Package ‘robis’

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Title Ocean Biodiversity Information System (OBIS) Client

Description Client for the Ocean Biodiversity Information System (<https://obis.org>).

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URL https://github.com/iobis/robis

BugReports https://github.com/iobis/robis/issues

Depends R (>= 3.1.3)

Imports httr, dplyr, jsonlite, leaflet, ggplot2, tidyr, httrcache, tibble, mapedit, sf, rlang, purrr, stringr, curl, data.table, tidyselect, xml2


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Suggests testthat, knitr, rmarkdown, spelling

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**R topics documented:**

- `area` .................................................. 2
- `checklist` ............................................. 3
- `dataset` ................................................ 4
- `dna_records` ......................................... 5
- `get_geometry` ........................................ 5
- `map_ggplot` .......................................... 6
- `map_leaflet` ......................................... 6
- `measurements` ....................................... 7
- `node` ................................................... 7
- `occurrence` .......................................... 8
- `robis` .................................................. 9
- `taxon` .................................................. 10

**Index**

```
area  Fetch a list of areas
```

**Description**

Fetch a list of areas

**Usage**

```r
area(verbosity = FALSE)
```

**Arguments**

- `verbose` logical. Optional parameter to enable verbose logging (default = FALSE).

**Value**

The areas.

**Examples**

```r
areas <- area(verbosity = FALSE)
```
checklist

Create a checklist.

Description

Create a checklist.

Usage

checklist(scientificname = NULL, taxonid = NULL, datasetid = NULL, nodeid = NULL, instituteid = NULL, areaid = NULL, startdate = NULL, enddate = NULL, startdepth = NULL, enddepth = NULL, geometry = NULL, redlist = NULL, hab = NULL, wrims = NULL, dropped = NULL, flags = NULL, exclude = NULL, verbose = FALSE)

Arguments

scientificname the scientific name.
taxonid the taxon identifier (WoRMS AphiaID).
datasetid the dataset identifier.
nodeid the OBIS node identifier.
instituteid the OBIS institute identifier.
areaid the OBIS area identifier.
startdate the earliest date on which occurrence took place.
enddate the latest date on which the occurrence took place.
startdepth the minimum depth below the sea surface.
enddepth the maximum depth below the sea surface.
geometry a WKT geometry string.
redlist include only IUCN Red List species.
hab include only IOC-UNESCO HAB species.
wrims include only WRiMS species.
dropped only include dropped records (TRUE), exclude dropped records (NULL) or include dropped records (include).
flags quality flags which need to be set.
exclude quality flags to be excluded from the results.
verbose logical. Optional parameter to enable verbose logging (default = FALSE).

Value

The checklist.
Examples

```r
taxa <- checklist(scientificname = "Tellinidae")
taxa <- checklist(geometry = "POLYGON ((2.3 51.8, 2.3 51.6, 2.6 51.6, 2.6 51.8, 2.3 51.8))")
taxa <- checklist(areaid = 10181)
```

Description

Create a list of datasets.

Usage

```r
dataset(scientificname = NULL, taxonid = NULL, datasetid = NULL,
        nodeid = NULL, instituteid = NULL, areaid = NULL, startdate = NULL,
        enddate = NULL, startdepth = NULL, enddepth = NULL, geometry = NULL,
        redlist = NULL, hab = NULL, wrims = NULL, exclude = NULL, verbose = FALSE)
```

Arguments

- `scientificname`: the scientific name.
- `taxonid`: the taxon identifier (WoRMS AphiaID).
- `datasetid`: the dataset identifier.
- `nodeid`: the OBIS node identifier.
- `instituteid`: the OBIS institute identifier.
- `areaid`: the OBIS area identifier.
- `startdate`: the earliest date on which occurrence took place.
- `enddate`: the latest date on which the occurrence took place.
- `startdepth`: the minimum depth below the sea surface.
- `enddepth`: the maximum depth below the sea surface.
- `geometry`: a WKT geometry string.
- `redlist`: include only IUCN Red List species.
- `hab`: include only IOC-UNESCO HAB species.
- `wrims`: include only WRiMS species.
- `exclude`: quality flags to be excluded from the results.
- `verbose`: logical. Optional parameter to enable verbose logging (default = FALSE).

Value

The datasets.
**dna_records**

Extract DNA records from occurrence data with a dna column.

**Usage**

dna_records(df, fields = "id")

**Arguments**

df the occurrence dataframe.
fields columns from the occurrence dataframe to include.

**Value**

The DNA records.

---

**get_geometry**

Get a WKT geometry by drawing on a map.

**Description**

Get a WKT geometry by drawing on a map.

**Usage**

get_geometry(provider_tiles = "Esri.WorldGrayCanvas")

**Arguments**

provider_tiles the base map provider.

**Value**

A WKT representation of a geometry.
map_ggplot

Create a ggplot2 map.

Description
Create a ggplot2 map.

Usage
map_ggplot(data, color = "#ff3399")

Arguments
data the occurrences from occurrence().
color color to be used for the dots.

Value
A ggplot object.

map_leaflet

Create a leaflet map.

Description
Create a leaflet map.

Usage
map_leaflet(data, color = "#ff3399",
provider_tiles = "Esri.WorldGrayCanvas", popup = function(x) { x["id"] },
antarctic = FALSE)

Arguments
data the occurrences from occurrence().
color color to be used for the dots.
provider_tiles the base map provider.
popup function generating the popup content.
antarctic use antarctic polar stereographic projection.

Value
A leaflet object.
## measurements

Extract measurements or facts from occurrence data with a mof column.

### Description

Extract measurements or facts from occurrence data with a mof column.

### Usage

```r
measurements(df, fields = "id")
```

### Arguments

- **df**: the occurrence dataframe.
- **fields**: columns from the occurrence dataframe to include.

### Value

The measurements.

## node

Fetch a list of nodes

### Description

Fetch a list of nodes

### Usage

```r
node(verbose = FALSE)
```

### Arguments

- **verbose**: logical. Optional parameter to enable verbose logging (default = FALSE).

### Value

The nodes

### Examples

```r
nodes <- node()
```
Description

Find occurrences.

Usage

occurrence(scientificname = NULL, taxonid = NULL, datasetid = NULL, nodeid = NULL, instituteid = NULL, areaid = NULL, startdate = NULL, enddate = NULL, startdepth = NULL, enddepth = NULL, geometry = NULL, measurementtype = NULL, measurementtypeid = NULL, measurementvalue = NULL, measurementvalueid = NULL, measurementunit = NULL, measurementunitid = NULL, redlist = NULL, hab = NULL, wrims = NULL, mof = NULL, dna = NULL, absence = NULL, event = NULL, dropped = NULL, flags = NULL, exclude = NULL, fields = NULL, qcfields = NULL, verbose = FALSE)

Arguments

- **scientificname**: the scientific name.
- **taxonid**: the taxon identifier (WoRMS AphiaID).
- **datasetid**: the dataset identifier.
- **nodeid**: the OBIS node identifier.
- **instituteid**: the OBIS institute identifier.
- **areaid**: the OBIS area identifier.
- **startdate**: the earliest date on which occurrence took place.
- **enddate**: the latest date on which the occurrence took place.
- **startdepth**: the minimum depth below the sea surface.
- **enddepth**: the maximum depth below the sea surface.
- **geometry**: a WKT geometry string.
- **measurementtype**: the measurement type to be included in the measurements data.
- **measurementtypeid**: the measurement type ID to be included in the measurements data.
- **measurementvalue**: the measurement value to be included in the measurements data.
- **measurementvalueid**: the measurement value ID to be included in the measurements data.
- **measurementunit**: the measurement unit to be included in the measurements data.
- **measurementunitid**: the measurement unit ID to be included in the measurements data.
redlist include only IUCN Red List species.
hab include only IOC-UNESCO HAB species.
wrims include only WRiMS species.
mof include measurements data (default = NULL).
dna include DNA data (default = NULL).
absence only include absence records (TRUE), exclude absence records (NULL) or include absence records (include).
event only include pure event records (TRUE), exclude pure event records (NULL) or include event records (include).
dropped only include dropped records (TRUE), exclude dropped records (NULL) or include dropped records (include).
flags quality flags which need to be set.
exclude quality flags to be excluded from the results.
fields fields to be included in the results.
qcfields include lists of missing and invalid fields (default = NULL).
verbose logical. Optional parameter to enable verbose logging (default = FALSE).

Value
The occurrence records.

Examples
records <- occurrence(scientificname = "Abra sibogai")
records <- occurrence(taxonid = 141438, startdate = as.Date("2007-10-10"))
records <- occurrence(taxon = 141438, geometry = "POLYGON ((0 0, 0 45, 45 45, 45 0, 0 0))")

robis R client for the OBIS API

Description
This is an R client for the Ocean Biodiversity Information System (OBIS) API which is documented at https://api.obis.org.
Code and issues for this package are managed at https://github.com/iobis/robis.

Author(s)
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Samuel Bosch
Description
Get taxon by taxon ID.

Usage
\texttt{taxon(taxonid, verbose = FALSE)}

Arguments
\begin{itemize}
  \item \texttt{taxonid} \hspace{1cm} the taxon identifier (WoRMS AphiaID).
  \item \texttt{verbose} \hspace{1cm} logical. Optional parameter to enable verbose logging (default = FALSE).
\end{itemize}

Value
Tibble containing taxon records.

Examples
\texttt{taxon(c(141433, 141434))}
Index

area, 2
checklist, 3
dataset, 4
dna_records, 5
get_geometry, 5
map_ggplot, 6
map_leaflet, 6
measurements, 7
node, 7
occurrence, 8
robis, 9
taxon, 10