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()
**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**

```r
findGeneByPaperCnt(cnt = 1)
```

**Arguments**

- `cnt`: minimal number of papers that mentioned gene

**Value**

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

**See Also**

- `getGenesByID`
- Other Gene functions: `findGeneByCompartmentPaperCnt`, `findGeneByPapers`, `findGenesByEntrez`, `findGenesByName`, `getAllGenes4Compartment`, `getGenes4Compartment`, `getGenesByID`

**Examples**

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

**findGeneByPapers**

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**

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

**Arguments**

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

**Examples**

res<- getAllGenes4Compartment(compartmentID = 1)
gnt<-getGeneInfoByIDs(res$GeneID)

pmids<-names(sort(table(gnt$PaperPMID))[1:5])
cntT <- findGeneByPapers(pmids,cnt=3)
head(cntT)

---

**findGenesByEntrez**

*Internal Gene representation for given list of gene Entrez IDs*

**Description**

Get internal gene representation for set of gene Entrez IDs. Function lookups for provided values in Human Entrez ID, Mouse Entrez ID and Rat Entrez ID 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**

findGenesByEntrez(entrez)

**Arguments**

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

**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.
findGenesByName

See Also

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

Examples

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

findGenesByName # Find GeneIDs for names

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

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(), findGenesByEntrez(), getAllGenes4Compartment(), getGenes4Compartment(), getGenesByID()

Examples

# Find GeneIDs for names
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

ggetAllGenes4BrainRegion(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

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()
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))

geneDiseaseByNames

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 diseases.

Usage
geneDiseaseByNames(names)

Arguments
names vector of Human gene names

Value
data.frame

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

Examples
t <- geneDiseaseByNames(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(getGeneInfoByEntrez(entrez)

Arguments

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

Value

data.frame with fields specified above.

See Also

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

Examples

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

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

geneInfoByIDs(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))

getGeneInfoByName Get gene information for set of gene names.

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 (species the original experiment was performed on), BrainRegion (Brain region where the specific genes were identified, according to the paper)

Usage

geneInfoByNames(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
getGeneInfoByPapers

Value
data.frame with fields specified above.

See Also

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

Examples

# 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

geneInfoByPapers(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

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

genes4BrainRegion  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

genes4BrainRegion(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: `getAllGenes4BrainRegion()`, `getBrainRegions()`, `getPPIbyIDs4BrainRegion()`

Other BrainRegion Gene functions: `getAllGenes4BrainRegion()`

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

genes4Compartment(ids, compartmentID)
getGenesByID

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>ids</td>
<td>Gene IDs</td>
</tr>
<tr>
<td>compartmentID</td>
<td>compartment ID</td>
</tr>
</tbody>
</table>

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

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

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

genesByID(ids)

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>ids</td>
<td>vector of GeneID values.</td>
</tr>
</tbody>
</table>
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))

getIGraphFromPPI Get Igraph representation of 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 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**

- **entrez**: list of Entrez IDs for genes to select
- **hdoid**: disease HDOID to get mutational association.

**Value**

data.frame as described in `getMutations4DiseaseByIDs`.

**See Also**

findGenesByEntrez

Other Mutation functions: `getMutations4DiseaseByIDs()`, `getMutations4DiseaseByName()`

**Examples**

```r
hdoid<- 'DOID:0060041'
etrez<-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)
getMutations4DiseaseByIDs

Arguments

ids internal GeneIDs to filter mutation data
hdoid disease HDOID 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**

```r
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**

- `entrez`: 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'.

---
getPPIbyIDs4BrainRegion

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 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(), getPPIbyName(), 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'.

**getPPIbyIDs4Compartment**

---

**Value**

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

**See Also**

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

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

**Examples**

```r
# getting all genes for mouse Striatum
gns <- getAllGenes4BrainRegion(brainRegion = "Striatum", taxID = 10090)
head(gns)

# getting full PPI network for postsynaptic compartment
ppi <- getPPIbyIDs4BrainRegion(
  gns$GeneID,
  brainRegion = "Striatum",
  taxID = 10090,
  type = "limited"
)
head(ppi)
```

---

**getPPIbyIDs4Compartment**

*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

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
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

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

---

### Description

Get synaptome papers overview

### Usage

```r
getPapers()
```

### Value

data.frame with following columns:

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

### Examples

```r
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

getTableFromPPI(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()`, `getPPIbyName()`

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**

```r
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**

```r
graphFromSynaptomeGeneTable(
geneTable,
LCC = FALSE,
simplify = FALSE,
type = c("induced", "limited")
)
```
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.
- **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

- network defined by the gene table

See Also

- `[getPPIbyIDs()]`

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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- J. Douglas Armstrong

References

\insertRefSorokina:2021hlsynaptome.db
See Also

Useful links:

- Report bugs at https://github.com/lptolik/synaptome.db/issues/
Index

* list(BrainRegion Gene functions)
  getAllGenes4BrainRegion, 5
  getGenes4BrainRegion, 14
* list(BrainRegion functions)
  getAllGenes4BrainRegion, 5
  getBrainRegions, 6
  getGenes4BrainRegion, 14
  getPPIbyIDs4BrainRegion, 22
* list(Compartment functions)
  getAllGenes4Compartment, 6
  getCompartments, 7
  getGenes4Compartment, 15
  getPPIbyIDs4Compartment, 23
* list(Compartment functions)
  getAllGenes4Compartment, 6
  getCompartments, 7
  getGenes4Compartment, 15
  getPPIbyIDs4Compartment, 23
* list(Gene functions)
  findGeneByCompartmentPaperCnt, 1, 2–4, 6, 16, 17
  findGeneByPaperCnt, 1, 2, 3, 4, 6, 16, 17
  findGeneByPapers, 1, 2, 3, 4, 6, 16, 17
  findGenesByEntrez(), 1, 2, 3, 4, 6, 16, 17
  findGenesByName(), 1, 2, 3, 4, 6, 16, 17
  findGenesByEntrez(), 1, 2, 3, 4, 6, 16, 17
  findGenesByID(), 1–4, 6, 16, 17
  getAllGenes4BrainRegion, 5, 7, 15, 23
  getAllGenes4Compartment, 1–4, 6, 7, 16, 17, 24
  getBrainRegions, 5, 6, 15, 23
  getCompartments, 6, 7, 16, 24
  getGeneDiseaseByEntres, 8, 9
  getGeneDiseaseByIDs, 8, 9
  getGeneDiseaseByName, 8, 9
  getGeneInfoByEntrez, 10, 11, 12–14
  getGeneInfoByIDs, 10, 11, 12, 14
  getGeneInfoByName, 10, 12, 13, 14
  getGeneInfoByPapers, 10, 12, 13, 14
  getGenes4BrainRegion, 5, 7, 14, 23
  getGenes4Compartment, 1–4, 6, 7, 15, 17, 24
  getGenesByEntrez(), 10, 12–14
  getGenesByIDs, 10, 11, 13, 14
  getGenesByPaperCnt, 10, 12, 13, 14
  getIGraphFromPPI, 17
  getIGraphFromPPI(), 17, 21–24, 26
  getIGraphFromPPI(), 17
  getIGraphFromPPI(), 21, 22, 24, 26
  getMutations4DiseaseByEntres, 18, 19, 20

getMutations4DiseaseByEntres, 18
getMutations4DiseaseByIDs, 18
getMutations4DiseaseByNames, 20

* list(PPI functions)
  getGeneInfoByEntrez, 10, 11, 12–14
  getGeneInfoByIDs, 10, 11, 12, 14
  getGeneInfoByName, 10, 12, 13, 14
  getGeneInfoByPapers, 10, 12, 13, 14
  getGenes4BrainRegion, 5, 7, 14, 23
  getGenes4Compartment, 1–4, 6, 7, 15, 17, 24
  getGenesByID, 1–4, 6, 16, 17, 26, 28
  getGenesByIDs(), 6, 16
  getIGraphFromPPI, 17, 21–24, 26
  getIGraphFromPPI(), 21, 22, 24, 26
  getMutations4DiseaseByEntres, 18, 19, 20
INDEX

getMutations4DiseaseByIDs, 18, 18, 20
getMutations4DiseaseByName, 18, 19, 20
getPapers, 25
getPPIbyEntrez, 17, 20, 22–24, 26
getPPIbyEntrez(), 17, 22, 24, 26
getPPIbyIDs, 17, 21, 21, 23, 24, 26
getPPIbyIDs(), 17, 21, 24, 26
getPPIbyIDs4BrainRegion, 5, 7, 15, 17, 21, 22, 22, 24, 26
getPPIbyIDs4Compartment, 6, 7, 16, 17, 21–23, 23, 24, 26
getPPIbyName, 17, 21–24, 24, 26
getPPIbyName(), 17, 21, 22, 26
getTableFromPPI, 17, 21–24, 26
graphFromSynaptomeByEntrez, 27
graphFromSynaptomeGeneTable, 27
igraph, 17

synaptome.data, 28
synaptome.db, 27, 28
synaptome.db-package (synaptome.db), 28