Package ‘ReactomeGraph4R’

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Title Interface for the Reactome Graph Database

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ReactomeGraph4R-package

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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

**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](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**

```r
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**

```r
## 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**

```r
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 a species
- **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")
matchInteractors

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 stdId 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$get_property_keys()
• relationship: a relationship between nodes, access the full list of relationships: con <- getOption("con"); con$get_relationships()
• 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
**matchPaperObjects**

**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**

```r
## 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**

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

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

```r
## 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="28797626", 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

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

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

```r
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

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

- **event.id**: stdId/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

```r
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

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

**Arguments**

- `event.id`  
  stdId 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**

```r
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**

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

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>id</td>
<td>stId or dbId of a Reactome object</td>
</tr>
<tr>
<td>displayName</td>
<td>displayName of a Reactome object</td>
</tr>
<tr>
<td>main</td>
<td>if set to TRUE, only <strong>first-class</strong> referrals returned</td>
</tr>
<tr>
<td>depth</td>
<td>number of depths</td>
</tr>
<tr>
<td>all.depth</td>
<td>if set to TRUE, connected objects in all depths returned</td>
</tr>
<tr>
<td>species</td>
<td>name or taxon id or dbId or abbreviation of a species</td>
</tr>
<tr>
<td>type</td>
<td>return results as a list of dataframes ('row'), or as a graph object ('graph')</td>
</tr>
</tbody>
</table>

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

```r
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

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

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>ids</td>
<td>Reactome stIds/dbIds, or non-Reactome ids</td>
</tr>
<tr>
<td>databaseName</td>
<td>database name</td>
</tr>
<tr>
<td>speedUp</td>
<td>set TRUE to use doParallel method</td>
</tr>
<tr>
<td>cluster</td>
<td>the number of cluster in makeCluster</td>
</tr>
</tbody>
</table>
unnestListCol

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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