

# Package: neotoma (via r-universe)

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**Type** Package

**Title** Access to the Neotoma Paleocological Database Through R

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**Description** NOTE: This package is deprecated. Please use the neotoma2 package described at <https://github.com/NeotomaDB/neotoma2>. Access paleocological datasets from the Neotoma Paleocological Database using the published API (<<http://wnapi.neotomadb.org/>>), only containing datasets uploaded prior to June 2020. The functions in this package access various pre-built API functions and attempt to return the results from Neotoma in a usable format for researchers and the public.

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**URL** <https://docs.ropensci.org/neotoma>,  
<https://github.com/ropensci/neotoma>

**BugReports** <https://github.com/ropensci/neotoma/issues>

**Depends** R (>= 2.10)

**Imports** plyr, reshape2, jsonlite, httr, xml2, analogue, leaflet, dplyr, sf, assertthat, methods

**Suggests** testthat, knitr

**RoxygenNote** 7.2.1

**Repository** <https://ropensci.r-universe.dev>

**RemoteUrl** <https://github.com/ropensci/neotoma>

**RemoteRef** master

**RemoteSha** fd935c440bb5809502bb3d41c034af0ce7a45ecc

## Contents

ages	3
bind	4
browse	5
browse.dataset	6
browse.dataset_list	7
browse.default	7
browse.download	8
browse.download_list	8
compile_downloads	9
compile_taxa	10
counts	12
depths	13
download	14
get_chroncontrol	15
get_chroncontrol.dataset	16
get_chroncontrol.dataset_list	17
get_chroncontrol.default	17
get_chroncontrol.download	18
get_chroncontrol.download_list	18
get_closest	19
get_contact	20
get_dataset	21
get_dataset.default	24
get_dataset.download	25
get_dataset.download_list	26
get_dataset.geochronologic	26
get_dataset.geochronologic_list	27
get_dataset.integer	27
get_dataset.numeric	28
get_dataset.site	28
get_download	29
get_download.dataset	31
get_download.dataset_list	31
get_download.default	32
get_download.site	32
get_geochron	33
get_publication	34
get_publication.dataset	35
get_publication.dataset_list	36
get_publication.default	36
get_publication.download	37
get_publication.download_list	37
get_site	38
get_site.dataset	39
get_site.dataset_list	40
get_site.default	40

get_site.download . . . . .	41
get_site.download_list . . . . .	41
get_site.geochronologic . . . . .	42
get_site.geochronologic_list . . . . .	42
get_site.integer . . . . .	43
get_site.numeric . . . . .	43
get_table . . . . .	44
get_taxa . . . . .	45
gp.table . . . . .	46
plot_leaflet . . . . .	46
pollen.equiv . . . . .	47
read.tilia . . . . .	48
read_bacon . . . . .	48
StratipLOT.download . . . . .	50
StratipLOT.download_list . . . . .	51
taxa . . . . .	52
taxon.list . . . . .	53
write_agefile . . . . .	54
<b>Index</b>	<b>56</b>

---

ages

*Access proxy age data*

---

## Description

Extracts age information from objects and returns them in a useful format.

## Usage

```
ages(obj, ...)
```

```
## S3 method for class 'download'
```

```
ages(obj, ...)
```

```
## S3 method for class 'download_list'
```

```
ages(obj, ...)
```

## Arguments

`obj` an R object from which counts are to be extracted.

`...` arguments passed to other methods.

## Details

Methods are available for "download" and "download\_list" objects.

**Value**

Either a data frame of ages or a list of such objects.

**Author(s)**

Simon Goring

**Examples**

```
## Not run:
ostracodes <- get_dataset(datasettype = 'ostracode')

ostro.dl <- get_download(ostracodes)
ostro.ages <- ages(ostro.dl)

## End(Not run)
```

---

bind

*Function to bind objects together into a longer object.*

---

**Description**

From multiple download\*s, dataset\*s or sites, join them together into a single object.

**Usage**

```
bind(x, ...)
```

**Arguments**

x                    An object returned by one of the get\_\* commands for download, site or dataset.  
...                   other objects of the same class.

**Details**

To support further synthesis and analysis `compile_download` works to transform a list returned by [get\\_download](#) into a large data frame with columns for site and sample attributes and also with the associated assemblage data at each sample depth. This function also does the same for single sites.

**Value**

This command returns a larger list.

**Author(s)**

Simon J. Goring <simon.j.goring@gmail.com>

## References

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

## Examples

```
## Not run:
# Search for sites with "Thuja" pollen that are older than 8kyr BP and
# that are on the west coast of North America:
t8kyr.poa <- get_dataset(taxonname="Thuja*",
                        loc=c(-150, 20, -100, 60), ageyoung = 8000)
t8kyr.canis <- get_dataset(taxonname="Canis*",
                          loc=c(-150, 20, -100, 60), ageyoung = 8000)

t8kyr.co_site <- bind(t8kyr.poa, t8kyr.canis)
plot(t8kyr.co_site)

####
# We want to look at four different dataset types across a forest-prairie
# boundary:
dataset_types <- c("ostracode surface sample",
                  "water chemistry",
                  "diatom surface sample",
                  "pollen surface sample")

# Run the `get_dataset` function for each of the different dataset types
dataset_lists <- lapply(dataset_types,
                        function(x) {
                          get_dataset(datasettype=x,
                                       loc = c(-100,43,-92,48))
                        })

# Using do.call here to make sure that I don't have to split the list out.
new_datasets <- do.call(bind, dataset_lists)

# And voila!
plot(new_datasets)

## End(Not run)
```

---

browse

*Open a browser window to display a Neotoma dataset within the Neotoma Explorer*

---

## Description

Using a download or dataset object, open up a browser window in the users default browser. Passing a download\_list or dataset\_list will open Neotoma Explorer with the first object and return a warning.

Using a numeric value, download, download\_list, dataset or dataset\_list object, open up a browser window in the users default browser. Very large objects

### Usage

```
browse(x)
```

### Arguments

x                    A numeric value, download, download\_list, dataset or dataset\_list object.

### Value

Returns a NULL value, opens a browser.

### Author(s)

Simon J. Goring <simon.j.goring@gmail.com>

### References

Neotoma Project Website: <http://www.neotomadb.org> API Reference: <http://wnapi.neotomadb.org/doc/resources/sites>

### Examples

```
## Not run:
# Where are the XRF data?

xrf.data <- get_dataset(datasettype='X-ray fluorescence (XRF)')
browse(xrf.data)

## End(Not run)
```

---

browse.dataset	<i>Open a browser window to display a Neotoma dataset within the Neotoma Explorer</i>
----------------	---

---

### Description

Using a numeric value, download, download\_list, dataset or dataset\_list object, open up a browser window in the users default browser. Very large objects

### Usage

```
## S3 method for class 'dataset'
browse(x)
```

**Arguments**

x                    A dataset object.

---

browse.dataset\_list    *Open a browser window to display a Neotoma dataset within the Neotoma Explorer*

---

**Description**

Using a numeric value, download, download\_list, dataset or dataset\_list object, open up a browser window in the users default browser. Very large objects

**Usage**

```
## S3 method for class 'dataset_list'  
browse(x)
```

**Arguments**

x                    A dataset\_list object.

---

browse.default        *Open a browser window to display a Neotoma dataset within the Neotoma Explorer*

---

**Description**

Using a numeric value, download, download\_list, dataset or dataset\_list object, open up a browser window in the users default browser. Very large objects

**Usage**

```
## Default S3 method:  
browse(x)
```

**Arguments**

x                    A numeric value with the dataset ID.

---

browse.download	<i>Open a browser window to display a Neotoma dataset within the Neotoma Explorer</i>
-----------------	---

---

### Description

Using a numeric value, download, download\_list, dataset or dataset\_list object, open up a browser window in the users default browser. Very large objects

### Usage

```
## S3 method for class 'download'  
browse(x)
```

### Arguments

x                    A download object.

---

browse.download_list	<i>Open a browser window to display a Neotoma dataset within the Neotoma Explorer</i>
----------------------	---

---

### Description

Using a numeric value, download, download\_list, dataset or dataset\_list object, open up a browser window in the users default browser. Very large objects

### Usage

```
## S3 method for class 'download_list'  
browse(x)
```

### Arguments

x                    A download\_list object.



---

compile\_downloads      *Compile download objects*

---

## Description

Function to convert multiple downloads into a single large table.

From the assemblage data for multiple cores, return a single data.frame with columns for site meta-data and assemblage data.

To support further synthesis and analysis `compile_download` works to transform a list returned by `get_download` into a large data frame with columns for site and sample attributes and also with the associated assemblage data at each sample depth. This function also does the same for single sites.

## Usage

```
compile_downloads(downloads)
```

## Arguments

`downloads`      A `download_list` as returned by `get_download`, or multiple downloads joined in a list.

## Value

This command returns a data frame.

## Author(s)

Simon J. Goring <[simon.j.goring@gmail.com](mailto:simon.j.goring@gmail.com)>

## References

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

Gavin DG, Oswald WW, Wahl ER, Williams JW. 2003. A statistical approach to evaluating distance metrics and analog assignments for pollen records. *Quaternary Research* 60: 356-367.

Whitmore J, Gajewski K, Sawada M, Williams JW, Shuman B, Bartlein PJ, Minckley T, Viau AE, Webb III T, Shafer S, Anderson P, Brubaker L. 2005. Modern pollen data from North America and Greenland for multi-scale paleoenvironmental applications. *Quaternary Science Reviews* 24: 1828-1848.

Williams J, Shuman B. 2008. Obtaining accurate and precise environmental reconstructions from the modern analog technique and North American surface pollen dataset. *Quaternary Science Reviews*. 27:669-687.

API Reference: <http://wnapi.neotomadb.org/doc/resources/contacts>

**Examples**

```
## Not run:
# Search for sites with "Thuja" pollen that are older than 8kyr BP and
# that are on the west coast of North America:
t8kyr.datasets <- get_dataset(taxonname='Thuja*',
                             loc=c(-150, 20, -100, 60),
                             ageyoung = 8000)

# Returns 3 records (as of 04/04/2013), get dataset for the first record,
# Gold Lake Bog.
thuja.sites <- get_download(t8kyr.datasets)

gold.p25 <- compile_taxa(thuja.sites, 'P25')

all.gold <- compile_downloads(gold.p25)

pollen.sums <- rowSums(all.gold[,11:ncol(all.gold)], na.rm=TRUE)

plot(x = all.gold$age,
     y = all.gold$Cupressaceae.Taxaceae / pollen.sums,
     col = all.gold$site.name,
     pch = 19)

## End(Not run)
```

---

 compile\_taxa

*Function to convert assemblage taxa to standardized lists.*


---

**Description**

From the assemblage data for the core return assemblage data with the assemblage taxa Currently implemented only for pollen data.

**Usage**

```
compile_taxa(object, list.name, alt.table = NULL, cf = TRUE, type = TRUE)
```

**Arguments**

object	A pollen object returned by <a href="#">get_download</a> .
list.name	The taxon compilation list, one of a set of lists from the literature (e.g., "P25", "WhitmoreFull"). More detail in section Details.
alt.table	A user provided table formatted with at least two columns, one called 'taxon' and the other named as in list.name.
cf	Should taxa listed as *cf*s (*e.g.*, *cf*. *Gilia*) be considered highly resolved?
type	Should taxa listed as types (*e.g.*, *Iva annua*-type) be considered highly resolved?

## Details

The data object uses the smaller pollen subset. As this package develops we will add the capacity to summarize data output from the translation. Currently we can return only subsets that have been defined in the literature. These lists include:

- "P25" This list is derived from Gavin et al., (2003), and includes 25 pollen taxa.
- "WS64" This list is derived from Williams and Shuman (2008).
- "WhitmoreFull" This is the full list associated with the Whitmore et al., (2005) North American Modern Pollen Database.
- "WhitmoreSmall" As above, but taxa for which both fully resolved and undifferentiated exist these taxa are summed.

## Value

This command returns a list object with the same structure as the parent pollen object returned by [get\\_download](#), or a matrix (or data frame) depending on whether object is one or the other. Any pollen taxon not included in the major taxa defined in the pollen gets returned as 'Other'.

## Author(s)

Simon J. Goring <[simon.j.goring@gmail.com](mailto:simon.j.goring@gmail.com)>

## References

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

Gavin DG, Oswald WW, Wahl ER, Williams JW. 2003. A statistical approach to evaluating distance metrics and analog assignments for pollen records. *Quaternary Research* 60: 356-367.

Whitmore J, Gajewski K, Sawada M, Williams JW, Shuman B, Bartlein PJ, Minckley T, Viau AE, Webb III T, Shafer S, Anderson P, Brubaker L. 2005. Modern pollen data from North America and Greenland for multi-scale paleoenvironmental applications. *Quaternary Science Reviews* 24: 1828-1848.

Williams J, Shuman B. 2008. Obtaining accurate and precise environmental reconstructions from the modern analog technique and North American surface pollen dataset. *Quaternary Science Reviews*. 27:669-687.

API Reference: <http://wnapi.neotomadb.org/doc/resources/contacts>

## Examples

```
## Not run:
# Search for sites with "Thuja" pollen that are older than 8kyr BP and
# that are on the west coast of North America:
t8kyr.datasets <- get_dataset(taxonname='Thuja*', loc=c(-150, 20, -100, 60), ageyoung = 8000)

# Returns 3 records (as of 04/04/2013), get dataset for the first record, Gold Lake Bog.
GOLDKBG <- get_download(t8kyr.datasets[[1]])

gold.p25 <- compile_taxa(GOLDKBG, 'P25')
```

```
## End(Not run)
```

---

counts	<i>Access proxy count data</i>
--------	--------------------------------

---

## Description

Extract pollen or other proxy counts from data objects and returns them in a useful format.

## Usage

```
counts(obj, ...)  
  
## S3 method for class 'download'  
counts(obj, ...)  
  
## S3 method for class 'download_list'  
counts(obj, ...)
```

## Arguments

obj	an R object from which counts are to be extracted.
...	arguments passed to other methods.

## Details

Methods are available for "download" and "download\_list" objects.

## Value

Either a data frame of counts or a list of such objects.

## Author(s)

Gavin Simpson

## Examples

```
## Not run:  
marion <- get_site('Marion Lake%')  
louise <- get_site('Louise Pond%')  
western.sites <- rbind(marion, louise)  
western.data <- get_dataset(western.sites)  
  
western.dl <- get_download(western.data)  
western.cnt <- counts(western.dl)  
sapply(western.cnt, dim)  
marion.cnt <- counts(western.dl[[1]])
```

```
dim(marion.cnt)

## End(Not run)
```

---

depths

*Extracts the depth values from a 'download' object*

---

### Description

Using a download object, return the sample depths (if available).

Using a numeric value, download, download\_list, dataset or dataset\_list object, open up a browser window in the users default browser. Very large objects

### Usage

```
depths(obj, ...)
```

## Default S3 method:  
depths(obj, ...)

## S3 method for class 'download'  
depths(obj, ...)

## S3 method for class 'download\_list'  
depths(obj, ...)

### Arguments

obj            A download object.

...            arguments passed to other methods.

### Value

Returns a vector of depths.

### Author(s)

Simon J. Goring <simon.j.goring@gmail.com>

### References

Neotoma Project Website: <http://www.neotomadb.org> API Reference: <http://wnapi.neotomadb.org/doc/resources/sites>

## Examples

```
## Not run:
# Provide a vector of depths to generate a new age model:
# The dataset id 684 is for Devils Lake, a record published by Louis Maher Jr.

pollen.data <- get_download(684)
pollen.chron <- get_chroncontrol(pollen.data)[[1]]

age_sds <- pollen.chron$chron.control$age - focal$chron.control$age.young,
get_curves <- ifelse(regexpr("Radiocarbon",
                           pollen.chron$chron.control$control.type) > -1,
                    'intcal13', 'normal')

new_chron <- Bchron::Bchronology(ages = pollen.chron$chron.control$age,
                                ageSds = age_sds
                                positions = pollen.chron$chron.control$depth,
                                calCurves = ,
                                predictPositions = depths(pollen.data))

## End(Not run)
```

---

download

*A class for download objects.*

---

## Description

A download is an object with the full record for a single dataset.

A download is an object with the full record for a single dataset.

## Details

TO DO

TO DO

## Author(s)

Simon Goring

---

get_chroncontrol	<i>Function to return chronological control tables used to build age models.</i>
------------------	--

---

### Description

Using the dataset ID, return all records associated with the data. At present, only returns the dataset in an unparsed format, not as a data table. This function will only download one dataset at a time.

### Usage

```
get_chroncontrol(x, chronology = 1, verbose = TRUE, add = FALSE)
```

### Arguments

x	A single numeric chronology ID, a vector of numeric dataset IDs as returned by <a href="#">get_dataset</a> or a download or download_list object.
chronology	When download objects have more than associated chronology, which chronology do you want? Default is 1.
verbose	logical, should messages on API call be printed?
add	logical, should this chron control be added to the download object?

### Value

This command returns either an object of class "try-error" containing the error returned from the Neotoma API call, or a full data object containing all the relevant information required to build either the default or prior chronology for a core. When download or download\_list objects are passed, the user can add the chroncontrol to the download object explicitly, in which case the function will return a download with chroncontrol embedded.

This is a list comprising the following items:

chron.control	A table describing the collection, including dataset information, PI data compatible with <a href="#">get_contact</a> and site data compatible with <a href="#">get_site</a> .
meta	Dataset information for the core, primarily the age-depth model and chronology. In cases where multiple age models exist for a single record the most recent chronology is provided here.

If Neotoma returns empty content, either the control table or the associated metadata (which happens in approximately 25

### Author(s)

Simon J. Goring <simon.j.goring@gmail.com>

### References

+ Neotoma Project Website: <http://www.neotomadb.org> + API Reference: <http://wnapi.neotomadb.org/doc/resources/contact>

**Examples**

```
## Not run:
# The point of pulling chronology tables is to re-build or examine the
# chronological information that was used to build the age-depth model for
# the core. You can do this by hand, but the `write_agefile` function works
# with `download` objects directly.

three_pines <- get_download(get_dataset(get_site("Three Pines Bog"),
                                     datasettype = "pollen"))
pines_chron <- get_chroncontrol(three_pines)

# Spline interpolation:
model <- smooth.spline(x = pines_chron[[1]]$chron.control$depth,
                      y = pines_chron[[1]]$chron.control$age)

new_ages <- predict(model, x = three_pines[[1]]$sample.meta$depth)

## End(Not run)
```

---

```
get_chroncontrol.dataset
```

*Function to return chronological control tables from a dataset.*

---

**Description**

Using a dataset, return the default chron-control table.

**Usage**

```
## S3 method for class 'dataset'
get_chroncontrol(x, chronology = 1, verbose = TRUE, add = FALSE)
```

**Arguments**

x	A dataset.
chronology	When download objects have more than associated chronology, which chronology do you want? Default is 1.
verbose	logical; should messages on API call be printed?
add	Should the chroncontrol be added to the download object (only accepts FALSE)



---

```
get_chroncontrol.dataset_list
```

*Function to return chronological control tables from a dataset\_list.*

---

### Description

Using a dataset\_list, return the default chron-control table.

### Usage

```
## S3 method for class 'dataset_list'
get_chroncontrol(x, chronology = 1, verbose = TRUE, add = FALSE)
```

### Arguments

x	A dataset_list object.
chronology	When download objects have more than associated chronology, which chronology do you want? Default is 1.
verbose	logical; should messages on API call be printed?
add	Should the chroncontrol be added to the download object (only accepts FALSE)

---

```
get_chroncontrol.default
```

*Function to return chronological control tables from a chronologic ID.*

---

### Description

Using the chronology ID, return the chron control table as a data.frame.

### Usage

```
## Default S3 method:
get_chroncontrol(x, chronology = 1, verbose = TRUE, add = FALSE)
```

### Arguments

x	A single numeric chronology ID or a vector of numeric chronology IDs as returned by get_datasets.
chronology	For download methods, which chronology controls should be used?
verbose	logical; should messages on API call be printed?
add	logical, should this chron control be added to the download object?

---

```
get_chroncontrol.download
```

*Function to return chronological control tables from a download object.*

---

### Description

Using a download, return the default chron-control table as a data.frame.

### Usage

```
## S3 method for class 'download'
get_chroncontrol(x, chronology = 1, verbose = TRUE, add = FALSE)
```

### Arguments

x	A single download object.
chronology	For download methods, which chronology controls should be used?
verbose	logical; should messages on API call be printed?
add	Should the chroncontrol be added to the download object (default FALSE)

---

```
get_chroncontrol.download_list
```

*Function to return chronological control tables from a download\_list object.*

---

### Description

Using a download\_list, return the default chron-control table as a data.frame.

### Usage

```
## S3 method for class 'download_list'
get_chroncontrol(x, chronology = 1, verbose = TRUE, add = FALSE)
```

### Arguments

x	A download_list object.
chronology	When download objects have more than associated chronology, which chronology do you want? Default is 1.
verbose	logical; should messages on API call be printed?
add	Should the chroncontrol be added to the download object (default FALSE)

---

get_closest	<i>Find the closest dataset records to a site, dataset or long/lat pair in Neotoma</i>
-------------	--

---

### Description

Passing in a download object the function outputs a Bacon or Clam formatted file to a user defined destination for age modelling with existing age-depth modeling software.

### Usage

```
get_closest(x, n, buffer, ...)
```

### Arguments

x	A vector long/lat pair, or a dataset, site or download.
n	The maximum number of records to return (in the case of ties the return may be larger)
buffer	The size of the buffer for dataset search (in meters)
...	optional arguments to pass into get_dataset.

### Details

The function uses the sf package to generate a circular buffer around a point of interest. From there a square bounding box is sent to Neotoma using the get\_dataset() function. To use the buffering function we must convert from long/lat to UTM coordinates, which we do by guessing the UTM zone of the point of interest. Details can be found in the function's R code hosted on GitHub: [https://github.com/ropensci/neotoma/blob/master/R/get\\_closest.R](https://github.com/ropensci/neotoma/blob/master/R/get_closest.R)

### Value

This command returns a dataset or dataset\_list, or NULL if no records exist within the bounding box.

### Author(s)

Simon J. Goring <simon.j.goring@gmail.com>, Andria Dawson <andria.dawson@gmail.com>

### References

Neotoma Project Website: <http://www.neotomadb.org> API Reference: <http://wnapi.neotomadb.org/doc/resources/contacts>

**Examples**

```
## Not run:
# The point of pulling chronology tables is to re-build or examine the chronological
# information that was used to build the age-depth model for the core.
# Find the closest records to Madison, WI:
get_closest(x = c(-89.4012, 43.0731), n = 10, buffer = 5000, datasettype = "pollen")

## End(Not run)
```

---

<code>get_contact</code>	<i>Get contact information.</i>
--------------------------	---------------------------------

---

**Description**

A function to obtain contact information for data contributors from the Neotoma Paleocological Database.

**Usage**

```
get_contact(contactid, contactname, contactstatus, familyname)
```

**Arguments**

<code>contactid</code>	Contact ID is a numerical value associated with the Neotoma Contact table's numerical Contact ID.
<code>contactname</code>	A character string indicating the data contributors' project, organization or personal name. May be a partial string and can include wildcards.
<code>contactstatus</code>	The current status of the contact. Possible values include: active, deceased, defunct, extant, inactive, retired, unknown.
<code>familyname</code>	A character string. Full or partial string indicating the contact's last name.

**Value**

The function takes parameters defined by the user and returns a list of contact information supplied by the Neotoma Paleocological Database. The user may define all or none of the possible fields. The function contains data checks for each defined parameter.

The function returns either a single item of class "try-error" describing the reason for failure (either mis-defined parameters or an error from the Neotoma API), or a table of contacts, with rows corresponding to the number of individual contacts returned by the Neotoma API. Each row entry includes the following parameters:

<code>contact.name</code>	Full name of the person, last name first (e.g. "Simpson, George Gaylord") or name of organization or project (e.g. "Great Plains Flora Association").
<code>contact.status</code>	Current status of the person, organization, or project. Field links to the Contact-Statuses lookup table.
<code>family.name</code>	Family or surname name of a person.

leading.initials	Leading initials for given or forenames without spaces (e.g. "G.G. ").
given.names	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").
title	A person's title (e.g. "Dr. ", "Prof. ", "Prof. Dr").
phone	Telephone number.
fax	Fax number.
email	Email address.
url	Universal Resource Locator, an Internet World Wide Web address.
address	Full mailing address.
notes	Free form notes or comments about the person, organization, or project.
contact.id	Unique database record identifier for the contact.
alias.id	The ContactID of a person's current name. If the AliasID is different from the ContactID, the ContactID refers to the person's former name.

**Author(s)**

Simon J. Goring <simon.j.goring@gmail.com>

**References**

Neotoma Project Website: <http://www.neotomadb.org> API Reference: <http://wnapi.neotomadb.org/doc/resources/contacts>

**Examples**

```
## Not run:
# To find all data contributors who are active:
active.cont <- get_contact(contactstatus = 'active')

# To find all data contributors who have the last name "Smith"
smith.cont <- get_contact(familyname = 'Smith')

## End(Not run)
```

---

get_dataset	<i>Obtain dataset information from the Neotoma Paleocological Database or an existing object.</i>
-------------	---

---

**Description**

A function to access the Neotoma API and return datasets corresponding to the parameters defined by the user.

**Usage**

```

get_dataset(
  x,
  datasettype,
  piid,
  altmin,
  altmax,
  loc,
  gpid,
  taxonids,
  taxonname,
  ageold,
  ageyoung,
  ageof,
  subdate
)

```

**Arguments**

x	An optional value, either a numeric site ID or object of class <code>download</code> , <code>download_list</code> or <code>site</code> .
datasettype	A character string corresponding to one of the allowed dataset types in the Neotoma Database. Allowed types include: "geochronologic", "loss-on-ignition", "pollen", "plant macrofossils", "vertebrate fauna", "mollusks", and "pollen surface sample". See note in Details below.
piid	Numeric value for the Principle Investigator's ID number.
altmin	Numeric value indicating the minimum altitude for the site (can be used alone or with <code>altmax</code> ).
altmax	Numeric value indicating the maximum altitude for the site (can be used alone or with <code>altmin</code> ).
loc	A numeric vector <code>c(lonW, latS, lonE, latN)</code> representing the bounding box within which to search for sites. The convention here is to use negative values for longitudes west of Greenwich or longitudes south of the equator
gpid	A character string or numeric value, must correspond to a valid geopolitical identity in the Neotoma Database. Use <code>get.tables('GeoPoliticalUnits')</code> for a list of acceptable values, or link here: <a href="http://wnapi.neotomadb.org/apdx/geopol.htm">http://wnapi.neotomadb.org/apdx/geopol.htm</a>
taxonids	A numeric identifier for the taxon. See <code>get_table</code> and use <code>get_table('Taxa')</code> for a list of acceptable values.
taxonname	A character string corresponding to a valid taxon identity in the Neotoma Database. See <code>get_table</code> and use <code>get_table('Taxa')</code> for a list of acceptable values.
ageold	The oldest date acceptable for the search (in years before present).
ageyoung	The youngest date acceptable for the search.
ageof	If a taxon ID or taxon name is defined this parameter must be set to "taxon", otherwise it may refer to "sample", in which case the age bounds are for any

	samples within datasets or "dataset" if you want only datasets that are within the bounds of ageold and ageyoung.
subdate	Date of dataset submission, either YYYY-MM-DD or MM-DD-YYYY.

### Details

With regards to datasettypes, because Neotoma is a "living" database, and new dataset types are being added in an ongoing manner as new research disciplines use the database, you can use `get_table("datasettypes")` to see the full list of available dataset types in the database.

### Value

More details on the use of these parameters can be obtained from <http://wnapi.neotomadb.org/doc/resources/datasets>.

A list of class 'dataset\_list', with each item corresponding to an individual record. Searches that return no items will result in a NULL value being returned. Otherwise each list item (each dataset record) includes the following components:

dataset.id	Unique database record identifier for the dataset.
dataset.name	Name of the dataset; not commonly used.
CollUnitHandle	Code name of the Collection Unit with which the dataset is associated. This code may be up to 10 characters. Data are frequently distributed by Collection Unit, and the Handle is used for file names.
CollUnitID	Unique database record identifier for the collection unit.
CollType	The collection type. Types include cores, sections, excavations, and animal middens.
DatasetType	The dataset type, such as: geochronologic, loss-on-ignition, pollen, plant macrofossils, vertebrate fauna, etc.
AgeOldest	The oldest of all sample ages (in calendar years before present) in the dataset.
AgeYoungest	The youngest of all sample ages (in calendar years before present) in the dataset.
SubDates	An array of objects that describe dataset submission events. If multiple submissions occurred then this is a table.
DatasetPIs	An array of objects that describe Principal Investigators associated with a dataset.
Site	An object describing the site where the dataset samples were taken.

### Author(s)

Simon J. Goring <[simon.j.goring@gmail.com](mailto:simon.j.goring@gmail.com)>

### References

Neotoma Project Website: <http://www.neotomadb.org> API Reference: <http://wnapi.neotomadb.org/doc/resources/contacts>

**Examples**

```
## Not run:
# Search for sites with "Thuja" pollen that are older than 8kyr BP and
# that are on the west coast of North America:
t8kyr.datasets <- get_dataset(taxonname='Thuja*',
                             loc=c(-150, 20, -100, 60),
                             ageyoung = 8000)

# Search for vertebrate fossils in Canada (gpid: 756) within the last 2kyr.
gpids <- get_table(table.name='GeoPoliticalUnits')
canID <- gpids[which(gpids$GeoPoliticalName == 'Canada'),1]

v2kyr.datasets <- get_dataset(datasettype='vertebrate fauna',
                              gpid=canID,
                              ageold = 2000)

## End(Not run)
```

---

get\_dataset.default    *Obtain dataset information from the Neotoma Paleocological Database or an existing object.*

---

**Description**

A function to access the Neotoma API and return datasets corresponding to the parameters defined by the user.

**Usage**

```
## Default S3 method:
get_dataset(
  x,
  datasettype,
  piid,
  altmin,
  altmax,
  loc,
  gpid,
  taxonids,
  taxonname,
  ageold,
  ageyoung,
  ageof,
  subdate
)
```



**Arguments**

x	A numeric value corresponding to the site ID.
datasettype	A character string corresponding to one of the allowed dataset types in the Neotoma Database. You can find the full list of allowed datasettypes using: <code>get_table("datasettypes")</code> .
piid	Numeric value for the Principle Investigator's ID number.
altmin	Numeric value indicating the minimum altitude for the site (can be used alone or with altmax).
altmax	Numeric value indicating the maximum altitude for the site (can be used alone or with altmin).
loc	A numeric vector <code>c(lonW, latS, lonE, latN)</code> representing the bounding box within which to search for sites. The convention here is to use negative values for longitudes west of Greenwich or longitudes south of the equator
gpid	A character string or numeric value, must correspond to a valid geopolitical identity in the Neotoma Database. Use <code>get.tables('GeoPoliticalUnits')</code> for a list of acceptable values, or link here: <a href="http://wnapi.neotomadb.org/apdx/geopol.htm">http://wnapi.neotomadb.org/apdx/geopol.htm</a>
taxonids	A numeric identifier for the taxon. See <code>get_table</code> and use <code>get_table('Taxa')</code> for a list of acceptable values.
taxonname	A character string corresponding to a valid taxon identity in the Neotoma Database. See <code>get_table</code> and use <code>get_table('Taxa')</code> for a list of acceptable values.
ageold	The oldest date acceptable for the search (in years before present).
ageyoung	The youngest date acceptable for the search.
ageof	If a taxon ID or taxon name is defined this parameter must be set to "taxon", otherwise it may refer to "sample", in which case the age bounds are for any samples within datasets or "dataset" if you want only datasets that are within the bounds of ageold and ageyoung.
subdate	Date of dataset submission, either YYYY-MM-DD or MM-DD-YYYY.

---

`get_dataset.download` *Obtain dataset information from an existing download object.*

---

**Description**

A function to access a dataset within a download object.

**Usage**

```
## S3 method for class 'download'
get_dataset(x, ...)
```

**Arguments**

x	An object of class download.
...	objects passed from the generic. Not used in the call.

---

```
get_dataset.download_list
```

*Obtain dataset information from a download\_list.*

---

### Description

A function to return datasets corresponding to the objects within a download\_list.

### Usage

```
## S3 method for class 'download_list'  
get_dataset(x, ...)
```

### Arguments

x	An object of class download_list.
...	objects passed from the generic. Not used in the call.

---

```
get_dataset.geochronologic
```

*Obtain dataset information from an object of class geochronologic.*

---

### Description

A function to access the Neotoma API and return datasets corresponding to the parameters defined by the user.

### Usage

```
## S3 method for class 'geochronologic'  
get_dataset(x, ...)
```

### Arguments

x	An object of class geochronologic.
...	objects passed from the generic. Not used in the call.

---

```
get_dataset.geochronologic_list
```

*Obtain dataset information from an object of class geochronologic\_list.*

---

**Description**

A function to access the Neotoma API and return datasets corresponding to the parameters defined by the user.

**Usage**

```
## S3 method for class 'geochronologic_list'  
get_dataset(x, ...)
```

**Arguments**

x                    An object of class geochronologic\_list.  
...                   objects passed from the generic. Not used in the call.

---

```
get_dataset.integer    Obtain dataset information from a vector of dataset IDs.
```

---

**Description**

A function to access the Neotoma API and return datasets corresponding to the parameters defined by the user.

**Usage**

```
## S3 method for class 'integer'  
get_dataset(x = NULL, ...)
```

**Arguments**

x                    A single numeric dataset id, or a numeric vector.  
...                   objects passed from the generic. Not used in the call.

get\_dataset.numeric     *Obtain dataset information from a vector of dataset IDs.*

---

### Description

A function to access the Neotoma API and return datasets corresponding to the parameters defined by the user.

### Usage

```
## S3 method for class 'numeric'  
get_dataset(x = NULL, ...)
```

### Arguments

x                    A single numeric dataset id, or a numeric vector.  
...                  objects passed from the generic. Not used in the call.

---

get\_dataset.site        *Obtain dataset information from an existing site object.*

---

### Description

A function to access the Neotoma API and return datasets corresponding to the parameters defined by the user.

### Usage

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

### Arguments

x                    An object of class site.  
...                  objects passed from the generic. Not used in the call.

---

get_download	<i>Function to return full download records using sites, datasets, or dataset IDs.</i>
--------------	--

---

### Description

Using the dataset ID, site object or dataset object, return all records associated with the data as a `download_list`.

### Usage

```
get_download(x, verbose = TRUE)
```

### Arguments

<code>x</code>	A single numeric dataset ID or a vector of numeric dataset IDs as returned by <code>get_datasets</code> , or a site, dataset, or <code>dataset_list</code> .
<code>verbose</code>	logical; should messages on API call be printed?

### Value

This command returns either object of class "try-error" (see [try](#)) defined by the error returned from the Neotoma API call, or an object of class `download_list`, containing a set of download objects, each with relevant assemblage information and metadata: The download object is a list of lists and data frames that describe an assemblage, the constituent taxa, the chronology, site and PIs who contributed the data. The following are important components:

<code>dataset</code>	A table describing the collection, including dataset information, PI data compatible with <a href="#">get_contact</a> and site data compatible with <a href="#">get_site</a> .
<code>sample.meta</code>	Dataset information for the core, primarily the age-depth model and chronology. In cases where multiple age models exist for a single record the most recent chronology is provided here.
<code>taxon.list</code>	The list of taxa contained within the dataset, unordered, including information that can be used in <a href="#">get_taxa</a>
<code>counts</code>	The assemblage data for the dataset, arranged with each successive depth in rows and the taxa as columns. All taxa are described in <code>taxon.list</code> , the chronology is in <code>sample.data</code>
<code>lab.data</code>	A data frame of laboratory data, such as exotic pollen spike, amount of sample counted, charcoal counts, etc.
<code>chronologies</code>	A list of existing chronologies. If only a single chronology exists for a record then this is the same as the age-model in <code>sample.meta</code> .

**Note**

The function returns a warning in cases where single taxa are defined by multiple taphonomic characteristics, for example grains that are identified separately as crumpled and torn in the same sample and sums these values within a sample. In the case that a geochronology dataset is passed to `get_download` the function returns a message and a NULL object (that is later excised). Use `get_geochron` for these objects. The chronologies can be augmented using the function `get_chroncontrol`, where the individual chronology objects in `chronologies` will consist of a table equivalent to `sample.meta` and a `chroncontrol` object.

**Author(s)**

Simon J. Goring <simon.j.goring@gmail.com>

**References**

Neotoma Project Website: <http://www.neotomadb.org> API Reference: <http://wnapi.neotomadb.org/doc/resources/contacts>

**Examples**

```
## Not run:
# Search for sites with "Pseudotsuga" pollen that are older than 8kyr BP and
# that are roughly within western British Columbia:
t8kyr.datasets <- get_dataset(taxonname='*Picea*', loc=c(-90, 41, -89, 44),
                             ageold = 20000, ageyoung=10000)

# Returns 20 records (as of 04/04/2013), get the dataset for all records:
pollen.records <- get_download(t8kyr.datasets)

# Standardize the taxonomies for the different records using the WS64 taxonomy.
compiled.sites <- compile_taxa(pollen.records, list.name='WS64')

# Extract the Pseudotsuga curves for the sites:
get.curve <- function(x, taxa) {
  if (taxa %in% colnames(x$count)) {
    count <- x$count[,taxa]/rowSums(x$count, na.rm=TRUE)
  } else {
    count <- rep(0, nrow(x$count))
  }
  data.frame(site = x$dataset$site.data$site.name,
            age = x$sample.meta$age,
            count = count)
}

curves <- do.call(rbind.data.frame,
                lapply(compiled.sites, get.curve, taxa = 'Larix/Pseudotsuga'))

# For illustration, remove the sites with no Pseudotsuga occurrence:
curves <- curves[curves$count > 0, ]

smooth.curve <- predict(loess(sqrt(count)~age, data=curves),
                       data.frame(age=seq(20000, 0, by = -100)))
```

```

plot(sqrt(count) ~ age, data = curves,
      ylab = '% Pseudotsuga/Larix', xlab='Calibrated Years BP', pch=19,
      col=rgb(0.1, 0.1, 0.1, 0.1), xlim=c(0, 20000))
lines(seq(20000, 0, by = -100), smooth.curve, lwd=2, lty=2, col=2)

# This figure shows us an apparent peak in Larix/Pseudotsuga pollen in the
# early-Holocene that lends support to a warmer, drier early-Holocene in
# western North America.

## End(Not run)

```

---

get\_download.dataset    *Function to return full download records using a dataset.*

---

### Description

Using a dataset, return all records associated with the data as a download\_list.

### Usage

```
## S3 method for class 'dataset'
get_download(x, verbose = TRUE)
```

### Arguments

x	An object of class dataset.
verbose	logical; should messages on API call be printed?

---

get\_download.dataset\_list  
*Function to return full download records using a dataset\_list.*

---

### Description

Using a dataset\_list, return all records associated with the data as a download\_list.

### Usage

```
## S3 method for class 'dataset_list'
get_download(x, verbose = TRUE)
```

### Arguments

x	An object of class dataset_list.
verbose	logical; should messages on API call be printed?

---

get\_download.default    *Function to return full download records using numeric dataset IDs.*

---

**Description**

Using the dataset ID, return all records associated with the data as a download\_list.

**Usage**

```
## Default S3 method:  
get_download(x, verbose = TRUE)
```

**Arguments**

x	A single numeric dataset ID or a vector of numeric dataset IDs as returned by get_datasets.
verbose	logical; should messages on API call be printed?

---

get\_download.site    *Function to return full download records using a site.*

---

**Description**

Using a site, return all records associated with the data as a download\_list.

**Usage**

```
## S3 method for class 'site'  
get_download(x, verbose = TRUE)
```

**Arguments**

x	An object of class site.
verbose	logical; should messages on API call be printed?



---

get_geochron	<i>Function to return geochronological data from records.</i>
--------------	---

---

### Description

Using the dataset ID, return all geochronological data associated with the dataID. At present, only returns the dataset in an unparsed format, not as a data table. This function will only download one dataset at a time.

### Usage

```
get_geochron(x, verbose = TRUE)
```

### Arguments

x	A numeric dataset ID or a vector of numeric dataset IDs, or an object of class of class <code>site</code> , <code>dataset</code> , <code>dataset_list</code> , <code>download</code> or <code>download_list</code> for which geochrons are required.
verbose	logical; should messages on API call be printed?

### Value

This command returns either an object of class "try-error" (see [try](#)) defined by the error returned from the Neotoma API call, or a geochronologic object, which is a list with two components, a dataset and a geochronology table, a `data.frame` with the following components:

<code>sample.id</code>	A unique identifier for the geochronological unit.
<code>age.type</code>	String. The age type, one of calendar years, radiocarbon years, etc.
<code>age</code>	Dated age of the material.
<code>e.older</code>	The older error limit of the age value. Commonly 1 standard deviation.
<code>e.young</code>	The younger error limit of the age value.
<code>delta13C</code>	The measured or assumed delta13C value for radiocarbon dates, if provided.
<code>material.dated</code>	A table describing the collection, including dataset information, PI data compatible with <a href="#">get_contact</a> and site data compatible with <a href="#">get_site</a> .
<code>geo.chron.type</code>	Text string, type of geochronological analysis, i.e., Radiocarbon dating, luminescence.
<code>notes</code>	Text string
<code>infinite</code>	Boolean, does the dated material return an "infinite" date?

A full data object containing all the relevant geochronological data available for a dataset.

### Author(s)

Simon J. Goring <[simon.j.goring@gmail.com](mailto:simon.j.goring@gmail.com)>

## References

Neotoma Project Website: <http://www.neotomadb.org> API Reference: <http://wnapi.neotomadb.org/doc/resources/contacts>

## Examples

```
## Not run:
# Search for the sites around Marion Lake, BC. I want to find sites within
# about 1km.

marion <- get_site(sitename = "Marion Lake*")

marion_close <- get_closest(marion, n = 10, buffer = 1)

# Returns 116 records (as of 13/07/2015). These are the pollen records though,
# we want the sites:
geochron.records <- get_geochron(marion_close)

# We want to extract all the radiocarbon ages from the records:

get_ages <- function(x){
  any.ages <- try(x[[2]]$age[x[[2]]$age.type == 'Radiocarbon years BP'])
  if(is(any.ages, 'try-error')) output <- NA
  if(!is(any.ages, 'try-error')) output <- unlist(any.ages)
  output
}

radio.chron <- unlist(sapply(geochron.records, get_ages))

hist(radio.chron[radio.chron<40000], breaks=seq(0, 25000, by = 1000),
     main = 'Radiocarbon dates for Pseudotsuga records',
     xlab = 'Radiocarbon date (14C years before 1950)')

## End(Not run)
```

---

get_publication	<i>A function to get publications for sites or datasets in the Neotoma Database using the API.</i>
-----------------	--

---

## Description

The function takes the parameters, defined by the user, and returns a table with publication information from the Neotoma Paleocological Database.

## Usage

```
get_publication(x, contactid, datasetid, author, pubtype, year, search)
```

**Arguments**

x	Numeric Publication ID value, either from <a href="#">get_dataset</a> or known.
contactid	Numeric Contact ID value, either from <a href="#">get_dataset</a> or <a href="#">get_contact</a>
datasetid	Numeric Dataset ID, known or from <a href="#">get_dataset</a>
author	Character string for full or partial author's name. Can include wildcards such as 'Smit*' for all names beginning with 'Smit'.
pubtype	Character string, one of eleven allowable types, see <a href="#">get_table</a> . For a list of allowed types run <code>get_table("PublicationTypes")</code> .
year	Numeric publication year.
search	A character string to search for within the article citation.

**Value**

A list is returned with two data frame components:

meta	A single row with Publication ID, type, year of publication and full citation.
Authors	data.frame of author names, order and IDs, can be of variable length.

**Author(s)**

Simon J. Goring <[simon.j.goring@gmail.com](mailto:simon.j.goring@gmail.com)>

**References**

Neotoma Project Website: <http://www.neotomadb.org> API Reference: <http://wnapi.neotomadb.org/doc/resources/contacts>

**Examples**

```
## Not run:
# To find all publications from 1998:
year.cont <- get_publication(year = 1998)

# To find all data contributors who have the last name "Smith"
smith.cont <- get_publication(author = 'Smith')

## End(Not run)
```

---

get\_publication.dataset

*A function to get publications for datasets in the Neotoma Database using the API.*

---

**Description**

The function takes a dataset and returns a table with publication information from the Neotoma Paleocological Database.

**Usage**

```
## S3 method for class 'dataset'
get_publication(x, ...)
```

**Arguments**

x                    an object of class dataset.  
 ...                  objects passed from the generic. Not used in the call.

---

```
get_publication.dataset_list
```

*A function to get publications for dataset\_lists in the Neotoma Database using the API.*

---

**Description**

The function takes a dataset\_list and returns a table with publication information from the Neotoma Paleocological Database.

**Usage**

```
## S3 method for class 'dataset_list'
get_publication(x, ...)
```

**Arguments**

x                    an object of class dataset\_list.  
 ...                  objects passed from the generic. Not used in the call.

---

```
get_publication.default
```

*A function to get publications for sites or datasets in the Neotoma Database using the API.*

---

**Description**

The function takes the parameters, defined by the user, and returns a table with publication information from the Neotoma Paleocological Database.

**Usage**

```
## Default S3 method:
get_publication(x, contactid, datasetid, author, pubtype, year, search)
```

**Arguments**

x	Numeric Publication ID value, either from <a href="#">get_dataset</a> or known.
contactid	Numeric Contact ID value, either from <a href="#">get_dataset</a> or <a href="#">get_contact</a>
datasetid	Numeric Dataset ID, known or from <a href="#">get_dataset</a>
author	Character string for full or partial author's name. Can include wildcards such as 'Smit*' for all names beginning with 'Smit'.
pubtype	Character string, one of eleven allowable types, see <a href="#">get_table</a> . For a list of allowed types run <code>get_table("PublicationTypes")</code> .
year	Numeric publication year.
search	A character string to search for within the article citation.

---

```
get_publication.download
```

*A function to get publications for downloads in the Neotoma Database using the API.*

---

**Description**

The function takes a download and returns a table with publication information from the Neotoma Paleocological Database.

**Usage**

```
## S3 method for class 'download'
get_publication(x, ...)
```

**Arguments**

x	an object of class download.
...	objects passed from the generic. Not used in the call.

---

```
get_publication.download_list
```

*A function to get publications for datasets in the Neotoma Database using the API.*

---

**Description**

The function takes a download\_list and returns a table with publication information from the Neotoma Paleocological Database.

**Usage**

```
## S3 method for class 'download_list'
get_publication(x, ...)
```

**Arguments**

x                    an object of class `download_list`.  
 ...                 objects passed from the generic. Not used in the call.

---

get_site	<i>Return Site Information.</i>
----------	---------------------------------

---

**Description**

Return site information from the Neotoma Paleoecological Database.

get\_site returns site information from the Neotoma Paleoecological Database based on parameters defined by the user.

**Usage**

```
get_site(sitename, altmin, altmax, loc, gpid, ...)
```

**Arguments**

sitename            character string representing the full or partial site name, or an object of class `dataset`, `dataset_list`, `download` or `download_list`

altmin             Minimum site altitude (in m).

altmax             Maximum site altitude (in m).

loc                 A numeric vector `c(lonW, latS, lonE, latN)` representing the bounding box within which to search for sites. The convention here is to use negative values for longitudes west of Greenwich or longitudes south of the equator.

gpid                A character string or numeric value, must correspond to a valid geopolitical identity in the Neotoma Database. Use `get.tables('GeoPoliticalUnits')` for a list of acceptable values, or link here: <http://wnapi.neotomadb.org/apdx/geopol.htm>

...                 Optional additional arguments

**Value**

A data frame:

siteid	Unique database record identifier for the site.
sitename	Name of the site.
long	Mean longitude, in decimal degrees, for a site (-180 to 180).
lat	Mean latitude, in decimal degrees, for a site (-90 to 90).

elev	Elevation in meters.
description	Free form description of a site, including such information as physiography and vegetation around the site.
long_acc	If the site is described by a bounding box this is the box width.
lat_acc	If the site is described by a bounding box this is the box height.

**Author(s)**

Simon J. Goring <simon.j.goring@gmail.com>

**References**

Neotoma Project Website: <http://www.neotomadb.org> API Reference: <http://wnapi.neotomadb.org/doc/resources/sites>

**Examples**

```
## Not run:
# What is the distribution of site elevations in Neotoma?
all.sites <- get_site() #takes a bit of time.

plot(density(all.sites$elev, from = 0, na.rm=TRUE),
main = 'Altitudinal Distribution of Neotoma Sites', xlab = 'Altitude (m)', log='x')

# Get site information from a dataset:
nw.datasets <- get_dataset(loc = c(-140, 50, -110, 65),
                           datasettype='pollen',
                           taxonname='Pinus*')

nw.sites <- get_site(nw.datasets)

## End(Not run)
```

---

get\_site.dataset      *Return Site Information from a numeric list of site ids.*

---

**Description**

Return site information from the Neotoma Paleocological Database.

**Usage**

```
## S3 method for class 'dataset'
get_site(sitename, ...)
```

**Arguments**

sitename      An object of class dataset.  
 ...          Arguments passed from the generic method, not used.

---

get\_site.dataset\_list *Return Site Information from a dataset\_list*

---

### Description

Return site information from the Neotoma Paleocological Database.

### Usage

```
## S3 method for class 'dataset_list'  
get_site(sitename, ...)
```

### Arguments

sitename	An object of class dataset_list.
...	Arguments passed from the generic method, not used.

---

get\_site.default *Return Site Information.*

---

### Description

Return site information from the Neotoma Paleocological Database.

### Usage

```
## Default S3 method:  
get_site(sitename, ...)
```

### Arguments

sitename	A character string representing the full or partial site name.
...	Arguments passed from the generic method, not used.



---

get_site.download	<i>Return Site Information from a download</i>
-------------------	--

---

**Description**

Return site information from the Neotoma Paleocological Database.

**Usage**

```
## S3 method for class 'download'  
get_site(sitename, ...)
```

**Arguments**

sitename	An object of class download.
...	Arguments passed from the generic method, not used.

---

get_site.download_list	<i>Return Site Information from a download_list</i>
------------------------	---

---

**Description**

Return site information from the Neotoma Paleocological Database.

**Usage**

```
## S3 method for class 'download_list'  
get_site(sitename, ...)
```

**Arguments**

sitename	An object of class download_list.
...	Arguments passed from the generic method, not used.

get\_site.geochronologic

*Return Site Information from a geochronologic*

---

### **Description**

Return site information from the Neotoma Paleocological Database.

### **Usage**

```
## S3 method for class 'geochronologic'  
get_site(sitename, ...)
```

### **Arguments**

sitename	An object of class geochronologic.
...	Arguments passed from the generic method, not used.

---

get\_site.geochronologic\_list

*Return Site Information from a geochronologic\_list*

---

### **Description**

Return site information from the Neotoma Paleocological Database.

### **Usage**

```
## S3 method for class 'geochronologic_list'  
get_site(sitename, ...)
```

### **Arguments**

sitename	An object of class geochronologic_list.
...	Arguments passed from the generic method, not used.

---

get_site.integer	<i>Return Site Information from a vector of integers.</i>
------------------	---

---

**Description**

Return site information from the Neotoma Paleocological Database.

**Usage**

```
## S3 method for class 'integer'  
get_site(sitename, ...)
```

**Arguments**

sitename	An integer or vector of integers.
...	Arguments passed from the generic method, not used.

---

get_site.numeric	<i>Return Site information from a vector of numeric elements.</i>
------------------	---

---

**Description**

Return site information from the Neotoma Paleocological Database.

**Usage**

```
## S3 method for class 'numeric'  
get_site(sitename = NULL, ...)
```

**Arguments**

sitename	A numeric value or vector of numeric elements.
...	Arguments passed from the generic method, not used.

---

`get_table`*Get Neotoma value tables.*

---

**Description**

Get Neotoma value tables.

**Usage**

```
get_table(table.name = NULL)
```

**Arguments**

`table.name` Call one of the available tables in the Neotoma Database. A full listing of tables can be found here: <http://wnapi.neotomadb.org/doc/resources/dbtables>. By default it returns all objects in the table.

**Details**

A table of values corresponding to the parameter of interest.

**Author(s)**

Simon J. Goring <[simon.j.goring@gmail.com](mailto:simon.j.goring@gmail.com)>

**References**

Neotoma Project Website: <http://www.neotomadb.org> API Reference: <http://wnapi.neotomadb.org/doc/resources/contacts>

**Examples**

```
## Not run:
taxon.table <- get_table('Taxa')

# Get the frequency of a random taxon in Neotoma.
tax_sample <- sample(nrow(taxon.table), 1)
cat("The taxon",
    taxon.table$TaxonName[tax_sample],
    "occurs in Neotoma",
    length(get_dataset(taxonname = taxon.table$TaxonName[tax_sample])),
    "times.")

## End(Not run)
```

---

get_taxa	<i>Get taxon information from Neotoma.</i>
----------	--

---

### Description

Get taxon information from Neotoma.

### Usage

```
get_taxa(taxonid, taxonname, status, taxagroup, ecolgroup)
```

### Arguments

taxonid	Numeric taxon identifier used in Neotoma
taxonname	A character string representing the full or partial name of taxa of interest.
status	The current status of the taxon, one of 'extinct', 'extant', 'all'.
taxagroup	The taxonomic grouping for the taxa. See <a href="http://wnapi.neotomadb.org/doc/resources/taxa">http://wnapi.neotomadb.org/doc/resources/taxa</a> for the list of approved groupings.
ecolgroup	The ecological group of the taxa. More detailed than taxagroup, can be obtained using <code>get_table("EcolGroupTypes")</code> .

### Value

Returns a data frame with the following components:

TaxonID	Unique database record identifier for a taxon
TaxonCode	Shorthand notation for a taxon identification
TaxonName	Name of the taxon
Author	Author(s) of the name. Used almost exclusively with beetle taxa
Extinct	True if extinct; false if extant
TaxaGroup	Code for taxa group to which taxon belongs
EcolGroups	Array of ecological group codes to which the taxon belongs
HigherTaxonID	TaxonID of the next higher taxonomic rank
PublicationID	Publication identification number
Notes	Free-form notes or comments about the taxon

### Author(s)

Simon J. Goring <[simon.j.goring@gmail.com](mailto:simon.j.goring@gmail.com)>

### References

Neotoma Project Website: <http://www.neotomadb.org> API Reference: <http://wnapi.neotomadb.org/doc/resources/contacts>

**Examples**

```
## Not run:  
## Return all species taxa with "Abies" in name - note wildcard  
taxa <- get_taxa(taxonname = "Abies*")  
  
## End(Not run)
```

---

gp.table	<i>A list of all the geopolitical entities in the Neotoma database.</i>
----------	---

---

**Description**

A list of geopolitical entities with associated numeric ID values.

**Usage**

```
gp.table
```

**Format**

a data.frame object

**Author(s)**

Simon J. Goring <simon.j.goring@gmail.com>

**Source**

The Neotoma database.

---

plot_leaflet	<i>Leaflet plots for neotoma data.</i>
--------------	--

---

**Description**

A plotting function to provide interactive data investigation using the leaflet tools. This package requires a connection to the internet for proper functioning.

**Usage**

```
plot_leaflet(x, providerTiles = "Stamen.TerrainBackground", ...)
```

**Arguments**

x	A neotoma data object
providerTiles	Default "Stamen.TerrainBackground", a character string indicating the tile background to be used for plotting.
...	Other terms to be passed to the function.

**Value**

A leaflet object

---

pollen.equiv	<i>A table to convert the pollen taxa identified by investigators to standardized lists.</i>
--------------	--

---

**Description**

A list of standardized (published) taxonomies from the literature to help standardize taxonomies for synthesis work.

**Usage**

```
data(pollen.equiv)
```

**Format**

a data.frame object

**Details**

Taxon conversion table (readable).

**Author(s)**

Simon J. Goring <simon.j.goring@gmail.com>; Jeremiah Marsicek

---

read.tilia	<i>Read proxy data from Tilia TLX files</i>
------------	---

---

**Description**

Read proxy data from a Tilia TLX format file.

**Usage**

```
read.tilia(file)
```

**Arguments**

file            a string representing a Tilia TLX format file.

**Value**

Return a 'download' object.

**Author(s)**

Simon J. Goring <simon.j.goring@gmail.com>

**Examples**

```
## Not run:  
crystal <- read.tilia('crystal.tlx')  
  
## End(Not run)
```

---

read_bacon	<i>Function to read in defined Bacon outputs.</i>
------------	---

---

**Description**

Reads in Bacon output and formats it for inclusion in a download object.



**Usage**

```
read_bacon(
  x,
  path = ".",
  add = FALSE,
  chron_name = "Bacon",
  as_default = TRUE,
  download = NULL,
  sections = NULL,
  age_field = "median",
  interp = TRUE
)
```

**Arguments**

x	A folder path that contains a Bacon age file.
path	The location of the Cores folder.
add	Should the results be added to an existing download? Defaults to FALSE.
chron_name	The name for the chronology if the Bacon file is being added to a download.
as_default	Should the chronology become the default?
download	The target download if add is TRUE.
sections	If there are multiple Bacon runs in a folder, identify the file by the number of sections in the run.
age_field	Should the age be assigned to the "median" or the "wmean"?
interp	If the depths don't match up, should we interpolate from the Bacon output? (default TRUE)

**Details**

The function expects that you are in a working directory containing a "Cores" which would then contain output files from Bacon runs. The output can either be added to an existing record (for example, replacing the default age model returned by Neotoma), or it can be loaded on its own. If the depths for the loaded file do not match with the depths in the 'download's 'sample.meta' then the user can use the 'interp' parameter to interpolate between depths. This method uses linear interpolation.

**Examples**

```
## Not run:
# Download the record for Lake O' Pines:
lake_o_dl <- get_download(15925)

# This assumes that you have Bacon installed in a folder and have
# set it to your working directory.

write_agefile(lake_o_dl[[1]], path = ".", chronology = 1,
              corename = "LAKEPINES", cal.prog = 'Bacon')
```

```

source("Bacon.R")

# These defaults just help the core run quickly, they're not
# necessarily good parameters.

Bacon("LAKEPINES", acc.mean = 10,
      thick = 50, depths.file = TRUE,
      suggest = FALSE, ask = FALSE)

lake_o_dl <- read_bacon("LAKEPINES", add = TRUE,
                      download = download, sections = 17)

## End(Not run)

```

---

StratipLOT.download    *Palaeoecological stratigraphic diagrams*

---

### Description

Draws paleoecological diagrams from a download object. Allows control of variable type (using the `tran` function from the `analogue` package), and taxonomic grouping.

### Usage

```

## S3 method for class 'download'
StratipLOT(x, yaxis = "age", method = "none", group = NULL, ...)

```

### Arguments

<code>x</code>	A download object.
<code>yaxis</code>	One of the columns in <code>sample.meta</code> , including <code>depth</code> , <code>age</code> , <code>age.younger</code> , or <code>age.older</code> , default <code>age</code> .
<code>method</code>	An option for axis transformation using <code>tran</code> from the <code>analogue</code> package. "none" by default.
<code>group</code>	An ecological group from the taxon table.
<code>...</code>	variables to be passed to <code>StratipLOT</code> .

### Details

A wrapper for the `analogue` package's `StratipLOT` function. Allowing the user to plot a stratigraphic diagram directly from a download object.

### Value

A trellis object.

## Examples

```
## Not run:
lake_o_dl <- get_download(15925)
StratipLOT(lake_o_dl[[1]])

## End(Not run)
```

---

StratipLOT.download\_list

*Palaeoecological stratigraphic diagrams*

---

## Description

Draws paleoecological diagrams from a `download_list` object. Allows control of variable type (using the `tran` function from the `analogue` package), and taxonomic grouping. This function only works for `download_list` objects that contain a single object.

## Usage

```
## S3 method for class 'download_list'
StratipLOT(x, yaxis = "age", method = "none", group = NULL, ...)
```

## Arguments

<code>x</code>	A <code>download_list</code> object.
<code>yaxis</code>	One of the columns in <code>sample.meta</code> , including <code>depth</code> , <code>age</code> , <code>age.younger</code> , or <code>age.older</code> , default <code>age</code> .
<code>method</code>	An option for axis transformation using <code>tran</code> from the <code>analogue</code> package. "none" by default.
<code>group</code>	An ecological group from the taxon table.
<code>...</code>	variables to be passed to <code>StratipLOT</code> .

## Details

A wrapper for the `analogue` package's `StratipLOT` function. Allowing the user to plot a stratigraphic diagram directly from a `download` object.

## Value

A trellis object.

**Examples**

```
## Not run:
lake_o_dl <- get_download(15925)
# This works:
StratipLOT(lake_o_dl)

lakes_o_nw <- get_download(get_site(sitename = "Lake B%"))
# This Fails:
# StratipLOT(lake_o_nw)

## End(Not run)
```

---

taxa

*Access proxy taxonomic data*


---

**Description**

Extracts taxa from download objects and returns them in a useful format.

**Usage**

```
taxa(obj, ...)
```

```
## S3 method for class 'download'
taxa(obj, ...)
```

```
## S3 method for class 'download_list'
taxa(obj, collapse = TRUE, hierarchy = FALSE, ...)
```

**Arguments**

obj	an R object from which counts are to be extracted.
...	arguments passed to other methods.
collapse	should the results be returned as a list, one for each site (FALSE), or a single dataframe of all taxa? Default is TRUE
hierarchy	Should the taxonomic hierarchy be included?

**Details**

Methods are available for "download" and "download\_list" objects.

**Value**

Either a data frame of taxa or a list of such objects.

**Author(s)**

Simon Goring

**Examples**

```
## Not run:
ostracodes <- get_dataset(datasettype = 'ostracode')

ostro.dl <- get_download(ostracodes)
ostro.taxa <- taxa(ostro.dl)

## End(Not run)
```

---

taxon.list

*Neotoma taxon list*

---

**Description**

The taxonomy table for datasets in neotoma, as would be returned by [get\\_table](#)

**Usage**

```
data(taxon.list)
```

**Format**

a data.frame object

**Author(s)**

Simon J. Goring <simon.j.goring@gmail.com>

**Source**

The Neotoma database.

---

write_agefile	<i>Write age control file to disk formatted for either Bacon or Clam</i>
---------------	--

---

### Description

Passing in a download object the function outputs a Bacon or Clam formatted file to a user defined destination for age modelling with existing age-depth modeling software.

### Usage

```
write_agefile(download, chronology = 1, path, corename, cal.prog = "Bacon")
```

### Arguments

download	A single site returned by get_download.
chronology	Default is 1, the default chronology for the core. If a core has more than one chronology the user can define a different set of chronological controls.
path	The location of the 'Cores' folder & working directory for Bacon. Do not include "Cores" in the path name.
corename	The intended handle for the core, to be used in writing to file.
cal.prog	The method intended to build the age model, either 'Bacon' or 'Clam'.

### Value

This command returns a file in location path/Cores containing all the relevant information required to build either the default or prior chronology for a core.

### Author(s)

Simon J. Goring <simon.j.goring@gmail.com>

### References

Neotoma Project Website: <http://www.neotomadb.org> API Reference: <http://wnapi.neotomadb.org/doc/resources/contacts>

### Examples

```
## Not run:
# Find a particular record:

three_pines <- get_download(get_dataset(get_site("Three Pines Bog"),
                                     datasettype = "pollen"))

# You will need to edit the `path` argument here to point to a directory that
# contains a `Cores` directory.

write_agefile(download = three_pines[[1]],
```

```
path = "./inst",  
corename = "THREEPINES",  
cal.prog = "Bacon")
```

```
## End(Not run)
```

# Index

## \* API

- get\_closest, 19
- write\_agefile, 54

## \* IO

- browse, 5
- depths, 13
- get\_chroncontrol, 15
- get\_contact, 20
- get\_dataset, 21
- get\_download, 29
- get\_geochron, 33
- get\_publication, 34
- get\_site, 38
- get\_table, 44
- get\_taxa, 45

## \* Neotoma

- get\_closest, 19
- write\_agefile, 54

## \* Palaeoecology

- get\_closest, 19
- write\_agefile, 54

## \* connection

- browse, 5
- depths, 13
- get\_chroncontrol, 15
- get\_contact, 20
- get\_dataset, 21
- get\_download, 29
- get\_geochron, 33
- get\_publication, 34
- get\_site, 38
- get\_table, 44
- get\_taxa, 45

## \* methods

- download, 14

## \* utilities

- bind, 4
- compile\_downloads, 9
- compile\_taxa, 10

- ages, 3

- bind, 4

- browse, 5

- browse.dataset, 6

- browse.dataset\_list, 7

- browse.default, 7

- browse.download, 8

- browse.download\_list, 8

- compile\_downloads, 9

- compile\_taxa, 10

- counts, 12

- depths, 13

- download, 14

- get\_chroncontrol, 15

- get\_chroncontrol.dataset, 16

- get\_chroncontrol.dataset\_list, 17

- get\_chroncontrol.default, 17

- get\_chroncontrol.download, 18

- get\_chroncontrol.download\_list, 18

- get\_closest, 19

- get\_contact, 15, 20, 29, 33, 35, 37

- get\_dataset, 15, 21, 35, 37

- get\_dataset.default, 24

- get\_dataset.download, 25

- get\_dataset.download\_list, 26

- get\_dataset.geochronologic, 26

- get\_dataset.geochronologic\_list, 27

- get\_dataset.integer, 27

- get\_dataset.numeric, 28

- get\_dataset.site, 28

- get\_download, 4, 9–11, 29

- get\_download.dataset, 31

- get\_download.dataset\_list, 31

- get\_download.default, 32

- get\_download.site, 32

- get\_geochron, 33



get\_publication, 34  
get\_publication.dataset, 35  
get\_publication.dataset\_list, 36  
get\_publication.default, 36  
get\_publication.download, 37  
get\_publication.download\_list, 37  
get\_site, 15, 29, 33, 38  
get\_site.dataset, 39  
get\_site.dataset\_list, 40  
get\_site.default, 40  
get\_site.download, 41  
get\_site.download\_list, 41  
get\_site.geochronologic, 42  
get\_site.geochronologic\_list, 42  
get\_site.integer, 43  
get\_site.numeric, 43  
get\_table, 22, 25, 35, 37, 44, 53  
get\_taxa, 29, 45  
gp.table, 46

plot\_leaflet, 46  
pollen.equiv, 47

read.tilia, 48  
read\_bacon, 48

StratipLOT.download, 50  
StratipLOT.download\_list, 51

taxa, 52  
taxon.list, 53  
try, 29, 33

write\_agefile, 54