

# Package: gson (via r-universe)

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**Title** Base Class and Methods for 'gson' Format

**Version** 0.1.0

**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

**License** Artistic-2.0

**Encoding** UTF-8

**RoxygenNote** 7.2.3

**NeedsCompilation** no

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**Repository** <https://guangchuangyu.r-universe.dev>

**RemoteUrl** <https://github.com/cran/gson>

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## Contents

gson . . . . .	2
GSON-class . . . . .	3
gsonList . . . . .	3
read.gmt . . . . .	4
read.gson . . . . .	4
show . . . . .	5

<b>Index</b>	<b>6</b>
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gson                      *construct a 'GSON' object*

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### 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)
```

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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>

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gsonList	<i>construct a 'GSONList' object</i>
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**Description**

construct a 'GSONList' object

**Usage**

```
gsonList(...)
```

**Arguments**

... input GSON objects

**Value**

A 'GSONList' instance

read.gmt                    *read.gmt*

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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

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read.gson                    *read and write gson file*

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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)
```

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show

*show method*

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**Description**

show method for GSON instance

**Usage**

```
show(object)
```

**Arguments**

object            A GSON object

**Value**

message

**Author(s)**

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

# Index

## \* classes

GSON-class, 3

gson, 2

GSON-class, 3

gsonList, 3

read.gmt, 4

read.gson, 4

show, 5

show, GSON-method (GSON-class), 3

write.gson (read.gson), 4