

Package ‘paleobioDB’

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Description 19 functions to wrap each endpoint of the PaleobioDB API, plus 8 functions to visualize and process the fossil data. The API documentation for the Paleobiology Database can be found in <<http://paleobiodb.org/data1.1/>>

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Type Package

License GPL-2

Title Download and Process Data from the Paleobiology Database

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URL <https://github.com/ropensci/paleobioDB>

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Imports rjson, gtools, RCurl, plyr, scales

Depends raster, maps

Suggests roxygen2, testthat

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'pbdb_geographic_functions.R' 'pbdb_querys.R'
'rest_api_tools.R' 'pbdb_rest_api_setup.R'
'pbdb_taxonomic_functions.R' 'pbdb_temporal_functions.R'

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paleobioDB

paleobioDB: An R-package for downloading, visualizing and processing data from the Paleobiology Database

Description

We have developed paleobioDB, an R-package designed to make easy and flexible queries of the Paleobiology Database, as well as to visualize and download selected data. This package will make it easy to access paleontological data in a way that should allow those data to be further analyzed, including via packages and libraries available in R.

Details

We programmed two different groups of functions. First, we developed a set of general and flexible functions to wrap the **PaleobioDB API**. These functions connect R with each of the endpoints of the PaleobioDB API. Second, based on these base functions, we programmed a second set of functions intended to explore and visualize the fossil occurrences in their geographic, temporal and taxonomic dimensions.

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References

Sara Varela, Javier Gonzalez-Hernandez, Luciano Fabris Sgarbi, Charles Marshall, Mark D. Uhen, Shanan Peters, Michael McClennen, 2014. paleobioDB: an R-package for downloading, visualizing and processing data from the Paleobiology Database (under review)

See Also

<http://paleobiodb.org>

Examples

```
## Not run:

canidae<- pbdb_occurrences (limit="all", base_name="canidae",
interval="Quaternary", show=c("coords", "phylo", "ident"))

## to explore the number of subtaxa
pbdb_subtaxa (canidae)

## to explore the temporal resolution of the fossil records
pbdb_temporal_resolution (canidae)

## returns a dataframe and a plot with the temporal span
## of the species, genera, etc.
pbdb_temp_range (canidae, rank= "genus", names=FALSE)

## returns a dataframe and a plot showing the species, genera, etc.
richness across time
pbdb_richness (canidae, rank= "species",
```

```

temporal_extent= c (0,10), res= 1)

## returns a dataframe and a plot showing the evolutionary
and extinction rates across time

## evolutionary rates= evo_ext=1
pbdb_orig_ext (canidae, rank="species", temporal_extent=c(0, 10),
res=1, orig_ext=1)

## extinction rates= evo_ext=2
pbdb_orig_ext (canidae, rank="species", temporal_extent=c(0, 10),
res=1, orig_ext=2)

## maps the fossil occurrences
pbdb_map (canidae, main = "Canidae", pch= 19, cex=0.7)

## maps the sampling effort
pbdb_map_occur (canidae, res= 5)

## maps the species, genera, etc. richness
pbdb_map_richness (canidae, rank="species", res= 5)

## End(Not run)

```

pbdb_collection *pbdb_collection*

Description

Returns information about a single collection record from the Paleobiology Database.

Usage

```
pbdb_collection (id, ...)
```

Arguments

<code>id</code>	identifier of the collection. This parameter is required.
<code>...</code>	documentation for all the parameters is available in http://paleobiodb.org/data1.1/colls/single go to <code>?pbdb_occurrences</code> to see an explanation about the main filtering parameters For example: <code>vocab set vocab="pbdb"</code> to show the complete name of the variables (by default variables have short 3-letter names) <code>show</code> to show extra variables (e.g. <code>"loc"</code> to show additional information about the geographic locality of the collection)

Value

a dataframe with a single occurrence

Examples

```
## Not run:
pbdb_collection (id=1003, vocab="pbdb", show="loc")

## End(Not run)
```

pbdb_collections *pbdb_collections*

Description

Returns information about multiple collections, selected according to the parameters you provide.

Usage

```
pbdb_collections (...)
```

Arguments

```
...                    documentation for all the parameters is available in http://paleobiodb.org/data1.1/colls/list
                      go to ?pbdb_occurrences to see an explanation about the main filtering parameters
```

Value

a dataframe with the collections that match the query

Examples

```
## Not run:
pbdb_collections (base_name="Cetacea", interval="Miocene")

## End(Not run)
```

pbdb_collections_geo *pbdb_collections_geo*

Description

This path returns information about geographic clusters of collections from the Paleobiology Database. These clusters are defined in order to facilitate the generation of maps at low resolutions. You can make a config request via <http://paleobiodb.org/data1.1/config> in order to get a list of the available summary levels.

Usage

```
pbdb_collections_geo (...)
```

Arguments

```
... documentation for all the parameters is available in http://paleobiodb.org/data1.1/colls/summary
go to ?pbdb_occurrences to see an explanation about the main filtering parameters
```

Value

a dataframe with the collections that match the query

Examples

```
## Not run:
pbdb_collections_geo (vocab="pbdb", lngmin=0.0,
  lngmax=15.0, latmin=0.0, latmax=15.0, level=2)

## End(Not run)
```

pbdb_interval	<i>pbdb_interval</i>
---------------	----------------------

Description

Returns information about a single interval, selected by identifier.

Usage

```
pbdb_interval (id, ...)
```

Arguments

```
id identifier of the temporal interval. This parameter is required.
... documentation for all the parameters is available in http://paleobiodb.org/data1.1/intervals/single
vocab set vocab="pbdb" to show the complete name of the variables (by default
variables have short 3-letter names)
```

Value

a dataframe with information from a single temporal interval

Examples

```
## Not run:
pbdb_interval (id=1, vocab="pbdb")

## End(Not run)
```

pbdb_intervals *pbdb_intervals*

Description

Returns information about multiple intervals, selected according to the parameters you provide.

Usage

```
pbdb_intervals (...)
```

Arguments

```
...                      documentation for all the parameters is available in http://paleobiodb.org/data1.1/intervals/lists.
For example: min_ma return only intervals that are at least this old max_ma return
only intervals that are at most this old order return the intervals in order start-
ing as specified. Possible values include older, younger. Defaults to younger.
vocab set vocab="pbdb" to show the complete name of the variables (by default
variables have short 3-letter names)
```

Value

a dataframe with information from several temporal intervals

Examples

```
## Not run:
pbdb_intervals (min_ma= 0, max_ma=2, vocab="pbdb")

## End(Not run)
```

pbdb_map *pbdb_map*

Description

Maps the fossil records

Usage

```
pbdb_map (data, col.int="white" ,pch=19, col.ocean="black", main=NULL,
col.point=c("light blue","blue"), ...)
```

Arguments

<code>data</code>	Input dataframe. This dataframe is the output of pbdb_occurrences function using the argument: <code>show = "coords"</code> . See too: Details and Examples
<code>col.int</code>	The colour of the mainland.
<code>pch</code>	See: par
<code>col.ocean</code>	The colour of the ocean.
<code>main</code>	To set the title of the map. See: par
<code>col.point</code>	Two or more colours. To generate the colour gradient used to show the number of occurrences per cell in map
<code>...</code>	Others parameters. See par and map

Details

The function opens a new window for the map

CAUTION! The argument `show = "coords"` in [pbdb_occurrences](#) function is required. We recommend the use of a cairo device ([X11](#)) for better visualization of the graphs. See **Examples**

Value

A map showing the distribution of the fossil records, with the points with a color gradient, according to the number of occurrences per cell.

See Also

See [pbdb_occurrences](#), [map](#), [par](#) and [colors](#) help pages

Examples

```
## Not run:
data<- pbdb_occurrences (limit="all", vocab= "pbdb",
base_name="Canis", show="coords")
X11(width=12, height=8)
pbdb_map(data)
pbdb_map(data,pch=1)
pbdb_map(data,pch=19,col.point=c("pink","red"), col.ocean="light blue",
main="canis")

## End(Not run)
```

pbdb_map_occur *pbdb_map_occur*

Description

Creates a RasterLayer object and a plot of the sampling effort (number of fossil records per cell).

Usage

```
pbdb_map_occur (data, res=5, col.int="white", col.ocean="black",
  col.eff=c("light blue","blue"), do.plot=TRUE, ...)
```

Arguments

data	Input dataframe. This dataframe is the output of pbdb_occurrences function using the argument: show="coords". See too: Details and Examples
res	the resolution of the RasterLayer object (in decimal degrees). See: raster
col.int	The colour of the mainland
col.ocean	The colour of the ocean
col.eff	Two or more colours. To generate the colour gradient used to show the number of occurrences per cell in map
do.plot	Logical; TRUE the function returns a RasterLayer and a plot.
...	Others parameters. See par and map

Details

CAUTION! The argument show = "coords" in [pbdb_occurrences](#) function is required. We recommend the use of a cairo device ([X11](#)) for better visualization of the graphs. See **Examples**

Value

A RasterLayer object and a plot with the sampling effort (number of fossil records per cell). This RasterLayer object have the resolution controlled by the argument res. The default is res=1.

See Also

See [pbdb_occurrences](#), [map](#), [par](#) and [colors](#) help pages

Examples

```
## Not run:
data<- pbdb_occurrences (limit="all", vocab= "pbdb", base_name="Canis",
  show="coords")
X11(width=13, height=7.8)
pbdb_map_occur (data,res=2)
## to obtain the raster file without plotting it
```

```
pbdb_map_occur (data,res=3,do.plot=F)

## End(Not run)
```

pbdb_map_richness *pbdb_map_richness*

Description

Creates a RasterLayer object and a plot with richness of species, genera, families, etc. per cell.

Usage

```
pbdb_map_richness (data, rank="species", do.plot=TRUE, res=5,
  col.int="white", col.ocean="black",
  col.rich=c("light blue","blue"),...)
```

Arguments

data	Input dataframe. This dataframe is the output of pbdb_occurrences function using the argument: <code>show = c("phylo", "coords", "ident")</code> . See too: Details and Examples
rank	To set which taxon rank you are interested for calculate richness. The options are: "species", "genus", "family", "order", "class" or "phylum")
do.plot	Logical; TRUE the function returns a RasterLayer and a plot.
res	The resolution of the RasterLayer object (in decimal degrees). See: raster
col.int	The colour of the mainland
col.ocean	The colour of the ocean
col.rich	Two or more colours. To generate the colour gradient used to show the richness per cell in map
...	Others parameters. See par and map

Details

CAUTION! The argument `show = "coords"` in [pbdb_occurrences](#) function is required. We recommend the use of a cairo device ([X11](#)) for better visualization of the graphs. See **Examples**

Value

A RasterLayer object and a plot with richness of species, genera, families, etc. per cell. This RasterLayer object have the resolution controlled by the argument `res`. The default is `res=1`.

See Also

See [pbdb_occurrences](#), [map](#), [par](#) and [colors](#) help pages

Examples

```
## Not run:
data<- pbdb_occurrences (limit=1000, vocab= "pbdb", base_name="mammalia",
show=c("phylo","coords","ident"))
X11(width=13, height=7.8)
pbdb_map_richness (data,res=8,rank="genus")
pbdb_map_richness (data,res=8,rank="family")
## to obtain the raster file and not plot the map
pbdb_map_richness (data,res=8,rank="family",do.plot=F)

## End(Not run)
```

pbdb_occurrence	<i>pbdb_occurrence</i>
-----------------	------------------------

Description

Returns information about a single occurrence record from the Paleobiology Database.

Usage

```
pbdb_occurrence (id, ...)
```

Arguments

id	identifier of the occurrence. This parameter is required.
...	documentation for all the parameters is available in http://paleobiodb.org/data1.1/occs/single Below, we describe the most common filters that paleontologists and ecologists might use. vocab set vocab="pbdb" to show the complete name of the variables (by default variables have short 3-letter names) show to show extra variables (e.g. coords)

Value

a dataframe with a single occurrence

Examples

```
## Not run:
pbdb_occurrence (id=1001)
pbdb_occurrence (id=1001, vocab="pbdb", show="coords")

## End(Not run)
```

pbdb_occurrences *pbdb_occurrences*

Description

Returns information about species occurrence records stored in the Paleobiology Database.

Usage

```
pbdb_occurrences (...)
```

Arguments

... documentation for all the parameters is available in <http://paleobiodb.org/data1.1/occs/list>
 Below, we describe the most common filters that paleontologists and ecologists might use. `limit` set limit to "all" to download all the occurrences. By default the limit is 500. `taxon_name` Return only records associated with the specified taxonomic name(s). You may specify multiple names, separated by commas. `base_name` Return records associated with the specified taxonomic name(s) and any of their children (e.g. `base_name="Canis"` will include `Canis` and `Canis lupus`). `lngmin` numeric. The longitude boundaries will be normalized to fall between -180 and 180. (Note that if you specify `lngmin` then you must also specify `lngmax`). Return only records whose geographic location falls within the given bounding box (defined by `lngmin`, `lngmax`, `latmin`, `latmax`). It generates two adjacent bounding boxes if the range crosses the antimeridian. `lngmax` numeric. The longitude boundaries will be normalized to fall between -180 and 180. `latmin` numeric. between -90 and 90. (Note that if you specify `latmin` then you must also specify `latmax`) `latmax` numeric. between -90 and 90. `min_ma` return only records whose temporal locality is at least this old, specified in Ma. `max_ma` return only records whose temporal locality is at most this old, specified in Ma. `interval` return only records whose temporal locality falls within the named geologic time interval (e.g. "Miocene"). `continent` return only records whose geographic location falls within the specified continent(s). `show` to show extra variables (e.g. `coords`, `phylo`, `ident`)

Value

a dataframe with the species occurrences

Examples

```
## Not run:
pbdb_occurrences (id=c(10, 11), show=c("coords", "phylo", "ident"))
pbdb_occurrences (limit="all", vocab= "pbdb",
taxon_name="Canis", show=c("coords", "phylo", "ident"))
pbdb_occurrences (limit="all", vocab= "pbdb",
base_name="Canidae", show=c("coords", "phylo", "ident"))

## End(Not run)
```

pbdb_orig_ext *pbdb_orig_ext*

Description

Plots the appearance of new taxa across time.

Usage

```
pbdb_orig_ext (data, rank,
temporal_extent, res, orig_ext,
colour="#0000FF30", bord="#0000FF", do.plot=TRUE)
```

Arguments

data	dataframe with our query to the paleoBD pbdb_occurrences . Important, it is required to show the name of the families, orders, etc. in the dataframe, to do that set: <code>show=c("phylo", "ident")</code> (see example).
rank	to set which taxon rank you are interested. By default rank= "species"
temporal_extent	vector to set the temporal extent (min, max)
res	numeric. to set the intervals of the temporal extent
orig_ext	1= origination, 2=extinction.
colour	to change the colour of the bars in the plot, skyblue2 by default.
bord	to set the colour of the border of the polygon
do.plot	TRUE/FALSE (TRUE by default).

Value

a dataframe with the number of first appearances and extinctions of the selected taxon rank across time, and a plot with the first appearances or extinctions of the selected taxon rank across time.

Examples

```
## Not run:
canidae<- pbdb_occurrences (limit="all", vocab="pbdb",
base_name="Canidae", show=c("phylo", "ident"))

# plot of the evolutive rates.
pbdb_orig_ext (canidae, rank="genus", temporal_extent=c(0, 10),
res=1, orig_ext=1)

# plot of the extinction rates.
pbdb_orig_ext (canidae, rank="species", temporal_extent=c(0, 10),
res=1, orig_ext=2)

## End(Not run)
```

pbdb_reference *pbdb_reference*

Description

Returns information about a single reference, selected by identifier

Usage

```
pbdb_reference (id, ...)
```

Arguments

`id` identifier of the reference. This parameter is required. #'

`...` documentation for all the parameters is available in <http://paleobiodb.org/data1.1/refs/single> go to `?pbdb_occurrences` to see an explanation about the main filtering parameters For example: `vocab set vocab="pbdb"` to show the complete name of the variables (by default variables have short 3-letter names)

Value

a dataframe with a single reference

Examples

```
## Not run:
pbdb_collection (id=1003, vocab="pbdb", show="loc")

## End(Not run)
```

pbdb_references *pbdb_references*

Description

Returns information about multiple references, selected according to the parameters you provide.

Usage

```
pbdb_references (...)
```

Arguments

... documentation for all the parameters is available in <http://paleobiodb.org/data1.1/refs/list>. For example: `author` Select only references for which any of the authors matches the specified name `year` Select only references published in the specified year `pubtitle` Select only references that involve the specified publication order Specifies the order in which the results are returned. You can specify multiple values separated by commas, and each value may be appended with `.asc` or `.desc`. Accepted values are: `author`, `year`, `pubtitle`, `created`, `modified`, `rank`.

Value

a dataframe with the information about the references that match the query

Examples

```
## Not run:
pbdb_references (author= "Polly")

## End(Not run)
```

`pbdb_ref_collections` *pbdb_ref_collections*

Description

Returns information about the references from which the selected collection data were entered.

Usage

```
pbdb_ref_collections (...)
```

Arguments

... documentation for all the parameters is available in <http://paleobiodb.org/data1.1/colls/refs>. For example: `id` A comma-separated list of collection identifiers. `author` Select only references for which any of the authors matches the specified name `year` Select only references published in the specified year `pubtitle` Select only references that involve the specified publication order Specifies the order in which the results are returned. You can specify multiple values separated by commas, and each value may be appended with `.asc` or `.desc`. Accepted values are: `author`, `year`, `pubtitle`, `created`, `modified`, `rank`.

Value

a dataframe with the information about the references that match the query

Examples

```
## Not run:
pbdb_ref_collections (id=1)

## End(Not run)
```

pbdb_ref_occurrences *pbdb_ref_occurrences*

Description

Returns information about the bibliographic references associated with fossil occurrences from the database.

Usage

```
pbdb_ref_occurrences (...)
```

Arguments

... documentation for all the parameters is available in <http://paleobiodb.org/data1.1/occs/refs> go to ?pbdb_occurrences to see an explanation about the main filtering parameters. For example: `author` Select only references for which any of the authors matches the specified name `year` Select only references published in the specified year `pubtitle` Select only references that involve the specified publication order `order` Specifies the order in which the results are returned. You can specify multiple values separated by commas, and each value may be appended with `.asc` or `.desc`. Accepted values are: `author`, `year`, `pubtitle`, `created`, `modified`, `rank`. (see documentation in <http://paleobiodb.org/data1.1/occs/refs>)

Value

a dataframe with the information about the references that match the query

Examples

```
## Not run:
pbdb_ref_occurrences (vocab="pbdb",
  taxon_name="Canis", year=2000)

## End(Not run)
```

pbdb_ref_taxa *pbdb_ref_taxa*

Description

This URL path returns information about the source references associated with taxa in the Paleobiology Database. You can use the same parameters that are available with `pbdb_taxa`, but Reference records are returned instead of Taxon records. One record is returned per reference, even if it is associated with multiple taxa.

Usage

```
pbdb_ref_taxa (...)
```

Arguments

... documentation for all the parameters is available. in <http://paleobiodb.org/data1.1/taxa/refs>. For instance:

- `name` Return information about the most fundamental taxonomic name matching this string.
- `id` Return information about the taxonomic name corresponding to this identifier. You may not specify both `name` and `id` in the same query.
- `exact` if this parameter is specified, then the taxon exactly matching the specified name or identifier is selected, rather than the senior synonym which is the default.
- `show` to show extra variables (see documentation for show in <http://paleobiodb.org/data1.1/taxa/refs>)
- `rel` set `rel="synonyms"` to select all synonyms of the base taxon or taxa; `rel="children"` to select the taxa immediately contained within the base taxon or taxa; `rel="common_ancestor"` to select the most specific taxon that contains all of the base taxa.
- `extant` TRUE/FALSE to select extinct/extant taxa.

Value

a dataframe with references from a list of taxa

Examples

```
## Not run:
pbdb_ref_taxa (name="Canidae", vocab="pbdb", show=c("attr", "app", "size", "nav"))

## End(Not run)
```

`pbdb_richness` *pbdb_richness*

Description

Plots the number of the interested.

Usage

```
pbdb_richness (data, rank, res, temporal_extent, colour, bord, do.plot)
```

Arguments

<code>data</code>	dataframe with our query to the paleoBD pbdb_occurrences . Important, it is required to show the name of the families, orders, etc. in the dataframe, to do that set: <code>show=c("phylo", "ident")</code> (see example).
<code>rank</code>	to set which taxon rank you are interested. By default <code>rank= "species"</code>
<code>res</code>	numeric. to set the intervals of the temporal extent
<code>temporal_extent</code>	vector to set the temporal extent (min, max)
<code>colour</code>	to change the colour of the bars in the plot, <code>skyblue2</code> by default.
<code>bord</code>	to set the colour of the border of the polygon
<code>do.plot</code>	TRUE/FALSE (TRUE by default).

Value

a plot and a dataframe with the richness aggregated by the taxon rank in the specified temporal extent and resolution.

Examples

```
## Not run:
data<- pbdb_occurrences (limit="all", vocab="pbdb",
base_name="Canidae", show=c("phylo", "ident"))
pbdb_richness (data, rank="species", res=1, temporal_extent=c(0,3))

## End(Not run)
```

pbdb_scale	<i>pbdb_scale</i>
------------	-------------------

Description

Returns information about a single time scale, selected by identifier.

Usage

```
pbdb_scale (id, ...)
```

Arguments

id	identifier of the temporal interval. This parameter is required.
...	documentation for all the parameters is available in http://paleobiodb.org/data1.1/scales/single . For example: vocab set vocab="pbdb" to show the complete name of the variables (by default variables have short 3-letter names)

Value

a dataframe with information from a single scale

Examples

```
## Not run:
pbdb_scale (id=1, vocab="pbdb")

## End(Not run)
```

pbdb_scales	<i>pbdb_scales</i>
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Description

Returns information about multiple time scales.

Usage

```
pbdb_scales(...)
```

Arguments

...	documentation for all the parameters is available in http://paleobiodb.org/data1.1/scales/list . For instance: vocab set vocab="pbdb" to show the complete name of the variables (by default variables have short 3-letter names)
-----	---

Value

a dataframe with information from the selected scales

Examples

```
## Not run:
## Get a dataframe with all the scales available in PBDB
## by setting no ids
pbdb_scales ()

## End(Not run)
```

pbdb_strata

pbdb_strata

Description

Returns information about geological strata, selected by name, rank, and/or geographic location.

Usage

```
pbdb_strata (...)
```

Arguments

... documentation for all the parameters is available in <http://paleobiodb.org/data1.1/strata/list>
 For example: name A full or partial name. You can use and _ as wildcards, but the query will be very slow if you put a wildcard at the beginning rank Return only strata of the specified rank: formation, group or member. lngmin numeric. The longitude boundaries will be normalized to fall between -180 and 180. (Note that if you specify lngmin then you must also specify lngmax). Return only records whose geographic location falls within the given bounding box (defined by lngmin, lngmax, latmin, latmax). It generate two adjacent bounding boxes if the range crosses the antimeridian. lngmax numeric. The longitude boundaries will be normalized to fall between -180 and 180. latmin numeric. between -90 and 90. (Note that if you specify latmin then you must also specify latmax) latmax numeric. between -90 and 90. loc Return only strata associated with some occurrence whose geographic location falls within the specified geometry, specified in WKT format. vocab set vocab="pbdb" to show the complete name of the variables (by default variables have short 3-letter names)

Value

a dataframe with information from the selected strata

Examples

```
## Not run:
pbdb_strata (lngmin=0, lngmax=15, latmin=0, latmax=15, rank="formation", vocab="pbdb")

## End(Not run)
```

pbdb_strata_auto *pbdb_strata_auto*

Description

Returns a list of strata matching the given prefix or partial name. This can be used to implement auto-completion for strata names, and can be limited by geographic location if desired.

Usage

```
pbdb_strata_auto (...)
```

Arguments

... documentation for all the parameters is available in <http://paleobiodb.org/data1.1/strata/auto>. For instance: name A full or partial name. You can use but the query will be very slow if you put a wildcard at the beginning rank Return only strata of the specified rank: formation, group or member. lngmin numeric. The longitude boundaries will be normalized to fall between -180 and 180. (Note that if you specify lngmin then you must also specify lngmax). Return only records whose geographic location falls within the given bounding box (defined by lngmin, lngmax, latmin, latmax). It generate two adjacent bounding boxes if the range crosses the antimeridian. lngmax numeric. The longitude boundaries will be normalized to fall between -180 and 180. latmin numeric. between -90 and 90. (Note that if you specify latmin then you must also specify latmax) latmax numeric. between -90 and 90. loc Return only strata associated with some occurrence whose geographic location falls within the specified geometry, specified in WKT format. vocab set vocab="pbdb" to show the complete name of the variables (by default variables have short 3-letter names)

Value

a dataframe with information from the strata that matches our letters.

Examples

```
## Not run:
pbdb_strata_auto (name= "Pin", vocab="pbdb")

## End(Not run)
```

pbdb_subtaxa

pbdb_subtaxa

Description

count the number of subtaxa within a given taxa. e.g. number of species within a genus.

Usage

```
pbdb_subtaxa (data, do.plot, col)
```

Arguments

`data` dataframe with our query to the paleoBD [pbdb_occurrences](#)

`do.plot` by default this function make a plot to visualize the distribution of taxa. Set to FALSE to skip the plot.

`col` set the colour of the histogram. skyblue2 by default.

Value

a plot and a dataframe with the number of subtaxa in the data.

Examples

```
## Not run:
canidae_quat<- pbdb_occurrences (limit="all",
base_name="Canidae", interval="Quaternary",
show=c("coords", "phylo", "ident"))
pbdb_subtaxa (canidae_quat)

## End(Not run)
```

pbdb_taxa

pbdb_taxa

Description

Returns information about multiple taxonomic names. This function can be used to query for all of the children or parents of a given taxon, among other operations.

Usage

```
pbdb_taxa (...)
```

Arguments

... documentation for all the parameters is available in <http://paleobiodb.org/data1.1/taxa/list>
 For example: `name` Return information about the most fundamental taxonomic name matching this string. `id` Return information about the taxonomic name corresponding to this identifier. You may not specify both `name` and `id` in the same query. `exact` if this parameter is specified, then the taxon exactly matching the specified name or identifier is selected, rather than the senior synonym which is the default. `show` to show extra variables: `attr` (The attribution of this taxon (author and year)), `app` (The age of first and last appearance of this taxon from the occurrences recorded in this database), `size` (The number of sub-taxa appearing in this database), `nav` (Additional information for the PBDB Navigator taxon browser) `rel` set `rel="synonyms"` to select all synonyms of the base taxon or taxa; `rel="children"` to select the taxa immediately contained within the base taxon or taxa; `rel="common_ancestor"` to select the most specific taxon that contains all of the base taxa. `extant` TRUE/FALSE to select extant/extinct taxa.

Value

a dataframe with information from a list of taxa

Examples

```
## Not run:
pbdb_taxa (name="Canidae", vocab="pbdb",
show=c("attr", "app", "size", "nav"))
pbdb_taxa (id =c(10, 11), vocab="pbdb",
show=c("attr", "app", "size", "nav"))
pbdb_taxa (id =c(10, 11), vocab="pbdb",
show=c("attr", "app", "size", "nav"), rel="common_ancestor")

## End(Not run)
```

pbdb_taxa_auto

pbdb_taxa_auto

Description

Returns a list of names matching the given prefix or partial name.

Usage

pbdb_taxa_auto (...)

Arguments

... see all parameters: http://paleobiodb.org/data1.1/taxa/auto_doc.html For example: name A partial name or prefix. It must have at least 3 significant characters, and may include both a genus (possibly abbreviated) and a species. limit set the limit to the number of matches

Value

a dataframe with information about the matches (taxon rank and number of occurrences in the database)

Examples

```
## Not run:
pbdb_taxa_auto (name="Cani", limit=10)

## End(Not run)
```

pbdb_taxon

pbdb_taxon

Description

Returns information about a single taxonomic name, identified either by name or by identifier.

Usage

```
pbdb_taxon (...)
```

Arguments

... documentation for all the parameters is available in <http://paleobiodb.org/data1.1/taxa/single> go to ?pbdb_taxa to see an explanation about the main filtering parameters. For example: name Return information about the most fundamental taxonomic name matching this string. The % and _ characters may be used as wildcards.

Value

a dataframe with information from a single taxon

Examples

```
## Not run:
pbdb_taxon (name="Canis", vocab="pbdb",
show=c("attr", "app", "size"))

## End(Not run)
```

```
pbdb_temporal_resolution  
      pbdb_temporal_resolution
```

Description

to show the temporal resolution of the fossil data

Usage

```
pbdb_temporal_resolution (data, do.plot=TRUE)
```

Arguments

data dataframe with our query to the paleoBD [pbdb_occurrences](#)
do.plot TRUE/FALSE. To show a frequency plot of the data (TRUE by default).

Value

a plot and a list with a summary of the temporal resolution of the data (min, max, 1st and 3rd quartils, median and mean), and the temporal resolution of each fossil record (Ma).

Examples

```
## Not run:  
data<- pbdb_occurrences (taxon_name= "Canidae", interval= "Quaternary")  
pbdb_temporal_resolution (data)  
  
## End(Not run)
```

```
pbdb_temp_range            pbdb_temp_range
```

Description

constructs a plot and a dataframe with the temporal range of the taxa (species, genera, families, etc.) within in a selected higher taxon.

Usage

```
pbdb_temp_range (data, rank, col = "#0000FF",  
names = TRUE, do.plot =TRUE)
```

Arguments

<code>data</code>	dataframe with our query to the paleoBD pbdb_occurrences . Important, it is required to show the name of the families, orders, etc. in the dataframe, to do that set: <code>show=c("phylo", "ident")</code> (see example).
<code>rank</code>	to set which taxon rank you are interested.
<code>col</code>	to change the colour of the bars in the plot, <code>skyblue2</code> by default.
<code>names</code>	TRUE/FALSE (TRUE by default). To include or not the name of the taxa in the plot
<code>do.plot</code>	TRUE/FALSE (TRUE by default).

Value

a plot and a dataframe with the time span of the taxa selected (species, genus, etc.)

Examples

```
## Not run:
canis_quaternary<- pbdb_occurrences (limit="all", base_name="Canis",
                                     interval="Quaternary", show=c("coords", "phylo", "ident"))
pbdb_temp_range (canis_quaternary, rank="species", names=FALSE)

## End(Not run)
```

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