# Package 'psygenet2r'

September 19, 2024

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

**Version** 1.37.1

**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)

**License** MIT + file LICENSE

**LazyData** true

**Imports** stringr, RCurl, igraph, ggplot2, reshape2, grid, parallel, biomaRt, BgeeDB, topGO, Biobase, labeling, GO.db

**Suggests** testthat, knitr, rmarkdown, BiocStyle

**NeedsCompilation** no

**VignetteBuilder** knitr

**biocViews** Software, BiomedicalInformatics, Genetics, Infrastructure, DataImport, DataRepresentation

**RoxygenNote** 7.1.1

**PackageStatus** Deprecated

**git_url** https://git.bioconductor.org/packages/psygenet2r

**git_branch** devel

**git_last_commit** 20b9d14

**git_last_commit_date** 2024-08-12

**Repository** Bioconductor 3.20

**Date/Publication** 2024-09-18

**Author** Alba Gutierrez-Sacristan [aut, cre],
Carles Hernandez-Ferrer [aut],
Jaun R. Gonzalez [aut],
Laura I. Furlong [aut]

**Maintainer** Alba Gutierrez-Sacristan <a.gutierrez.sacristan@gmail.com>

# 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 Psy-GeNET.

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

`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 ca |
| | totalGenesBarColor | Blue | Determines the color of the bar for total genes for a disease cate |

---

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 associed 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 greate |
| | 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)
```

## 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]
```

# Index