Package ‘rglobi’

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Type Package
Title R Interface to Global Biotic Interactions
Description A programmatic interface to the web service methods provided by Global Biotic Interactions (GloBI). 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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get_child_taxa

**Description**

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

**Usage**

```r
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

**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`
**get_data_fields**

List data fields identified in GloBI database

---

**Description**

Returns data frame with supported data fields

**Usage**

```r
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

---

**get_interactions**

Get Species Interaction from GloBI

---

**Description**

Get Species Interaction from GloBI

**Usage**

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

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

```r
## 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

```r
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

Examples

```r
## Not run:
get_interactions_by_taxa(sourcetaxon = "Rattus")
get_interactions_by_taxa(sourcetaxon = "Aves", targettaxon = "Rattus")
get_interactions_by_taxa(source_taxon = "Rattus rattus",
bbox = c(-67.87,12.79,-57.08,23.32))

## End(Not run)
```
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, ...)

---

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, ...)

---
get_interaction_areas

Arguments

bbox Coordinates in EPSG:4326 decimal degrees defining "left, bottom, right, top" of bounding box

Value

Returns data frame of interactions

See Also

Other areas: get_interaction_areas

Examples

```r
## 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, ...)

Arguments

bbox Coordinates in EPSG:4326 decimal degrees defining "left, bottom, right, top" of bounding box

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

Value

Returns data frame of coordinates

See Also

Other areas: get_interactions_in_area
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.

Description

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

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
**get_interaction_table**

**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

**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
## 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
get_predators_of(taxon = "Rattus rattus", ...)

get_prey_of

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_predators_of`

Examples

```r
## Not run:
get_prey_of("Rattus rattus")
get_prey_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", ...)
```

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

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

## End(Not run)
```

<table>
<thead>
<tr>
<th>query</th>
<th>Executes a Cypher Query Against GloBI’s Neo4j Instance</th>
</tr>
</thead>
</table>

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

**Usage**

```r
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
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