

Package ‘ReactomeGraph4R’

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Title Interface for the Reactome Graph Database

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Description Pathways, reactions, and biological entities in Reactome knowledge are systematically represented as an ordered network. Instances are represented as nodes and relationships between instances as edges; they are all stored in the Reactome Graph Database. This package serves as an interface to query the interconnected data from a local Neo4j database, with the aim of minimizing the usage of Neo4j Cypher queries.

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ReactomeGraph4R-package
<i>ReactomeGraph4R: Interface for the Reactome Graph Database</i>

Description

Pathways, reactions, and biological entities in Reactome knowledge are systematically represented as an ordered network. Instances are represented as nodes and relationships between instances as edges; they are all stored in the Reactome Graph Database. This package serves as an interface to query the interconnected data from a local Neo4j database, with the aim of minimizing the usage of Neo4j Cypher queries.

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See Also

Useful links:

- <https://github.com/reactome/ReactomeGraph4R>
- Report bugs at <https://github.com/reactome/ReactomeGraph4R/issues>

login	<i>Log in to the local neo4j server</i>
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Description

Before running `login()`, you have to successfully finish the Reactome Neo4j database setup and build a connection on your local machine (details see: <https://github.com/reactome/ReactomeGraph4R>). This command is to create a `neo4r` object that is used to communicate between R and Neo4j, also to do a sanity check for the connection.

Usage

```
login(con = NULL)
```

Arguments

`con` an existed connexion object. It is not necessary to log in for the first time.

Value

connection to the local neo4j database

Examples

```
## Not run:  
# The first step to the graph database!  
login()  
  
## End(Not run)  
# you can also check the neo4r connexion object by running:  
getOption("con")
```

matchDiseases	<i>MATCH diseases of PhysicalEntity/Reaction/Pathway</i>
---------------	--

Description

To find Diseases related to a PhysicalEntity or an Event, or get PhysicalEntities/Events associated with a Disease in reverse

Usage

```
matchDiseases(  
  id = NULL,  
  displayName = NULL,  
  species = NULL,  
  type = c("row", "graph")  
)
```

Arguments

id	stId or dbId of a PhysicalEntity/Event/Disease
displayName	displayName of a PhysicalEntity/Event/Disease
species	name or taxon id or dbId or abbreviation of aspecies
type	return results as a list of dataframes ('row'), or as a graph object ('graph')

Value

Disease(s) related to the given PhysicalEntity/Reaction/Pathway; or instances related to the given Disease

See Also

Other match: [matchHierarchy\(\)](#), [matchInteractors\(\)](#), [matchObject\(\)](#), [matchPEroles\(\)](#), [matchPaperObjects\(\)](#), [matchPrecedingAndFollowingEvents\(\)](#), [matchReactionsInPathway\(\)](#), [matchReferrals\(\)](#)

Examples

```
disease <- "neuropathy"
# matchDiseases(displayName=disease, species="M. musculus", type="row")
# matchDiseases(id="R-HSA-162588", type="graph")
```

matchHierarchy	<i>MATCH hierarchy</i>
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Description

Reactome data are organized in a hierarchical way: Pathway-Reaction-Entity. This function retrieves the hierarchical data of a given Event (Pathway or Reaction) or Entity (PhysicalEntity or ReferenceEntity).

Usage

```
matchHierarchy(
  id = NULL,
  displayName = NULL,
  databaseName = "Reactome",
  species = NULL,
  type = c("row", "graph")
)
```

Arguments

id	stId or dbId of an Event/Entity; or an external id
displayName	displayName of Event/PhysicalEntity/ReferenceEntity
databaseName	database name
species	name or taxon id or dbId or abbreviation of specified species
type	return results as a list of dataframes ('row'), or as a graph object ('graph')

Value

hierarchical instances of the given id and databaseName

See Also

Other match: [matchDiseases\(\)](#), [matchInteractors\(\)](#), [matchObject\(\)](#), [matchPEroles\(\)](#), [matchPaperObjects\(\)](#), [matchPrecedingAndFollowingEvents\(\)](#), [matchReactionsInPathway\(\)](#), [matchReferrals\(\)](#)

Examples

```
## use the Reactome displayName of a UniProt object
uniprot.name <- "UniProt:P04637 TP53"
# matchHierarchy(displayName=uniprot.name,
#                 databaseName="UniProt", type="row")
# matchHierarchy(id="R-HSA-1369062", type="graph")
```

matchInteractors	<i>MATCH interactors</i>
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Description

To retrieve interactions of a given PhysicalEntity (PE), it first finds the ReferenceEntity matched with the PE, then get the Interactions having "interactor" relationship with the ReferenceEntity.

Usage

```
matchInteractors(
  pe.id = NULL,
  pe.displayName = NULL,
  species = NULL,
  type = c("row", "graph")
)
```

Arguments

pe.id	stId or dbId of a PhysicalEntity
pe.displayName	displayName of a PhysicalEntity
species	name or taxon id or dbId or abbreviation of specified species
type	return results as a list of dataframes ('row'), or as a graph object ('graph')

Value

interactions of a given PhysicalEntity

See Also

Other match: [matchDiseases\(\)](#), [matchHierarchy\(\)](#), [matchObject\(\)](#), [matchPEroles\(\)](#), [matchPaperObjects\(\)](#), [matchPrecedingAndFollowingEvents\(\)](#), [matchReactionsInPathway\(\)](#), [matchReferrals\(\)](#)

Examples

```
pe.id <- 996766
# matchInteractors(pe.id)
```

matchObject

Basic query for database objects

Description

This function can fetch instance by setting the following arguments:

- **id**: a Reactome dbId/stId, or non-Reactome id (e.g. UniProt)
- **displayName**: a display name of a Reactome object
- **schemaClass**: a specific schema class, see [Data Schema](#)
- **property**: a property of a node or relationship, access the full list of properties: `con <- getOption("con"); con$get_`
- **relationship**: a relationship between nodes, access the full list of relationships: `con <- getOption("con"); con$get_`
- Species information can see [here](#), or run `View(matchObject(schemaClass = "Species")[['databaseObject']])` to view a full table

Usage

```
matchObject(
  id = NULL,
  displayName = NULL,
  schemaClass = NULL,
  species = NULL,
  returnedAttributes = NULL,
  property = NULL,
  relationship = NULL,
  limit = NULL,
  databaseName = "Reactome"
)
```

Arguments

id	Reactome stId or dbId, or non-Reactome identifier
displayName	displayName of a database object
schemaClass	schema class of a database object
species	name or taxon id or dbId or abbreviation of specified species
returnedAttributes	specific attribute(s) to be returned. If set to NULL, all attributes returned
property	a list of property keys and values, e.g. <code>list(isChimeric = TRUE, isInDisease = TRUE)</code>
relationship	relationship type(s)
limit	the number of returned objects
databaseName	database name. All databases see here

Value

Reactome database object(s) that meets all specified conditions

See Also

[multiObjects](#) for multiple ids

Other match: [matchDiseases\(\)](#), [matchHierarchy\(\)](#), [matchInteractors\(\)](#), [matchPERoles\(\)](#), [matchPaperObjects\(\)](#), [matchPrecedingAndFollowingEvents\(\)](#), [matchReactionsInPathway\(\)](#), [matchReferrals\(\)](#)

Examples

```
## fetch instance by class
# all.species <- matchObject(schemaClass = "Species")

## fetch instance by name
# matchObject(displayName = "RCOR1 [nucleoplasm]",
#             returnedAttributes=c("stId", "speciesName"))

## fetch instance by id
## Reactome id
# matchObject(id = "R-HSA-9626034")
## non-Reactome id
# matchObject(id = "P60484", databaseName = "UniProt")

## fetch instances by relationship
# matchObject(relationship="inferredTo", limit=10)

## fetch instances by property
property.list <- list(hasEHLD = TRUE, isInDisease = TRUE)
# matchObject(property = property.list,
#             returnedAttributes = c("displayName", "stId", "isInDisease", "hasEHLD"),
#             limit=20)
```

matchPaperObjects	<i>MATCH objects related to a paper</i>
-------------------	---

Description

Fetch Reactome instances related to a paper by its PubMed id or title

Usage

```
matchPaperObjects(
  pubmed.id = NULL,
  displayName = NULL,
  type = c("row", "graph")
)
```

Arguments

pubmed.id	PubMed identifier of a paper
displayName	paper title
type	return results as a list of dataframes ('row'), or as a graph object ('graph')

Value

Reactome instances associated with a paper

See Also

Other match: [matchDiseases\(\)](#), [matchHierarchy\(\)](#), [matchInteractors\(\)](#), [matchObject\(\)](#), [matchPEroles\(\)](#), [matchPrecedingAndFollowingEvents\(\)](#), [matchReactionsInPathway\(\)](#), [matchReferrals\(\)](#)

Examples

```
## fetch Reactome instances by paper title
paper <- "Chaperone-mediated autophagy at a glance"
# matchPaperObjects(displayName=paper)

## fetch Reactome instances by pubmed id
# matchPaperObjects(pubmed.id="20797626", type="graph")
# matchPaperObjects(pubmed.id="23515720", type="row")
```

matchPEroles

MATCH roles of PhysicalEntity

Description

This function retrieves the role(s) of a given PhysicalEntity including:

- Input
- Output
- Regulator
- Catalyst

Usage

```
matchPEroles(
  pe.id = NULL,
  pe.displayName = NULL,
  species = NULL,
  type = c("row", "graph")
)
```


Arguments

`pe.id` `stId` or `dbId` of a `PhysicalEntity`
`pe.displayName` `displayName` of a `PhysicalEntity`
`species` `name` or `taxon id` or `dbId` or `abbreviation` of a `species`
`type` return results as a list of dataframes (**'row'**), or as a graph object (**'graph'**)

Value

information of the given `PhysicalEntity` and its role(s)

See Also

Other `match`: `matchDiseases()`, `matchHierarchy()`, `matchInteractors()`, `matchObject()`, `matchPaperObjects()`, `matchPrecedingAndFollowingEvents()`, `matchReactionsInPathway()`, `matchReferrals()`

Examples

```

stId <- "R-HSA-8944354"
# matchPEroles(pe.id = stId, type = "graph")

# matchPEroles(pe.displayName = "2SUM01:MITF [nucleoplasm]",
#               species = "pig", type = "row")

```

`matchPrecedingAndFollowingEvents`

MATCH the preceding/following Events

Description

This method can find preceding and following `ReactionLikeEvents` (RLEs) of a specific Event with the relationship `'precedingEvent'`. The argument `"depth"` is used to describe the "variable length relationships" in Neo4j, default is 1 (i.e. immediately connected); or you can set `all.depth = TRUE` to retrieve the whole context.

Usage

```

matchPrecedingAndFollowingEvents(
  event.id = NULL,
  event.displayName = NULL,
  species = NULL,
  depth = 1,
  all.depth = FALSE,
  type = c("row", "graph")
)

```

Arguments

<code>event.id</code>	stId/dbId of an Event
<code>event.displayName</code>	displayName of an Event
<code>species</code>	name or taxon id or dbId or abbreviation of specified species
<code>depth</code>	number of depths
<code>all.depth</code>	if set to TRUE, all RLE(s) connected to the given Event in all depths returned
<code>type</code>	to return results as a list of dataframes ('row'), or as a graph object ('graph')

Value

preceding/following Events connected to the given Event in specified depth(s), default depth = 1

See Also

Other match: [matchDiseases\(\)](#), [matchHierarchy\(\)](#), [matchInteractors\(\)](#), [matchObject\(\)](#), [matchPEroles\(\)](#), [matchPaperObjects\(\)](#), [matchReactionsInPathway\(\)](#), [matchReferrals\(\)](#)

Examples

```
stId <- "R-HSA-983150"
# matchPrecedingAndFollowingEvents(event.id=stId, depth=2, type="row")
```

matchReactionsInPathway

MATCH Reactions in associated Pathway

Description

This method could find all Reactions connected with a given Pathway by the relationship 'hasEvent'. Also, the input can be a Reaction, the result would then be Pathway(s) linked via 'hasEvent' together with other Reactions linked with the Pathways(s).

Usage

```
matchReactionsInPathway(
  event.id = NULL,
  event.displayName = NULL,
  species = NULL,
  type = c("row", "graph")
)
```

Arguments

`event.id` stId or dbId of an Event
`event.displayName` displayName of an Event

`species` name or taxon id or dbId or abbreviation of a species

`type` return results as a list of dataframes (**'row'**), or as a graph object (**'graph'**)

Value

Reactions connected to the given Pathway/Reaction via 'hasEvent' relationships

See Also

Other match: [matchDiseases\(\)](#), [matchHierarchy\(\)](#), [matchInteractors\(\)](#), [matchObject\(\)](#), [matchPERoles\(\)](#), [matchPaperObjects\(\)](#), [matchPrecedingAndFollowingEvents\(\)](#), [matchReferrals\(\)](#)

Examples

```

reaction <- "R-HSA-1369062"
# matchReactionsInPathway(event.id=reaction, type="graph")
# matchReactionsInPathway("R-HSA-5682285", type="row")

```

matchReferrals	<i>MATCH biological referrals</i>
----------------	-----------------------------------

Description

This method retrieves Reactome objects that are connected with the given object in a *reverse* relationship. For example, to find Pathways containing the given Reaction.

Usage

```

matchReferrals(
  id = NULL,
  displayName = NULL,
  main = TRUE,
  depth = 1,
  all.depth = FALSE,
  species = NULL,
  type = c("row", "graph")
)

```

Arguments

id	stId or dbId of a Reactome object
displayName	displayName of a Reactome object
main	if set to TRUE, only first-class referrals returned
depth	number of depths
all.depth	if set to TRUE, connected objects in all depths returned
species	name or taxon id or dbId or abbreviation of a species
type	return results as a list of dataframes ('row'), or as a graph object ('graph')

Details

For now it just focuses on biological referrals in the following Classes: "Event", "PhysicalEntity", "Regulation", "CatalystActivity", "ReferenceEntity", "Interaction", "AbstractModifiedResidue".

Value

referrals of the given instance

See Also

Other match: [matchDiseases\(\)](#), [matchHierarchy\(\)](#), [matchInteractors\(\)](#), [matchObject\(\)](#), [matchPEroles\(\)](#), [matchPaperObjects\(\)](#), [matchPrecedingAndFollowingEvents\(\)](#), [matchReactionsInPathway\(\)](#)

Examples

```
stId <- "R-HSA-112479"
# matchReferrals("R-HSA-112479", main=FALSE, all.depth=TRUE, type="row")
```

multiObjects

Retrieve multiple Reactome objects

Description

The [matchObject](#) function takes only one id/name at a time, this method allows you to input many ids and get an aggregated table for their detailed information. It can only accept **ids** for now.

Usage

```
multiObjects(ids, databaseName = "Reactome", speedUp = FALSE, cluster = 2)
```

Arguments

ids	Reactome stIds/dbIds, or non-Reactome ids
databaseName	database name
speedUp	set TRUE to use doParallel method
cluster	the number of cluster in makeCluster

Value

Reactome database objects for the given ids

See Also

[matchObject](#) for details

Examples

```
## "ids" can be Reactome or non-Reactome ids
ids <- c("P02741", "P08887", "P08505", "Q9GZQ8")
#res <- multiObjects(ids, databaseName="UniProt", speedUp=TRUE)
```

unnestListCol

Unnest a column of lists in a dataframe

Description

Unnest a column of lists in a dataframe

Usage

```
unnestListCol(df, column = "properties")
```

Arguments

df	dataframe where a column to be unnested
column	specific column to be unnested

Value

an unnested dataframe for network visualization

Examples

```
# nodes <- unnestListCol(graph$nodes, "properties")
```

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