Package 'gson'

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Title Base Class and Methods for 'gson' Format

Version 0.2.1

Description Provides a lightweight container and exchange format for gene set collections. It stores gene set membership, names, gene identifiers, species, versions, and source metadata, with utilities for reading, writing, validating, and converting gene set data for enrichment analysis and related workflows.

Imports jsonlite, methods, rlang, stats, utils, yulab.utils (>= 0.0.7)

Suggests digest, fs, testthat (>= 3.0.0)

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Contents

as.data.frame.GSON 2
gson 2
GSON-class 3
gsonList 4
read.gmt 4
read.gson 5
show 6
validate_gson 6
[[.GSON 7

Index **8**

as.data.frame.GSON *Coerce GSON to a data frame*

Description

Coerce GSON to a data frame

Usage

```
## S3 method for class 'GSON'
as.data.frame(x, row.names = NULL, optional = FALSE, ...)
```

Arguments

x	A GSON object.
row.names	Unused.
optional	Unused.
...	Unused.

Value

A data frame with gene set-gene memberships and optional names.

gson *construct a 'GSON' object*

Description

construct a 'GSON' object

Usage

```
gson(
  gsid2gene,
  gsid2name = NULL,
  gene2name = NULL,
  schema_version = "1.0",
  species = NULL,
  gsname = NULL,
  version = NULL,
  accessed_date = NULL,
  keytype = NULL,
  urlpattern = 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
schema_version	GSON file schema version
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
urlpattern	URL pattern
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 *Class "GSON" This class represents gene set information.*

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'

schema_version version of the GSON file schema

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

`urlpattern` URL pattern to browse gene set online

`info` extra information

Author(s)

Guangchuang Yu https://yulab-smu.top

`gsonList` *construct a 'GSONList' object*

Description

construct a 'GSONList' object

Usage

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

Arguments

`...`	input GSON objects

Value

A 'GSONList' instance

`read.gmt` *read.gmt*

Description

parse gmt file to a data.frame

write a GSON object to GMT format

Usage

```
read.gmt(gmtfile)

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

write.gmt(x, file = "")
```

Arguments

gmtfile	gmt file
output	one of 'data.frame' or 'GSON'
x	A GSON object
file	output GMT file

Value

data.frame

Author(s)

Guangchuang Yu

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read.gson *read and write gson file*

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 *show method*

Description

show method for GSON instance

Usage

```
show(object)
```

Arguments

object	A GSON object

Value

message

Author(s)

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validate_gson *Validate a GSON object*

Description

validate_gson() checks the core data contract of a GSON gene set collection. It is useful after constructing an object manually or reading one from an external source.

Usage

```
validate_gson(x, error = TRUE)
```

Arguments

x	A GSON object.
error	Logical. If TRUE, throw an error when validation fails. If FALSE, return a character vector of validation messages.

Value

TRUE if the object is valid. If error = FALSE, returns a character vector of validation messages when invalid.

Examples

```
x <- gson(data.frame(gsid = "GS1", gene = "gene1"))
validate_gson(x)
```

`[[.GSON` *Extract genes from a GSON object*

Description

Extract genes from a GSON object

Usage

```
## S3 method for class 'GSON'
x[[i, ...]]
```

Arguments

`x`	A `GSON` object.
`i`	A gene set ID or numeric index.
`...`	Unused.

Value

A character vector of genes.

Index

∗ **classes**
    GSON-class, 3
[[.GSON, 7

as.data.frame.GSON, 2

gson, 2
GSON-class, 3
gsonList, 4

read.gmt, 4
read.gson, 5

show, 6
show,GSON-method *(*GSON-class*)*, 3

validate_gson, 6

write.gmt *(*read.gmt*)*, 4
write.gson *(*read.gson*)*, 5