Package: rglobi (via r-universe)

August 29, 2024

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

Date 2023-10-06

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)

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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

Contents

`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

```
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_type(), get_interactions(), get_predators_of(), get_prey_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_prey_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

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

```
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_prey_of()

Examples

```
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

```
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

```
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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