

Package ‘ReactomeContentService4R’

December 5, 2021

Title Interface for the Reactome Content Service

Version 1.3.0

Description Reactome is a free, open-source, open access, curated and peer-reviewed knowledgebase of bio-molecular pathways. This package is to interact with the Reactome Content Service API. Pre-built functions would allow users to retrieve data and images that consist of proteins, pathways, and other molecules related to a specific gene or entity in Reactome.

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Encoding UTF-8

URL <https://github.com/reactome/ReactomeContentService4R>

BugReports <https://github.com/reactome/ReactomeContentService4R/issues>

Roxygen list(markdown = TRUE)

RoxygenNote 7.1.1

Imports httr, jsonlite, utils, magick (>= 2.5.1), data.table, doParallel, foreach, parallel

Suggests pdftools, testthat, knitr, rmarkdown

VignetteBuilder knitr

Language en-US

biocViews DataImport, Pathways, Reactome

git_url <https://git.bioconductor.org/packages/ReactomeContentService4R>

git_branch master

git_last_commit be1e016

git_last_commit_date 2021-10-26

Date/Publication 2021-12-05

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discover	<i>Search engines discovery schema</i>
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Description

Search engines discovery schema

Usage

```
discover(event.id)
```

Arguments

event.id stable id or db id of an Event

Value

a list of the event schema

Examples

```
discover("R-HSA-73893")
```

exportEventFile	<i>File exporter</i>
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Description

Export Reactome pathway diagrams in SBGN or SBML format.

Usage

```
exportEventFile(  
  id,  
  format = c("sbgn", "sbml"),  
  writeToFile = TRUE,  
  file = NULL  
)
```

Arguments

id	a stable or db id of an Event (Pathway or Reaction)
format	either in "sbgn" (SBGN, Systems Biology Graphical Notation) or "sbml" (SBML, Systems Biology Markup Language)
writeToFile	If set to TRUE, the returned data would be written into a file. If file=NULL, the output file will be automatically saved into the working directory and named based on the id and format
file	full path of the output file

Value

a character object with the content of SBGN/SBML for a given id, or a SBGN/SBML file saved into the specified path. If the output is empty character or list, please check on [ContentService](#) or contact HelpDesk <help@reactome.org>.

See Also

Other exporter: [exportImage\(\)](#)

Examples

```
exportEventFile("R-HSA-432047", "sbgn", writeToFile=FALSE)  
## Not run: exportEventFile("R-HSA-68616", "sbml", file="orc.assembly.sbml")
```

 exportImage

Image exporter

Description

The diagram exporter allows researchers to include images of their favorite pathway diagrams into their publications, posters or presentations. For details see Reactome [diagram exporter](#) guide.

Usage

```
exportImage(
  id = NULL,
  output = c("diagram", "fireworks", "reaction"),
  species = NULL,
  format = c("png", "jpg", "jpeg", "svg", "gif"),
  quality = 5,
  flg = NULL,
  flgInteractors = TRUE,
  sel = NULL,
  title = TRUE,
  margin = 15,
  ehld = TRUE,
  diagramProfile = "Modern",
  token = NULL,
  resource = "TOTAL",
  analysisProfile = "Standard",
  expColumn = NULL,
  fireworksCoverage = FALSE,
  file = NULL,
  ...
)
```

Arguments

id	stable or db id of a ReactionLikeEvent for "reaction" output, or id of an Event for "diagram"
output	type of exported image including "diagram", "fireworks", "reaction"
species	name or db id or taxon id of a species. Used in "fireworks" output
format	output format including "png", "jpg", "jpeg", "svg", "gif"
quality	result image quality between 1-10, default is 5
flg	gene name, protein or chemical identifier or Reactome identifier used to flag elements in the diagram
flgInteractors	defines whether to take into account interactors for the flagging
sel	highlight element(s) selection in the diagram
title	whether the name of the pathway is shown below

margin	defines the image margin between 0-20, default is 15
ehld	whether textbook-like illustration are taken into account
diagramProfile	color profile, "modern" or "standard"
token	token from Reactome Analysis Service
resource	the analysis resource for which the results will be overlaid on top of the given pathways overview
analysisProfile	analysis color profile including "Standard", "Strosobar", "Copper%20plus"
expColumn	the specific expression analysis results column to be overlaid. If it is not specified (null), the first one is selected. If it is not specified (null) and format is gif, then an animated gif is generated with all the columns.
fireworksCoverage	set TRUE to overlay analysis coverage values in a fireworks image
file	full path of the output file
...	additional parameters passed to <code>magick::image_write()</code>

Value

an image saved into the specified path or a magick image object. More magick processing see the [package](#).

See Also

[magick](#) to further process the image object

Other exporter: [exportEventFile\(\)](#)

Examples

```
# fireworks
exportImage(species="9606", output="fireworks",
            format="jpg", quality=7)

## Not run:
# animated gifs of EHLs
# can use your own token from your Reactome Analysis
gif <- exportImage(id="R-HSA-69278", output="diagram", format="gif",
                  sel="R-HSA-69242", token="MjAyMDA2MTcyMDM5NDBfMzU2")
print(gif)

# reaction
exportImage(id="R-HSA-6787403", output="reaction", format="svg",
            flg="MT01", analysisProfile="Copper%20plus", file="R-HSA-6787403.svg")

## End(Not run)
```

`getEntities`*PhysicalEntity queries*

Description

This method retrieves instances related to `PhysicalEntity`.

Usage

```
getEntities(  
  id,  
  retrieval = c("subunits", "complexes", "componentOf", "otherForms"),  
  resource = "Reactome",  
  subunitsExcludeStructures = FALSE  
)
```

Arguments

<code>id</code>	stable or db id of a Reactome <code>PhysicalEntity</code> , or id from resources other than Reactome
<code>retrieval</code>	entities to be retrieved, including "subunits", "complexes", "componentOf", "otherForms"
<code>resource</code>	resource other than Reactome, e.g. UniProt, Ensembl
<code>subunitsExcludeStructures</code>	whether contained Complexes and EntitySets are excluded when retrieving "subunits"

Details

Details on options of `retrieval` arg:

- **subunits**: retrieves subunits that constitute any given Complex
- **complexes**: retrieves Complexes that contain the given `id` and `resource`
- **componentOf**: retrieves structures (Complexes and Sets) that include the given Entity as their component
- **otherForms**: retrieves Entities containing all other forms of the given `PhysicalEntity`

Value

a dataframe containing requested information

See Also

Other `getContent`: [getEventsHierarchy\(\)](#), [getOrthology\(\)](#), [getParticipants\(\)](#), [getPathways\(\)](#), [getPerson\(\)](#), [getSchemaClass\(\)](#), [getSpecies\(\)](#), [query\(\)](#)

Examples

```
getEntities("R-HSA-5674003", retrieval="subunits")
getEntities("P00533", retrieval="complexes", resource="UniProt")
```

getEventsHierarchy *EventsHierarchy queries*

Description

Events (Pathways and Reactions) in Reactome are organized in a hierarchical structure for every species. By following all `hasEvent` relationships, this method retrieves the full event hierarchy for any given **main species**.

Usage

```
getEventsHierarchy(main.species)
```

Arguments

`main.species` name or taxon/db id or abbreviation of **main species** in Reactome

Value

a nested dataframe containing full event hierarchy for a given main species

See Also

[getSpecies](#) to get the main species list

Other `getContent`: [getEntities\(\)](#), [getOrthology\(\)](#), [getParticipants\(\)](#), [getPathways\(\)](#), [getPerson\(\)](#), [getSchemaClass\(\)](#), [getSpecies\(\)](#), [query\(\)](#)

Examples

```
## Not run:
getEventsHierarchy("chicken")
getEventsHierarchy("XTR")

## End(Not run)
```

getOrthology *Orthology related queries*

Description

This function retrieves the orthology for any given Event or Entity in the specified species. More information on inferred events see <https://www.reactome.org/pages/documentation/electronically-inferred-events/>.

Usage

```
getOrthology(id, species)
```

Arguments

id	a stable or db id of an Event or Entity
species	name or taxon id or dbId or abbreviation of species

Value

a list containing the orthology for given Event or Entity in the specified species

See Also

Other getContent: [getEntities\(\)](#), [getEventsHierarchy\(\)](#), [getParticipants\(\)](#), [getPathways\(\)](#), [getPerson\(\)](#), [getSchemaClass\(\)](#), [getSpecies\(\)](#), [query\(\)](#)

Examples

```
getOrthology("R-HSA-5674003", "pig")
```

getParticipants *Participants related queries*

Description

Data in Reactome are organized in a hierarchical manner - Pathways contain Reactions, Reactions contain PhysicalEntities. This function is to get the participants of a given Event.

Usage

```
getParticipants(  
  event.id,  
  retrieval = c("AllInstances", "PhysicalEntities", "ReferenceEntities",  
               "EventsInPathways")  
)
```


Arguments

event.id	a stable or db id of an Event (pathways and reactions)
retrieval	participants to be retrieved, including "AllInstances", "PhysicalEntities", "ReferenceEntities", "EventsInPathways"

Details

Details on options of retrieval arg:

- **AllInstances**: retrieves all participants (PhysicalEntities) from a given Event and their ReferenceEntities
- **PhysicalEntities**: retrieves all the PhysicalEntities that take part in a given Event
- **ReferenceEntities**: retrieves the ReferenceEntities for all PhysicalEntities in every constituent Pathway/Reaction
- **EventsInPathways**: recursively retrieves all the Events contained in any given Event

Value

a dataframe containing requested participants

See Also

Other getContent: [getEntities\(\)](#), [getEventsHierarchy\(\)](#), [getOrthology\(\)](#), [getPathways\(\)](#), [getPerson\(\)](#), [getSchemaClass\(\)](#), [getSpecies\(\)](#), [query\(\)](#)

Examples

```
getParticipants("R-HSA-6804741", "AllInstances")
getParticipants("R-HSA-69306", "EventsInPathways")
```

getPathways *Pathway related queries*

Description

To get the Events that contain the given PhysicalEntity or Event (i.e. subpathway).

Usage

```
getPathways(id, species = NULL, allForms = FALSE, top.level = FALSE)
```

Arguments

id	a stable or db id of a PhysicalEntity or Event present in the pathways
species	name or taxon id or dbId or abbreviation of species
allForms	if set to TRUE, all low level pathways that contain the given PhysicalEntity (not Event) in all forms returned
top.level	if set to TRUE, only top-level pathways returned

Value

a dataframe containing requested pathways

See Also

Other getContent: [getEntities\(\)](#), [getEventsHierarchy\(\)](#), [getOrthology\(\)](#), [getParticipants\(\)](#), [getPerson\(\)](#), [getSchemaClass\(\)](#), [getSpecies\(\)](#), [query\(\)](#)

Examples

```
getPathways("R-HSA-199420", "Homo sapiens")
```

getPerson

Person queries

Description

Retrieves a specific person's property by his/her name or OrcidId or dbId.

Usage

```
getPerson(name = NULL, id = NULL, attributes = NULL)
```

Arguments

name	Person's first or/and last name
id	Person's Orcid Id or DbId
attributes	Property for a person. Return all available attributes if it is not specified.

Value

a list of requested information

See Also

Other getContent: [getEntities\(\)](#), [getEventsHierarchy\(\)](#), [getOrthology\(\)](#), [getParticipants\(\)](#), [getPathways\(\)](#), [getSchemaClass\(\)](#), [getSpecies\(\)](#), [query\(\)](#)

Examples

```
getPerson(name="Robin Haw", attributes=c("displayName", "affiliation"))
```

getSchemaClass	<i>Schema class queries</i>
----------------	-----------------------------

Description

Fetch instances by Class. All Classes see [Reactome data schema](#).

Usage

```
getSchemaClass(  
  class,  
  species = NULL,  
  all = FALSE,  
  rows = 1000,  
  minimised = FALSE,  
  reference = FALSE  
)
```

Arguments

class	schema class name
species	name or taxon id or dbId or abbreviation of species. Only Event and PhysicalEntity classes can specify species
all	to return ALL entries or not, default is FALSE
rows	the number of entries retrieved, default is 1000
minimised	to retrieve simplified entries (db id, stable id, displayName, type) or not, default is FALSE
reference	to retrieve simplified reference objects (db id, external identifier, external database name) or not, default is FALSE. Only for ReferenceEntity or ExternalOntology class

Value

a sorted dataframe containing entries that belong to the specified schema class

See Also

Other getContent: [getEntities\(\)](#), [getEventsHierarchy\(\)](#), [getOrthology\(\)](#), [getParticipants\(\)](#), [getPathways\(\)](#), [getPerson\(\)](#), [getSpecies\(\)](#), [query\(\)](#)

Examples

```
## Not run:  
getSchemaClass(class="Drug", all=TRUE)  
  
## End(Not run)  
getSchemaClass(class="Regulation", rows=20, minimised=TRUE)  
getSchemaClass(class="Complex", species="pig", rows=10)
```

`getSpecies`*Species queries*

Description

This method retrieves the list of all or main species in Reactome knowledgebase.

Usage

```
getSpecies(main = FALSE)
```

Arguments

`main` determine whether return main species, which are those have either manually curated or computationally inferred pathways

Value

a dataframe of species information

See Also

Other `getContent`: [getEntities\(\)](#), [getEventsHierarchy\(\)](#), [getOrthology\(\)](#), [getParticipants\(\)](#), [getPathways\(\)](#), [getPerson\(\)](#), [getSchemaClass\(\)](#), [query\(\)](#)

Examples

```
# get a list of main species
getSpecies(main=TRUE)
```

`listSearchItems`*List filter items*

Description

To list the available filtering options for `searchQuery()`, and their counts.

Usage

```
listSearchItems(
  items = c("all", "species", "types", "compartments", "keywords"),
  facet = FALSE
)
```

Arguments

items	categories of query, including "species", "types", "compartments", "keywords", or "all"
facet	return faceting information or not

Value

available search items

See Also

[searchQuery](#) to search in Reactome

Examples

```
listSearchItems()
```

nonReactomeId	<i>Non-Reactome id mappings</i>
---------------	---------------------------------

Description

Mappings between non-Reactome identifiers and Reactome objects.

Usage

```
map2RefEntities(external.id)
```

```
map2Events(external.id, resource, species, mapTo = c("pathways", "reactions"))
```

```
event2Ids(event.id)
```

Arguments

external.id	an id from external dabatases, e.g. ChEBI, UniProt
resource	database name other than Reactome (e.g. UniProt, GeneCards)
species	name or taxon id or dbId or abbreviation of species
mapTo	retrieve Pathways or Reactions where an identifier can be mapped to
event.id	a stable or db id of an Event (Pathways and Reactions)

Details

Descriptions of functions:

- [map2RefEntities](#) maps a non-Reactome id to ReferenceEntities that store the given external id
- [map2Events](#) fetches Events related to a given non-Reactome id
- [event2Ids](#) gets all non-Reactome ids associated with a given Event

Value

a list of ReferenceEntity information
a dataframe of Events associated with the given id
non-Reactome ids associated with a given Event

Examples

```
## Not run:  
map2RefEntities("15377") #ChEBI id  
  
## End(Not run)  
map2Events("Q7Z569", resource="GeneCards", species="human", mapTo="reactions")  
event2Ids("R-HSA-69541")
```

query

Common data retrieval

Description

This function retrieves a Reactome Database object that has all its properties and direct relationships (relationships of depth 1) filled, while it also includes any second level relationships regarding regulations and catalysts.

Usage

```
query(id)
```

Arguments

id a stable or db id of **any** Reactome entry

Value

a list containing comprehensive information (all attributes) for a given id

See Also

[searchQuery](#) to search in Reactome

Other getContent: [getEntities\(\)](#), [getEventsHierarchy\(\)](#), [getOrthology\(\)](#), [getParticipants\(\)](#), [getPathways\(\)](#), [getPerson\(\)](#), [getSchemaClass\(\)](#), [getSpecies\(\)](#)

Examples

```
query("R-HSA-60140")
```

searchQuery	<i>Search query</i>
-------------	---------------------

Description

Search for Reactome objects by name or identifiers.

Usage

```
searchQuery(  
  query,  
  species = NULL,  
  types = NULL,  
  compartments = NULL,  
  keywords = NULL,  
  cluster = TRUE,  
  range = NULL  
)
```

Arguments

query	name or dbId or stId of a search term from any class
species	name or taxon id or dbId or abbreviation of species
types	type filter, such as "Protein", "Complex", "Reaction", etc
compartments	compartment filter, such as "cytosol", "plasma membrane", "nucleoplasm", etc
keywords	keyword filter, such as "binds", "phosphorylates", "transports", etc
cluster	cluster returned data or not
range	start row and the number of rows to include, e.g. range = c(0, 2)

Value

a list of information about the search term

See Also

[listSearchItems](#) for available filters

Examples

```
searchQuery(query="Biological oxidation", species="Mus musculus", types=c("Pathway", "Reaction"))
```

`spellCheck`*Spell-check suggestions for a given query*

Description

Spell-check suggestions for a given query

Usage

```
spellCheck(query)
```

Arguments

`query` a search term

Value

spell-check suggestions for a given search term

Examples

```
spellCheck("intelukin")
```


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