synaptome.db

November 11, 2026

`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

getGenesByID

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

`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

```
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

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

Arguments

`pmids`	vector of PMIDs to search for genes
`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(), 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 Entres 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.

See Also

Other Lookup functions: `findGenesByName()`

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

```
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

```
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()
```

`getCompartments` *Get full list of compartments*

Description

Get list of synaptic compartments considered in the database. Returns table with compartments: "Presynaptic", "Postsynaptic", "Synaptosome", and their internal IDs.

Usage

```
getCompartments()
```

Value

data.frame described above

See Also

Other Compartment functions: `getAllGenes4Compartment()`, `getGenes4Compartment()`, `getPPIbyIDs4Compartment()`

Examples

```
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)
```

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 diseases.

Usage

```
getGeneDiseaseByName(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

```
getGeneInfoByEntrez(entrez)
```

Arguments

`entrez`	`vector` of Entres 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))
```

`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.

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

Usage

```
getGeneInfoByName(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

```
# 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

```
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,

- 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

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

```
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 *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.

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, obtaioed 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(), getPPIbyIDs(), getPPIbyIDs4BrainRegion(), getPPIbyIDs4Compartment(), 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

```
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

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

```
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

```
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.

Usage

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

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(), getPPIbyIDs(), getPPIbyIDs4BrainRegion(), getPPIbyIDs4Compartment(
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("limited", "induced"))
```

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 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("limited", "induced")
)
```

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'.

Value

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

See Also

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

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

Examples

```
# 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

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

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'.

Value

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

See Also

Other PPI functions: getIGraphFromPPI(), getPPIbyEntrez(), getPPIbyIDs(), getPPIbyIDs4BrainRegion(), 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("limited", "induced"))
```

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(), getPPIbyIDs(), getPPIbyIDs4BrainRegion(), getPPIbyIDs4Compartment(), 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

```
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
- Rat Name 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()`, `getPPIbyIDs()`, `getPPIbyIDs4BrainRegion()`, `getPPIbyIDs4Compartment()`, `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

```
graphFromSynaptomeByEntrez(
  entrez,
  LCC = TRUE,
  simplify = TRUE,
  type = c("limited", "induced")
)
```

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
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

Examples

```
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,
  type = c("limited", "induced")
)
```

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

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

synaptome.db *synaptome.db: programmatic access to the Synaptic proteome database*

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.

Author(s)

Maintainer: Oksana Sorokina <oksana.sorokina@ed.ac.uk>

Authors:

- Anatoly Sorokin <lptolik@gmail.com>
- J. Douglas Armstrong

References

\insertRefSorokina:2021hlsynaptome.db

See Also

Useful links:

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

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