Package ‘GeneBook’

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**Type** Package

**Title** Multi-Types Gene ID Converting/Annotating

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**Description** An implementation of the advanced gene
search in R. This package has basic annotation information. Also, it contains a relative intact gene database which was obtained from the Human Gene Database <https://www.genecards.org>. It allows users to search gene symbol or alias and convert gene interested to the consistent gene symbols. It also provides users with gene WIKI introduction.

**NeedsCompilation** no

**Depends** R (>= 3.5.0)

**Imports** dplyr, stringr, svDialogs, repmis

**License** GPL (>= 3.0)

**LazyData** true

**RoxygenNote** 6.1.1

**Repository** CRAN

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**R topics documented:**

- GeneBook-package
- dir.choose
- f.dir.create
Description

An implementation of the advanced gene search in R. This package has basic annotation information. Also, it contains a relative intact gene database which was obtained from the Human Gene Database <https://www.genecards.org>. It allows users to search gene symbol or alias and convert gene interested to the consistent gene symbols. It also provides users with gene WIKI introduction.

Details

GeneBook package applies to the strings of genes. It can convert gene ID and its alias to a consistent symbol and provide information about how accurate the conversion is. Furthermore, it can tell detailed information about genes. This package relies on our database which includes data from GeneCards Human Gene Database.

GeneCard_main: The main function to export converted genes and genes description after import a file including genes interested

GeneCard_ID_Convert: Convert genes to consistent symbols

GeneCard_Symbol_Details: Function to get the detailed information of gene

Author(s)

Li Xu, Zhang Wen, Siyan Chen, Hans Bibiko, Will Lowe

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**dir.choose**

*Function to choose directory for both Mac users*

**Description**

This function replaces function choose.dir() which allows the user to choose directory. No arguments needs.

**Usage**

```r
dir.choose()
```

**Value**

value returning path of directory chosen by users

**Note**

Function dir.choose() is derived from the work of others

**Author(s)**

Hans Bibiko

**References**

https://grokbase.com/t/r/r-sig-mac/12bxhv5xcz/equivalent-of-choose-dir

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**f.dir.create**

*Create Output Path for a Folder*

**Description**

Function to create output path. Users will be asked to choose directory and input the name of a folder. No arguments needs.

**Usage**

```r
f.dir.create()
```

**Value**

value returning list of path of directory and name of folder
**genecard_description_summary**

*Gene Description*

**Description**

A dataset containing the consistent gene symbol, type and description

**Usage**

*genecard_description_summary*

**Format**

A dataframe contains 59,918 observations and 7 columns

**Source**

Human Gene Database

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**genecard_id**

*Gene ID*

**Description**

This dataset contains the gene ID and subnames of almost 745936 genes

**Usage**

*genecard_id*

**Format**

A dataframe containing 2 columns and 745,936 observations

**Source**

Human Gene Database
### Description

Function for transferring a single gene or multiple genes to the consistent gene symbols.

### Usage

GeneCard_ID_Convert(x)

### Arguments

- x: An R string. Gene symbol or aliases for the gene

### Details

The gene conversion is based on the GeneCards Human Gene Database

### Value

Value return is a matrix including Previous ID, Symbol and Label. The label tells how accuracy the conversion is

### Examples

#### One Gene ID Convert

```r
x = "AD2"
GeneCard_ID_Convert(x)
```

#### Multiple Gene ID Convert

```r
test_symbol = c("ADAMTS7", "CDKN2BAS", "SH2B3", "SLC22A3", "LPAL2", "LPA", "LDLR", "SMARCA4", "PHACTR1", "ZC3HC1", "ABO", "WDR12", "SORT1", "TCF21", "RASD1", "PEMT", "RAI1", "PPAP2B")
as.matrix(test_symbol)->test_symbol

mat_id_convert = c()
for(i in 1:nrow(test_symbol)) {
    GeneCard_ID_Convert(test_symbol[i])->out
    mat_id_convert=rbind(mat_id_convert,out)
}
```
```r
cbind(test_symbol, mat_id_convert) -> test_results
colnames(test_results) <- c("previous_ID", "Symbol", "Label")
head(test_results)
```

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**GeneCard_main**

*MAIN FUNCTION FOR THE PACKAGE for Mac Users*

**Description**

It allows users to choose the file which includes a column of genes interested and create a folder for output. File can be CSV or RDA. This function will export two tables of the converted gene symbols and gene description. No arguments needs

**Usage**

GeneCard_main()

**Details**

This function depends on the function of choose.dir() and f.dir.creat()

**Value**

Value returning is a folder with path and name assigned by users. Two TXT files are under the folder including a file of converted genes and a file of genes description

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**genecard_miss**

*missing gene*

**Description**

A dataset containing the missing gene ID of almost 170 genes

**Usage**

genecard_miss

**Format**

A dataframe containing 168 observation
GeneCard_Symbol_Details

GET DETAILS OF GENE SYMBOLS

Description
Function to get the detailed information of the gene interested

Usage
GeneCard_Symbol_Details(x)

Arguments
x
R string of converted gene by function GeneCard_ID_Convert

Details
This function works only for the genes with consistent symbols. Please use function GeneCard_ID_Convert first and then apply function GeneCard_Symbol_Details to get the detailed information of the gene.

Value
Value return is a dataframe with 7 columns describing the properties of genes

Examples
## One Gene Details
x = "TRBVI4"
GeneCard_Symbol_Details(x)

get_os

Get Information about Operating System

Description
Generic function tells R operating system information. No argument needs

Usage
get_os()

Value
value returning is a string providing the Information about users' Operating System
Note

Function get_os() is derived from the work of others

Author(s)

Will Lowe

References

http://conjugateprior.org/2015/06/identifying-the-os-from-r/

Examples

get_os()
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