Package 'Autoseed'

April 24, 2020

Type Package

Title Retrieve Disease-Related Genes from Public Sources

Version 0.1.0

Description For researchers to quickly and comprehensively acquire disease genes, so as to understand the mechanism of disease,
we developed this program to acquire disease-related genes.
The data is integrated from three public databases. The three databases are 'eDGAR', 'DrugBank' and 'MalaCards'. The 'eDGAR' is a comprehensive database, containing data on the relationship between disease and genes.
'DrugBank' contains information on 13443 drugs and 5157 targets. 'MalaCards' integrates human disease information, including disease-related genes.

Depends R (>= 3.5.0)

LazyData TRUE

License GPL (>= 3)

Encoding UTF-8

RoxygenNote 7.1.0

NeedsCompilation no

Author Jiawei Wu [aut, cre],
Xu Li [aut]

Maintainer Jiawei Wu <jared_wood@163.com>

Repository CRAN

Date/Publication 2020-04-24 09:40:02 UTC

R topics documented:

AutoSeed *Get disease-related genes from eDGAR, DrugBank and MalaCards*

Description

Get disease-related genes from eDGAR, DrugBank and MalaCards

Usage

```
AutoSeed(search)
```

Arguments

search   Name of the disease

Value

result$edgar: Containing Disease Name, OMIM ID and Genesymbol (Data comes from the eDGAR)
result$malacards: Containing genes related to the disease (Data comes from the MalaCards) result$drugbank: Containing genes related to the disease (Data comes from the DrugBank)

Examples

```
result = AutoSeed("diabetes")
```

---

drugbank *Relationship between gene and disease*

Description

The data was collected in the drugbank. We got 27728 relationships between various disease and their related genes.

Usage

```
data("drugbank")
```

Format

A data frame with 27728 observations on the following 2 variables.

Details

There are two columns in the data. The first column is genes and the second column is diseases.

Source

<https://www.drugbank.ca/>

Examples

```
data(drugbank)
```

---

drugbank_disease_gene   *Get disease-related genes from DrugBank.*

Description

Get disease-related genes from DrugBank.

Usage

```
drugbank_disease_gene(search)
```

Arguments

search   Name of the disease, character

Value

The genes related to the disease, list

Examples

```
result = drugbank_disease_gene("diabetes")
```

---

edgar   *Relationship between the gene and disease in edgar*

Description

The function "edgar_disease_gene()" will generate the relationship between gene and disease depend on this dataset.

Usage

```
data("edgar")
```

Format

A data frame with 1038340 observations on the following 2 variables.

Details

We got a total of 1038340 diseases and genes. There are two columns in the data. The first column is genes and the second column is diseases.

Source

<http://edgar.biocomp.unibo.it/gene_disease_db/>

Examples

```
data(edgar)
```

---

edgar_disease_gene   *Get disease-related genes from eDGAR*

Description

Get disease-related genes from eDGAR

Usage

```
edgar_disease_gene(disease)
```

Arguments

disease   Name of the disease, character

Value

a vector containing genesymbol related to the disease

Examples

```
result = edgar_disease_gene("diabetes")
```

---

mala	*The relationship between gene and disease*

Description

The data was collected in the Malacards. We got 241306 relationships between various disease and their related genes.

Usage

```
data("mala")
```

Format

A data frame with 241306 observations on the following 2 variables.

Details

We got a total of 241306 diseases and genes. There are two columns in the data. The first column is disease and the second column is gene.

Source

<https://doi.org/10.1093/nar/gkw1012>

Examples

```
data(mala)
```

---

malacards_disease_gene

Get disease-related genes from MalaCards

Description

Get disease-related genes from MalaCards

Usage

```
malacards_disease_gene(disease)
```

Arguments

disease   Name of the disease

Value

The genes related to the disease, character vector

Examples

```
result = malacards_disease_gene("diabetes")
```

Index