Package ‘rWikiPathways’

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

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Author Egon Willighagen [aut, cre] (<https://orcid.org/0000-0001-7542-0286>), Alex Pico [aut] (<https://orcid.org/0000-0001-5706-2163>)

Maintainer Egon Willighagen <egon.willighagen@gmail.com>

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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

`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 workding 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

`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 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 spcifically 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/b

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/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

```
{
findPathwayUrlsByXref('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` *Get Curation Tags on a Pathway*

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, timestampe and user

Examples

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

`getEveryCurationTag` *Get Every Instance of a Curation Tag*

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, timestampe 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` *Get Ontology Terms by Pathway*

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, timestampe and user

Examples

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

`getPathway` *Get Pathway*

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/b

Value

A `list` of Xrefs identifiers

Examples

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

`listOrganisms` *List Organisms*

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

```
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` *List Pathway Names*

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` *List Pathways*

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 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` *Read GMT File for Names*

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-namee associations

See Also

readGMT

Examples

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

`readPathwayGMT` *Read Pathway GMT File*

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` *WikiPathways GET*

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

`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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