**Package ‘rglobi’**

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**Encoding** UTF-8

**Language** en-US

**Type** Package

**Title** R Interface to Global Biotic Interactions

**Description** A programmatic interface to the web service methods provided by Global Biotic Interactions (GloBI) (<https://www.globalbioticinteractions.org/>). GloBI provides access to spatial-temporal species interaction records from sources all over the world. rglobi provides methods to search species interactions by location, interaction type, and taxonomic name. In addition, it supports Cypher, a graph query language, to allow for executing custom queries on the GloBI aggregate species interaction data set.

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**URL** https://docs.ropensci.org/rglobi/, https://github.com/ropensci/rglobi

**BugReports** https://github.com/ropensci/rglobi/issues

**VignetteBuilder** knitr

**Depends** R (>= 3.0.1)

**License** MIT + file LICENSE

**Imports** rjson (>= 0.2.13), readr (>= 1.3.1), RCurl (>= 0.3.4), curl (>= 0.3.3)

**Suggests** testthat(>= 0.7), openssl, httr, markdown, knitr

**RoxygenNote** 6.1.1

**NeedsCompilation** no

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get_child_taxa

Returns all known child taxa with known interaction of specified taxa and rank.

Usage

get_child_taxa(taxon.names, rank = "Species", skip = 0, limit = 25, 
opts = list())

Arguments

taxon.names list of taxa of which child taxa should be included.
rank selected taxonomic rank of child taxa
skip number of child taxon names to skip before returning result. May be used for pagination.
limit maximum number of child taxon names returned
opts list of options including web service configuration like "port" and "host"

Value

list of child taxon names
get_data_fields

See Also

Other interactions: get_interaction_matrix, get_interaction_table, get_interaction_types, get_interactions_by_taxa, get_interactions_by_type, get_interactions, get_predators_of, get_prey_of

Examples

## Not run:
get_child_taxa(list("Aves"))

## End(Not run)

get_data_fields  List data fields identified in GloBI database

Description

Returns data frame with supported data fields

Usage

get_data_fields(opts = list(), read_csv = read_csv_online)

Arguments

opts  list of named options to configure GloBI API

read_csv  function used to find csv associated to query url, defaulting to online query method

Value

Returns data frame of supported data fields

Examples

## Not run:
get_data_fields()

## End(Not run)
get_interactions

Get Species Interaction from GloBI

Description

Get Species Interaction from GloBI

Usage

get_interactions(taxon = "Homo sapiens", interaction.type = "preysOn",
...)

Arguments

taxon canonical scientific name of source taxon (e.g. Homo sapiens)
interaction.type the preferred interaction type (e.g. preysOn)
... list of options to configure GloBI API

Value

species interactions between source and target taxa

See Also

Other interactions: get_child_taxa, get_interaction_matrix, get_interaction_table, get_interaction_types,
get_interactions_by_taxa, get_interactions_by_type, get_predators_of, get_prey_of

Examples

## Not run:
get_interactions("Homo sapiens", "preysOn")
get_interactions("Insecta", "parasiteOf")

## End(Not run)

get_interactions_by_taxa

Return interactions involving specific taxa

Description

Returns interactions involving specific taxa. Secondary (target) taxa and spatial boundaries may also be set
Usage

get_interactions_by_taxa(sourcetaxon, targettaxon = NULL, interactiontype = NULL, accordingto = NULL, showfield = c("source_taxon_external_id", "source_taxon_name", "source_taxon_path", "source_specimen_life_stage", "interaction_type", "target_taxon_external_id", "target_taxon_name", "target_taxon_path", "target_specimen_life_stage", "latitude", "longitude", "study_citation", "study_external_id", "study_source_citation"), otherkeys = NULL, bbox = NULL, returnobservations = F, opts = list(), read_csv = read_csv_online)

Arguments

- **sourcetaxon**: Taxa of interest (consumer, predator, parasite); may be specified as "Genus species" or higher level (e.g., Genus, Family, Class).
- **targettaxon**: Taxa of interest (prey, host); may be specified as "Genus species" or higher level (e.g., Genus, Family, Class).
- **interactiontype**: Interaction types of interest (prey, host); may be specified as listed by get_interaction_types()
- **accordingto**: Data source of interest
- **showfield**: Data fields of interest (e.g., source_taxon_external_id, source_taxon_name); may be specified as listed by get_data_fields()
- **otherkeys**: list of key-value pairs to query any field not covered by other parameters; keys may be specified as listed by get_data_fields()
- **bbox**: Coordinates in EPSG:4326 decimal degrees defining "left, bottom, right, top" of bounding box
- **returnobservations**: if true, all individual observations are returned, else only distinct relationships
- **opts**: list of named options to configure GloBI API
- **read_csv**: function used to find csv associated to query url, defaulting to online query method

Value

Returns data frame of interactions

Note

For data sources in which type of interactions were not specified, the interaction is labeled "interacts_with"

See Also

Other interactions: get_child_taxa, get_interaction_matrix, get_interaction_table, get_interaction_types, get_interactions_by_type, get_interactions, get_predators_of, get_prey_of
get_interactions_by_type

Get Species Interactions by Interaction Type from GloBI

Description

Get Species Interactions by Interaction Type from GloBI

Usage

get_interactions_by_type(interactiontype = c("interactsWith"), ...)

Arguments

interactiontype
  the requested interaction type (e.g. preysOn)

...
  list of options to configure GloBI API

Value

species interactions given provided interaction type(s)

See Also

Other interactions: get_child_taxa, get_interaction_matrix, get_interaction_table, get_interaction_types, get_interactions_by_taxa, get_interactions, get_predators_of, get_prey_of

Examples

## Not run:
get_interactions_by_type(interactiontype = c("eats", "eatenBy"))
get_interactions_by_type(interactiontype = "parasiteOf")

## End(Not run)
get_interactions_in_area

Return all interactions in specified area

Description

Returns all interactions in data base in area specified in arguments

Usage

get_interactions_in_area(bbox, ...)

Arguments

bbox Coordinates in EPSG:4326 decimal degrees defining "left, bottom, right, top" of bounding box
...
list of named options to configure GloBI API

Value

Returns data frame of interactions

See Also

Other areas: get_interaction_areas

Examples

## Not run:
get_interactions_in_area(bbox = c(-67.87, 12.79, -57.08, 23.32))

## End(Not run)

get_interaction_areas

Find locations at which interactions were observed

Description

Returns all locations (latitude,longitude) of interactions in data base or area specified in arguments

Usage

get_interaction_areas(bbox = NULL, read_csv = read_csv_online, ...)

Examples

## Not run:
get_interaction_areas(bbox = c(-67.87, 12.79, -57.08, 23.32))

## End(Not run)
get_interaction_matrix

Get Interaction Matrix. Constructs an interaction matrix indicating whether source taxa (rows) or target taxa (columns) are known to interact with given type.

Usage

get_interaction_matrix(source.taxon.names = list("Homo sapiens"),
                      target.taxon.names = list("Mammalia"), interaction.type = "eats",
                      opts = list(), read_csv = read_csv_online)

Arguments

source.taxon.names
  list of source taxon names (e.g. list('Mammalia', 'Aves', 'Ariopsis felis'))

target.taxon.names
  list of target taxon names
get_interaction_table

interaction.type
- the preferred interaction type (e.g. preysOn)

opts
- list of options to configure GloBI API

read_csv
- function used to find csv associated to query url, defaulting to online query method

Value
- matrix representing species interactions between source and target taxa

See Also
- Other interactions: get_child_taxa, get_interaction_table, get_interaction_types, get_interactions_by_taxa, get_interactions_by_type, get_interactions, get_predators_of, get_prey_of

Examples

```r
## Not run:
get_interaction_matrix("Homo sapiens", "Mammalia", "interactsWith")

## End(Not run)
```

get_interaction_table

Returns all known child taxa with known interaction of specified source and target taxa on any rank.

Description

Returns all known child taxa with known interaction of specified source and target taxa on any rank.

Usage

```r
get_interaction_table(source.taxon.names = list(),
                     target.taxon.names = list(), interaction.type = "preysOn",
                     skip = 0, limit = 100, opts = list())
```

Arguments

- source.taxon.names: list of taxon names for source
- target.taxon.names: list of taxon names for target
- interaction.type: kind of interaction
- skip: number of records skipped before including record in result table, used in pagination
- limit: maximum number of interaction to include
- opts: connection parameters and other options
get_interaction_types

Value
table of matching source, target and interaction types

See Also
Other interactions: get_child_taxa, get_interaction_matrix, get_interaction_types, get_interactions_by_taxa, get_interactions_by_type, get_interactions, get_predators_of, get_prey_of

Examples
```r
## Not run:
get_interaction_table(source.taxon.names = list("Aves"), target.taxon.names = list('Insecta'))
## End(Not run)
```

get_interaction_types List interactions identified in GloBI database

Description
Returns data frame with supported interaction types

Usage
get_interaction_types(opts = list(), read_csv = read_csv_online)

Arguments
- **opts**: list of named options to configure GloBI API
- **read_csv**: function used to find csv associated to query url, defaulting to online query method

Value
Returns data frame of supported interaction types

See Also
Other interactions: get_child_taxa, get_interaction_matrix, get_interaction_table, get_interactions_by_taxa, get_interactions_by_type, get_interactions, get_predators_of, get_prey_of

Examples
```r
## Not run:
get_interaction_types()
## End(Not run)
```
get_predators_of  

*Get a List of Predators of a Given Prey Taxon*

**Description**

Get a List of Predators of a Given Prey Taxon

**Usage**

```r
get_predators_of(taxon = "Rattus rattus", ...)
```

**Arguments**

- `taxon`  
  scientific name of prey taxon. Can be any taxonomic rank (e.g. Rattus rattus, Decapoda)
- `...`  
  list of named options to configure the GloBI API

**Value**

list of recorded prey-predator interactions that involve the desired prey taxon.

**See Also**

Other interactions: `get_child_taxa`, `get_interaction_matrix`, `get_interaction_table`, `get_interaction_types`, `get_interactions_by_taxa`, `get_interactions_by_type`, `get_interactions`, `get_prey_of`

**Examples**

```r
## Not run:
get_predators_of("Rattus rattus")
get_predators_of("Primates")
## End(Not run)
```

---

get_prey_of  

*Get a List of Prey for given Predator Taxon*

**Description**

Get a List of Prey for given Predator Taxon

**Usage**

```r
get_prey_of(taxon = "Homo sapiens", ...)
```

**Examples**

```r
## Not run:
get_prey_of("Homo sapiens")
## End(Not run)
```
Arguments

taxon  scientific name of predator taxon. Can be any taxonomic rank (e.g. Homo sapiens, Animalia)
  ...
  list of named options to configure GloBI API

Value

  list of recorded predator-prey interactions that involve the desired predator taxon

See Also

  Other interactions: get_child_taxa, get_interaction_matrix, get_interaction_table, get_interaction_types, get_interactions_by_taxa, get_interactions_by_type, get_interactions, get_predators_of

Examples

    ## Not run:
    get_prey_of("Homo sapiens")
    get_prey_of("Primates")

    ## End(Not run)

---

query  

*Executes a Cypher Query Against GloBI’s Neo4j Instance*

Description

Executes a Cypher Query Against GloBI’s Neo4j Instance

Usage

    query(cypherQuery, opts = list())

Arguments

  cypherQuery  Cypher query (see http://github.com/globalbioticinteractions/globalbioticinteractions/wiki/cypher for examples)

  opts  list of named options to configure GloBI API

Value

  result of cypher query string
Index

* areas
  get_interaction_areas, 7
  get_interactions_in_area, 7
* database
  get_data_fields, 3
  get_interaction_areas, 7
  get_interaction_types, 10
  get_interactions_by_taxa, 4
  get_interactions_in_area, 7
* data
  get_data_fields, 3
* interactions
  get_child_taxa, 2
  get_interaction_matrix, 8
  get_interaction_table, 9
  get_interaction_types, 10
  get_interactions, 4
  get_interactions_by_taxa, 4
  get_interactions_by_type, 6
  get_predators_of, 11
  get_prey_of, 11
  get_child_taxa, 2, 4–6, 9–12
  get_data_fields, 3
  get_interaction_areas, 7, 7
  get_interaction_matrix, 3–6, 8, 10–12
  get_interaction_table, 3–6, 9, 10–12
  get_interaction_types, 3–6, 9, 10, 11, 12
  get_interactions, 3, 4, 5, 6, 9–12
  get_interactions_by_taxa, 3, 4, 4, 6, 9–12
  get_interactions_by_type, 3–5, 6, 9–12
  get_interactions_in_area, 7, 8
  get_predators_of, 3–6, 9, 10, 11, 12
  get_prey_of, 3–6, 9–11, 11
query, 12