen count")

## End(Not run)
```

`samples, sites-method` *samples*

Description

Obtain all samples within a sites object

Usage

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

Arguments

`x` sites object

Examples

```
## Not run:
marion <- get_sites(sitename = "Marion Lake") %>%
  get_datasets() %>%
  filter(datasettype == "pollen") %>%
  get_downloads()
pollen <- samples(marion)
plot(value ~ I(-1 * age),
      data = pollen[pollen$variablename == "Cupressaceae",],
      xlab = "Years before present",
      ylab = "Cupressaceae pollen count")

## End(Not run)
```

`samples-class` *S4 class for the set of samples*

Description

The grouped class for samples from the Neotoma Paleoecology Database.

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

selectMatch,publication,logical-method	<i>Select the best match (between a local record and a Neotoma match)</i>
----------------------------------------	---------------------------------------------------------------------------

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).

selectMatch,publication,numeric-method	<i>Select the best match (between a local record and a Neotoma match)</i>
----------------------------------------	---------------------------------------------------------------------------

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.

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.

Usage

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

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.

Examples

```
## Not run:
# Create a site called "My Lake", to
x = st_as_sf(st_sfc(st_point(c(5,5))))
my_site <- set_site(sitename = "My Lake",
                    geography = x,
                    description = "my lake",
                    altitude = 30)

## End(Not run)
```

set_collunit	<i>set Site Information for Fossil Sites</i>
--------------	----------------------------------------------

Description

set Site Information for Fossil Sites

Usage

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

Arguments

x	object to be set as collunit
collectionunitid	collection unit identifier
notes	notes
handle	handle
colldate	collection date
location	location of the collection unit
waterdepth	depth at where the sample is taken
gpslocation	location with GPS

collunittype type of collection unit
 collectiondevice device used to collect the sample
 collectionunitname name of the collection unit
 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

Examples

```
## Not run:
# Create a dataset
my_dataset <- set_dataset(database = "EPD",
                           datasettype = "pollen",
                           notes = "my lake"0)

## End(Not run)
```

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.

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

set_dataset

set Site Information for Fossil Sites

Description

set Site Information for Fossil Sites

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

Examples

```
## Not run:
# Create a dataset
my_dataset <- set_dataset(database = "EPD",
                           datasettype = "pollen",
                           notes = "my lake"0)

## End(Not run)
```

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.

set_default,chronologies-method

Change the default age model for a record.

Description

Change the default age model for a record.

Usage

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

Arguments

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

set_publications

Create a new publication (or publication set)

Description

A function to create new publication objects by hand.

Usage

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

set_sample	<i>set Sample Information</i>
------------	-------------------------------

Description

set Sample Information

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

Examples

```
## Not run:
# Create a site called "My Lake", to
x = st_as_sf(st_sfc(st_point(c(5,5))))
my_site <- set_site(sitename = "My Lake",
  geography = x,
  description = "my lake",
  altitude = 30)

## End(Not run)
```

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.

Examples

```
## Not run:
# 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")

## End(Not run)
```

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	A character description of site.
collunits	Collection units in the site

Examples

```
## Not run:
# Create a site called "My Lake", to
x = st_as_sf(st_sfc(st_point(c(5,5))))
my_site <- set_site(sitename = "My Lake",
                    geography = x,
                    description = "my lake",
                    altitude = 30)

## End(Not run)
```

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
--------	-----------------

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

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.

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.

show,dataset-method	<i>Show Dataset Method</i>
---------------------	----------------------------

Description

Show Dataset Method

Usage

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

Arguments

object	dataset object
--------	----------------

show,datasets-method	<i>Show Datasets object as a dataframe</i>
----------------------	--------------------------------------------

Description

Show Datasets object as a dataframe

Usage

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

Arguments

object	datasets object
--------	-----------------

show,publication-method	<i>Print publications to screen.</i>
-------------------------	--------------------------------------

Description

Print publications to screen.

Usage

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

Arguments

object	A publication object.
--------	-----------------------

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

show,site-method

Show a site object as a dataframe

Description

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

Usage

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

Arguments

object site object

Examples

```
## Not run:
some_site <- get_sites(sitename = "Site%")
as.data.frame(some_site[[1]])

## End(Not run)
```

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
--------	--------------

Examples

```
## Not run:
some_site <- get_sites(sitename = "Site%")
as.data.frame(some_site)

## End(Not run)
```

show,specimen-method	<i>Show Specimen Method</i>
----------------------	-----------------------------

Description

Show Specimen Method

Usage

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

Arguments

object	specimen 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

showMatch *Show matches for objects.*

Description

Show matches for objects.

Usage

```
showMatch(x)
```

Arguments

x object to show matches for

showMatch,publication-method
 Show matched publication objects.

Description

Show matched publication objects.

Usage

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

Arguments

x A publication object.

site-class	<i>An S4 class for site information from the Neotoma Paleoecology Database.</i>
------------	---------------------------------------------------------------------------------

Description

An S4 class for site information from the Neotoma Paleoecology Database.

sites-class	<i>An S4 class for multi-site information from the Neotoma Paleoecology Database.</i>
-------------	---------------------------------------------------------------------------------------

Description

An S4 class for multi-site information from the Neotoma Paleoecology Database.

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

Description

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

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
---	--------------

```
specimens,collunit-method
      specimens
```

Description

Obtain elements from collunit

Usage

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

Arguments

x collunit object

```
specimens,collunits-method
      specimens
```

Description

Obtain elements from collunits

Usage

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

Arguments

x collunits object

```
specimens,site-method  s
```

Description

Obtain elements on the specimens level

Usage

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

Arguments

x site object

specimens,sites-method	
	<i>specimens</i>

Description

Information table for Specimens

Usage

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

Arguments

x Use a sites element that has specimens added.

Value

The function returns a specimens summary table.

Author(s)

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

Examples

```
## Not run:  
# To return a specimens table do:  
my_specimens <- get_specimens(19832)  
my_tbl <- specimens(my_specimens)  
  
## End(Not run)
```

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

Description

The grouped class for specimens from the Neotoma Paleoecology Database.

summary, sites-method	<i>Summary of objects within a sites object.</i>
-----------------------	--------------------------------------------------

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

taxa	<i>taxa</i>
------	-------------

Description

Show the samples table

Usage

```
taxa(object)
```

Arguments

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

Author(s)

Socorro Dominguez <sedv8808@gmail.com>

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	<i>Extract taxonomic data from a single site.</i>
------------------	---------------------------------------------------

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

```
## Not run:
somesites <- get_sites(datasestype = "pollen", limit = 3) %>%
  get_downloads()
diatomtaxa <- taxa(somesites[[1]])

## End(Not run)
```

taxa,sites-method	<i>Extract taxonomic data from a set of sites.</i>
-------------------	----------------------------------------------------

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

```
## Not run:
somesites <- get_sites(datasettype = "diatom", limit = 3) %>%
  get_downloads()
diatomtaxa <- taxa(somesites)
common_taxa <- diatomtaxa %>%
  dplyr::filter(sites == 3)

## End(Not run)
```

testNull

Clear NULL values and replace with value predefined value.

Description

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

Usage

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

Arguments

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

Value

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

Examples

```
## Not run:
# Passing a null value into the function returns 12:
a <- testNull(val = NULL, out = 12)
# Passing a non-NULL value returns that value:
b <- testNull(val = 11, out = 12)

## End(Not run)
```

toJSON

toJSON

Description

Export toJSON

Usage

```
toJSON(x)
```

Arguments

x Sites object to extract taxa table from

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 <sedv8808@gmail.com>

Examples

```
## Not run:
# To find all sites that contain the string "Alex%"
alex.sites <- get_sites(sitename="Alex%")
Convert the object to json
toJSON(alex.sites)

## End(Not run)
```

toWide

*toWide***Description**

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

Usage

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

Arguments

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

Examples

```
## Not run:
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, all_data=TRUE) %>%
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')

## End(Not run)
```

use_na	<i>Change NA values from logic to a prescribed type.</i>
--------	----------------------------------------------------------

Description

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

Usage

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

Arguments

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

write.csv,chronologies-method
<i>write CSV</i>

Description

write CSV

Usage

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

Arguments

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

```
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.

```
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.

```
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().

```
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.

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

Description

Get or remove sites by numeric index

Usage

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

Arguments

x	The collunits object
i	The numeric index

`[,datasets,numeric,ANY-method`*Get or remove datasets by numeric index*

Description

Get or remove datasets by numeric index

Usage

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

Arguments

x	The datasets object
i	The numeric index

[,site,character,ANY-method]

Get site field by character index

Description

Get site field by character index

Usage

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

Arguments

x	The site object
i	The column indicator

[,site,numeric,ANY-method]

Get site field by numeric index

Description

Get site field by numeric index

Usage

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

Arguments

x	The site object
i	The column indicator

```
[,sites,numeric,ANY-method
```

Get or remove sites by numeric index

Description

Get or remove sites by numeric index

Usage

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

Arguments

x	The sites object
i	The numeric index

Examples

```
## Not run:  
some_site <- get_sites(sitename = "Site%")  
some_site[2]  
  
## End(Not run)
```

```
[,specimens,numeric,ANY-method
```

Get or remove specimens by numeric index

Description

Get or remove specimens by numeric index

Usage

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

Arguments

x	The specimens object
i	The numeric index

```
[<-,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.

```
[<-,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.

```
[<-,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.

```
[<-,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.

```
[<-,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.

```
[<-,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.

```
[<-,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.

```
[<-,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.

```
[[,chronologies,numeric,ANY-method
      Extract
```

Description

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

Usage

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

Arguments

x	chronologies object
i	iteration in chronologies list

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

Description

Obtain one of the elements within a collunits list

Usage

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

Arguments

x	collunits object
i	iteration in collunits list

[[,contacts,numeric,ANY-method

Extract or Replace Parts of an Object

Description

Extract or Replace Parts of an Object

Usage

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

Arguments

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

[[,datasets,numeric,ANY-method

Slicer

Description

Obtain one of the elements within a datasets list

Usage

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

Arguments

x	datasets object
i	iteration in datasets list

```
[[,publications,numeric,ANY-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,ANY'
x[[i]]
```

Arguments

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

```
[[,samples,numeric,ANY-method
```

Slicer

Description

Obtain one of the elements within a samples list

Usage

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

Arguments

x	samples object
i	iteration in samples list

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

Description

Obtain one of the elements within a sites list

Usage

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

Arguments

x	sites object
i	iteration in sites list

Examples

```
## Not run:
some_site <- get_sites(sitename = "Site%")
some_site[[2]]

## End(Not run)
```

```
[[,specimens,numeric,ANY-method
      Slicer
```

Description

Obtain one of the elements within a specimens list

Usage

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

Arguments

x	specimens object
i	iteration in specimens list

```
[[<-,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

```
[[<-,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

[[<-,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

[[<-,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

```
[[<-,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

```
$,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

\$.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

\$.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

\$.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

<i>\$,contact-method</i>	<i>Extract or Replace Parts of an Object</i>
--------------------------	----------------------------------------------

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.

<i>\$,contacts-method</i>	<i>Extract or Replace Parts of an Object</i>
---------------------------	----------------------------------------------

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.

<i>\$,dataset-method</i>	<i>\$</i>
--------------------------	-----------

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

\$.datasets-method	<i>\$ for datasets</i>
--------------------	------------------------

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.

\$.publication-method	<i>Extract an element from a publication</i>
-----------------------	----------------------------------------------

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)

\$.sample-method	<i>\$</i>
------------------	-----------

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

\$,samples-method	<i>\$for samples</i>
-------------------	----------------------

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

\$,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

\$,sites-method	<i>\$for sites</i>
-----------------	--------------------

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

\$.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

\$.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.

\$<-,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.

\$<-,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.

\$<-,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.

<code>\$<- ,site-method</code>	<i>Assign site field by numeric index</i>
-----------------------------------	-------------------------------------------

Description

Assign site field by numeric index

Usage

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

Arguments

<code>x</code>	The site object.
<code>name</code>	name of the slot
<code>value</code>	The value to be used.

<code>\$<- ,specimen-method</code>	<i>Assign specimen field by numeric index</i>
---------------------------------------	-----------------------------------------------

Description

Assign specimen field by numeric index

Usage

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

Arguments

<code>x</code>	The specimen object.
<code>name</code>	name of the slot.
<code>value</code>	The value to be used.