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: Interface for the Reactome Graph Database

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 *Log in to the local neo4j server*

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 *MATCH diseases of PhysicalEntity/Reaction/Pathway*

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 *MATCH hierarchy*

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 *MATCH interactors*

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$g`
- **relationship**: a relationship between nodes, access the full list of relationships: `con <- getOption("con"); con$g`
- 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. `list(isChimeric = TRUE, isInDisease = TRUE)`
`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")

## fecth 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 *MATCH objects related to a paper*

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 = "2SUMO1: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

`event.id`	stId/dbId of an Event
`event.displayName`	displayName of an Event
`species`	name or taxon id or dbId or abbreviation of specified species
`depth`	number of depths
`all.depth`	if set to `TRUE`, all RLE(s) connected to the given Event in all depths returned
`type`	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 *MATCH biological referrals*

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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