findGeneByCompartmentPaperCnt

Get gene table of frequently found genes within compartments

Description

Get gene table and paper count for genes mentioned cnt or more times in different compartment-paper pairs.

Usage

findGeneByCompartmentPaperCnt(cnt = 1)

Arguments

cnt

minimal number of times mentioned gene

Value

data.frame with 9 columns: 8 specified in getGenesByID and Npmid column for the paper count.

See Also

genesByID

Other Gene functions: findGeneByPaperCnt(), findGeneByPapers(), findGenesByEntrez(), findGenesByName(), getAllGenes4Compartment(), getGenes4Compartment(), getGenesByID()

Examples

cntT <- findGeneByPaperCnt(47)
head(cntT)
findGeneByPaperCnt

Get gene table of frequently found genes

Description
Get gene table and paper count for genes mentioned \( cnt \) or more times in different papers.

Usage
findGeneByPaperCnt\( (cnt = 1) \)

Arguments
\begin{itemize}
\item \texttt{cnt} \hspace{1cm} \text{minimal number of papers that mentioned gene}
\end{itemize}

Value
data.frame with 9 columns: 8 specified in \texttt{getGenesByID} and \texttt{Npmid} column for the paper count.

See Also
getGenesByID

Other Gene functions: \texttt{findGeneByCompartmentPaperCnt()}, \texttt{findGeneByPapers()}, \texttt{findGenesByEntrez()}, \texttt{findGenesByName()}, \texttt{getAllGenes4Compartment()}, \texttt{getGenes4Compartment()}, \texttt{getGenesByID()}

Examples
\begin{verbatim}
cntT <- findGeneByPaperCnt(47)
head(cntT)
\end{verbatim}
findGenesByEntrez

Value
data.frame with 9 columns: 8 specified in getGenesByID and Npmid column for the paper count.

See Also
genesByID
Other Gene functions: findGeneByCompartmentPaperCnt(), findGeneByPaperCnt(), findGenesByEntrez(), findGenesByName(), getAllGenes4Compartment(), getGenes4Compartment(), getGenesByID()
**findGenesByName**

**Description**

Get internal gene representation for set of gene names. Function lookups for provided values in Human Name, Mouse Name and Rat Name columns and return following features for all found genes: GeneID (internal database ID), MGI ID, Human Entrez ID, Mouse Entrez ID, Rat Entrez ID, Human gene name, Mouse gene name and Rat gene name.

**Usage**

```r
findGenesByName(name)
```

**Arguments**

- `name` vector of gene names.

**Details**

Could be used as an intermediate step for building Protein-Protein interaction map from the list of Gene IDs returned in the first column. Also, this function provides a useful sanity check, e.g. how many Gene IDs correspond to the specific gene name or Entrez ID, which could be specie-specific.

**Value**

`data.frame` with columns specified above.

**See Also**

Other Lookup functions: `findGenesByEntrez()`  
Other Gene functions: `findGeneByCompartmentPaperCnt()`, `findGeneByPaperCnt()`, `findGeneByPapers()`, `findGenesByName()`, `getAllGenes4Compartment()`, `getGenes4Compartment()`, `getGenesByID()`

**Examples**

```r
# get information for specific gene
# t <- findGenesByEntrez(c(1742, 1741, 1739, 1740))
```

```r
t <- findGenesByName(c("Src", "Srcin1", "Fyn"))
```
**getAllGenes4BrainRegion**

*Get all genes for brain region for particular specie*

### Description

Get all genes annotated for specific brain region for specific specie. Function lookups Brain Region ID and Specie Tax ID columns and returns main information like internal Gene IDs, MGI ID, Human Entrez ID, Human Gene Name, Mouse Entrez ID, Mouse Gene Name, Localisation (presynaptic, postsynaptic, synaptosomal), PaperPMID and BrainRegion.

### Usage

```r
getAllGenes4BrainRegion(brainRegion, taxID)
```

### Arguments

- `brainRegion`: ID for specific brain region
- `taxID`: specie ID

### Value

data.frame with the following columns:

- GeneID
- Localisation
- MGI
- HumanEntrez
- MouseEntrez
- HumanName
- MouseName
- PMID
- Paper
- Year
- SpeciesTaxID
- BrainRegion

### See Also

Other BrainRegion functions: `getBrainRegions()`, `getGenes4BrainRegion()`, `getPPIbyIDs4BrainRegion()`

Other BrainRegion Gene functions: `getGenes4BrainRegion()`

### Examples

```r
gns <- getAllGenes4BrainRegion(brainRegion = "Striatum", taxID = 10090)
head(gns)
```
getAllGenes4Compartment

 Extract all genes found in compartment

Description
Get all genes annotated for specific compartment. Function returns main information like internal Gene IDs, MGI ID, Human Entrez ID, Human Gene Name, Mouse Entrez ID, Mouse Gene Name, Rat Entrez ID, Rat Gene Name.

Usage
getAllGenes4Compartment(compartmentID)

Arguments
compartmentID  ID for specific compartment

Value
data.frame described in getGenesByID()

See Also
Other Gene functions: findGeneByCompartmentPaperCnt(), findGeneByPaperCnt(), findGeneByPapers(), findGenesByEntrez(), findGenesByName(), getGenes4Compartment(), getGenesByID()
Other Compartment functions: getCompartments(), getGenes4Compartment(), getPPIbyIDs4Compartment()

Examples
G <- getAllGenes4Compartment(compartmentID = 1) # 5560 rows

getBrainRegions
Get list of all Brain regions in the database

Description
Get full list of brain regions considered in the database. Returns table with regions and their respective IDs.

Usage
getBrainRegions()
getCompartments

Value

data.frame with following columns:

- ID: Brain region internal ID
- Name: name of the region
- Description: extended description of the region
- InterlexID
- ParentID: ID of the containing brain region

See Also

Other BrainRegion functions: `getAllGenes4BrainRegion()`, `getGenes4BrainRegion()`, `getPPIbyIDs4BrainRegion()`

Examples

t <- getBrainRegions()

c <- getCompartments()
getGeneDiseaseByEntres

_Disease information for Human Entrez IDs_

**Description**

Get Human disease information (HDO provided) for the set of Human Entrez IDs. Function lookups for diseases associated with Human Entrez IDs and returns list of available diseases.

**Usage**

```
getGeneDiseaseByEntres(entrez)
```

**Arguments**

- `entrez` vector of Human Entrez gene IDs

**Value**

data.frame with following columns:

- HumanEntrez
- HumanName
- HDOID
- Description

**See Also**

Other Disease functions: `getGeneDiseaseByIDs()`, `getGeneDiseaseByName()`

**Examples**

```
t <- getGeneDiseaseByEntres(c(8573, 1742, 1739)) # (95 rows)
```

getGeneDiseaseByIDs

_Disease information for internal gene IDs._

**Description**

Get Human disease information (HDO provided) for the set of internal gene IDs. Function lookups for diseases associated with internal GeneIDs and returns list of available diseases.

**Usage**

```
getGeneDiseaseByIDs(ids)
```
getGeneDiseaseByName

Arguments
ids vector of gene IDs.

Value
data.frame with following columns:
  - HumanEntrez
  - HumanName
  - HDOID
  - Description

See Also
Other Disease functions: getGeneDiseaseByEntres(), getGeneDiseaseByName()

Examples
t <- getGeneDiseaseByIDs(c(48, 585, 710))

getGeneDiseaseByName Disease information for Human Gene Names

Description
Get Human disease information (HDO provided) for the set of Human Gene Names. Function
lookups for diseases associated with internal Human gene names and returns list of available dis-
eases.

Usage
geneDiseaseByName(names)

Arguments
names vector of Human gene names

Value
data.frame

See Also
Other Disease functions: getGeneDiseaseByEntres(), getGeneDiseaseByIDs()

Examples
t <- getGeneDiseaseByName(c("CASK", "DLG2", "DLG1")) # (115 rows)
getGeneInfoByEntrez

Gene information for given list of gene Entrez IDs

Description

Get gene information for set of gene Entrez IDs. Function lookup for name in Human Entrez ID and Mouse Entrez Id data and return following features for all found genes: GeneID (internal database ID), Localisation (presynaptic, postsynaptic, synaptosome), MGI (MGI ID), HumanEntrez (Human Entrez ID), MouseEntrez (Mouse Entrez ID), HumanName (Human gene name), MouseName (Mouse gene name), PaperPMID (PMID IDs for the publications where the genes were reported), Paper (papers where specific genes were reported in a format FIRSTAUTHOR_YEAR), Year, SpeciesTaxID (specie the original experiment was performed on), BrainRegion (Brain region where the specific genes were identified, according to the paper)

Usage

geneInfoByEntrez(entrez)

Arguments

etrez vector of Entrez IDs. Function accepts both integers and characters.

Value

data.frame with fields specified above.

See Also

Other GeneInfo functions: getGeneInfoByIDs(), getGeneInfoByNames(), getGeneInfoByPapers()

Examples

# get information for specific gene
t <- getGeneInfoByEntrez(1742)

# get information for specific character string Entrez representation
t <- getGeneInfoByEntrez("1742")

# get information for the list of genes
t <- getGeneInfoByNames(c(1741, 1742, 1739, 1740))
getGeneInfoByIDs

Get GeneInfo table for set of GeneIDs

Description
Function lookup for internal GeneID values and return following features for all found genes: GeneID (internal database ID), Localisation (one of the following: presynaptic, postsynaptic, synaptosome), MGI (MGI ID), HumanEntrez (Human Entrez ID), MouseEntrez (Mouse Entrez ID), HumanName (Human gene name), MouseName (Mouse gene name), PaperPMID (PMID IDs for the publications where the genes were reported), Paper (papers where specific genes were reported in a format FIRSTAUTHOR_YEAR), Year, SpeciesTaxID (specie the original experiment was performed on), BrainRegion (Brain region where the specific genes were identified, according to the paper)

Usage
getGeneInfoByIDs(ids)

Arguments
ids vector of Gene IDs.

Details
This function then returns following features for all found genes:

- GeneID,
- Localisation,
- MGI,
- HumanEntrez,
- MouseEntrez,
- HumanName,
- MouseName,
- PaperPMID,
- Paper,
- Year,
- SpeciesTaxID,
- BrainRegion

Value
data.frame with column specified above.
getGeneInfoByName

See Also

Other GeneInfo functions: `getGeneInfoByEntrez()`, `getGeneInfoByName()`, `getGeneInfoByPapers()`

Examples

gdf <- getGeneInfoByIDs(c(46, 6, 15, 1))

description

Function lookup for name in Human Gene name, Rat Gene name and Mouse Gene name data and return following features for all found genes: GeneID (internal database ID), Localisation (one of the following: presynaptic, postsynaptic, synaptosome), MGI (MGI ID), HumanEntrez (Human Entrez ID), MouseEntrez (Mouse Entrez ID), HumanName (Human gene name), MouseName (Mouse gene name), PaperPMID (PMID IDs for the publications where the genes were reported), Paper (papers where specific genes were reported in a format FIRSTAUTHOR_YEAR), Year, SpeciesTaxID (specie the original experiment was performed on), BrainRegion (Brain region where the specific genes were identified, according to the paper)

Usage

geneInfoByName(name)

Arguments

name vector of gene names

Details

This function then returns following features for all found genes:

- GeneID,
- Localisation,
- MGI,
- HumanEntrez,
- MouseEntrez,
- HumanName,
- MouseName,
- PaperPMID,
- Paper,
- Year,
- SpeciesTaxID,
- BrainRegion
Value

data.frame with fields specified above.

See Also

Other GeneInfo functions: `getGeneInfoByEntrez()`, `getGeneInfoByIDs()`, `getGeneInfoByPapers()`

Examples

```r
# get information for specific gene
t <- getGeneInfoByName("CASK")

# get information for the list of genes
t <- getGeneInfoByName(c("CASK", "DLG2"))
```

---

**getGeneInfoByPapers**  Get gene information for set of genes mentioned by certain papers.

**Description**

Function lookup for specified PubMedIDs in the gene reference data and return following features for genes referenced by requested papers at least `cnt` times: GeneID (internal database ID), Localisation (one of the following: presynaptic, postsynaptic, synaptosome), MGI (MGI ID), HumanEntrez (Human Entrez ID), MouseEntrez (Mouse Entrez ID), HumanName (Human gene name), MouseName (Mouse gene name), PaperPMID (PMID IDs for the publications where the genes were reported if it is within `pmids` list), Paper (papers where specific genes were reported in a format `FIRSTAUTHOR_YEAR`), Year, SpeciesTaxID (specie the original experiment was performed on), BrainRegion (Brain region where the specific genes were identified, according to the paper)

**Usage**

```r
getGeneInfoByPapers(pmids, cnt = 1)
```

**Arguments**

- `pmids`  vector of PMIDs to search for genes
- `cnt`  minimal number of papers that mentioned gene

**Details**

This function then returns following features for all found genes:

- GeneID,
- Localisation,
- MGI,
- HumanEntrez,
getGenes4BrainRegion

• MouseEntrez,
• HumanName,
• MouseName,
• PaperPMID,
• Paper,
• Year,
• SpeciesTaxID,
• BrainRegion

Value
data.frame with fields specified above.

See Also
Other GeneInfo functions: getGeneInfoByEntrez(), getGeneInfoByIDs(), getGeneInfoByName()

Examples
```
res<- getAllGenes4Compartment(compartmentID = 1)
gnt<-getGeneInfoByIDs(res$GeneID)
pmids<-names(sort(table(gnt$PaperPMID))[1:5])
cntT <- getGeneInfoByPapers(pmids,cnt=3)
head(cntT)
```

getGenes4BrainRegion  Select genes from the list that found in brain region of particular specie

Description
Select genes from your list annotated for specific brain region. Should be used with findGenesByEntrez() or findGenesByName() functions to obtain list of internal IDs for your list of genes. Function lookups the Gene table for specified localisation and returns main gene information like internal Gene IDs, MGI ID, Human Entrez ID, Human Gene Name, Mouse Entrez ID, Mouse Gene Name, PaperPMID, Localisation and BrainRegion.

Usage
```
getGenes4BrainRegion(ids, brainRegion, taxID)
```

Arguments
```
ids internal IDs for list of genes
brainRegion ID for the brain region of interest
taxID taxon ID specie tax ID
```
getGenes4Compartment

Value

data.frame with the following columns:

- GeneID
- Localisation
- MGI
- HumanEntrez
- MouseEntrez
- HumanName
- MouseName
- PMID
- Paper
- Year
- SpeciesTaxID
- BrainRegion

See Also

Other BrainRegion functions: getGenes4BrainRegion(), getBrainRegions(), getPPIbyIDs4BrainRegion()

Other BrainRegion Gene functions: getGenes4BrainRegion()

Examples

Genes <- getGenes4BrainRegion(c(1, 15, 156, 1500, 3000, 7000),
    brainRegion = "Striatum", taxID = 10090)
# 5 rows

---

getGenes4Compartment  Select genes from the list that found in compartment

Description

Select all genes from your list annotated for specific compartment. Should be used with findGenesByEntrez() or findGenesByName() functions to obtain list of internal IDs for your list of genes. Function lookups the Gene table for specified localisation and returns main gene information like internal Gene IDs, MGI ID, Human Entrez ID, Human Gene Name, Mouse Entrez ID, Mouse Gene Name, Rat Entrez ID, Rat Gene Name.

Usage

genes <- getGenes4Compartment(ids, compartmentID)
Arguments

ids Gene IDs
compartmentID compartment ID

Value
data.frame described in getGenesByID()

See Also
Other Gene functions: findGeneByCompartmentPaperCnt(), findGeneByPaperCnt(), findGeneByPapers(), findGenesByEntrez(), findGenesByName(), getAllGenes4Compartment(), getGenesByID()
Other Compartment functions: getAllGenes4Compartment(), getCompartments(), getPPIbyIDs4Compartment()

Examples

Genes <- getGenes4Compartment(c(1, 15, 156, 1500, 3000, 7000),
  compartmentID = 1
)

getGenesByID(ids)

getGenesByID

Get gene table from list of GeneIDs.

Description
Takes internal gene IDs as input and return the following features for all found genes:

GeneID internal database ID
MGI MGI ID
HumanEntrez Human Entrez ID
MouseEntrez Mouse Entrez ID
HumanName Human gene name
MouseName Mouse gene name
RatEntrez Rat Entrez ID
Rat Name Rat gene name

Usage
getGenesByID(ids)

Arguments
ids vector of GeneID values.
**getIGraphFromPPI**

- **Value**
  
  data.frame with 8 columns specified above.

- **See Also**
  
  Other Gene functions: findGeneByCompartmentPaperCnt(), findGeneByPaperCnt(), findGeneByPapers(), findGenesByEntrez(), findGenesByName(), getAllGenes4Compartment(), getGenes4Compartment()

- **Examples**
  
  gdf <- getGenesByID(c(46, 6, 15, 1))

---

**Description**

Combine information from PPI data.frame obtained with functions like getPPIbyName or getPPIbyEntrez with information about genes obtained from getGenesByID to make interpretable undirected PPI graph in igraph format. In this format network could be further analysed and visualized by algorithms in igraph package.

- **Usage**
  
  getIGraphFromPPI(ppi)

- **Arguments**
  
  - **ppi**
    
    PPI data.frame with columns A and B, obtained from functions like getPPIbyName

- **Value**
  
  igraph object with specified PPI network.

- **See Also**
  
  getPPIbyName(), getPPIbyEntrez() and getPPIbyIDs() to get PPI data.frame, getTableFromPPI() to get interpretable table representation of the PPI data.frame.
  
  Other PPI functions: getPPIbyEntrez(), getPPIbyIDs4BrainRegion(), getPPIbyIDs4Compartment(), getPPIbyIDs(), getPPIbyName(), getTableFromPPI()

- **Examples**
  
  library(igraph)
  g <- getIGraphFromPPI(
    getPPIbyIDs(c(48, 129, 975, 4422, 5715, 5835), type = "lim")
  )
  plot(g, vertex.label = V(g)$RatName, vertex.size = 35)
getMutations4DiseaseByEntres

*Get mutational information for Gene and Disease*

**Description**

Function looks up the information for particular set of Entrez IDs and disease HDOID.

**Usage**

`getMutations4DiseaseByEntres(entrez, hdoid)`

**Arguments**

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>entrez</code></td>
<td>list of Entrez IDs for genes to select</td>
</tr>
<tr>
<td><code>hdoid</code></td>
<td>disease HDOID to get mutational association.</td>
</tr>
</tbody>
</table>

**Value**

data.frame as described in `getMutations4DiseaseByIDs`.

**See Also**

`findGenesByEntrez`

Other Mutation functions: `getMutations4DiseaseByIDs()`, `getMutations4DiseaseByNames()`

**Examples**

```r
hdoid<-'DOID:0060041'
entrez<-c("23859", "17754", "18673", "268566", "12293", "320840", "24012")
mdf<-getMutations4DiseaseByEntres(entrez, hdoid)
is.null(mdf)
```

getMutations4DiseaseByIDs

*Get mutational information for Gene and Disease*

**Description**

Function looks up the information for particular set of GeneIDs and disease HDOID.

**Usage**

`getMutations4DiseaseByIDs(ids, hdoid)`

**Arguments**

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>ids</code></td>
<td>list of GeneIDs for genes to select</td>
</tr>
<tr>
<td><code>hdoid</code></td>
<td>disease HDOID to get mutational association.</td>
</tr>
</tbody>
</table>

**Value**

data.frame as described in `getMutations4DiseaseByIDs`.

**See Also**

`findGenesByEntrez`

Other Mutation functions: `getMutations4DiseaseByEntres()`, `getMutations4DiseaseByNames()`

**Examples**

```r
hdoid<-'DOID:0060041'
entrez<-c("23859", "17754", "18673", "268566", "12293", "320840", "24012")
mdf<-getMutations4DiseaseByEntres(entrez, hdoid)
is.null(mdf)
```
getMutations4DiseaseByIDs

Arguments

ids internal GeneIDs to filter mutation data
hdoid disease HOID to get mutational association.

Details

This function then returns following features for all found genes:

- GeneID,
- MGI,
- MouseEntrez,
- MouseName,
- HumanName,
- HumanEntrez,
- HDOID,
- Disease,
- Chromosome,
- Position,
- Variant,
- FunctionClass,
- cDNAvariant,
- ProteinVariant,
- DENOVO,
- SFARI,
- EpilepsyGene,
- ClinVar,
- PMID,
- Paper

Value

data.frame with fields specified above.

See Also

Other Mutation functions: getMutations4DiseaseByEntres(), getMutations4DiseaseByName()

Examples

hdoid<-'DOID:0060041'
ids<-c(6,32,127,181,240,267,558)
mdf<-getMutations4DiseaseByIDs(ids, hdoid)
is.null(mdf)
getMutations4DiseaseByName

*Get mutational information for Gene and Disease*

**Description**

Function lookups for provided values in Human Name, Mouse Name and Rat Name columns, extract known mutations, filter requested HDOID and return data.frame in the format described in getMutations4DiseaseByIDs.

**Usage**

getMutations4DiseaseByName(name, hdoid)

**Arguments**

- **name**
  - gene names to look for
- **hdoid**
  - disease HDOID to get mutational association.

**Value**

data.frame as described in getMutations4DiseaseByIDs.

**See Also**

findGenesByName

Other Mutation functions: getMutations4DiseaseByEntres(), getMutations4DiseaseByIDs()

**Examples**

```r
hdoid<- 'DOID: 0060041'
name<- c("Dlg2", "Map1a", "Phb", "Gphn", "Cacna2d1", "Negr1", "Rgs7")
mdf<- getMutations4DiseaseByName(name, hdoid)
is.null(mdf)
```

---

getPPIbyEntrez

*Extract the PPIs for my list of genes defined by Entrez IDs*

**Description**

Get Protein-Protein interactions (PPIs) for the set of ID. Function lookups for PPIs for the list of Entrez IDs and returns either “induced” (all available interactions for these genes) or “limited” (only interactions between genes specified in the query) table of interacting genes A and B, where A and B are respective Internal IDs.
getPPIbyIDs

Usage

getPPIbyEntrez(entrez, type = c("induced", "limited"))

Arguments

tenrez Entrez IDs

type type of the PPI network should be either induced (for all the PPIs for specific genes, including external genes) or limited (for PPIs between the genes specified in the query). Type could be shortened to recognizable minimum like 'ind' or 'lim'.

Value
data.frame with interactors internal GeneID in columns A and B

See Also

getPPIbyName() and getPPIbyIDs() to get PPI data.frame, getIGraphFromPPI() to get igraph representation of the PPI data.frame and getTableFromPPI() to get interpretable table representation of the PPI data.frame.

Other PPI functions: getIGraphFromPPI(), getPPIbyIDs4BrainRegion(), getPPIbyIDs4Compartment(), getPPIbyIDs(), getPPIbyName(), getTableFromPPI()

Examples

t <- getPPIbyEntrez(c(1739, 1740, 1742, 1741), type = "ind")

getPPIbyIDs

Extract the PPIs for my list of genes defined by GeneID

Description

Get Protein-Protein interactions (PPIs) for the set of internal GeneIDs. Function lookups for PPIs for specific GeneID and returns either “induced” (all interaction for this GeneID) or “limited” (only interactions between GeneIDs specified in the query) table of A and B interacting genes, where A and B are respective GeneIDs.

Usage

getPPIbyIDs(ids, type = c("induced", "limited"))

Arguments

ids Gene IDs

type type of the PPI network should be either induced (for all the PPIs for specific genes, including external genes) or limited (for PPIs between the genes specified in the query). Type could be shortened to recognizable minimum like 'ind' or 'lim'.
Value

data.frame with interactors internal GeneID in columns A and B

See Also

getPPIbyName() and getPPIbyEntrez() to get PPI data.frame, getIGraphFromPPI() to get
graph representation of the PPI data.frame and getTableFromPPI() to get interpretable table
representation of the PPI data.frame.

Other PPI functions: getIGraphFromPPI(), getPPIbyEntrez(), getPPIbyIDs4BrainRegion(),
getPPIbyIDs4Compartment(), getPPINbyName(), getTableFromPPI()

Examples

t <- getPPIbyIDs(c(48, 585, 710), type = "limited") # (16 rows)
t <- getPPIbyIDs(c(48, 585, 710), type = "induced") # 306 rows

getPPIbyIDs4BrainRegion

Prepare induced or limited network for brain region

Description

Prepare PPI network for genes from your list annotated for specific brain region. Should be used
with findGenesByEntrez() or findGenesByName() functions to obtain list of internal IDs for
your list of genes. Could be used with getAllGenes4BrainRegion functions to obtain all genes
belonging to respective brain region. Function lookups the PPI table for gene IDs from the list and
returns “limited” or “induced” interactors GeneIDs for the specified region.

Usage

getPPIbyIDs4BrainRegion(
  ids,
  brainRegion,
  taxID,
  type = c("induced", "limited")
)

Arguments

  ids        gene IDs
  brainRegion region ID
  taxID      taxon ID
  type       type of the PPI network should be either induced (for all the PPIs for specific
genes, including external genes) or limited (for PPIs between the genes specified in the query). Type could be shortened to recognizable minimum like 'ind' or 'lim'.
prepare induced or limited network for compartment

**Description**

Prepare PPI network for genes from your list annotated for specific compartment. Should be used with findGenesByEntrez or findGenesByName functions to obtain list of internal IDs for your list of genes. Could be used with getAllGenes4Compartment functions to obtain all genes belonging to respective compartment. Function lookups the PPI table for gene IDs from the list and returns “limited” or “induced” interactors GeneIDs from the same compartment.

**Usage**

```r
getPPIbyIDs4Compartment(ids, compartmentID, type = c("induced", "limited"))
```

**Arguments**

- `ids` : internal gene IDs
- `compartmentID` : ID for specific compartment
- `type` : type of the PPI network should be either ‘induced’ (for all the PPIs for specific genes, including external genes) or ‘limited’ (for PPIs between the genes specified in the query). Type could be shortened to recognizable minimum like ‘ind’ or ‘lim’.
getPPIbyName

Value

data.frame with interactors internal GeneID in columns A and B

See Also

Other PPI functions: `getIGraphFromPPI()`, `getPPIbyEntrez()`, `getPPIbyIDs4BrainRegion()`, `getPPIbyIDs()`, `getPPIbyName()`, `getTableFromPPI()`

Other Compartment functions: `getAllGenes4Compartment()`, `getCompartments()`, `getGenes4Compartment()`

Examples

```r
ppi <- getPPIbyIDs4Compartment(c(1, 15, 156, 1500, 3000, 7000),
                                compartmentID = 1, type = "induced"
) # 201 rows
```

getPPIbyName

Extract the PPIs for my list of genes defined by Gene name

Description

Get Protein-Protein interactions (PPIs) for the set of gene names. Function lookups for PPIs for the list of GeneIDs and returns either “induced” (all interaction for this GeneID) or “limited” (only interactions between GeneIDs specified in the query) table of interacting genes A and B, where A and B are respective gene names.

Usage

```r
getPPIbyName(name, type = c("induced", "limited"))
```

Arguments

- **name**: Gene names
- **type**: type of the PPI network should be either induced (for all the PPIs for specific genes, including external genes) or limited (for PPIs between the genes specified in the query). Type could be shortened to recognizable minimum like 'ind' or 'lim'.

Value

data.frame with interactors internal GeneID in columns A and B

See Also

`getPPIbyEntrez()` and `getPPIbyIDs()` to get PPI data.frame, `getIGraphFromPPI()` to get igraph representation of the PPI data.frame and `getTableFromPPI()` to get interpretable table representation of the PPI data.frame.

Other PPI functions: `getIGraphFromPPI()`, `getPPIbyEntrez()`, `getPPIbyIDs4BrainRegion()`, `getPPIbyIDs4Compartment()`, `getPPIbyIDs()`, `getTableFromPPI()`
Examples

t <- getPPIbyName(
  c("CASK", "DLG4", "GRIN2A", "GRIN2B", "GRIN1"),
  type = "lim"
)

getPapers

Get synaptome papers overview

Description

Get synaptome papers overview

Usage

getPapers()

Value

data.frame with following columns:

- PaperPMID
- SpeciesTaxID
- Year
- Name
- Localisation
- BrainRegion
- Method
- Ngenes

Examples

p <- getPapers()
head(p)
getTableFromPPI

Get table representation of the PPI.

Description

Combine information from PPI data.frame obtained with functions like `getPPIbyName` or `getPPIbyEntrez` with information about genes obtained from `getGenesByID` to make interpretable table representation.

Usage

getableFromPPI(ppi)

Arguments

  ppi        PPI data.frame with columns A and B, obtained from functions like `getPPIbyName`

Value

  table with the following columns added for both interactors (A and B):

  - GeneID internal database ID
  - MGI MGI ID
  - HumanEntrez Human Entrez ID
  - MouseEntrez Mouse Entrez ID
  - HumanName Human gene name
  - MouseName Mouse gene name
  - RatEntrez Rat Entrez ID
  - RatName Rat gene name

See Also

  `getPPIbyName()`, `getPPIbyEntrez()` and `getPPIbyIDs()` to get PPI data.frame, `getIGraphFromPPI()` to get igraph representation of the PPI data.frame.

  Other PPI functions: `getIGraphFromPPI()`, `getPPIbyEntrez()`, `getPPIbyIDs4BrainRegion()`, `getPPIbyIDs4Compartment()`, `getPPIbyIDS()`.

Examples

tbl <- getTableFromPPI(getPPIbyIDs(c(48, 585, 710), type = "limited"))
graphFromSynaptomeByEntrez

Utility function to create network from synaptome.db data

Description

Utility function to create network from synaptome.db data

Usage

graphFromSynaptomeByEntrez(entrez, LCC = TRUE, simplify = TRUE)

Arguments

- `entrez`: vector of EntrezIDs for network vertices
- `LCC`: if TRUE only largest connected component is returned
- `simplify`: if TRUE loops and multiple edges will be removed

Value

network defined by the gene table

Examples

```r
library(synaptome.db)
cid<-match('Presynaptic', getCompartments()$Name)
geneTable<-getAllGenes4Compartment(cid)
gg<-graphFromSynaptomeByEntrez(geneTable$HumanEntrez)
```

graphFromSynaptomeGeneTable

Utility function to create network from synaptome.db data

Description

Utility function to create network from synaptome.db data

Usage

graphFromSynaptomeGeneTable(geneTable, LCC = FALSE, simplify = FALSE)

Arguments

- `geneTable`: data.frame described in getGenesByID
- `LCC`: if TRUE only largest connected component is returned
- `simplify`: if TRUE loops and multiple edges will be removed
Value

network defined by the gene table

Examples

```r
library(synaptome.db)
cid<-match('Presynaptic', getCompartments()$Name)
geneTable<-getAllGenes4Compartment(cid)
gg<-graphFromSynaptomeGeneTable(geneTable)
```

Description

The package obtains a local copy of the Synaptic proteome database from AnnotationHub package `synaptome.data` and provides a set of utility R functions to query and analyse its content.

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References

\insertRefSorokina:2021hlsynaptome.db

See Also

Useful links:
  • Report bugs at https://github.com/lptolik/synaptome.db/issues/
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