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

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Contents

add_chronology	6
add_chronology,collunit,chronology,data.frame-method	7
as.data.frame,authors-method	8
as.data.frame,chronologies-method	8
as.data.frame,chronology-method	9

as.data.frame,collunit-method	9
as.data.frame,collunits-method	10
as.data.frame,contact-method	10
as.data.frame,contacts-method	11
as.data.frame,dataset-method	11
as.data.frame,datasets-method	12
as.data.frame,publication-method	12
as.data.frame,publications-method	13
as.data.frame,site-method	13
as.data.frame,sites-method	14
as.data.frame,taxa-method	14
as.data.frame,taxon-method	15
as.list,sites-method	15
author-class	16
authors-class	16
build_specimen	17
c,chronologies-method	17
c,collunits-method	18
c,contact-method	18
c,contacts-method	19
c,datasets-method	19
c,missingOrNULL-method	20
c,publications-method	20
c,samples-method	21
c,sites-method	21
c,taxa-method	22
check_contacts	22
check_contacts.contacts	23
chroncontrols	23
chroncontrols,site-method	24
chroncontrols,sites-method	24
chronologies	25
chronologies,collunit-method	25
chronologies,collunits-method	26
chronologies,site-method	26
chronologies,sites-method	27
chronologies-class	27
chronology-class	27
cite_data	28
cite_data,site-method	28
cite_data,sites-method	29
collunit-class	29
collunits	30
collunits,site-method	30
collunits,sites-method	31
collunits-class	31
contact-class	31
contacts-class	32

coordinates	32
coordinates,sites-method	33
dataset-class	33
datasets	34
datasets,collunit-method	34
datasets,collunits-method	35
datasets,site-method	35
datasets,sites-method	36
datasets-class	36
doi	36
doi,publication-method	37
doi,site-method	37
doi,sites-method	38
filter	38
filter.sites	40
getids	41
getids.collunit	42
getids.collunits	42
getids.site	43
getids.sites	43
get_contacts	44
get_contacts.default	44
get_contacts.numeric	45
get_datasets	45
get_datasets.default	47
get_datasets.numeric	48
get_datasets.site	48
get_datasets.sites	49
get_downloads	49
get_downloads.numeric	51
get_downloads.sites	52
get_manual	52
get_publications	53
get_publications.default	54
get_publications.numeric	54
get_publications.publication	55
get_publications.publications	56
get_sites	57
get_sites.default	59
get_sites.numeric	60
get_stats	60
get_table	61
get_taxa	62
get_taxa.default	62
get_taxon	63
get_taxon.default	63
get_taxon.numeric	64
length,chronologies-method	64

length,collunits-method	65
length,datasets-method	65
length,publications-method	66
length,samples-method	66
length,sites-method	67
length,taxa-method	67
missingOrNULL-class	68
names,collunit-method	68
names,contact-method	68
names,dataset-method	69
names,publication-method	69
names,publications-method	70
names,site-method	70
names,taxon-method	71
pingNeotoma	71
plot,sites-method	72
plotLeaflet	72
plotLeaflet,site-method	73
plotLeaflet,sites-method	73
publication-class	74
publications-class	74
repositories-class	75
repository-class	75
sample-class	75
samples	76
samples,collunit-method	76
samples,collunits-method	77
samples,site-method	77
samples,sites-method	78
samples-class	78
selectMatch	79
selectMatch,publication,logical-method	79
selectMatch,publication,numeric-method	80
set_chronology	80
set_collunit	81
set_contact	83
set_dataset	84
set_default	85
set_default,chronologies-method	86
set_publications	86
set_sample	88
set_server	89
set_site	90
show,collunit-method	91
show,collunits-method	91
show,contact-method	92
show,contacts-method	92
show,dataset-method	93

show,datasets-method	93
show,publication-method	94
show,publications-method	94
show,site-method	95
show,sites-method	95
show,taxa-method	96
show,taxon-method	96
showMatch	97
showMatch,publication-method	97
site-class	98
sites-class	98
specimen-class	98
specimens-class	98
summary,sites-method	99
taxa	99
taxa,collunit-method	100
taxa,collunits-method	100
taxa,site-method	101
taxa,sites-method	101
taxa-class	102
taxon-class	102
toWide	103
write.csv,chronologies-method	104
write.csv,collunits-method	104
write.csv,datasets-method	105
write.csv,sites-method	105
write.csv,taxa-method	106
[,collunits,numeric-method	106
[,datasets,numeric-method	107
[,site,character-method	107
[,site,numeric-method	108
[,sites,numeric-method	108
[,taxa,numeric-method	109
[<-,collunit,character,ANY,ANY-method	109
[<-,collunit,numeric,ANY,ANY-method	110
[<-,dataset,character,ANY,ANY-method	110
[<-,dataset,numeric,ANY,ANY-method	111
[<-,sample,character,ANY,ANY-method	111
[<-,site,character,ANY,ANY-method	112
[<-,site,numeric,ANY,ANY-method	112
[<-,taxon,character,ANY,ANY-method	113
[<-,taxon,numeric,ANY,ANY-method	113
[[,chronologies,numeric-method	114
[[,collunits,numeric-method	114
[[,contacts,numeric-method	115
[[,datasets,numeric-method	115
[[,publications,numeric-method	116
[[,samples,numeric-method	116

[[,sites,numeric-method	117
[[,taxa,numeric-method	117
[[<-,collunits,ANY,ANY,ANY-method	118
[[<-,datasets,ANY,ANY,ANY-method	118
[[<-,publications,ANY,ANY,ANY-method	119
[[<-,samples,ANY,ANY,ANY-method	119
[[<-,sites,ANY,ANY,ANY-method	120
[[<-,taxa,ANY,ANY,ANY-method	120
\$.chronologies-method	121
\$.chronology-method	121
\$.collunit-method	122
\$.collunits-method	122
\$.contact-method	123
\$.contacts-method	123
\$.dataset-method	124
\$.datasets-method	124
\$.publication-method	125
\$.sample-method	125
\$.samples-method	126
\$.site-method	126
\$.sites-method	127
\$.taxa-method	127
\$.taxon-method	128
\$<-,chronology-method	128
\$<-,collunit-method	129
\$<-,dataset-method	129
\$<-,site-method	130
\$<-,taxon-method	130

Index 131

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

Value

chronology object defined by user,

add_chronology,collunit,chronology,data.frame-method

Add a new chronology into an existing collectionunit.

Description

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

Usage

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

Arguments

object	A collection unit object
x	A chronology object generated using set_chronology()
y	A data.frame of sample ages, with required columns: "analysisunitid", "age", "agetype", "ageolder", and "ageyounger".

Details

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

Value

chronologies with new added chronology

as.data.frame,authors-method

Convert a publication author to a data.frame

Description

Convert a publication author to a data.frame

Usage

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

Arguments

x An author

Value

data.frame with publications metadata

as.data.frame,chronologies-method

as.data.frame chronologies

Description

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

Usage

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

Arguments

x chronologies object

Value

data.frame with chronologies metadata

`as.data.frame,chronology-method`*Create a data.frame from a chronology object.*

Description

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

Usage

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

Arguments

x chronology object

Value

data.frame

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

Description

show as dataframe

Usage

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

Arguments

x site object

Value

data.frame object with a collection units metadata

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

Description

show as dataframe as prep to save as csv

Usage

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

Arguments

x collunits object

Value

data.frame of multiple collection units metadata.

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

Description

Transform a contacts object to a data.frame()

Usage

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

Arguments

x A contact object.

Value

data.frame object with contact metadata

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

Description

Transform a contacts object to a data.frame()

Usage

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

Arguments

x A contacts object.

Value

data.frame object with multiple contacts metadata

`as.data.frame,dataset-method`*as.data.frame dataset*

Description

show as dataframe as prep to save as csv

Usage

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

Arguments

x dataset object

Value

data.frame with dataset metadata

as.data.frame,datasets-method
as.data.frame datasets

Description

show as dataframe as prep to save as csv

Usage

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

Arguments

x datasets object

Value

data.frame with datasets metadata

as.data.frame,publication-method
Convert a publication to a data.frame

Description

Convert a publication to a data.frame

Usage

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

Arguments

x A publication object.

Value

data.frame with publications' metadata.

`as.data.frame,publications-method`*Convert publications to a data.frame*

Description

Convert publications to a data.frame

Usage

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

Arguments

x A publications object.

Value

data.frame with publications' metadata.

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

Description

show as dataframe as prep to save as csv

Usage

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

Arguments

x site object

Value

data.frame object with site metadata

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

Description

shows object as data.frame

Usage

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

Arguments

x sites object

Value

data.frame object with sites metadata

as.data.frame, taxa-method
as.data.frame taxa

Description

show as dataframe as prep to save as csv

Usage

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

Arguments

x taxa object

Value

data.frame with taxa metadata

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

Description

show as dataframe as prep to save as csv

Usage

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

Arguments

x taxon object

Value

data.frame with taxon metadata

```
as.list,sites-method    as.list sites
```

Description

show as dataframe as prep to save as csv

Usage

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

Arguments

x sites object

Value

list object with sites metadata

author-class

An S4 class for the authors of a Neotoma publication.

Description

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

Value

object of class `author`

Examples

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

authors-class

An S4 class for a set of Neotoma author objects.

Description

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

Value

object of class `authors`

Examples

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

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

Description

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

Usage

```
build_specimen(x)
```

Arguments

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

Value

A simple specimen object

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

Description

c Method - Combine chronologies objects

Usage

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

Arguments

x	chronologies object 1
y	chronologies object 2

Value

concatenated chronologies

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

Description

c Method - Combine collunits objects

Usage

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

Arguments

x	collunits object 1
y	collunits object 2

Value

concatenated collection units without duplicates

c,contact-method	<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

Value

contacts concatenated object

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

Value

concatenated and clean objects

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

Value

concatenated datasets object

c,missingOrNULL-method

c Method for NULL values

Description

c Method for NULL values

c Method for NULL values

Usage

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

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

Arguments

x	NULL object
y	sites/datasets object

Value

concatenated collunits object

list of concatenated items when the first object is NULL

c,publications-method *Combine publication objects.*

Description

Combine publication objects.

Usage

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

Arguments

x	A publications object.
y	A publications object

Value

concatenated publications object

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

Description

c Method - Combine datasets objects

Usage

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

Arguments

x	datasets object 1
y	datasets object 2

Value

concatenated samples 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

Value

concatenated and cleaned sites object

c, taxa=method	<i>c Method - Combine taxa objects</i>
----------------	--

Description

c Method - Combine taxa objects

Usage

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

Arguments

x	taxa object 1
y	taxa object 2

Value

concatenated taxa object

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

Description

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

Usage

```
check_contacts(x, ...)
```

Arguments

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

Value

contacts object

check_contacts.contacts	<i>Get contact information for Neotoma contributors</i>
-------------------------	---

Description

Get contact information for Neotoma contributors

Usage

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

Arguments

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

Value

contacts object

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

Description

Show the samples table

Usage

```
chroncontrols(x)
```

Arguments

- x Sites object to extract chroncontrols table from

Value

data.frame with chroncontrols information

`chroncontrols,site-method`*Recover information about the chron controls for a collectionunit.*

Description

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

Usage

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

Arguments

x site object

Value

data.frame with chronological controls

`chroncontrols,sites-method`*Recover information about the chron controls for a collectionunit.*

Description

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

Usage

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

Arguments

x sites object

Value

data.frame with chronological controls

chronologies	<i>Obtain the chronology from a record or multiple records.</i>
--------------	---

Description

Obtain the chronology from a record or multiple records.

Usage

```
chronologies(x)
```

Arguments

x	sites object that contains chronologies
---	---

Value

chronologies object with all chronologies used.

chronologies, collunit-method	<i>Extract chronologies from a collunit object.</i>
-------------------------------	---

Description

Extract chronologies from a collunit object.

Usage

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

Arguments

x	A collunit object
---	-------------------

Value

chronologies from a collunit object

chronologies,collunits-method

Extract chronologies from a collunits object.

Description

Extract chronologies from a collunits object.

Usage

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

Arguments

x A collunits object

Value

chronologies from a collunits object

chronologies,site-method

Extract chronologies from a site object.

Description

Extract chronologies from a site object.

Usage

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

Arguments

x A site object

Value

chronologies from a site object

`chronologies,sites-method`*Extract chronologies from a sites object.*

Description

Extract chronologies from a sites object.

Usage

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

Arguments

x A sites object

Value

chronologies from a sites object

`chronologies-class`*S4 class for chronologies information*

Description

The grouped class for chronologies from the Neotoma Paleoecology Database.

Value

object of class chronologies

`chronology-class`*S4 class for chronologies information*

Description

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

Value

object of class chronology

cite_data	<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.
---	------------------------------------

Value

data.frame with citation data

cite_data,site-method	<i>Obtain data citations from a single record.</i>
-----------------------	--

Description

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

Usage

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

Arguments

x	sites object
---	--------------

Value

data.frame object with citation information.

Examples

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

`cite_data,sites-method`*Obtain data citations from multiple records.*

Description

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

Usage

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

Arguments

`x` sites object

Value

data.frame object with citation information.

Examples

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

`collunit-class`*S4 class for collection units information.*

Description

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

Value

object of class `collunit`

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

Description

Extract collection units from a sites object

Usage

```
collunits(object)
```

Arguments

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

Value

collunits detail from a sites object

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

Description

Extract collunits from a site object.

Usage

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

Arguments

object	A site object
--------	---------------

Value

collunits from a site object

collunits,sites-method

Extract collunits from a sites object.

Description

Extract collunits from a sites object.

Usage

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

Arguments

object A sites object

Value

collunits from a sites object

collunits-class

An S4 class for Neotoma Collection Units

Description

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

contact-class

An S4 class for Neotoma contacts

Description

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

Value

object of class contact

Examples

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

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

Description

An unordered list of individual S4 contact objects.

Value

object of class contacts

Examples

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

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

Description

Obtain coordinates from a sites object.

Usage

```
coordinates(obj, ...)
```

Arguments

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

Value

dataframe with coordinate values

`coordinates,sites-method`*Return the latitude and longitude of sites*

Description

Return the latitude and longitude of sites

Usage

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

Arguments

<code>obj</code>	A sites object
<code>...</code>	Additional parameters associated with the call.

Value

`data.frame` object with site coordinates.

`dataset-class`*S4 class for dataset information*

Description

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

Value

object of class `dataset`

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

Description

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

Usage

```
datasets(object)
```

Arguments

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

Value

datasets object specific to the metadata contained in datasets

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

Description

Extract datasets from a collunit object.

Usage

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

Arguments

object	A collunit object
--------	-------------------

Value

datasets from a collunit object

`datasets, collunits-method`*Extract datasets from a collunits object.*

Description

Extract datasets from a collunits object.

Usage

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

Arguments

object A collunits object

Value

datasets from a collunits object

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

Description

Extract datasets from a site object.

Usage

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

Arguments

object A site object

Value

datasets from a site object

Value

doi object with DOI information

doi,publication-method

Get a publication DOI.

Description

Get a publication DOI.

Usage

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

Arguments

x A publication object.

Value

DOI from a publication

doi,site-method

Obtain dataset DOIs from records.

Description

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

Usage

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

Arguments

x a Neotoma2 site object

Value

data.frame object with DOIs information.

Examples

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

doi, sites-method	<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 'sites'
doi(x)
```

Arguments

x a Neotoma2 site object

Value

data.frame object with DOIs information.

Examples

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

filter	<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

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

Arguments

<code>x</code>	A site, dataset or download.
<code>...</code>	arguments to filter by.

Value

filtered sites object

filter.sites

Apply a filter for Neotoma sites objects.

Description

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

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

Usage

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

Arguments

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

Value

filtered sites object

Examples

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

getids

Get object IDs

Description

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

Usage

```
getids(x, order = TRUE)
```

Arguments

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

Value

`data.frame` containing siteid, datasetid, and collunitid

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

Description

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

Usage

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

Arguments

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

Value

data.frame containing siteid, datasetid, and collunitid

Examples

```
marion <- get_sites(sitename = "Marion Lake")  
collunitids <- getids(collunits(marion)[[1]])
```

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

Description

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

Usage

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

Arguments

x	A Neotoma2 collunits object.
order	sort items by siteid, collunitid, datasetid

Value

data.frame containing siteid, datasetid, and collunitid

Examples

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

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

Description

Get object IDs from a site object.

Usage

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

Arguments

x	A Neotoma2 site object.
order	sort items by siteid, collunitid, datasetid

Value

data.frame containing siteid, datasetid, and collunitid

getids.sites	<i>Get object IDs from sites</i>
--------------	----------------------------------

Description

Get object IDs from sites

Usage

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

Arguments

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

Value

data.frame containing siteid, datasetid, and collunitid

get_contacts	<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)

Value

contacts object

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)

Value

contacts object

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)

Value

contacts object

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

Description

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

Usage

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

Arguments

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

Details

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

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

Value

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

Author(s)

Socorro Dominguez <dominguezvid@wisc.edu>

Examples

```
# To find all datasets with a min altitude of 12 and a max altitude of 25:
sites_12to25 <- get_datasets(altmin=12, altmax=25)
# To find all datasets in Brazil
brazil <- '{"type": "Polygon",
"coordinates": [[
  [-73.125, -9.102096738726443],
  [-56.953125, -33.137551192346145],
  [-36.5625, -7.710991655433217],
  [-68.203125, 13.923403897723347],
  [-73.125, -9.102096738726443]]]}'
brazil_datasets <- get_datasets(loc = brazil[1], limit=2)
# To obtain the dataset metadata:
datasets(brazil_datasets)
# There is insufficient metadata at this point to obtain information
# about taxa present at the site. We must use get_downloads() to
# obtain the full set of sample information:
# This fails: taxa(brazil_datasets)
```

get_datasets.default *Get Dataset Default*

Description

Get Dataset Default

Usage

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

Arguments

x	Use a single number to extract dataset information
...	accepted arguments, see details for more information.

Value

sites object with full metadata up to the dataset level

get_datasets.numeric *Get Dataset Numeric*

Description

Get Dataset Numeric

Usage

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

Arguments

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

Value

sites object with full metadata up to the dataset level

Examples

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

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

Description

Get Dataset from a site object.

Usage

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

Arguments

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

Value

sites object with full metadata up to the dataset level

Examples

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

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()

Value

sites object with full metadata up to the dataset level

Examples

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

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 <dominguezvid@wisc.edu>

Examples

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

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

```
get_downloads.numeric  get_downloads
```

Description

get_downloads

Usage

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

Arguments

x	Use a single number to extract site information
...	arguments in ellipse form

Value

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

get_downloads.sites *get_downloads sites*

Description

get_downloads sites

Usage

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

Arguments

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

Value

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

get_manual *get_manual*

Description

Open up the Neotoma manual homepage.

Usage

```
get_manual()
```

Value

NULL side effect for opening browser with the manual

Author(s)

Simon Goring <goring@wisc.edu>

Examples

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

get_publications	<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.

Value

publications object

Examples

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

```
get_publications.default
```

Get publication information from Neotoma

Description

Get publication information from Neotoma

Usage

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

Arguments

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

Value

publications object

Examples

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

```
get_publications.numeric
```

Get publications using their unique identifier.

Description

Get publications using their unique identifier.

Usage

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

Arguments

`x` integer A contact ID

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

Value

publications object

Examples

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

```
get_publications.publication
```

Update information for a publications object.

Description

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

Usage

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

Arguments

`x` integer A publication

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

Value

updated publication object

Examples

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

```
get_publications.publications
```

Update metadata for a set of publication objects.

Description

Update metadata for a set of publication objects.

Usage

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

Arguments

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

Value

publications object

Examples

```
# Take a publication object and purposely degrade the metadata:
bad_pub <- get_publications(c(666, 667, 668))
# Note this only changes the reported year, not the citation string.
bad_pub[[1]]@year <- "1923"
bad_pub[[1]]@publicationid <- NA_integer_
updated_pubs <- get_publications(bad_pub)
# Only the first publication object has any matches. It's the only one
```

```
# that is missing its publicaitonid.
attr(updated_pubs[[1]], "matches")
attr(updated_pubs[[2]], "matches")
# we see the proper citation in the record:
updated_pubs[[1]] <- attr(updated_pubs[[1]], "matches")[[1]]
```

get_sites

get_sites

Description

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

Usage

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

Arguments

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

Details

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

- `siteid` The unique site ID (integer) in Neotoma. Can be passed as a vector of site IDs.
- `sitename` The site name, or approximate match using the `%` wildcard.
- `database` The constituent database for the record. See `get_table("constituentdatabases")`
- `altmin` The minimum altitude range for site elevation (in meters).
- `altmax` The maximum altitude range for site elevation (in meters).
- `datasetid` The unique dataset ID (integer) in Neotoma. Can be passed as a vector of dataset IDs.
- `datasettype` Neotoma contains data for a number of datasettypes. This returns a subset of data types. For a complete list of available datasettypes, run `neotoma2::get_table('datasettypes')`
- `doi` The dataset DOI for a dataset contained within a site. Can be passed as a vector of DOIs.

- **gpid** The geopolitical name or identifier containing a site. Can be passed as a vector of names.
- **keywords** Keywords for samples within a set of sites. For example "modern" indicates a sample within the record uses the keyword "modern".
- **contacts** Contact names or IDs associated with a site.
- **ageyoung** A minimum spanning age for the record, in years before radiocarbon present (1950).
- **ageold** A maximum spanning age for the record, in years before radiocarbon present (1950).
- **ageof** An age which must be contained within the range of sample ages for a site.
- **taxa** The names of taxa which must be present within samples in a record.
- **all_data** The API only downloads the first 25 records of the query. For the complete records, use `all_data=TRUE`. This call will then return a data object that contains site metadata for one or more sites, along with limited metadata describing the collection units and datasets located at that site.

Value

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

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

Author(s)

Socorro Dominguez <dominguezvid@wisc.edu>

Examples

```
## Find sites with a min altitude of 12m and a max altitude of 25m
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 sites 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_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))
}

```

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.

Value

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

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

Author(s)

Socorro Dominguez <dominguezvid@wisc.edu>

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

Value

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

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

Examples

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

get_stats	<i>get_stats</i>
-----------	------------------

Description

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

Usage

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

Arguments

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

Details

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

Value

data.frame with summary statistics

Author(s)

Socorro Dominguez <dominguezvid@wisc.edu>
Simon Goring <goring@wisc.edu>

Examples

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

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

Description

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

Usage

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

Arguments

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

Value

selected table values from the Database

Examples

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

get_taxa	<i>get_taxa</i>
----------	-----------------

Description

a sites object with the requested taxa.

Usage

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

Arguments

- x string taxa name or names
- ... accepted arguments, see details for more information.

Value

A Neotoma2 sites object with datasets with the requested taxa.

get_taxa.default	<i>Get Taxa Default</i>
------------------	-------------------------

Description

Get Taxa Default

Usage

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

Arguments

- x Use a taxon ID to extract site information
- ... accepted arguments, see details for more information.

Value

sites object containing the requested taxa

get_taxon	<i>get_taxon</i>
-----------	------------------

Description

a sites object with the requested taxa.

Usage

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

Arguments

x	string taxa name or names
...	accepted arguments, see details for more information.

Value

A Neotoma2 sites object with datasets with the requested taxa.

get_taxon.default	<i>Get Taxa Default</i>
-------------------	-------------------------

Description

Get Taxa Default

Usage

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

Arguments

x	Use a taxon ID to extract site information
...	accepted arguments, see details for more information.

Value

sites object containing the requested taxa

get_taxon.numeric	<i>Get Taxa Numeric</i>
-------------------	-------------------------

Description

Get Taxa Numeric

Usage

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

Arguments

x	Use a taxon ID to extract sites information
...	Additional parameters to get_taxa

Value

sites object with requested taxa

Examples

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

length,chronologies-method	<i>Length Method chronologies</i>
----------------------------	-----------------------------------

Description

Length Method chronologies

Usage

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

Arguments

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

Value

integer describing length

length,collunits-method

Length Method collunits

Description

Length Method collunits

Usage

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

Arguments

x collunits object

Value

length of a collunits object

length,datasets-method

Length Method datasets

Description

Length Method datasets

Usage

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

Arguments

x datasets object

Value

int that showcases the length of a datasets object

length,publications-method

Get the number of publications in a publications object.

Description

Get the number of publications in a publications object.

Usage

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

Arguments

x A publications object.

Value

int of the length of the publications object

length,samples-method *Length Method samples*

Description

Length Method samples

Usage

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

Arguments

x samples object

Value

int representing the length of samples object

length,sites-method	<i>Length Method Sites</i>
---------------------	----------------------------

Description

Length Method Sites

Usage

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

Arguments

x sites object

Value

int with the length of sites object

length,taxa-method	<i>Length Method taxa</i>
--------------------	---------------------------

Description

Length Method taxa

Usage

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

Arguments

x taxa object

Value

int that showcases the length of a taxa object

missingOrNull-class *c Method - Combine objects, including NULL*

Description

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

names,collunit-method *Get slot names*

Description

Get all names for named elements within a collunit object.

Usage

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

Arguments

x A collection unit object.

Value

NULL. Shows the names of the slots

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

Description

Get names of contacts slots

Usage

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

Arguments

x A contact object.

Value

names of slots

names,dataset-method *Get slot names*

Description

Get all names for named elements within a dataset object.

Usage

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

Arguments

x A dataset object.

Value

list with all names of dataset slots

names,publication-method
Get slot names for a publication object.

Description

Get slot names for a publication object.

Usage

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

Arguments

x A publication object.

Value

string with publication slots' names

names,publications-method

Get slot names for a publication object.

Description

Get slot names for a publication object.

Usage

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

Arguments

x A publications object.

Value

string with publications slots' names

names,site-method

Get slot names

Description

Get all names for named elements within a site object.

Usage

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

Arguments

x A site object.

Value

names of the slots of a site object

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

Description

Get all names for named elements within a taxon object.

Usage

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

Arguments

x A taxon object.

Value

list with all names of taxon slots

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

Description

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

Usage

```
pingNeotoma(server = "neotoma")
```

Arguments

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

Value

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

Examples

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

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

Description

Plot site coordinates using a basic plot.

Usage

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

Arguments

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

Value

plot object with site coordinates.

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

Description

Plot sites on a leaflet map

Usage

```
plotLeaflet(object)
```

Arguments

object	Sites object to plot
--------	----------------------

Value

leaflet map with site markers

Author(s)

Socorro Dominguez <dominguezvid@wisc.edu>

plotLeaflet,site-method
plotLeaflet

Description

Plot a site on a leaflet map

Usage

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

Arguments

object Site object to plot

Value

leaflet map

Examples

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

plotLeaflet,sites-method
plotLeaflet

Description

Plot sites on a leaflet map

Usage

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

Arguments

object Sites object to plot

Value

leaflet map

Examples

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

publication-class	<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.

Value

object of class publication

Examples

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

publications-class	<i>An S4 class for multi-publication information from the Neotoma 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.

Value

object of class publications

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

Description

The grouped class for repositories from the Neotoma Paleoecology Database.

Value

object of class repositories

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

Description

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

Value

object of class repository

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

Description

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

Value

object of class sample

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

Description

Obtain samples from a record or multiple records.

Usage

```
samples(x)
```

Arguments

x	sites object
---	--------------

Value

data.frame with record information at sample level

samples, collunit-method	<i>samples</i>
--------------------------	----------------

Description

Obtain elements from collunit

Usage

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

Arguments

x	collunit object
---	-----------------

Value

data.frame with sample records

samples, collunits-method

Get samples from a collectionunit or set of collection units:

Description

Obtain elements from collunits

Usage

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

Arguments

x collunits object

Value

data.frame with sample records

samples, site-method *samples*

Description

Obtain elements on the samples level

Usage

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

Arguments

x site object

Value

data.frame with sample records

Examples

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

`samples, sites-method` *samples*

Description

Obtain all samples within a sites object

Usage

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

Arguments

x sites object

Value

data.frame with sample records

Examples

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

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

Description

The grouped class for samples from the Neotoma Paleoecology Database.

Value

object of class `samples`

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

Description

Select the best match for an object.

Usage

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

Arguments

x	object
n	n elements that are a best match

Value

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

```
selectMatch(publication, logical-method)
```

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

Description

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

Usage

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

Arguments

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

Value

the best match to the selected publication.

```
selectMatch,publication,numeric-method
```

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

Description

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

Usage

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

Arguments

x	A publication object
n	The match number.

Value

the best match to the selected publication.

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

Description

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

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

Usage

```
set_chronology(
  x = NA,
  chronologyid = NA_integer_,
  notes = NA_character_,
  contact = list(),
  agemodel = NA_character_,
  ageboundolder = NA_integer_,
  ageboundyounger = NA_integer_,
  isdefault = NA_integer_,
```

```

    dateprepared = as.Date(character(0)),
    modelagetype = NA_character_,
    chronologyname = NA_character_,
    chroncontrols = data.frame(0)
  )

```

Arguments

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

Value

chronology object

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

Description

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

Usage

```

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

```

Arguments

x	object to be set as collunit
collectionunitid	collection unit identifier
notes	notes
handle	handle
colldate	collection date
location	location of the collection unit
waterdepth	depth at where the sample is taken
gpslocation	location with GPS
collunittype	type of collection unit
collectiondevice	device used to collect the sample
collectionunitname	name of the collection unit
depositionalenvironment	depositional environment
datasets	datasets that the collection unit has
chronologies	chronologies taken from the collection unit
defaultchronology	best chronology model identifier to be used with this collection unit

Value

collunit object

Examples

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

set_contact

*Set contact information for a new record.***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 indentifiers across objects, and because we want to avoid conflicts between naming systems, a universally unique identifier (UUID) is created for the object ID. This is not to be updated to the database.

Usage

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

Arguments

x	Object to be set as a contact
contactid	An arbitrary Contact identification number.
familyname	Family or surname name of a person.
leadinginitials	Leading initials for given or forenames without spaces (e.g. G.G.).
givennames	Given or forenames of a person (e.g. George Gaylord). Initials with spaces are used if full given names are not known (e.g. G. G).

suffix	Suffix of a person's name (e.g. Jr., III).
ORCID	A unique ORCID (see https://orcid.org).
title	A person's title (e.g. Dr., Prof., Prof. Dr).
institution	The institution where an individual works.
email	An individuals email address
phone	Their phone number
contactstatus	Are they "active" or "retired"?
fax	Do people still use fax machines?
url	Their homepage
address	A physical address
notes	Notes about the individual

Value

contact object

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

Description

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

Usage

```
set_dataset(
  x = NA,
  datasetid = NA_integer_,
  datasetname = NA_character_,
  database = NA_character_,
  doi = NA,
  datasettype = NA_character_,
  age_range_old = NA_integer_,
  age_range_young = NA_integer_,
  age_units = NA_character_,
  notes = NA_character_,
  pi_list = NA,
  samples = NULL,
  specimens = NULL
)
```

Arguments

x	object to be set as dataset,
datasetid	dataset identifier
datasetname	name of the dataset
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
age_units	age units
notes	notes
pi_list	pi list
samples	taxa objects
specimens	specimens slot

Value

dataset object

Examples

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

set_default

Set the default chronology within a collectionunit.

Description

Set the default chronology within a collectionunit.

Usage

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

Arguments

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

Value

sites object with new default chronology

set_default,chronologies-method

Change the default age model for a record.

Description

Change the default age model for a record.

Usage

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

Arguments

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

Value

chronologies object with a new defaulted chronology

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

Description

A function to create new publication objects by hand.

Usage

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

```

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

```

Arguments

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

state	State of publication.
country	Country of publication.
originallanguage	Original language of publication.
notes	Publication notes.
author	name of the author of publication.
Value	
publication object	
set_sample	<i>set Sample Information</i>

Description

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

Usage

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

Arguments

x	Object to be set as a sample
ages	ages
igsn	IGSN character
datum	dataframe of datum
depth	integer representing depth
sampleid	ID for sample
thickness	thickness of core

samplename	sample's name
sampleanalyst	Analyst's contact name
analysisunitid	Which analysis unit it is
analysisunitname	Analysis Unit's name

Value

sample object

Examples

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

set_server	<i>Set Neotoma API Source or Server</i>
------------	---

Description

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

Usage

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

Arguments

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

Value

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

Examples

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

set_site

*set Site Information for Fossil Sites***Description**

set Site Information for Fossil Sites

Usage

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

Arguments

x	Object to be set as a site
siteid	The unique site id for a site. If this site is new to Neotoma then leave the ID as NA (the default).
sitename	Actual site name as a character string.
geography	An sf object representing the site location, either as a polygon or point.
altitude	altitude/elevation of the site.
geopolitical	The geopolitical unit in which the site is located.
area	The area of the site or depositional basin in <i>ha</i> . Can be calculated from the polygon.
notes	additional information of the site
description	Function to create new site objects for personal analysis. The new object will not be uploaded to the database.
collunits	Collection units in the site

Value

site object

Examples

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

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

Description

Show the collection unit information

Usage

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

Arguments

object collunit object

Value

null used for side effects. Printing a data.frame

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

Description

Show the collection unit information

Usage

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

Arguments

object collunits object

Value

null used for side effects. Printing a data.frame

show,contact-method	<i>Show contact object</i>
---------------------	----------------------------

Description

Show contact object
Show a contact object

Usage

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

Arguments

object	a contact object
--------	------------------

Value

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

show,contacts-method	<i>Show a contacts object.</i>
----------------------	--------------------------------

Description

Show a contacts object.

Usage

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

Arguments

object	A contacts object.
--------	--------------------

Value

null - side effect for printing contacts object

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

Description

Show Dataset Method

Usage

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

Arguments

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

Value

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

show,datasets-method	<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
--------	-----------------

Value

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

show,publication-method

Print publications to screen.

Description

Print publications to screen.

Usage

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

Arguments

object A publication object.

Value

NULL - side effect function of printing a data.frame

show,publications-method

Show the contents of a publication object.

Description

Show the contents of a publication object.

Usage

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

Arguments

object A publications object

Value

NULL - side effect function of printing a data.frame

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

Description

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

Usage

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

Arguments

object	site object
--------	-------------

Value

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

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

Description

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

Usage

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

Arguments

object	sites object
--------	--------------

Value

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

show, taxa-method	<i>Show Taxa Method</i>
-------------------	-------------------------

Description

Show Taxa Method

Usage

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

Arguments

object taxon object

Value

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

show, taxon-method	<i>Show Taxon Method</i>
--------------------	--------------------------

Description

Show Taxon Method

Usage

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

Arguments

object taxon object

Value

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

showMatch	<i>Show matches for objects.</i>
-----------	----------------------------------

Description

Show matches for objects.

Usage

```
showMatch(x)
```

Arguments

x	object to show matches for
---	----------------------------

Value

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

showMatch,publication-method	<i>Show matched publication objects.</i>
------------------------------	--

Description

Show matched publication objects.

Usage

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

Arguments

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

Value

NULL printed matches with other publications

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

Description

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

Value

object of class site

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

Description

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

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

Description

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

Value

object of class specimen

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

Description

The grouped class for specimens from the Neotoma Paleoecology Database.

Value

object of class specimens

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

Value

data.frame object with site summary information

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

Description

Show the samples table

Usage

```
taxa(object)
```

Arguments

- object Sites object to extract taxa table from

Value

data.frame with taxa records

taxa,collunit-method *Extract taxonomic data from a set of sites.*

Description

Extract taxonomic data from a set of sites.

Usage

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

Arguments

object A collunit object.

Value

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

taxa,collunits-method *Extract taxonomic data from a set of sites.*

Description

Extract taxonomic data from a set of sites.

Usage

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

Arguments

object A collunits object.

Value

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

taxa,site-method	<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

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

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

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

<code>taxa-class</code>	<i>S4 class for taxa information</i>
-------------------------	--------------------------------------

Description

Taxa class for taxa information from the Neotoma Paleoecology Database.

Value

object of class `taxon`

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

Description

Taxon class for single taxon information from the Neotoma Paleoecology Database.

Value

object of class `taxon`

toWide	<i>toWide</i>
--------	---------------

Description

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

Usage

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

Arguments

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

Value

wide data.frame obtained from long samples data.frame

Examples

```
fourcorners <- '{"type": "Polygon",  
"coordinates": [[  
[-109.36060497194846, 37.69552879956651],  
[-107.813845732192, 37.69552879956651],  
[-107.813845732192, 36.80303716260222],  
[-109.36060497194846, 36.80303716260222],  
[-109.36060497194846, 37.69552879956651]  
]]}'  
  
# Download all vertebrate localities within a bounding box.  
fc_sites <- neotoma2::get_sites(loc = fourcorners[1])
```

```
fc_ds <- neotoma2::get_datasets(fc_sites) %>%
neotoma2::filter(datasettype=="vertebrate fauna")

fc_dl <- neotoma2::get_downloads(fc_ds)
fc_dl1 <- fc_dl[[1]]

fc_smp <- samples(fc_dl1)
toWide(fc_smp, ecologicalgroups=c('AVES', 'RODE'),
elementtypes='bone/tooth', unit='present/absent')
```

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

Description

write CSV

Usage

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

Arguments

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

Value

null, called for side effects

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

Description

write CSV

Usage

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

Arguments

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

Value

null side effect for saving a CSV file.

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

Description

write CSV

Usage

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

Arguments

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

Value

null -side effect for printing a CSV file

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

Description

write CSV

Usage

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

Arguments

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

Value

NULL side effect from saving a csv file

write.csv,taxa-method *write CSV*

Description

write CSV

Usage

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

Arguments

x taxa object
... Additional parameters associated with the call.

Value

null -side effect for printing a CSV file

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

Description

Retrieve sites by numeric index

Usage

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

Arguments

x The collunits object
i The numeric index

Value

null used for side effects. Printing a data.frame

[,datasets,numeric-method
<i>Get or remove datasets by numeric index</i>

Description

Get or remove datasets by numeric index

Usage

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

Arguments

x	The datasets object
i	The numeric index

Value

Get or remove datasets by numeric index

[,site,character-method
<i>Get site field by character index</i>

Description

Get site field by character index

Usage

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

Arguments

x	The site object
i	The column indicator

Value

sliced site object

[,site,numeric-method	<i>Get site field by numeric index</i>
-----------------------	--

Description

Get site field by numeric index

Usage

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

Arguments

- x The site object
- i The column indicator

Value

sliced site object

[,sites,numeric-method	<i>Get or remove sites by numeric index</i>
------------------------	---

Description

Get or remove sites by numeric index

Usage

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

Arguments

- x The sites object
- i The numeric index

Value

sliced site object

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

Description

Get or remove taxa by numeric index

Usage

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

Arguments

x	The taxa object
i	The numeric index

Value

Get or remove taxa by 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.

Value

sliced element

```
[<-,collunit,numeric,ANY,ANY-method
```

Assign collunit field by numeric index

Description

Assign collunit field by numeric index

Usage

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

Arguments

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

Value

sliced value

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

Assign dataset field by numeric index

Description

Assign dataset field by numeric index

Usage

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

Arguments

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

Value

dataset slot with new assigned character value

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

Assign dataset field by numeric index

Description

Assign dataset field by numeric index

Usage

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

Arguments

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

Value

dataset slot with new assigned numeric value

[<-,sample,character,ANY,ANY-method

Assign sample field by numeric index

Description

Assign sample field by numeric index

Usage

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

Arguments

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

Value

sample object with reassigned character values

```
[<-,site,character,ANY,ANY-method
  Assign site field by numeric index
```

Description

Assign site field by numeric index

Usage

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

Arguments

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

Value

site object with reassigned character values

```
[<-,site,numeric,ANY,ANY-method
  Assign site field by numeric index
```

Description

Assign site field by numeric index

Usage

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

Arguments

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

Value

sites object with reassigned numeric values

[<-,taxon,character,ANY,ANY-method

Assign taxon field by numeric index

Description

Assign taxon field by numeric index

Usage

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

Arguments

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

Value

taxon slot with new assigned character value

[<-,taxon,numeric,ANY,ANY-method

Assign taxon field by numeric index

Description

Assign taxon field by numeric index

Usage

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

Arguments

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

Value

taxon slot with new assigned numeric value

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

Description

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

Usage

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

Arguments

x	chronologies object
i	iteration in chronologies list

Value

selected chronology object

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

Description

Obtain one of the elements within a collunits list

Usage

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

Arguments

x	collunits object
i	iteration in collunits list

Value

sliced collunits object

[[,contacts,numeric-method

Extract or Replace Parts of an Object

Description

Extract or Replace Parts of an Object

Usage

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

Arguments

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

Value

sliced contacts

[[,datasets,numeric-method

Slicer

Description

Obtain one of the elements within a datasets list

Usage

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

Arguments

x	datasets object
i	iteration in datasets list

Value

sliced dataset object

```
[[,publications,numeric-method
```

Obtain one of the elements within a publication list.

Description

Obtain one of the elements within a publication list.

Usage

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

Arguments

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

Value

selected publications object from index

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

Slicer

Description

Obtain one of the elements within a samples list

Usage

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

Arguments

x	samples object
i	iteration in samples list

Value

samples sliced object

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

Description

Obtain one of the elements within a sites list

Usage

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

Arguments

x	sites object
i	iteration in sites list

Value

sliced site object

Examples

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

```
[[,taxa,numeric-method  
      Slicer
```

Description

Obtain one of the elements within a taxa list

Usage

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

Arguments

x	taxa object
i	iteration in taxa list

Value

sliced taxa object

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

Description

Obtain one of the elements within a collunits list

Usage

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

Arguments

x	collunits object
i	iteration in collunits list
value	The value to be used

Value

Modified collunits

[[<-,datasets,ANY,ANY,ANY-method
Insert dataset

Description

Obtain one of the elements within a datasets list

Usage

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

Arguments

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

Value

One dataset slot's value

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

Assign value to an element in a publication list.

Description

Assign value to an element in a publication list.

Usage

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

Arguments

x	A publications object.
i	A numeric index for the requested publication
value	The value to be used

Value

publications with new assigned value.

[[<-,samples,ANY,ANY,ANY-method

Insert sample

Description

Obtain one of the elements within a samples list

Usage

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

Arguments

x	samples object
i	iteration in samples list
value	The value to be used

Value

samples object with reassigned values

<code>[[<-,sites,ANY,ANY,ANY-method</code>
<i>Insert site</i>

Description

Obtain one of the elements within a sites list

Usage

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

Arguments

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

Value

sites object with reassigned values

<code>[[<-,taxa,ANY,ANY,ANY-method</code>
<i>Insert taxon</i>

Description

Obtain one of the elements within a taxa list

Usage

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

Arguments

x	taxa object
i	iteration in taxa list
value	The value to be used

Value

One taxon slot's value

\$.chronologies-method	<i>Extract</i>
------------------------	----------------

Description

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

Usage

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

Arguments

x	chronologies object
name	name of the slot

Value

A multiple chronologies

\$.chronology-method	<i>Extract</i>
----------------------	----------------

Description

Extract chronology metadata by slot name.

Usage

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

Arguments

x	chronology object
name	name of the slot

Value

value of the slot name

<code>\$.collunit-method</code>	<code>\$</code>
---------------------------------	-----------------

Description

Obtain slots of a collunit without using at-mark

Usage

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

Arguments

<code>x</code>	collunit object
<code>name</code>	name of the slot

Value

null prints element of a slot

<code>\$.collunits-method</code>	<i>\$ for collunits</i>
----------------------------------	-------------------------

Description

Obtain slots of a collunit without using at-mark

Usage

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

Arguments

<code>x</code>	collunits object
<code>name</code>	name of the slot

Value

null prints element of a slot

\$.contact-method	<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.

Value

value in the selected slot

\$.contacts-method	<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.

Value

object value from the slot

<code>\$.dataset-method</code>	<code>\$</code>
--------------------------------	-----------------

Description

Obtain slots of a dataset without using at-mark

Usage

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

Arguments

<code>x</code>	dataset object
<code>name</code>	name of the slot

Value

Obtain a dataset's slot value using `$`

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

Description

Obtain slots of a dataset without using at-mark

Usage

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

Arguments

<code>x</code>	datasets object
<code>name</code>	name of the slot.

Value

Obtain a datasets' slot value using `$`

\$.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)

Value

value in the selected slot

\$.sample-method	\$
------------------	----

Description

Obtain slots of a sample without using at-mark

Usage

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

Arguments

x	sample object
name	name of the slot

Value

value at selected slot

<code>\$,samples-method</code>	<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

Value

value at selected slot

<code>\$,site-method</code>	<code>\$</code>
-----------------------------	-----------------

Description

Obtain slots of a site without using at-mark

Usage

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

Arguments

x	site object
name	name of the slot

Value

value at chosen slot in the site object

\$.sites-method	<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

Value

value at chosen slot in the site object

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

Description

Obtain slots of a taxon without using at-mark

Usage

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

Arguments

x	taxa object
name	name of the slot.

Value

Obtain a taxa' slot value using \$

<code>\$,taxon-method</code>	<code>\$</code>
------------------------------	-----------------

Description

Obtain slots of a taxon without using at-mark

Usage

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

Arguments

<code>x</code>	taxon object
<code>name</code>	name of the slot

Value

Obtain a taxon’s slot value using `$`

<code>\$<- ,chronology-method</code>	<i>Replace part of an object</i>
---	----------------------------------

Description

Assign values to slots within a chronology object.

Usage

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

Arguments

<code>x</code>	A chronology object
<code>name</code>	The name of the chronology slot.
<code>value</code>	A value to be assigned to the chronology slot.

Value

reassigned chronology object

`$<- ,collunit-method` *Assign collunit field by numeric index*

Description

Assign collunit field by numeric index

Usage

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

Arguments

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

Value

assign a new value to a slot

`$<- ,dataset-method` *Assign dataset field by numeric index*

Description

Assign dataset field by numeric index

Usage

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

Arguments

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

Value

Assign new dataset by numeric index

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

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

Value

site object with reassigned values

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

Description

Assign taxon field by numeric index

Usage

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

Arguments

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

Value

Assign new taxon by numeric index

Index

[,collunits,numeric-method, 106
[,datasets,numeric-method, 107
[,site,character-method, 107
[,site,numeric-method, 108
[,sites,numeric-method, 108
[,taxa,numeric-method, 109
[<-,collunit,character,ANY,ANY-method, 109
[<-,collunit,numeric,ANY,ANY-method, 110
[<-,dataset,character,ANY,ANY-method, 110
[<-,dataset,numeric,ANY,ANY-method, 111
[<-,sample,character,ANY,ANY-method, 111
[<-,site,character,ANY,ANY-method, 112
[<-,site,numeric,ANY,ANY-method, 112
[<-,taxon,character,ANY,ANY-method, 113
[<-,taxon,numeric,ANY,ANY-method, 113
[[,chronologies,numeric-method, 114
[[,collunits,numeric-method, 114
[[,contacts,numeric-method, 115
[[,datasets,numeric-method, 115
[[,publications,numeric-method, 116
[[,samples,numeric-method, 116
[[,sites,numeric-method, 117
[[,taxa,numeric-method, 117
[[<-,collunits,ANY,ANY,ANY-method, 118
[[<-,datasets,ANY,ANY,ANY-method, 118
[[<-,publications,ANY,ANY,ANY-method, 119
[[<-,samples,ANY,ANY,ANY-method, 119
[[<-,sites,ANY,ANY,ANY-method, 120
[[<-,taxa,ANY,ANY,ANY-method, 120
\$,chronologies-method, 121
\$,chronology-method, 121
\$,collunit-method, 122
\$,collunits-method, 122
\$,contact-method, 123
\$,contacts-method, 123
\$,dataset-method, 124
\$,datasets-method, 124
\$,publication-method, 125
\$,sample-method, 125
\$,samples-method, 126
\$,site-method, 126
\$,sites-method, 127
\$,taxa-method, 127
\$,taxon-method, 128
\$<-,chronology-method, 128
\$<-,collunit-method, 129
\$<-,dataset-method, 129
\$<-,site-method, 130
\$<-,taxon-method, 130

add_chronology, 6
add_chronology,collunit,chronology,data.frame-method, 7

as.data.frame,authors-method, 8
as.data.frame,chronologies-method, 8
as.data.frame,chronology-method, 9
as.data.frame,collunit-method, 9
as.data.frame,collunits-method, 10
as.data.frame,contact-method, 10
as.data.frame,contacts-method, 11
as.data.frame,dataset-method, 11
as.data.frame,datasets-method, 12
as.data.frame,publication-method, 12
as.data.frame,publications-method, 13
as.data.frame,site-method, 13
as.data.frame,sites-method, 14
as.data.frame,taxa-method, 14
as.data.frame,taxon-method, 15
as.list,sites-method, 15
author-class, 16
authors-class, 16

- build_specimen, 17
- c, chronologies-method, 17
- c, collunits-method, 18
- c, contact-method, 18
- c, contacts-method, 19
- c, datasets-method, 19
- c, missingOrNULL-method, 20
- c, publications-method, 20
- c, samples-method, 21
- c, sites-method, 21
- c, taxa-method, 22
- check_contacts, 22
- check_contacts.contacts, 23
- chroncontrols, 23
- chroncontrols.site-method, 24
- chroncontrols.sites-method, 24
- chronologies, 25
- chronologies.collunit-method, 25
- chronologies.collunits-method, 26
- chronologies.site-method, 26
- chronologies.sites-method, 27
- chronologies-class, 27
- chronology-class, 27
- cite_data, 28
- cite_data.site-method, 28
- cite_data.sites-method, 29
- collunit-class, 29
- collunits, 30
- collunits.site-method, 30
- collunits.sites-method, 31
- collunits-class, 31
- contact-class, 31
- contacts-class, 32
- coordinates, 32
- coordinates.sites-method, 33
- dataset-class, 33
- datasets, 34
- datasets.collunit-method, 34
- datasets.collunits-method, 35
- datasets.site-method, 35
- datasets.sites-method, 36
- datasets-class, 36
- doi, 36
- doi.publication-method, 37
- doi.site-method, 37
- doi.sites-method, 38
- filter, 38
- filter.sites, 40
- get_contacts, 44
- get_contacts.default, 44
- get_contacts.numeric, 45
- get_datasets, 45
- get_datasets.default, 47
- get_datasets.numeric, 48
- get_datasets.site, 48
- get_datasets.sites, 49
- get_downloads, 49
- get_downloads.numeric, 51
- get_downloads.sites, 52
- get_manual, 52
- get_publications, 53
- get_publications.default, 54
- get_publications.numeric, 54
- get_publications.publication, 55
- get_publications.publications, 56
- get_sites, 57
- get_sites.default, 59
- get_sites.numeric, 60
- get_stats, 60
- get_table, 61
- get_taxa, 62
- get_taxa.default, 62
- get_taxon, 63
- get_taxon.default, 63
- get_taxon.numeric, 64
- getids, 41
- getids.collunit, 42
- getids.collunits, 42
- getids.site, 43
- getids.sites, 43
- length, chronologies-method, 64
- length, collunits-method, 65
- length, datasets-method, 65
- length, publications-method, 66
- length, samples-method, 66
- length, sites-method, 67
- length, taxa-method, 67
- missingOrNULL-class, 68
- names, collunit-method, 68
- names, contact-method, 68
- names, dataset-method, 69

names,publication-method, [69](#)
names,publications-method, [70](#)
names,site-method, [70](#)
names,taxon-method, [71](#)

pingNeotoma, [71](#)
plot,sites-method, [72](#)
plotLeaflet, [72](#)
plotLeaflet,site-method, [73](#)
plotLeaflet,sites-method, [73](#)
publication-class, [74](#)
publications-class, [74](#)

repositories-class, [75](#)
repository-class, [75](#)

sample-class, [75](#)
samples, [76](#)
samples,collunit-method, [76](#)
samples,collunits-method, [77](#)
samples,site-method, [77](#)
samples,sites-method, [78](#)
samples-class, [78](#)
selectMatch, [79](#)
selectMatch,publication,logical-method,
 [79](#)
selectMatch,publication,numeric-method,
 [80](#)
set_chronology, [80](#)
set_collunit, [81](#)
set_contact, [83](#)
set_dataset, [84](#)
set_default, [85](#)
set_default,chronologies-method, [86](#)
set_publications, [86](#)
set_sample, [88](#)
set_server, [89](#)
set_site, [90](#)
show,collunit-method, [91](#)
show,collunits-method, [91](#)
show,contact-method, [92](#)
show,contacts-method, [92](#)
show,dataset-method, [93](#)
show,datasets-method, [93](#)
show,publication-method, [94](#)
show,publications-method, [94](#)
show,site-method, [95](#)
show,sites-method, [95](#)
show,taxa-method, [96](#)

show,taxon-method, [96](#)
showMatch, [97](#)
showMatch,publication-method, [97](#)
site-class, [98](#)
sites-class, [98](#)
specimen-class, [98](#)
specimens-class, [98](#)
summary,sites-method, [99](#)

taxa, [99](#)
taxa,collunit-method, [100](#)
taxa,collunits-method, [100](#)
taxa,site-method, [101](#)
taxa,sites-method, [101](#)
taxa-class, [102](#)
taxon-class, [102](#)
toWide, [103](#)

write.csv,chronologies-method, [104](#)
write.csv,collunits-method, [104](#)
write.csv,datasets-method, [105](#)
write.csv,sites-method, [105](#)
write.csv,taxa-method, [106](#)