Package: gson (via r-universe)

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Title Base Class and Methods for 'gson' Format

Version 0.2.0

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, tidyr, utils, yulab.utils (>= 0.0.7)

Suggests digest, fs, testthat (>= 3.0.0)

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Contents

`[[.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.

`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

`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)

Guangchuang Yu `https://yulab-smu.top`

`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)
```

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