Package 'psygenet2r'

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Title psygenet2r - An R package for querying PsyGeNET and to perform comorbidity studies in psychiatric disorders

Version 1.36.0

Description Package to retrieve data from PsyGeNET database (www.psygenet.org) and to perform comorbidity studies with PsyGeNET's and user's data.

Depends R (>= 3.4)

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Contents

`DataGeNET.Psy-class` *Class DataGeNET.Psy*

Description

Class `DataGeNET.Psy` is the basic object use in `psygenet2r` package. It is the main data container to using the different functions to query PsyGeNET database and generate teir output. The constructors of this class are the functions `psygenetGene` and `psygenetDisease`.

Slots

`type` Character containing `'gene'` of `'disease'`. It is used to eprform the correct query to PsyGeNET.

`search` Character containing `'single'` of `'list'`.It is used to eprform the correct query to PsyGeNET.

`database` Character containing the name of the database that will be queried. It can take the values `'MODELS'` to use Comparative Toxigenomics Database, data from mouse and rat; `'GAD'` to use Genetic Association Database; `'CTD'` to use Comparative Toxigenomics Database, data from human; `'PsyCUR'` to use Psychiatric disorders Gene association manually curated; `'CURATED'` to use Human, manually curated databases (PsyCUR and CTD); or `'ALL'` to use all these databases.

`term` Charcter with the term(s) to search into the database(s).

`qresult` `data.frame` with the obtained result

See Also

psygenetGene, psygenetDisease, DataGeNET.Psy-methods

`enrichedPD` *Enrichment of a user's input (genes) in PsyGeNET's diseases.*

Description

Test the enrichment of a given gene list on Psychiatric Disorders from PsyGeNET.

Usage

```
enrichedPD(gene, database = "ALL", verbose = FALSE, warnings = FALSE)
```

Arguments

`gene`	Name or vector of names (that can be both code or uml) to specific genes from PsyGeNET.
`database`	Name of the database that will be queried. It can take the values `'psycur15'` to use data validated by experts for first release of PsyGeNET; `'psycur16'` to use data validated by experts for second release of PsyGeNET; or `'ALL'` to use both databases. Default `'ALL'`.
`verbose`	By default `FALSE`. Change it to `TRUE` to get a on-time log from the function.
`warnings`	By default `TRUE`. Change it to `FALSE` to not see the warnings.

Value

A `data.frame` with the enricment at each Psychiatric Disorder

Examples

```
enrichedPD(c("ADCY2", "AKAP13", "ANK3"), "ALL")
```

extract *Raw data from* DataGeNET.Psy *and* JaccardIndexPsy.

Description

Obtain the raw data from a PsyGeNET's query stored in a DataGeNET.Psy object or the raw data with all the Jaccard Index for the disease of interest of an JaccardIndexPsy object.

Usage

```
extract(object, ...)

## S4 method for signature 'DataGeNET.Psy'
extract(object)

## S4 method for signature 'JaccardIndexPsy'
extract(object, order.cl = "pval", ...)
```

Arguments

object	Object of class DataGeNET.Psy or JaccardIndexPsy
...	NO USED
order.cl	Order resulting data.frame by the name of this column.

Value

A data.frame containing the raw result from PsyGeNET or a data.frame with the result Jaccard Index for each disease.

A data.frame containing the raw result from PsyGeNET

A data.frame with the result Jaccard Index for each disease.

Methods (by class)

- DataGeNET.Psy: Extract function for DataGeNET.Psy
- JaccardIndexPsy: Extract function for JacardIndexPsy

Examples

```
data(qr)
extract(qr)[1:2, ] # get internat data.frame
## Not run:
#Being x an JaccardIndexPsy
extract(x)

## End(Not run)
```

`extractSentences` *Method to obtain the sentences that support a gene-disease association from a* `DataGeNET.Psy` *object.*

Description

PsyGeNET contains a list of sentences that support a gene-disease association from public literature. The internal table of a `DataGeNET.Psy` object contains this information. The method `extractSentences` allows to extract those sentences that support a gene-disease association given a `DataGeNET.Psy` object and a disorder of interest.

Usage

```
extractSentences(object, disorder, verbose)

## S4 method for signature 'DataGeNET.Psy'
extractSentences(object, disorder, verbose = FALSE)
```

Arguments

`object`	Object of class `DataGeNET.Psy`.
`disorder`	The disorder of interest. Only those sentences supporting a gene-disease association with this specific disorder will be extracted. Disorder must be provided by using "Disease Id" or "Disease Name". The "Disease Id" can be provided with or without the "uml" tag. Example of a "Disease Name": "schizophrenia"; Example of a "Disease Id": "umls:C0036341", that is equivalent of using "C0036341".
`verbose`	If set to `TRUE` informative messages are show.

Value

A data frame showing the sentences.

Methods (by class)

- `DataGeNET.Psy`: Get sentences or evidences

Examples

```
data(qr)
extractSentences(qr, "Depression")
```

`geneAttrPlot` *Ploting the relation between genes and disease-categories*

Description

Given a set of genes or a result of `psygenetGene` creates four types of plots showing the relation of the genes with the disease's category in psyGeNET.

Usage

```
geneAttrPlot(x, type = "pie", ..., verbose = FALSE)
```

Arguments

`x`	Vector of genes of interest of `DataGeNET.Psy` resulting of `psyegnetDisease`.
`type`	Type of the drawn chart. By default it is `"pie"`. It can takes `"pie"` to plot a pie chart with the number of genes for each psychiatric category, `"disease category"` for visualizing a barplot with the total and specific number of genes for each psychiatric disorder, `"evidence index"` for a barplot showing for each psychiatric disorder the number of gene-disease associations according to the Evidence index and `"gene"` for visualizing a barplot with the total and specific number of diseases associated to each gene.
`...`	(Check NOTE section) Passed to inner functions for different plots.
`verbose`	By default `FALSE`. Change it to `TRUE` to get a on-time log from the function.

Value

A plot for a `DataGeNET.Psy` in terms of the panther-class.

Note

The "Evidence Index" is gotten from PsyGeNET. For more information about it and its calculation, pease visit `psygenet.org`. Argument `...` can be filled with specific argument depending on the type of plot:

Type	Argument	Color	Description
gene	cuiBarColor	Purple	Determines the color of the bar for diseases
	diseaseCategoryBarColor	Yellow	Determines the color of the bar for psychiatric categories
disease category	uniqueGenesBarColor	Orange	Determines the color of the bar for unique genes for a disease categ
	totalGenesBarColor	Blue	Determines the color of the bar for total genes for a disease category

getUMLs *Query PsyGeNET for given gene(s) and generates an* DataGeNET.Psy

Description

Given the name of one or multiple gene and retrives their information from PsyGeNET and creates an object of type DataGeNET.Psy.

Usage

```
getUMLs(word, database = "ALL")
```

Arguments

word	Disese to convert to UMLS using PsyGeNET database.
database	Name of the database that will be queried. It can take the values 'psycur15' to use data validated by experts for first release of PsyGeNET; 'psycur16' to use data validated by experts for second release of PsyGeNET; or 'ALL' to use both databases. Default 'ALL'.

Value

The corresponding UMLs for the input disease/s

Examples

```
umls <- getUMLs( word = "depressive", database = "ALL" )
```

jaccardEstimation *Calculation of the Jaccard Index between ideseases*

Description

This function is able to calculate the Jacard Index between: 1. muliple disases, 2. a set og genes and multiple diseases, 3. a set of genes and multiple main psychiatric disorders and 4. multiple diseases and multiple main psychiatric disorders.

Usage

```
jaccardEstimation(pDisease, sDisease, database = "ALL", nboot = 100,
  ncores = 1, verbose = FALSE)
```

Arguments

pDisease	vector of diseases, vector of genes, vector of main psychiatric disorder.
sDisease	vector of diseases, vector of genes, vector of main psychiatric disorder. Only necessary when comparing genes vs. diseases, genes vs. main psychiatric disorders or diseases vs. main psychiatric disorders. To compare multiple diseases only use pDisease.
database	Name of the database that will be queried. It can take the values 'psycur15' to use data validated by experts for first release of PsyGeNET; 'psycur16' to use data validated by experts for second release of PsyGeNET; or 'ALL' to use both databases.
nboot	Number of iterations sued to compute the pvalue associted to the calculated Jaccard Index (default 100).
ncores	Number of cores used to calculate the pvalue associated to the computed Jaccard Index (default 1).
verbose	By default FALSE. Change it to TRUE to get a on-time log from the function.

Details

Warning: The main psychiatric disorders are understood as a single set of genes composed by the genes of all the diseases that the main psychiatric disorder cotains.

Value

An object of class JaccardIndexPsy with the computed calculation of the JaccardIndex.

Examples

```
ji <- jaccardEstimation( c( "COMT", "CLOCK", "DRD3" ), "umls:C0005586", "ALL" )
```

JaccardIndexPsy-class *Class JaccardIndexPsy*

Description

Class JaccardIndexPsy is theresult of the process to look for a Jaccard Index between muliple diseases in psygenet2r package.

Slots

nit Number of iterations to calculate the estimated Jaccard index

type Slot to save type of query (disease-disease, gene-disease)

table data.frame containing the result table of Jaccard indexes

i1 [internal use] vector with names of first component

i2 [internal use] vector with names of second component

See Also

psygenetGene, psygenetDisease, JaccardIndexPsy-methods

Examples

```
ji <- jaccardEstimation( c( "COMT", "CLOCK", "DRD3" ), "umls:C0005586", "ALL" )
```

`ndisease` *Getter from* `DataGeNET.Psy`.

Description

Obtain the number of unique diseases in a `DataGeNET.Psy`.

Usage

```
ndisease(object)

## S4 method for signature 'DataGeNET.Psy'
ndisease(object)
```

Arguments

`object`	Object of class `DataGeNET.Psy`.

Value

The number of unique diseases

Methods (by class)

- `DataGeNET.Psy`: Get number of diseases

Examples

```
data(qr)
ndisease(qr)
```

ngene *Getter from* DataGeNET.Psy.

Description

Obtain the number of unique genes in a DataGeNET.Psy.

Usage

```
ngene(object)

## S4 method for signature 'DataGeNET.Psy'
ngene(object)
```

Arguments

object	Object of class DataGeNET.Psy.

Value

The number of unique genes

The number of unique genes

Methods (by class)

- DataGeNET.Psy: Get number of genes

Examples

```
data(qr)
ngene(qr)
```

pantherGraphic *Query PsyGeNET for given genes and creates a representation in base of their panther-class*

Description

Given a vector of genes of interest (or using a DataGeNET.Psy object), this function creates a representation of a the panther-class these genes belongs to.

Usage

```
pantherGraphic(x, database = "ALL", evidenceIndex, verbose = FALSE)
```

Arguments

x	Vector of genes of interest of DataGeNET.Psy resulting of psyegnetDisease.
database	Name of the database that will be queried. It can take the values 'psycur15' to use data validated by experts for first release of PsyGeNET; 'psycur16' to use data validated by experts for second release of PsyGeNET; or 'ALL' to use both databases. Default 'ALL'.
evidenceIndex	threshold to take into account a gene in the analysis
verbose	By default FALSE. Change it to TRUE to get a on-time log from the function.

Value

A plot for a DataGeNET.Psy in terms of the panther-class.

Examples

```
d.alch <- pantherGraphic( c( "COMT", "CLOCK", "DRD3" ), "ALL" )
```

---

plot,DataGeNET.Psy,ANY-method

Plots the content of a DataGeNET.Psy *object*

Description

This functions llows to create a variety of plots for DataGeNEt.Psy and JaccardIndexPsy objects.

Usage

```
## S4 method for signature 'DataGeNET.Psy,ANY'
plot(x, y,
  layout = igraph::layout.fruchterman.reingold, type = "GDA network",
  verbose = FALSE, ...)
```

Arguments

x	Object of class DataGeNET.Psy
y	NOT USED
layout	Function to design the location of the different nodes. By default layout.fruchterman.reingold from igraph is used.
type	Type of the drawn chart. By default it is "GDA network" but it also can be "GDCA network", "GDCA heatmap", "GDA heatmap" and "publications". The first two are network representations of the second two. While the last one draws a barplot with the number of PMIDs between genes and diseases.
verbose	By default FALSE. If set to TRUE information on the drawing process will be shown.
...	(Check NOTE section) Passed to inner functions for different plots.

Value

A plot for DataGeNET.Psy.

Note

The "Evidence Index" is gotten from PsyGeNET. For more information about it and its calculation, pease visit psygenet.org. Argument ... can be filled with specific argument depending on the type of plot:

Type	Argument	Color	Description
GDA network	geneColor	Yellow	Determines the color of the gene nodes
	diseaseColor	Blue	Determines the color of the disease nodes
GDA heatmap	highColor	Blue	Determines the color of the heatmap for the highest value
	lowColor	White	Determines the color of the heatmap for the lowest value
GDCA network	ei0color	Yellow	Determines the color for those associations with evidence index 0
	eiAmbiguitcolor	Grey	Determines the color for those associations with evidence index greater tha
	ei1color	Blue	Determines the color for those associations with evidence index 1
GDCA heatmap	AUDcolor	#FF3C32	
	BDcolor	#FFC698	
	DEPcolor	#9BE75E	
	SCHZcolor	#1F6024	
	CUDcolor	#5AB69C	
	SIDEPcolor	#50B8D6	
	CanUDcolor	#5467C3	
	SYPSYcolor	#A654C3	
	geneColor	Orange	

Examples

```
data(qr)
plot(qr) # for all-disease plot
plot(qr, type = 'GDCA network') # for MPI plot
```

---

plot,JaccardIndexPsy,ANY-method

Plot the content of a JaccardIndexPsy *object.*

Description

This functions llows to create a variety of plots for DataGeNEt.Psy and JaccardIndexPsy objects.

Usage

```
## S4 method for signature 'JaccardIndexPsy,ANY'
plot(x, y, cutOff, zero.remove = TRUE,
  noTitle = FALSE, lowColor = "white", highColor = "mediumorchid4",
  verbose = FALSE, ...)
```

Arguments

x	Object of class JaccardIndexPsy.
y	NOT USED
cutOff	Number to filter the shown results.
zero.remove	By deffault TRUE. It removes those relations with a Jaccard Index of 0.
noTitle	By default FALSE. If set to true no title will be added to the plot.
lowColor	By default "white". It can be changed to any other color.
highColor	By default "mediumorchid4". It can be changed to any other color.
verbose	By default FALSE. If set to TRUE information on the drawing process will be shown.
...	NOT USED

Value

A plot for JaccardIndexPsy.

Examples

```
## Not run:
#Being x an JaccardIndexPsy
qr <- plot(x)

## End(Not run)
```

---

psygenet2r *psygenet2r: Package to query PsyGeNET database and to perform comorbidity studies*

Description

psygenet2r has two categories of functions: querying functions and analysis and plotting functions.

querying functions

The functions to retrieve data from PsyGeNET are psygenetDisease and psygenetGene. There are some other support functions like psygenetGeneSentences.

analysis and plotting functions

The functions extract and extractSentences allows to retrieve the row data obtained from on-line resources. The functions plot and pantherGraphic draws a variety of charts to illustrate the obtained results. The function enrichedPD was built to perform enrichment studies on PsyGeNET data. Finally the function jaccardEstimation computes a Jaccard Index from a given input on PsyGeNET data.

psygenetDisease *Query PsyGeNET for given disease(s) and generates an* `DataGeNET.Psy`

Description

Given the name of one or multiple diseases and retrives their information from PsyGeNET and creates an object of type `DataGeNET.Psy`.

Usage

```
psygenetDisease(disease, database = "ALL", evidenceIndex = c(">", 0),
  verbose = FALSE, warnings = TRUE)
```

Arguments

`disease`	Name or vector of names (that can be both code or uml) to specific diseases from PsyGeNET. The diseases non existing in PsyGeNET will be removed from the output.
`database`	Name of the database that will be queried. It can take the values `'psycur15'` to use data validated by experts for first release of PsyGeNET; `'psycur16'` to use data validated by experts for second release of PsyGeNET; or `'ALL'` to use both databases. Default `'ALL'`.
`evidenceIndex`	A vector with two elements: 1) character with greather `'>'` or with lower `'<'` meaing greather or equal and lower or equal; 2) the evidence index cut-off to be compared. By default: `c('>', 0)`.
`verbose`	By default `FALSE`. Change it to `TRUE` to get a on-time log from the function.
`warnings`	By default `TRUE`. Change it to `FALSE` to don't see the warnings.

Value

An object of class `DataGeNET.Psy`

Note

The "Evidence Index" is gotten from PsyGeNET. For more information about it and its calculation, pease visit `psygenet.org`.

Examples

```
d.sch <- psygenetDisease( "schizophrenia", "ALL" )
```

psygenetDiseaseSentences *Query PsyGeNET for given disease(s) and extract the pmids sentences that report a gene-disease asssociation.*

Description

Given a disease or a disease list, retrives the pmids and sentences for each gene-disease association from PsyGeNET and creates an object of type DataGeNET.Psy.

Usage

```
psygenetDiseaseSentences(diseaseList, database = "ALL", verbose = FALSE)
```

Arguments

diseaseList	Name or vector of names (that can be both code or uml) to specific diseases from PsyGeNET. The diseases non existing in PsyGeNET will be removed from the output.
database	Name of the database that will be queried. It can take the values 'psycur15' to use data validated by experts for first release of PsyGeNET; 'psycur16' to use data validated by experts for second release of PsyGeNET; or 'ALL' to use both databases. Default 'ALL'.
verbose	By default FALSE. Change it to TRUE to get a on-time log from the function.

Value

An object of class DataGeNET.Psy

Examples

```
diseasesOfInterest <- c( "Bipolar Disorder","Depressive Disorder, Major" )
psyDisSen <- psygenetDiseaseSentences( diseaseList = diseasesOfInterest,
                                       database = "ALL" )
```

psygenetGene *Query PsyGeNET for given gene(s) and generates an* DataGeNET.Psy

Description

Given the name of one or multiple gene and retrives their information from PsyGeNET and creates an object of type DataGeNET.Psy.

Usage

```
psygenetGene(gene, database = "ALL", evidenceIndex = c(">", 0),
  verbose = FALSE, warnings = TRUE)
```

Arguments

gene	Name or vector of names (that can be both code or symbol) to specific genes from PsyGeNET. The genes non existing in PsyGeNET will be removed from the output.
database	Name of the database that will be queried. It can take the values 'psycur15' to use data validated by experts for first release of PsyGeNET; 'psycur16' to use data validated by experts for second release of PsyGeNET; or 'ALL' to use both databases. Default 'ALL'.
evidenceIndex	A vector with two elements: 1) character with greather '>' or with lower '<' meaing greather or equal and lower or equal; 2) the evidence index cut-off to be compared. By default: c('>', 0).
verbose	By default FALSE. Change it to TRUE to get a on-time log from the function.
warnings	By default TRUE. Change it to FALSE to not see the warnings.

Value

An object of class DataGeNET.Psy

Note

The "Evidence Index" is gotten from PsyGeNET. For more information about it and its calculation, pease visit psygenet.org.

Examples

```
d.alch <- psygenetGene( "ALDH2", "ALL" )
```

---

psygenetGeneSentences *Query PsyGeNET for given gene(s) and extract the pmids sentences that report a gene-disease asssociation.*

Description

Given a gene or a gene list, retrives the pmids and sentences for each gene-disease association from PsyGeNET and creates an object of type DataGeNET.Psy.

Usage

```
psygenetGeneSentences(geneList, database = "ALL", verbose = FALSE)
```

Arguments

geneList	Name or vector of names (that can be both code or symbol) to specific genes from PsyGeNET. The genes non existing in PsyGeNET will be removed from the output.
database	Name of the database that will be queried. It can take the values 'psycur15' to use data validated by experts for first release of PsyGeNET; 'psycur16' to use data validated by experts for second release of PsyGeNET; or 'ALL' to use both databases. Default 'ALL'.
verbose	By default FALSE. Change it to TRUE to get a on-time log from the function.

Value

An object of class DataGeNET.Psy

Examples

```
genesOfInterest <- c("PECR", "ADH1C", "CAST", "ERAP1", "PPP2R2B",
                     "ESR1", "GATA4", "CDH13")
psyGeneSen <- psygenetGeneSentences( geneList = genesOfInterest,
                                     database = "ALL")
```

---

qr DataGeNET.Psy *obtained from quering PsyGeNET for gene '4852'.*

Description

A dataset obtained from PsyGeNET after being queried with psygenetGene usig the term '4852' on "ALL" database.

Usage

```
data("qr")
```

Format

The format is: Formal class 'DataGeNET.Psy' [package "psygenet2r"] with 5 slots .. type : chr "gene" .. search : chr "" .. database: chr "ALL" .. term : chr "4852" .. qresult :'data.frame'

Value

A DataGeNET.Psy object.

Source

http://psygenet.org

Examples

```
ngene(qr)
ndisease(qr)
```

---

topAnatEnrichment *Enrichment of a user's input (genes) in anatomical terms (TopAnat).*

Description

Test the enrichment of a given gene list on Psychiatric Disorders from PsyGeNET.

Usage

```
topAnatEnrichment(gene, datatype = c("rna_seq", "affymetrix", "est",
  "in_situ"), statistic = "fisher", cutOff = 1, verbose = FALSE,
  warnings = FALSE)
```

Arguments

gene	Name or vector of names (that can be both code or uml) to specific genes from PsyGeNET.
datatype	It can take the values 'rna_seq', 'affymetrix', "est" or "in situ". Default c("rna_seq","affymetrix","est","in_situ").
statistic	By default it is "fisher". But it can be changed to "ks", "t", "globaltest", "sum" or "ks.ties". All from runTest.
cutOff	Default 1.
verbose	By default FALSE. Change it to TRUE to get a on-time log from the function.
warnings	By default TRUE. Change it to FALSE to not see the warnings.

Value

A data.frame with the enrichment results

Examples

```
## Not run:
topAnatEnrichment(gene=c("ADCY2", "AKAP13", "ANK3"))

## End(Not run)
```

`universe` *Vector with gene universe for Jaccard Index*

Description

Vector with all the gene names from DisGeNET database (http://www.disgenet.org) used as gene universe for Jaccard Index computation.

Usage

```
universe
```

Format

An object of class `character` of length 8947.

Details

data("universe", package = "psygenet2r")

Value

A `character` vector.

Source

http://www.disgenet.org

Examples

```
length(universe)
universe[1:10]
```

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