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

VignetteBuilder knitr

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get\_child\_taxa

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# Description

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

# 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
```

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# **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())
```

#### **Arguments**

opts

list of named options to configure GloBI API

# 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**

#### **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())
```

#### **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			

#### Value

opts

Returns data frame of interactions

# Note

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

list of named options to configure GloBI API

#### See Also

 $\label{lem:opt:constraints} Other interactions: \verb|get_child_taxa|, \verb|get_interaction_matrix|, \verb|get_interaction_table|, \verb|get_interaction_table|,$ 

```
## Not run:
get_interactions_by_taxa(sourcetaxon = "Rattus")
get_interactions_by_taxa(sourcetaxon = "Aves", targettaxon = "Rattus")
get_interactions_by_taxa(sourcetaxon = "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, ...)
```

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# 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, ...)
```

#### **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 coordinates

# See Also

```
Other areas: get_interactions_in_area
```

#### **Examples**

```
## Not run:
get_interaction_areas ()
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.

# **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())
```

# **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
```

#### 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

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

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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

```
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

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

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```
get_interaction_types List interactions identified in GloBI database
```

### **Description**

Returns data frame with supported interaction types

# Usage

```
get_interaction_types(opts = list())
```

# Arguments

opts

list of named options to configure GloBI API

#### 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", ...)
```

## **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

get\_prey\_of

#### 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**

```
## 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

```
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

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

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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/jhpoelen/eol-globi-data/wiki/cypher for ex-

amples)

opts list of named options to configure GloBI API

# Value

result of cypher query string

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