

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

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 | <i>Log in to the local neo4j server</i> |
|-------|---|

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

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 | <i>MATCH interactors</i> |
|------------------|--------------------------|

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 *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 = "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

| | |
|-------------------|---|
| 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 | <i>Unnest a column of lists in a dataframe</i> |
|---------------|--|

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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