

# Package ‘GeneBook’

August 1, 2019

**Type** Package

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

**Version** 1.0

**Date** 2019-07-28

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

**Maintainer** Siyan Chen <siyanc123@gmail.com>

**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

**Date/Publication** 2019-08-01 13:30:05 UTC

## R topics documented:

GeneBook-package . . . . .	2
dir.choose . . . . .	3
f.dir.create . . . . .	3

genecard_description_summary . . . . .	4
genecard_id . . . . .	4
GeneCard_ID_Convert . . . . .	5
GeneCard_main . . . . .	6
genecard_miss . . . . .	6
GeneCard_Symbol_Details . . . . .	7
get_os . . . . .	7
<b>Index</b>	<b>9</b>

---

GeneBook-package      *Multi-Types Gene ID Converting/Annotating*

---

## 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. fThis 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

Maintainer: Siyan Chen <[siyanc123@gmail.com](mailto:siyanc123@gmail.com)>

---

dir.choose	<i>Function to choose directory for both Mac users</i>
------------	--

---

**Description**

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

**Usage**

```
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>

---

f.dir.create	<i>Create Output Path for a Folder</i>
--------------	--

---

**Description**

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

**Usage**

```
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

---

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

---

GeneCard\_ID\_Convert    *GENE ID CONVERT*

---

### 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
x = "AD2"
GeneCard_ID_Convert(x)

## Multiple Gene ID Convert

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)
}
```

```
cbind(test_symbol, mat_id_convert)->test_results
colnames(test_results)<-c("previous_ID", "Symbol", "Label")
head(test_results)
```

---

GeneCard_main	<i>MAIN FUNCTION FOR THE PACKAGE for Mac Users</i>
---------------	--

---

### 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

---

genecard_miss	<i>missing gene</i>
---------------	---------------------

---

### 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 = "TRBV14"
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()
```

# Index

## \*Topic **datasets**

genecard\_description\_summary, [4](#)

genecard\_id, [4](#)

genecard\_miss, [6](#)

## \*Topic **package**

GeneBook-package, [2](#)

dir.choose, [3](#)

f.dir.create, [3](#)

GeneBook (GeneBook-package), [2](#)

GeneBook-package, [2](#)

genecard\_description\_summary, [4](#)

genecard\_id, [4](#)

GeneCard\_ID\_Convert, [5](#)

GeneCard\_main, [6](#)

genecard\_miss, [6](#)

GeneCard\_Symbol\_Details, [7](#)

get\_os, [7](#)