

Package ‘gson’

August 9, 2022

Title Base Class and Methods for 'gson' Format

Version 0.0.7

Description Proposes a new file format ('gson') for storing gene set and related information, and provides read, write and other utilities to process this file format.

Imports jsonlite, methods, rlang, stats, tidyr, utils

ByteCompile true

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Encoding UTF-8

RoxygenNote 7.2.1

NeedsCompilation no

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Repository CRAN

Date/Publication 2022-08-09 08:00:08 UTC

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gson *construct a 'GSON' object*

Description

construct a 'GSON' object

Usage

```
gson(  
  gsid2gene,  
  gsid2name = NULL,  
  gene2name = NULL,  
  species = NULL,  
  gsname = NULL,  
  version = NULL,  
  accessed_date = NULL,  
  keytype = NULL,  
  info = NULL  
)
```

Arguments

gsid2gene	A data frame with first column of gene set IDs and second column of genes
gsid2name	A data frame with first column of gene set IDs and second column of gene set names
gene2name	A data frame with first column of genes and second column of gene symbols
species	Which species of the genes belongs to
gsname	Name of the gene set (e.g., GO, KEGG, etc.)
version	version of the gene set
accessed_date	date to obtain the gene set data
keytype	keytype of genes
info	extra information

Value

A 'GSON' instance

Examples

```
wpfile <- system.file('extdata', "wikipathways-20220310-gmt-Homo_sapiens.gmt", package='gson')  
x <- read.gmt.wp(wpfile)  
gsid2gene <- data.frame(gsid=x$wpid, gene=x$gene)  
gsid2name <- unique(data.frame(gsid=x$wpid, name=x$name))  
species <- unique(x$species)  
version <- unique(x$version)  
gson(gsid2gene=gsid2gene, gsid2name=gsid2name, species=species, version=version)
```

GSON-class	<i>Class "GSON" This class represents gene set information.</i>
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Description

Class "GSON" This class represents gene set information.

Slots

gsid2gene data.frame with two columns of 'gsid' and 'gene'
 gsid2name data.frame with two columns of 'gsid' and 'name'
 gene2name data.frame with two columns of 'gene' and 'name'
 species species of the annotation
 gsname gene set name, e.g., GO, KEGG
 version version of the gene set
 accessed_date time to obtain the gene set data
 keytype keytype of genes
 info extra information

Author(s)

Guangchuang Yu <https://yulab-smu.top>

read.gmt	<i>read.gmt</i>
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Description

parse gmt file to a data.frame

Usage

```
read.gmt(gmtfile)
read.gmt.wp(gmtfile, output = "data.frame")
```

Arguments

gmtfile	gmt file
output	one of 'data.frame' or 'GSON'

Value

data.frame

Author(s)

Guangchuang Yu

read.gson	<i>read and write gson file</i>
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Description

read and write gson file

Usage`read.gson(file)``write.gson(x, file = "")`**Arguments**

file	A gson file
x	A GSON instance

Value

A GSON instance

Examples

```
wpfile <- system.file('extdata', "wikipathways-20220310-gmt-Homo_sapiens.gmt", package='gson')
x <- read.gmt.wp(wpfile, output = "GSON")
f = tempfile(fileext = '.gson')
write.gson(x, f)
read.gson(f)
```

show	<i>show method</i>
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Description

show method for GSON instance

Usage`show(object)`**Arguments**

object	A GSON object
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Value

message

Author(s)

Guangchuang Yu <https://yulab-smu.top>

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