

Package ‘rWikiPathways’

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Type Package

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Suggests testthat, BiocStyle, knitr, rmarkdown

Description Use this package to interface with the WikiPathways API. It provides programmatic access to WikiPathways content in multiple data and image formats, including official monthly release files and convenient GMT read/write functions.

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URL <https://github.com/wikipathways/rwikipathways>

BugReports <https://github.com/wikipathways/rwikipathways/issues>

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`downloadPathwayArchive`*Download Pathway Archive*

Description

Access the monthly archives of pathway content from WikiPathways.

Usage

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

Arguments

<code>date</code>	(optional) The timestamp for a monthly release (e.g., 20171010) or "current" (default) for latest release.
<code>organism</code>	(optional) A particular species. See listOrganisms .
<code>format</code>	(optional) Either gpml (default), gmt or svg.
<code>destpath</code>	(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

See Also

`readPathwayGMT`

Examples

```
downloadPathwayArchive() ## open in browser  
downloadPathwayArchive(format="gmt") ## open in browser  
downloadPathwayArchive(date="20171010", format="svg") ## open in browser  
downloadPathwayArchive(date="20171010", organism="Mus musculus", format="svg") ## download file  
downloadPathwayArchive(organism="Mus musculus") ## download file
```

findPathwayIdsByLiterature

Find Pathway WPIDs By Literature

Description

Retrieve list of pathway WPIDs containing the query citation.

Usage

```
findPathwayIdsByLiterature(query)
```

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')
}
```

findPathwayIdsByText *Find Pathway WPIDs By Text*

Description

Retrieve list of pathway WPIDs containing the query text.

Usage

```
findPathwayIdsByText(query)
```

Arguments

query A character string to search for, e.g., "cancer"

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, systemCode)
```

Arguments

<code>identifier</code>	(character) The official ID specified by a data source or system
<code>systemCode</code>	(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/

Details

Note: there will be multiple listings of the same pathway if the Xref is present mutiple times.

Value

A list of WPIDs

See Also

`findPathwaysByXref`

Examples

```
{  
  findPathwayIdsByXref('ENSG00000232810', 'En')  
}
```

findPathwayNamesByLiterature

Find Pathway Names By Literature

Description

Retrieve list of pathway names containing the query citation.

Usage

```
findPathwayNamesByLiterature(query)
```

Arguments

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

Details

Note: there will be multiple listings of the same pathway name if copies exist for multiple species.

Value

A list of lists

See Also

findPathwaysByLiterature

Examples

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

findPathwayNamesByText

Find Pathway Names By Text

Description

Retrieve list of pathway names containing the query text.

Usage

```
findPathwayNamesByText(query)
```

Arguments

query A character string to search for, e.g., "cancer"

Details

Note: there will be multiple listings of the same pathway name if copies exist for multiple species.

Value

A list of pathway names

See Also

findPathwaysByText

Examples

```
{
  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, systemCode)
```

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/b>

Details

Note: there will be multiple listings of the same pathway if the Xref is present mutiple times.

Value

A list of lists

See Also

findPathwaysByXref

Examples

```
{  
  findPathwayNamesByXref('ENSG00000232810', 'En')  
}
```

findPathwaysByLiterature

Find Pathways By Literature

Description

Retrieve pathways containing the query citation.

Usage

```
findPathwaysByLiterature(query)
```

Arguments

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

Details

The score is from a lucene index search engine, ranging from 0 to 1 with higher scores for better matches. The two literature columns are lists of pubmed ids and titles for the citations matching the query per pathway. The graphId column lists the id for any objects in the GPML pathway model that have been specifically annotated with the matching citations.

Value

A dataframe of pathway attributes in addition to query result score and literature details

Examples

```
{  
  findPathwaysByLiterature('19649250')  
  findPathwaysByLiterature('smith')  
  findPathwaysByLiterature('cancer')  
}
```

findPathwaysByText *Find Pathways By Text*

Description

Retrieve pathways containing the query text.

Usage

```
findPathwaysByText(query)
```

Arguments

query A character string to search for, e.g., "cancer"

Details

The score is from a lucene index search engine, ranging from 0 to 1 with higher scores for better matches.

Value

A dataframe of pathway attributes in addition to query result score

Examples

```
{
  findPathwaysByText('cancer')
}
```

findPathwaysByXref *Find Pathways By Xref*

Description

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

Usage

```
findPathwaysByXref(identifier, systemCode)
```

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/>

Details

Note: there will be multiple listings of the same pathway if the Xref is present mutiple times.

The score is from a lucene index search engine, ranging from 0 to 1 with higher scores for better matches.

Value

A dataframe of pathway attributes in addition to query result score

Examples

```
{
  findPathwaysByXref('ENSG00000232810', 'En')
}
```

findPathwayUrlsByLiterature

Find Pathway URLs By Literature

Description

Retrieve list of pathway URLs containing the query citation.

Usage

```
findPathwayUrlsByLiterature(query)
```

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

```
{
  findPathwayUrlsByLiterature('19649250')
  findPathwayUrlsByLiterature('smith')
  findPathwayUrlsByLiterature('cancer')
}
```

findPathwayUrlsByText *Find Pathway URLs By Text*

Description

Retrieve list of pathway URLs containing the query text.

Usage

```
findPathwayUrlsByText(query)
```

Arguments

query A character string to search for, e.g., "cancer"

Value

A list of urls

See Also

findPathwaysByText

Examples

```
{  
  findPathwayUrlsByText('cancer')  
}
```

findPathwayUrlsByXref *Find Pathway URLs By Xref*

Description

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

Usage

```
findPathwayUrlsByXref(identifier, systemCode)
```

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/>

Details

Note: there will be multiple listings of the same pathway if the Xref is present mutiple times.

Value

A list of lists

See Also

findPathwaysByXref

Examples

```
{
  findPathwayUrIsByXref('ENSG00000232810', 'En')
}
```

getCurationTagNames *Get Curation Tag Names on a Pathway*

Description

Retrieve names of curation tags for a specific pathway.

Usage

```
getCurationTagNames(pathway)
```

Arguments

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

Value

A list of tag names

Examples

```
{
  getCurationTagNames('WP554')
}
```

getCurationTags	<i>Get Curation Tags on a Pathway</i>
-----------------	---------------------------------------

Description

Retrieve information about curation tags for a specific pathway.

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

Examples

```
{
  getCurationTags('WP554')
}
```

getEveryCurationTag	<i>Get Every Instance of a Curation Tag</i>
---------------------	---

Description

Retrieve information about every instance of a given curation tag.

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

Examples

```
{
  getEveryCurationTag('Curation:FeaturedPathway')
}
```

getOntologyTermIds *Get Ontology Term IDs by Pathway*

Description

Retrieve identifiers of ontology terms for a specific pathway.

Usage

```
getOntologyTermIds(pathway)
```

Arguments

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

Value

A list of term identifiers

Examples

```
{
  getOntologyTermIds('WP554')
}
```

getOntologyTermNames *Get Ontology Term Names by Pathway*

Description

Retrieve names of ontology terms for a specific pathway.

Usage

```
getOntologyTermNames(pathway)
```

Arguments

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

Value

A list of term names

Examples

```
{
  getOntologyTermNames('WP554')
}
```

getOntologyTerms	<i>Get Ontology Terms by Pathway</i>
------------------	--------------------------------------

Description

Retrieve information about ontology terms for a specific pathway.

Usage

```
getOntologyTerms(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

Examples

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

getPathway	<i>Get Pathway</i>
------------	--------------------

Description

Retrieve a specific pathway in the GPML format

Usage

```
getPathway(pathway, revision = 0)
```

Arguments

pathway WikiPathways identifier (WPID) for the pathway to download, e.g. WP4
revision (integer, optional) Number to indicate a specific revision to download

Value

GPML

Examples

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

getPathwayHistory *Get Pathway History*

Description

Retrieve the revision history of a pathway.

Usage

```
getPathwayHistory(pathway, timestamp)
```

Arguments

pathway	WikiPathways identifier (WPID) for the pathway to download, e.g. WP4
timestamp	(integer) Limit by time, only history items after the given time, e.g., 20180201 for revisions since Feb 1st, 2018. Any length of timestamp is accepted, upto 14 digits, e.g., 2018, 201802, 20180201063011, etc.

Value

A list of revisions, including user and comment

Examples

```
{
  getPathwayHistory('WP554', 20180201)
}
```

getPathwayIdsByCurationTag
Get Pathway WPIDs by Curation Tag

Description

Retrieve pathway WPIDs for every pathway with a given curation tag.

Usage

```
getPathwayIdsByCurationTag(tag)
```


Arguments

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

Value

A list of pathway WPIDs

Examples

```
{
  getPathwayIdsByCurationTag('Curation:FeaturedPathway')
}
```

getPathwayIdsByOntologyTerm
Get Pathway WPIDs by Ontology Term

Description

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

Usage

```
getPathwayIdsByOntologyTerm(term)
```

Arguments

term (character) Official name of ontology term, e.g., "PW:0000045"

Value

A list of pathway WPIDs

Examples

```
{
  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

```
getPathwayIdsByParentOntologyTerm(term)
```

Arguments

term (character) Official name of ontology term, e.g., "PW:0000045"

Value

A list of pathway WPIDs

Examples

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

getPathwayInfo *Get Pathway Info*

Description

Retrieve information for a specific pathway

Usage

```
getPathwayInfo(pathway)
```

Arguments

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

Value

A dataframe of pathway WPID, URL, name, species and latest revision

Examples

```
{
  getPathwayInfo('WP554')
}
```

`getPathwaysByCurationTag`*Get Pathways by Curation Tag*

Description

Retrieve pathway information for every pathway with a given curation tag.

Usage

```
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

Examples

```
{
  getPathwaysByCurationTag('Curation:FeaturedPathway')
}
```

`getPathwaysByOntologyTerm`*Get Pathways by Ontology Term*

Description

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

Usage

```
getPathwaysByOntologyTerm(term)
```

Arguments

term (character) Official name of ontology term, e.g., "PW:0000045"

Value

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

Examples

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

getPathwaysByParentOntologyTerm

Get Pathways by Parent Ontology Term

Description

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

Usage

```
getPathwaysByParentOntologyTerm(term)
```

Arguments

term (character) Official name of ontology term, e.g., "PW:0000045"

Value

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

Examples

```
{
  getPathwaysByParentOntologyTerm('PW:0000045')
}
```

getRecentChanges *Get Recent Changes*

Description

Retrieve recent changes to pathways at WikiPathways.

Usage

```
getRecentChanges(timestamp)
```

Arguments

timestamp (14 digits, YYYYMMDDhhmmss) Limit by time, only history items after the given time, e.g., 20180201000000 for changes since Feb 1st, 2018.

Value

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

Examples

```
{
  getRecentChanges('20180201000000')
}
```

getRecentChangesIds *Get WPIDs of Recent Changes*

Description

Retrieve WPIDs of recently changed pathways at WikiPathways.

Usage

```
getRecentChangesIds(timestamp)
```

Arguments

timestamp (14 digits, YYYYMMDDhhmmss) Limit by time, only history items after the given time, e.g., 20180201000000 for changes since Feb 1st, 2018.

Value

A list of WPIDs

Examples

```
{
  getRecentChangesIds('20180201000000')
}
```

getRecentChangesNames *Get Pathway Names of Recent Changes*

Description

Retrieve names of recently changed pathways at WikiPathways.

Usage

```
getRecentChangesNames(timestamp)
```

Arguments

timestamp	(14 digits, YYYYMMDDhhmmss) Limit by time, only history items after the given time, e.g., 20180201000000 for changes since Feb 1st, 2018.
-----------	---

Value

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

Examples

```
{
  getRecentChangesNames('20180201000000')
}
```

getXrefList *Get Xref List*

Description

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

Usage

```
getXrefList(pathway, systemCode)
```

Arguments

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

Value

A list of Xrefs identifiers

Examples

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

listOrganisms	<i>List Organisms</i>
---------------	-----------------------

Description

Retrieve the list of organisms supported by WikiPathways

Usage

```
listOrganisms()
```

Value

A list of organisms

Examples

```
{
  listOrganisms()
}
```

listPathwayIds	<i>List Pathway WPIDs</i>
----------------	---------------------------

Description

Retrieve list of pathway WPIDs per species.

Usage

```
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

```
{  
  listPathwayIds('Mus musculus')  
}
```

listPathwayNames	<i>List Pathway Names</i>
------------------	---------------------------

Description

Retrieve list of pathway names per species.

Usage

```
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')  
}
```

listPathways	<i>List Pathways</i>
--------------	----------------------

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	<i>List Pathway URLs</i>
-----------------	--------------------------

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 genes. If you want another data frame with terms and names, then see readGMTnames.

Value

Data frame of term-gene associations

See Also

readGMTnames

Examples

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

readGMTnames	<i>Read GMT File for Names</i>
--------------	--------------------------------

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

See Also

readGMT

Examples

```
readGMTnames(system.file("extdata", "my_gmt_file.gmt", package="rWikiPathways"))
```

readPathwayGMT	<i>Read Pathway GMT File</i>
----------------	------------------------------

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",  
  "wikipathways-20201010-gmt-Homo_sapiens.gmt", package="rWikiPathways"))
```

wikipathwaysAPI

Open Swagger docs for WikiPathways API

Description

Opens swagger docs in default browser for available API calls.

Usage

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

Arguments

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

Value

New tab in default browser

Examples

```
{
  wikipathwaysAPI()
}
```

wikipathwaysGET	<i>WikiPathways GET</i>
-----------------	-------------------------

Description

Constructs the query, makes GET call and processes the result

Usage

```
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.

Value

query result content

Examples

```
{
  wikipathwaysGET('listOrganisms')
}
```

`writeGMT`*Write GMT File*

Description

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

Usage

```
writeGMT(df, outfile)
```

Arguments

<code>df</code>	Data frame with columns ordered as Identifiers, optional Description column and Genes. Identifiers must be first and Genes must be last.
<code>outfile</code>	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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