

Package ‘psygenet2r’

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

Version 1.9.1

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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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 their output. The constructors of this class are the functions psygenetGene and psygenetDisease.

Slots

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

search Character containing 'single' of 'list'. It is used to perform 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 Character with the term(s) to search into the database(s).

result data.frame with the obtained result

See Also

psygenetGene, psygenetDisease, DataGeNET.Psy-methods

enrichedPD	<i>Enrichment of a user's input (genes) in PsyGeNET's diseases.</i>
------------	---

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 enrichment at each Psychiatric Disorder

Examples

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

extract	<i>Raw data from DataGeNET.Psy and JaccardIndexPsy.</i>
---------	---

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 JaccardIndexPsy

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 evidences from a DataGeNET.Psy object.*

Description

Internally, PsyGeNET uses a series of collected evidences from public literature. The internal table of a DataGeNET.Psy object can contains this information. The method extractSentences allows to extrat this information.

Usage

```
extractSentences(object, disorder, verbose)

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

Arguments

object	Object of class DataGeNET.Psy.
disorder	A disorder to check if any evidence exists.
verbose	If set to TRUE informative messages are show.

Value

A data frame showing the evidence.

Methods (by class)

- DataGeNET.Psy: Get sentences or evidences

Examples

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

geneAttrPlot

Plotting 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 (default "pie") It can takes "pie",
 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.

getUMLs

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

Description

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

Usage

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

Arguments

word	Disease 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 the result of the process to look for a Jaccard Index between multiple 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	<i>Query PsyGeNET for given genes and creates a representation in base of their panther-class</i>
----------------	---

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", score, 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'.
score	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	<i>Plots the content of a DataGeNET.Psy or JaccardIndexPsy object.</i>
-------------------------------	--

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 = igrph::layout.fruchterman.reingold, type = "disease",
     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 "disease" but it also can be "individual disease", "disease", "disease class", "barplot", "heatmapGenes" or "heatmap".
verbose	By default FALSE. If set to TRUE information on the drawing process will be shown.
...	Passed to inner functions for different plots.

Value

A plot for DataGeNET.Psy.

Examples

```
data(qr)
plot(qr) # for all-disease plot
plot(qr, type = 'disease class') # 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, 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.
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	<i>psygenet2r: Package to query PsyGeNET database and to perform comorbidity studies</i>
------------	--

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	<i>Query PsyGeNET for given disease(s) and generates an DataGeNET.Psy</i>
-----------------	---

Description

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

Usage

```
psygenetDisease(disease, database = "ALL", score = 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'.
score	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`

Examples

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

psygenetDiseaseSentences

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

Description

Given a disease or a disease list, retrieves 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 retrieves their information from PsyGeNET and creates an object of type DataGeNET.Psy.

Usage

```
psygenetGene(gene, database = "ALL", score = 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'.
score	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

Examples

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

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

Description

Given a gene or a gene list, retrieves 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	<i>DataGeNET.Psy obtained from quering PsyGeNET for gene '4852'.</i>
----	--

Description

A dataset obtained from PsyGeNET after being queried with `psygenetGene` using 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	<i>Enrichment of a user's input (genes) in anatomical terms (TopAnat).</i>
-------------------	--

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	Default 'fisher'.
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)
```

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