

# Package: rglobi (via r-universe)

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**Encoding** UTF-8

**Language** en-US

**Type** Package

**Title** 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.

**Version** 0.3.4

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

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

**RoxygenNote** 7.2.3

**Repository** <https://ropensci.r-universe.dev>

**RemoteUrl** <https://github.com/ropensci/rglobi>

**RemoteRef** main

**RemoteSha** ea9eac637e7dfcc3667f06a5eae7cb11376814df

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get_data_fields	<i>List data fields identified in GloBI database</i>
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### 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

```
get_data_fields()
```

---

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\\_interaction\\_matrix\(\)](#), [get\\_interaction\\_types\(\)](#), [get\\_interactions\\_by\\_taxa\(\)](#), [get\\_interactions\\_by\\_type\(\)](#), [get\\_predators\\_of\(\)](#), [get\\_prey\\_of\(\)](#)

**Examples**

```
get_interactions("Homo sapiens", "preysOn")
get_interactions("Insecta", "parasiteOf")
```

---

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 = FALSE,
  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\\_interaction\\_matrix\(\)](#), [get\\_interaction\\_types\(\)](#), [get\\_interactions\\_by\\_taxa\(\)](#), [get\\_interactions\(\)](#), [get\\_predators\\_of\(\)](#), [get\\_preym\\_of\(\)](#)

**Examples**

```
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))
```

---

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\\_interaction\\_matrix\(\)](#), [get\\_interaction\\_types\(\)](#), [get\\_interactions\\_by\\_taxa\(\)](#), [get\\_interactions\(\)](#), [get\\_predators\\_of\(\)](#), [get\\_preym\\_of\(\)](#)

**Examples**

```
get_interactions_by_type(interactiontype = c("eats", "eatenBy"))
get_interactions_by_type(interactiontype = "parasiteOf")
```

---

`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**

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

**Value**

Returns data frame of interactions

**See Also**

Other areas: [get\\_interaction\\_areas\(\)](#)

**Examples**

```
get_interactions_in_area(bbox = c(-67.87, 12.79, -57.08, 23.32))
```

---

`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
...	list of named options to configure GloBI API

**Value**

Returns data frame of coordinates

**See Also**

Other areas: [get\\_interactions\\_in\\_area\(\)](#)

**Examples**

```
get_interaction_areas ()  
get_interaction_areas (bbox=c(-67.87, 12.79, -57.08, 23.32))
```

---

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\\_interaction\\_types\(\)](#), [get\\_interactions\\_by\\_taxa\(\)](#), [get\\_interactions\\_by\\_type\(\)](#), [get\\_interactions\(\)](#), [get\\_predators\\_of\(\)](#), [get\\_prey\\_of\(\)](#)

**Examples**

```
get_interaction_matrix("Homo sapiens", "Mammalia", "interactsWith")
```

---

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\\_interaction\\_matrix\(\)](#), [get\\_interactions\\_by\\_taxa\(\)](#), [get\\_interactions\\_by\\_type\(\)](#), [get\\_interactions\(\)](#), [get\\_predators\\_of\(\)](#), [get\\_preym\\_of\(\)](#)

**Examples**

```
get_interaction_types()
```

---

<code>get_predators_of</code>	<i>Get a List of Predators of a Given Prey Taxon</i>
-------------------------------	--

---

**Description**

Get a List of Predators of a Given Prey Taxon

**Usage**

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

**Arguments**

<code>taxon</code>	scientific name of prey taxon. Can be any taxonomic rank (e.g. <i>Rattus rattus</i> , <i>Decapoda</i> )
<code>...</code>	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\\_interaction\\_matrix\(\)](#), [get\\_interaction\\_types\(\)](#), [get\\_interactions\\_by\\_taxa\(\)](#), [get\\_interactions\\_by\\_type\(\)](#), [get\\_interactions\(\)](#), [get\\_preym\\_of\(\)](#)

**Examples**

```
get_predators_of("Rattus rattus")  
get_predators_of("Primates")
```

---

`get_prej_of`*Get a List of Prey for given Predator Taxon*

---

**Description**

Get a List of Prey for given Predator Taxon

**Usage**

```
get_prej_of(taxon = "Homo sapiens", ...)
```

**Arguments**

<code>taxon</code>	scientific name of predator taxon. Can be any taxonomic rank (e.g. Homo sapiens, Animalia)
<code>...</code>	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\\_interaction\\_matrix\(\)](#), [get\\_interaction\\_types\(\)](#), [get\\_interactions\\_by\\_taxa\(\)](#), [get\\_interactions\\_by\\_type\(\)](#), [get\\_interactions\(\)](#), [get\\_predators\\_of\(\)](#)

**Examples**

```
get_prej_of("Homo sapiens")
get_prej_of("Primates")
```

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