Package ‘rWikiPathways’

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downloadPathwayArchive

**Description**

Access the monthly archives of pathway content from WikiPathways.

**Usage**

```r
downloadPathwayArchive(
  date = "current",
  organism = NULL,
  format = c("gpml", "gmt", "svg"),
  destpath = "./"
)
```

**Arguments**

- `date` (optional) The timestamp for a monthly release (e.g., 20171010) or "current" (default) for latest release.
- `organism` (optional) A particular species. See `listOrganisms`.
- `format` (optional) Either gpml (default), gmt or svg.
- `destpath` (optional) Destination path for file to be downloaded to. Default is current working directory.

**Details**

If you do not specify an organism, then an archive file will not be downloaded. Rather, the archive will be opened in a tab in your default browser.

**Value**

Filename of downloaded file or an opened tab in default browser.
findPathwayIdsByLiterature

Find Pathway WPIDs By Literature

Description

Retrieve list of pathway WPIDs containing the query citation.

Usage

findPathwayIdsByLiterature(query = NULL)

Arguments

query The character string to search for, e.g., a PMID, title keyword or author name.

Value

A list of WPIDs

See Also

findPathwaysByLiterature

Examples

{
    findPathwayIdsByLiterature('19649250')
    findPathwayIdsByLiterature('smith')
    findPathwayIdsByLiterature('cancer')
}
findPathwayIDsByOrcid  Find Pathway WPIDs By ORCID

Description
Retrieve list of pathway WPIDs containing the query ORCID

Usage
findPathwayIDsByOrcid(query = NULL)

Arguments
query The character ORCID to search for.

Value
A list of WPIDs

See Also
findPathwaysByOrcid

Examples
def
findPathwayIDsByOrcid('0000-0001-9773-4008')
}

findPathwayIdsByText  Find Pathway WPIDs By Text

Description
Retrieve list of pathway WPIDs containing the query text.

Usage
findPathwayIdsByText(query = NULL, field = NULL)

Arguments
query A character string to search for, e.g., "cancer"
field Optional character string to restrict search to a single field, e.g., title, description, wpid, species, revision, authors, datanodes, annotations, or citedIn.
findPathwayIdsByXref

Value
A list of WPIDs

See Also
findPathwaysByText

Examples

```
{  
  findPathwayIdsByText('cancer')
}
```

findPathwayIdsByXref  Find Pathway WPIDs By Xref

Description
Retrieve list of pathway WPIDs containing the query Xref by identifier and system code.

Usage
```
findPathwayIdsByXref(identifier = NULL, systemCode = NULL)
```

Arguments
- **identifier** (character) The official ID specified by a data source or system
- **systemCode** (character) The BridgeDb code associated with the data source or system, e.g., En (Ensembl), L (Entrez), Ch (HMDB), etc. See column two of https://github.com/bridgedb/datasources/blob/main/datasources.tsv.

Value
A list of WPIDs

See Also
findPathwaysByXref

Examples

```
{  
  findPathwayIdsByXref('ENSG00000100031','En')
}
```
findPathwayNamesByLiterature

Find Pathway Names By Literature

Description
Retrieve list of pathway names containing the query citation.

Usage
findPathwayNamesByLiterature(query = NULL)

Arguments
query The character string to search for, e.g., a PMID, title keyword or author name.

Value
A list of lists

See Also
findPathwaysByLiterature

Examples
{
  findPathwayNamesByLiterature('19649250')
  findPathwayNamesByLiterature('smith')
  findPathwayNamesByLiterature('cancer')
}

findPathwayNamesByOrcid

Find Pathway Names By ORCID

Description
Retrieve list of pathway names containing the query ORCID

Usage
findPathwayNamesByOrcid(query = NULL)

Arguments
query The character ORCID to search for.
findPathwayNamesByText

Find Pathway Names By Text

Description
Retrieve list of pathway names containing the query text.

Usage
findPathwayNamesByText(query = NULL, field = NULL)

Arguments
query A character string to search for, e.g., "cancer"
field Optional character string to restrict search to a single field, e.g., title, description, wpid, species, revision, authors, datanodes, annotations, or citedIn.

Value
A list of pathway names

See Also
findPathwaysByOrcid

Examples
{
findPathwayNamesByOrcid('0000-0001-9773-4008')
}

{
findPathwayNamesByText('cancer')
}
findPathwayNamesByXref

Find Pathway Names By Xref

Description
Retrieve list of pathway names containing the query Xref by identifier and system code.

Usage
findPathwayNamesByXref(identifier = NULL, systemCode = NULL)

Arguments
identifier  (character) The official ID specified by a data source or system
systemCode  (character) The BridgeDb code associated with the data source or system, e.g.,
En (Ensembl), L (Entrez), Ch (HMDB), etc. See column two of https://github.com/bridgedb/datasources/blob/main/datasources.tsv.

Value
A list of lists

See Also
findPathwaysByXref

Examples
{
  findPathwayNamesByXref('ENSG00000100031', 'En')
}

findPathwaysByLiterature

Find Pathways By Literature

Description
Retrieve pathways containing the query citation.

Usage
findPathwaysByLiterature(query = NULL)
Arguments

query  The character string to search for, e.g., a PMID, title keyword, journal abbreviation, year, or author name.

Value

A dataframe of pathway attributes including the matching citations

Examples

{
    findPathwaysByLiterature('15134803')
    findPathwaysByLiterature('Schwartz GL')
    findPathwaysByLiterature('Eur J Pharmacol')
    findPathwaysByLiterature('antihypertensive drug responses')
}

findPathwaysByOrcid  Find Pathways By ORCID

Description

Retrieve pathways containing the query ORCID

Usage

findPathwaysByOrcid(query = NULL)

Arguments

query  The character ORCID to search for.

Value

A dataframe of pathway attributes including the matching ORCIDs

Examples

{
    findPathwaysByOrcid('0000-0001-9773-4008')
}
findPathwaysByText  

Find Pathways By Text

Description
Retrieve pathways matching the query text.

Usage
findPathwaysByText(query = NULL, field = NULL)

Arguments

query  A character string to search for, e.g., "cancer". Case insensitive.
field  Optional character string to restrict search to a single field, e.g., id, name, description, species, revision, authors, datanodes, annotations, or citedIn.

Details
Searches id, name, description, species, revision date, authors, datanode labels, ontology annotations, and citedIn (e.g., PMCIDs).

Value
A dataframe of pathway attributes including the matching attributes

Examples
{  
  findPathwaysByText('cancer')
  findPathwaysByText('cancer','name')
}

findPathwaysByXref  

Find Pathways By Xref

Description
Retrieve pathways containing the query Xref by identifier and system code.

Usage
findPathwaysByXref(identifier = NULL, systemCode = NULL)
findPathwayUrlsByLiterature

Arguments

- **identifier** (character) The official ID specified by a data source or system
- **systemCode** (character) The BridgeDb code associated with the data source or system, e.g., En (Ensembl), L (NCBI gene), H (HGNC), U (UniProt), Wd (Wikidata), Ce (ChEBI), Ik (InChi). See column two of https://github.com/bridgedb/datasources/blob/main/datasources.tsv.

Value

A dataframe of pathway attributes including the matching identifiers

Examples

```r
findPathwaysByXref('ENSG00000100031','En')
```

findPathwayUrlsByLiterature

*Find Pathway URLs By Literature*

Description

Retrieve list of pathway URLs containing the query citation.

Usage

```r
findPathwayUrlsByLiterature(query = NULL)
```

Arguments

- **query** The character string to search for, e.g., a PMID, title keyword or author name.

Value

A list of lists

See Also

findPathwaysByLiterature

Examples

```r
findPathwayUrlsByLiterature('19649250')
findPathwayUrlsByLiterature('smith')
findPathwayUrlsByLiterature('cancer')
```
findPathwayUrlsByOrcid

**Find Pathway URLs By ORCID**

**Description**

Retrieve list of pathway URLs containing the query ORCID

**Usage**

```r
findPathwayUrlsByOrcid(query = NULL)
```

**Arguments**

- **query**
  - The character ORCID to search for.

**Value**

A list of lists

**See Also**

findPathwaysByOrcid

**Examples**

```r
{
  findPathwayUrlsByOrcid('0000-0001-9773-4008')
}
```

---

findPathwayUrlsByText

**Find Pathway URLs By Text**

**Description**

Retrieve list of pathway URLs containing the query text.

**Usage**

```r
findPathwayUrlsByText(query = NULL, field = NULL)
```

**Arguments**

- **query**
  - A character string to search for, e.g., "cancer"
- **field**
  - Optional character string to restrict search to a single field, e.g., title, description, wpid, species, revision, authors, datanodes, annotations, or citedIn.
findPathwayUrlsByXref

Find Pathway URLs By Xref

Description

Retrieve list of pathway URLs containing the query Xref by identifier and system code.

Usage

findPathwayUrlsByXref(identifier = NULL, systemCode = NULL)

Arguments

identifier (character) The official ID specified by a data source or system
systemCode (character) The BridgeDb code associated with the data source or system, e.g., En (Ensembl), L (Entrez), Ch (HMDB), etc. See column two of https://github.com/bridgedb/datasources/blob/main/datasources.tsv

Value

A list of lists

See Also

findPathwaysByXref

Examples

{
  findPathwayUrlsByXref('cancer')
}

{
  findPathwayUrlsByXref('ENSG00000100031','En')
}
**getCounts**

*Get Counts for WikiPathways Stats*

**Description**

Retrieve information about various total counts at WikiPathways.

**Usage**

```r
getCounts()
```

**Value**

A `data.frame` of counts

**Examples**

```r
{
  getCounts()
}
```

---

**getCurationStatus**

*Get Curation Status of a Pathway*

**Description**

Retrieve information about curation status for a specific pathway.

**Usage**

```r
getcurationStatus(pathway)
```

**Arguments**

- `pathway` WikiPathways identifier (WPID) for the pathway, e.g. WP554

**Value**

A `data.frame` of status details

**Examples**

```r
{
  getcurationStatus('WP554')
}
```
getCurationTagNames  
DEPRECATED: Get Curation Tag Names on a Pathway

Description
This function is provided for compatibility with older web services only and will be defunct at the next release.

Usage
getCurationTagNames(pathway)

Arguments
pathway  WikiPathways identifier (WPID) for the pathway to download, e.g. WP4

Value
A list of tag names

getCurationTags  
DEPRECATED: Get Curation Tags on a Pathway

Description
This function is provided for compatibility with older web services only and will be defunct at the next release.

Usage
getcurationTags(pathway)

Arguments
pathway  WikiPathways identifier (WPID) for the pathway to download, e.g. WP4

Value
A list of tag name, display name, revision, text, timestamp and user
getEveryCurationTag  
**DEPRECATED: Get Every Instance of a Curation Tag**

**Description**
This function is provided for compatibility with older web services only and will be defunct at the next release.

**Usage**
getEveryCurationTag(tag)

**Arguments**
tag  
(character) Official name of curation tag, e.g., "Curation:FeaturedPathway"

**Value**
A list of tag name, display name, revision, text, timestamp and user

---

getOntologyTermIds  
*Get Ontology Term IDs by Pathway*

**Description**
Retrieve identifiers of ontology terms for a specific pathway.

**Usage**
getOntologyTermIds(pathway = NULL)

**Arguments**
pathway  
WikiPathways identifier (WPID) for the pathway to download, e.g. WP4

**Value**
A list of term identifiers

**Examples**

```r
{
  getOntologyTermIds('WP554')
}
```
**getOntologyTermNames**  
*Get Ontology Term Names by Pathway*

**Description**
Retrieve names of ontology terms for a specific pathway.

**Usage**
```r
getOntologyTermNames(pathway = NULL)
```

**Arguments**
- **pathway**
  - WikiPathways identifier (WPID) for the pathway to download, e.g. WP4

**Value**
A list of term names

**Examples**
```r
{
  getOntologyTermNames('WP554')
}
```

---

**getOntologyTerms**  
*Get Ontology Terms by Pathway*

**Description**
Retrieve information about ontology terms for a specific pathway.

**Usage**
```r
getOntologyTerms(pathway = NULL)
```

**Arguments**
- **pathway**
  - WikiPathways identifier (WPID) for the pathway, e.g. WP554. If NULL, then ontology term information for all pathways is returned.

**Value**
A `data.frame` pathway id and term information
**getPathway**

**Get Pathway**

**Examples**

```r
{
    getOntologyTerms('WP554')
}
```

**Description**

Retrieve a specific pathway in the GPML format.

**Usage**

```r
gcurrentIndex(pathway, revision = 0)
```

**Arguments**

- **pathway**
  
  WikiPathways identifier (WPID) for the pathway to retrieve, e.g. WP554

- **revision**
  
  <ignored> Only the latest version is available.

**Value**

GPML as string

**Examples**

```r
{
    getPathway('WP554')
}
```

**getPathwayHistory**

**Get Pathway History**

**Description**

View the revision history of a pathway.

**Usage**

```r
gcurrentIndexHistory(pathway = NULL, timestamp = NULL)
```

**Arguments**

- **pathway**
  
  WikiPathways identifier (WPID) for the pathway, e.g. WP554

- **timestamp**
  
  <ignored>
Value

Opens the GitHub history for a pathway

Examples

```r
#getPathwayHistory('WP554')
```

---

**getPathwayIdsByCommunity**

*Get Pathway IDs By Community*

**Description**

Retrieve the list of pathway IDs per community

**Usage**

```r
getPathwayIdsByCommunity(community_tag = NULL)
```

**Arguments**

- `community_tag`: Abbreviated name of community

**Value**

A list of pathway IDs

**Examples**

```r
{  
  getPathwayIdsByCommunity("AOP")
}
```
getPathwayIdsByCurationTag

**DEPRECATED: Get Pathway WPIDs by Curation Tag**

**Description**

This function is provided for compatibility with older web services only and will be defunct at the next release.

**Usage**

`getPathwayIdsByCurationTag(tag)`

**Arguments**

- `tag` *(character)* Official name of curation tag, e.g., "Curation:FeaturedPathway"

**Value**

A list of pathway WPIDs

---

getPathwayIdsByOntologyTerm

**Get Pathway WPIDs by Ontology Term**

**Description**

Retrieve pathway WPIDs for every pathway with a given ontology term.

**Usage**

`getPathwayIdsByOntologyTerm(term = NULL)`

**Arguments**

- `term` *(character)* Official ID of ontology term, e.g., "PW:0000045"

**Value**

A list of pathway WPIDs

**Examples**

```{r}
getPathwayIdsByOntologyTerm('PW:0000045')
```
getPathwayIdsByParentOntologyTerm

*Get Pathway WPIDs by Parent Ontology Term*

**Description**
Retrieve pathway WPIDs for every pathway with a child term of given ontology term

**Usage**
```r
getPathwayIdsByParentOntologyTerm(term = NULL)
```

**Arguments**
- **term** (character) Official name of ontology term, e.g., "signaling pathway"

**Value**
A list of pathway WPIDs

**Examples**
```r
{
  getPathwayIdsByParentOntologyTerm('signaling pathway')
}
```

getPathwayInfo

*Get Pathway Info*

**Description**
Retrieve information for a specific pathway

**Usage**
```r
getPathwayInfo(pathway = NULL)
```

**Arguments**
- **pathway** WikiPathways identifier (WPID) for the pathway to download, e.g. WP554. If NULL, then all pathways are returned.

**Value**
A dataframe of pathway WPID, URL, name, species, revision, authors, description, and citedIn
**getPathwayNamesByCommunity**

*Get Pathway Names By Community*

**Description**
Retrieve the list of pathway names per community

**Usage**
```r
getPathwayNamesByCommunity(community_tag = NULL)
```

**Arguments**
- `community_tag`: Abbreviated name of community

**Value**
A list of pathway names

**Examples**
```r
{  
getPathwayNamesByCommunity('WP554')  
}
```

**getPathwaysByCommunity**

*Get Pathways By Community*

**Description**
Retrieve pathways per community

**Usage**
```r
getPathwaysByCommunity(community_tag = NULL)
```

**Arguments**
- `community_tag`: Abbreviated name of community
**getPathwaysByOntologyTerm**

**Value**

A data.frame of pathway information

**Examples**

```r
{
  getPathwaysByCommunity("AOP")
}
```

---

**getPathwaysByCurationTag**

*DEPRECATED: Get Pathways by Curation Tag*

**Description**

This function is provided for compatibility with older web services only and will be defunct at the next release.

**Usage**

```r
getPathwaysByCurationTag(tag)
```

**Arguments**

- `tag` (character) Official name of curation tag, e.g., "Curation:FeaturedPathway"

**Value**

A list of pathway information, including WPID, url, name, species and revision

---

**getPathwaysByOntologyTerm**

*Get Pathways by Ontology Term*

**Description**

Retrieve pathway information for every pathway with a given ontology term.

**Usage**

```r
getPathwaysByOntologyTerm(term = NULL)
```

**Arguments**

- `term` (character) Official ID of ontology term, e.g., "PW:0000045"
**getPathwaysByParentOntologyTerm**

**Value**

A `data.frame` of pathway information

**Examples**

```r
{  
  getPathwaysByOntologyTerm('PW:0000045')
}
```

---

**getDescription**

Get Pathways by Parent Ontology Term

**Description**

Retrieve pathway information for every pathway with a child term of given ontology term.

**Usage**

```r
ggetPathwaysByParentOntologyTerm(term = NULL)
```

**Arguments**

- `term` (character) Official name of ontology term, e.g., "signaling pathway"

**Value**

A `data.frame` of pathway information

**Examples**

```r
{  
  getPathwaysByParentOntologyTerm('signaling pathway')
}
```
getRecentChanges

Get Recent Changes

Description
Retrieve recently changed pathways at WikiPathways.

Usage
getRecentChanges(timestamp = NULL)

Arguments
timestamp (8 digits, YYYYMMDD) Limit by time, only pathways changed after the given date, e.g., 20180201 for changes since Feb 1st, 2018.

Value
A data.frame of recently changed pathways, including id, name, url, species and revision.

getPathwayUrlsByCommunity

Get Pathway URLs By Community

Description
Retrieve the list of pathway URLs per community

Usage
getPathwayUrlsByCommunity(community_tag = NULL)

Arguments
community_tag Abbreviated name of community

Value
A list of pathway URLs

Examples
{
  getPathwayUrlsByCommunity("AOP")
}


getRecentChangesIds  

Examples

```
{  
    getRecentChanges('20180201')  
}
```

getRecentChangesIds  
Get WPIDs of Recent Changes

Description

Retrieve WPIDs of recently changed pathways at WikiPathways.

Usage

getRecentChangesIds(timestamp)

Arguments

timestamp  
(8 digits, YYYYMMDD) Limit by time, only pathways changed after the given date, e.g., 20180201 for changes since Feb 1st, 2018.

Value

A list of WPIDs

Examples

```
{  
    getRecentChangesIds('20180201')  
}
```

generateRecentChangesNames  
Get Pathway Names of Recent Changes

Description

Retrieve names of recently changed pathways at WikiPathways.

Usage

getRecentChangesNames(timestamp)

Arguments

timestamp  
(8 digits, YYYYMMDD) Limit by time, only pathways changed after the given date, e.g., 20180201 for changes since Feb 1st, 2018.
**getXrefList**

**Value**

A list of pathway names. Note: pathway deletions will be listed as blank names.

**Examples**

```r
{
  getRecentChangesNames('20180201')
}
```

---

**getXrefList**

*Get Xref List*

**Description**

Retrieve the Xref identifiers for a specific pathway in a particular system code

**Usage**

```r
getXrefList(pathway = NULL, systemCode = NULL, compact = FALSE)
```

**Arguments**

- **pathway**
  - WikiPathways identifier (WPID) for the pathway to download, e.g. WP554

- **systemCode**
  - (character) The BridgeDb code associated with the data source or system, e.g., En (Ensembl), L (NCBI gene), H (HGNC), S (UniProt), Wd (Wikidata), Ce (ChEBI), Ik (InChI). See column two of https://github.com/bridgedb/datasources/blob/main/datasources.tsv.

- **compact**
  - (Boolean) Whether to return compact identifiers, like ncbigene:1215. If FALSE (default), then just the identifier is returned, like 1215

**Value**

A list of Xref identifiers

**Examples**

```r
{
  xrefs = getXrefList("WP2338", "L")
}
```
listCommunities

Description
Retrieve the list of communities hosted by WikiPathways

Usage
listCommunities()

Value
A data.frame of community information

Examples
{
  listCommunities()
}

listOrganisms

Description
Retrieve the list of organisms supported by WikiPathways

Usage
listOrganisms()

Value
A list of organisms

Examples
{
  listOrganisms()
}
listPathwayIds  
*List Pathway WPIDs*

**Description**
Retrieve list of pathway WPIDs per species.

**Usage**
```r
listPathwayIds(organism ="")
```

**Arguments**
- `organism` (character, optional) A particular species. See `listOrganisms`. Default is all species.

**Details**
Basically returns a subset of `listPathways` result

**Value**
A list of WPIDs

**See Also**
listPathways

**Examples**
```r
{
  listPathwayIds("Mus musculus")
}
```

---

listPathwayNames  
*List Pathway Names*

**Description**
Retrieve list of pathway names per species.

**Usage**
```r
listPathwayNames(organism ="")
```
Arguments

organism (character, optional) A particular species. See listOrganisms. Default is all species.

Details

Basically returns a subset of listPathways result.

Value

A list of names

See Also

listPathways

Examples

{
  listPathwayNames('Mus musculus')
}

Description

Retrieve list of pathways per species, including WPID, name, species, URL and latest revision number.

Usage

listPathways(organism = "")

Arguments

organism (character, optional) A particular species. See listOrganisms. Default is all species.

Value

A dataframe of pathway information

Examples

{
  listPathways('Mus musculus')
}
listPathwayUrls  

List Pathway URLs

Description
Retrieve list of pathway URLs per species.

Usage
listPathwayUrls(organism = "")

Arguments
organism (character, optional) A particular species. See listOrganisms. Default is all species.

Details
Basically returns a subset of listPathways result

Value
A list of URLs

See Also
listPathways

Examples
{
  listPathwayUrls('Mus musculus')
}

readGMT  

Read GMT File

Description
Reads any generic GMT file to produce a data frame of term-gene associations useful in enrichment analyses and other applications.

Usage
readGMT(file)
Arguments

file Path to GMT file

Details

The returned data frame includes only terms and names. If you want another data frame with terms and names, then see readGMT.

Value

Data frame of term-gene associations

See Also

readGMT

Examples

#readGMT(system.file("extdata","my_gmt_file.gmt", package="rWikiPathways"))
#readGMT("path_to_your_gmt_file.gmt")

---

**Description**

Reads any generic GMT file to produce a data frame of term-name associations useful in enrichment analyses and other applications.

**Usage**

readGMTnames(file)

**Arguments**

file Path to GMT file

**Details**

The returned data frame includes only terms and names. If you want another data frame with terms and genes, then see readGMT.

**Value**

Data frame of term-name associations
readPathwayGMT

Description

Reads a WikiPathways GMT file to produce a data frame of pathway-gene associations useful in enrichment analyses and other applications.

Usage

readPathwayGMT(file)

Arguments

file Path to GMT file

Details

The returned data frame includes pathway name, version, identifier, and organism. The gene content is provided as NCBI Entrez Gene identifiers. The input file can be retrieved by using downloadPathwayArchive(organism="Homo sapiens",format="gmt").

Value

Data frame of pathway-gene associations

References

Adapted from the generic GMT reader provided by clusterProfiler, https://github.com/YuLab-SMU/clusterProfiler/blob/master/R/GMT.R

See Also

downloadPathwayArchive

Examples

#readPathwayGMT(system.file("extdata", "my_gmt_file.gmt", package="rWikiPathways"))
#readPathwayGMT("path_to_your_gmt_file.gmt")
DEPRECATED: Open Swagger docs for WikiPathways API

Description
This function is provided for compatibility with older web services only and will be defunct at the next release.

Usage
```r
wikipathwaysAPI(base.url = .baseUrl)
```

Arguments
- `base.url` (optional) Ignore unless you need to specify a custom domain.

Value
New tab in default browser

DEPRECATED: WikiPathways GET

Description
This function is provided for compatibility with older web services only and will be defunct at the next release.

Usage
```r
wikipathwaysGET(
  operation,
  parameters = NULL,
  format = c("json", "xml", "html", "jpg", "pdf", "dump"),
  base.url = .baseUrl
)
```

Arguments
- `operation` A character string to be converted to the query namespace
- `parameters` A named list of values to be converted to query parameters
- `format` (character) The format of the return, e.g., json (default), xml, html, jpg, pdf, dump
- `base.url` (optional) Ignore unless you need to specify a custom domain.
writeGMT

Write GMT File

Description

 Writes a GMT (Gene Matrix Transposed) file from a data frame.

Usage

writeGMT(df, outfile)

Arguments

df  Data frame with columns ordered as Identifiers, optional Description column and Genes. Identifiers must be first and Genes must be last.

outfile  Path to output GMT file

Details

 The input data frame must include at least two columns: Identifiers (first column) and Genes (last column). The Identifiers will be duplicated to fill the Description column in the output GMT file if none is provided. If more than three columns are provided, then the first n columns will be concatenated with number of columns.

Value

 None

References

Adapted from the GMT writer in MAGeCKFlute, https://github.com/WubingZhang/MAGeCKFlute/blob/master/R/readGMT.R

See Also

readPathwayGMT

Examples

#my.df <- data.frame(id=c("WP1000","WP1000","WP1000","WP1001","WP1001"),
#  description=c("cancer","cancer","cancer","diabetes","diabetes"),
#  gene=c("574413","2167","4690","5781","11184"))
#writeGMT(my.df, "my_gmt_file.gmt")
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