Package ‘rglobi’

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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.
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get_data_fields

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| 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

**Examples**

```r
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
get_interactions_by_taxa

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: \texttt{get_interaction_matrix()}, \texttt{get_interaction_types()}, \texttt{get_interactions_by_type()}, \texttt{get_interactions()}, \texttt{get_predators_of()}, \texttt{get_prey_of()}

Examples

```r
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))
```

```r
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 database in area specified in arguments.

**Usage**

```r
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**

```r
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 database or area specified in arguments.

**Usage**

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

**Examples**

```r
get_interaction_areas(bbox = NULL, read_csv = read_csv_online, ...)
```
get_interaction_matrix

**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**

```r
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**

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

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_prey_of()`

Examples

```r
get_interaction_types()
```

---

**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_interaction_matrix()`, `get_interaction_types()`, `get_interactions_by_taxa()`, `get_interactions_by_type()`, `get_interactions()`, `get_prey_of()`

Examples

```r
get_predators_of("Rattus rattus")
get_predators_of("Primates")
```
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_interaction_matrix(), get_interaction_types(), get_interactions_by_taxa(),
get_interactions_by_type(), get_interactions(), get_predators_of()

Examples
get_prey_of("Homo sapiens")
get_prey_of("Primates")
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