Package ‘paxtoolsr’

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Type Package

Title PaxtoolsR: Access Pathways from Multiple Databases through BioPAX and Pathway Commons

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SystemRequirements Java (>= 1.6)

License LGPL-3

Description The package provides a set of R functions for interacting with BioPAX OWL files using Paxtools and the querying Pathway Commons (PC) molecular interaction database that are hosted by the Computational Biology Center at Memorial Sloan-Kettering Cancer Center (MSKCC). Pathway Commons databases include: BIND, BioGRID, CORUM, CTD, DIP, DrugBank, HPRD, HumanCyc, IntAct, KEGG, MirTarBase, Panther, PhosphoSitePlus, Reactome, RECON, TRANSFAC.

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LazyData true

biocViews GeneSetEnrichment, GraphAndNetwork, Pathways, Software, SystemsBiology, NetworkEnrichment, Network, Reactome, KEGG

URL https://github.com/BioPAX/paxtoolsr

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addAttributeList  

Description
Add attributes using a list of vectors to an igraph object

Usage
addAttributeList(g, attr, l)

Arguments
- g: an igraph object
- attr: the name of the attribute
- l: the list of vectors

Value
the modified igraph object

convertSifnxIds  

Description
Convert IDs in a SIFNX

Usage
convertSifnxIds(sifnx, participantType = "ProteinReference", idType = "NCBI Gene", mapping = NULL, naRm = TRUE)

Arguments
- sifnx: a SIFNX object (e.g. from the downloadPc2 function)
- participantType: the type of participant on which the conversion will occur. Important because not all ID types apply to all entities and otherwise those entities would be labeled as missing an ID.
- idType: an ID type for conversion (not used if mapping parameter used)
- mapping: a two column data.frame with columns mapping$PARTICIPANT (old IDs to convert from) and mapping$ID (new IDs to convert to)
- naRm: remove edges where NA's were introduced due to failed conversions

Value
a SIFNX list with nodes and edges. Only edges will have converted IDs
**convertToDF**

**convertSifToSpia**  
*Convert SIF Interaction Types to SPIA types*

**Description**

Convert SIF Interaction Types to SPIA types

**Usage**

```r
convertSifToSpia(edges)
```

**Arguments**

- `edges`  
a data.frame of interactions; must have INTERACTION_TYPE column

**Value**

the edges data.frame with the converted interaction types

---

**convertToDF**  
*Convert Results from readSifnx to data.frame*

**Description**

Convert Results from readSifnx to data.frame

**Usage**

```r
convertToDF(lst)
```

**Arguments**

- `lst`  
a list returned from readSifnx

**Value**

a list entries converted to data.frame
**convertToDT**  
*Convert Results from readSifnx to data.table*

**Description**  
Convert Results from readSifnx to data.table

**Usage**  
convertToDT(lst)

**Arguments**  
- **lst**: a list returned from readSifnx

**Details**  
The SIFNX format is an evolving format. Older datasets may not have all the columns this function expects. In these cases, the columns will be added with all NULL entries.

**Value**  
a list entries converted to data.table

---

**downloadFile**  
*Check Cache and Download File*

**Description**  
Check Cache and Download File

**Usage**  
downloadFile(baseUrl, fileName, destDir = NULL, cacheEnv = "PAXTOOLSR_CACHE", verbose = FALSE)

**Arguments**  
- **baseUrl**: a string, entire download URL except filename
- **fileName**: a string, the filename of file to be downloaded
- **destDir**: a string, the path where a file should be saved
- **cacheEnv**: a string, the environment variable that points to the specific cache
- **verbose**: show debugging information

**Details**  
Description of file formats: http://www.pathwaycommons.org/pc2/formats
Value

a boolean TRUE if the file was downloaded or already exists, FALSE otherwise

See Also

readSif, readBiopax, readSbgn, readSifnx, readGmt

Examples

```r
downloadFile("http://google.com/", fileName="index.html", destDir=tempdir())
```

```
downloadPc2(selectedFileName = NULL, destDir = NULL, returnNames = NULL,
version = "current", verbose = FALSE)
```

Arguments

- `selectedFileName`: a string, a name of a file to skip the interactive selection
- `destDir`: a string, the destination directory for the file to be downloaded (Default: NULL). If NULL, then file will be downloaded to cache directory file.path(Sys.getenv("HOME"), ".paxtoolsRCache")
- `returnNames`: return a vector of names matching the given regular expression
- `version`: a version number for a previous version of Pathway Commons data; versions 3 and above
- `verbose`: a flag to display debugging information (Default: FALSE)

Value

an R object using one of the read* methods provided in this package corresponding to the file downloaded

Examples

```r
## Not run:
downloadPc2()
downloadPc2(returnNames="ext.*sif")
downloadPc2("PathwayCommons.8.inoh.GSEA.hgnc.gmt.gz", verbose=TRUE)
```

## End(Not run)
**downloadSignedPC**

*Download a SIF file containing only signed interactions*

**Description**

Download a SIF file containing only signed interactions

**Usage**

```r
downloadSignedPC(destDir = NULL)
```

**Arguments**

- `destDir` a string, the destination directory for the file to be downloaded (Default: NULL). If NULL, then file will be downloaded to cache directory file.path(Sys.getenv("HOME"), ".paxtoolsRCache")

**Value**

a SIF containing interactions that are considered signed (i.e. interactions causing an increase on decrease in a molecular species)

**Examples**

```r
# downloadSignedPC()
```

---

**extractIds**

*Extract IDs from an Extended SIF*

**Description**

Extract IDs from an Extended SIF

**Usage**

```r
extractIds(nodes, participantType = "ProteinReference", idType = "hgnc symbol")
```

**Arguments**

- `nodes` extended SIF nodes entries as a data.table (from convertToDT)
- `participantType` a vector of types of participants to search; useful to only search protein (ProteinReference) or small molecule (SmallMoleculeReference) related entries.
- `idType` the type of ID to search for; case-insensitive

**Details**

IMPORTANT: Only the first matching ID will be returned. In some cases, multiple IDs will exist.
Value

a named vector of the first matches for the given ID type

Examples

tmp <- readSifnx(system.file("extdata", "test_sifnx.txt", package="paxtoolsr"))
results <- extractIds(tmp$nodes)

---

fetch

Fetch a set of IDs from a BioPAX OWL file

Description

This function will create a subsetted object with specified URIs.

Usage

fetch(inputFile, outputFile = NULL, idList)

Arguments

inputFile: a string of the name of the input BioPAX OWL file
outputFile: a string with the name of the output BioPAX OWL file
idList: a vector of IDs from the BioPAX OWL file

Details

Only entities in the input BioPAX file will be used in the fetch. IDs used must be URIs for the entities of interest. Additional properties such as cross-references for fetched entities will be included in the output.

Value

an XMLInternalDocument representing a BioPAX OWL file

Examples

outFile <- tempfile()
ids <- c("http://identifiers.org/uniprot/P36894",
         "http://identifiers.org/uniprot/Q13873")
results <- fetch(system.file("extdata", "REACT_12034-3.owl", package="paxtoolsr"),
                 outFile, ids)
filterSif

*Keep interactions in SIF network based on certain criteria*

**Description**

Keep interactions in SIF network based on certain criteria

**Usage**

`filterSif(sif, interactionTypes = NULL, dataSources = NULL, ids = NULL, edgelist = NULL)`

**Arguments**

- `sif`: a binary SIF as a data.frame with three columns: "PARTICIPANT_A", "INTERACTION_TYPE", "PARTICIPANT_B"
- `interactionTypes`: a vector of interaction types to be kept (List of interaction types: http://www.pathwaycommons.org/pc2/formats)
- `dataSources`: a vector of data sources to be kept
- `ids`: a vector of IDs to be kept
- `edgelist`: a two-column data.frame where each row is an interaction to be kept. Directionality is ignored (e.g. Edge A B will return interactions A B and B A from SIF)

**Value**

filtered interactions with three columns: "PARTICIPANT_A", "INTERACTION_TYPE", "PARTICIPANT_B". The intersection of multiple filters is returned. The return class is the same as the input: data.frame or data.table

**Examples**

```r
results <- readSif(system.file("extdata", "test_sif.txt", package="paxtoolsr"))
intTypes <- c("controls-state-change-of", "controls-expression-of", "catalysis-precedes")
filteredNetwork <- filterSif(results, intTypes)

tmp <- readSifnx(system.file("extdata", "test_sifnx_250.txt", package = "paxtoolsr"))
results <- filterSif(tmp$edges, dataSources=c("INOH", "KEGG"))
results <- filterSif(tmp$edges, ids=c("CHEBI:17640", "MCM3"))
results <- filterSif(tmp$edges, dataSources=c("IntAct"), ids=c("CHEBI:17640", "MCM3"))

tmp <- readSifnx(system.file("extdata", "test_sifnx_250.txt", package = "paxtoolsr"))
edgelist <- read.table(system.file("extdata", "test_edgelist.txt", package = "paxtoolsr"), sep="\t", header=FALSE, stringsAsFactors=FALSE)
results <- filterSif(tmp$edges, edgelist=edgelist)
```
**getCacheFiles**

List files in cache directory

**Description**
List files in cache directory

**Usage**
getCacheFiles()

**Value**
a vector of the files in the cache directory

**Examples**
getCacheFiles()

---

**getErrorMessage**

Get Error Message for a Pathway Commons Error

**Description**
Get Error Message for a Pathway Commons Error

**Usage**
getErrorMessage(code)

**Arguments**
code a three digit numerical error code

**Value**
an error message for the code

**Examples**
results <- getErrorMessage("452")
getNeighbors

Get the neighbors of a set of IDs in a BioPAX file

Description
This function retrieves a set of neighbors for a set of IDs in a BioPAX file.

Usage
getNeighbors(inputFile, outputFile = NULL, idList)

Arguments
inputFile  a string with the name of the input BioPAX OWL file
outputFile a string with the name of the output BioPAX OWL file
idList     a vector of IDs from the BioPAX OWL file

Details
Only entities in the input BioPAX file will be searched for neighbors. IDs used must be URIs for the entities of interest.

Value
an XMLInternalDocument representing a BioPAX OWL file

Examples
outFile <- tempfile()
results <- getNeighbors(system.file("extdata",
  "raf_map_kinase_cascade_reactome.owl", package="paxtoolsr"),
  outFile,
  c("HTTP://WWW.REACTOME.ORG/BIOPAX/48887#PROTEIN2360_1_9606",
   "HTTP://WWW.REACTOME.ORG/BIOPAX/48887#PROTEIN1631_1_9606"))

getPc
Get Pathway Commons BioPAX elements

Description
This command retrieves full pathway information for a set of elements such as pathway, interaction or physical entity given the RDF IDs.

Usage
getc(uri, format = "BIOPAX", verbose = FALSE)
getPcUrl

Arguments

uri a vector that includes valid/existing BioPAX element’s URI (RDF ID; for utility classes that were “normalized”, such as entity references and controlled vocabularies, it is usually a Identifiers.org URL. Multiple IDs are allowed per query, for example, c("http://identifiers.org/uniprot/Q06609", "http://identifiers.org/uniprot/Q549Z0") See also about MIRIAM and Identifiers.org in details.

format output format (Default: BIOPAX). Valid options can be found using pcFormats

verbose a boolean, display the command used to query Pathway Commons

Details

Get commands only retrieve the BioPAX elements that are directly mapped to the ID. Use the "traverse query to traverse BioPAX graph and obtain child/owner elements.

Information on MIRIAM and Identifiers.org [http://www.pathwaycommons.org/pc2/#miriam](http://www.pathwaycommons.org/pc2/#miriam)

Value

a XMLInternalDocument object

See Also

pcFormats

Examples

uri <- "http://identifiers.org/uniprot/O14503"
#results <- getPc(uri)

uri <- c("http://identifiers.org/uniprot/O14503", "http://identifiers.org/uniprot/Q9P2X7")
#results <- getPc(uri, verbose=TRUE)

getPcUrl

Get base Pathway Commons URL

Description

Get base Pathway Commons URL

Usage

getcUrl()

Details

paxtoolsr will support versions Pathway Commons 5 and later. Old versions of the webservice will not be operational. Users can parse older BioPAX outputs as an alternative.

Value

a string with base Pathway Commons URL
getShortestPathSif

Examples

url <- getPcUrl()

getShortestPathSif

Get the shortest between two IDs (HGNC or CHEBI)

Description

Get the shortest between two IDs (HGNC or CHEBI)

Usage

g etShortestPathSif(sif, idA, idB, mode = c("all", "out", "in"),
weights = NULL, filterFun, ...)

Arguments

sif a SIF network
idA HGNC or CHEBI (CHEBI:XXXXX) ID
idB HGNC or CHEBI (CHEBI:XXXXX) ID
mode see shortest_paths() in igraph
weights see shortest_paths() in igraph
filterFun a function to filter multiple paths of the same length
... additional arguments passed on to filterFun

Value

a data.frame representing a SIF network

getSifInteractionCategories

Get a list of categories of SIF interactions

Description

Get a list of categories of SIF interactions

Usage

g etSifInteractionCategories()

Details

Description of interaction types: http://www.pathwaycommons.org/pc2/formats Categories provided: BetweenProteins, BetweenProteinsOther (often from high-throughput experiments), BetweenProteinSmallMolecule, BetweenSmallMolecules, SignedInteractions
Value

a list of interactions in categories

Examples

sifCat <- getSifInteractionCategories()

sifCat[["BetweenProteins"]]

---

**graphPc**

*Get Pathway Commons BioPAX elements*

Description

This function will retrieve a set of BioPAX elements given a graph query match.

Usage

```r
graphPc(kind, source, target = NULL, direction = NULL, limit = NULL,
format = NULL, datasource = NULL, organism = NULL, verbose = FALSE)
```

Arguments

- **kind**: graph query. Valid options can be found using `pcGraphQueries` See Details for information on graph queries.
- **source**: source object’s URI/ID. Multiple source URIs/IDs are allowed per query, for example `c("http://identifiers.org/uniprot/Q06609", "http://identifiers.org/uniprot/Q549Z0")` See a note about MIRIAM and Identifiers.org in details
- **target**: [Required for PATHSFROMTO graph query] target URI/ID. Multiple target URIs are allowed per query; for example `c("http://identifiers.org/uniprot/Q06609", "http://identifiers.org/uniprot/Q549Z0")` See a note about MIRIAM and Identifiers.org in details
- **direction**: [Optional, for NEIGHBORHOOD and COMMONSTREAM algorithms] - graph search direction. Valid options: `pcDirections`.
- **limit**: graph query search distance limit (default: 1).
- **format**: output format. Valid options: `pcFormats`.
- **datasource**: datasource filter (same as for ‘search’).
- **organism**: organism filter (same as for ‘search’).
- **verbose**: a boolean, display the command used to query Pathway Commons

Value

depending on the the output format a different object may be returned. `pcFormats`

See Also

`pcFormats`, `pcDirections`
idMapping

Examples

source <- "http://identifiers.org/uniprot/O14503"
#results <- graphPc(source=source, kind="neighborhood", format="EXTENDED_BINARY_SIF")

idMapping Map IDs to Primary Uniprot or ChEBI IDs

Description

Unambiguously maps, e.g., HGNC gene symbols, NCBI Gene, RefSeq, ENS*, and secondary UniProt identifiers to the primary UniProt accessions, or - ChEBI and PubChem IDs to primary ChEBI. You can mix different standard ID types in one query.

Usage

idMapping(ids, verbose = FALSE)

Arguments

ids a vector of IDs
verbose a boolean, display the command used to query Pathway Commons

Details

This is a specific id-mapping (not general-purpose) for reference proteins and small molecules; it was first designed for internal use, such as to improve BioPAX data integration and allow for graph queries accept not only URIs but also standard IDs. The mapping tables were derived exclusively from Swiss-Prot (DR fields) and ChEBI data (manually created tables and other mapping types and sources can be added in the future versions if necessary).

Value

a list of where each entry is a HGNC symbol provided and the each value is a primary UniProt or ChEBI ID.

Examples

genes <- c("BRCA2", "TP53")
#results <- idMapping(genes)
integrateBiopax  

Integrate two BioPAX OWL files (DEPRECATED)

Description

This function merges two BioPAX OWL files.

Usage

integrateBiopax(inputFile1, inputFile2, outputFile = NULL)

Arguments

inputFile1  
a string of the name of the input BioPAX OWL file

inputFile2  
a string of the name of the input BioPAX OWL file

outputFile  
a string of the name of the output integrated BioPAX OWL file

Details

This method is deprecated. Use mergeBiopax instead.

Value

an XMLInternalDocument representing a BioPAX OWL file

See Also

mergeBiopax

Examples

outFile <- tempfile()
results <- integrateBiopax(system.file("extdata", "raf_map_kinase_cascade_reactome.owl", package="paxtoolsr"),
                         system.file("extdata", "dna_replication.owl", package="paxtoolsr"),
                         outFile)

loadSifInIgraph  

Load SIF as igraph Network

Description

Load SIF as igraph Network

Usage

loadSifInIgraph(sif, directed = TRUE)
Arguments

sif a binary SIF as a data.frame with three columns: "PARTICIPANT_A", "INTERACTION_TYPE", "PARTICIPANT_B"
directed a boolean weather the returned graph should be directed (DEFAULT: TRUE)

Details

Users are likely to run into issues if the input SIF has factor levels

Value

a directed igraph network with interaction types

Examples

results <- readSif(system.file("extdata", "test_sif.txt", package="paxtoolsr"))
g <- loadSifInIgraph(results)

mapValues

Map values from One Vector to Another

Description

Map values from One Vector to Another

Usage

mapValues(data, oldValue, newValue)

Arguments

data a vector of strings where values will be replaced
oldValue a vector that matches values in the data vector
newValue a vector of new values that will replace the old values

Value

return the vector with the mapped values. If there was no corresponding entry then replace it with an NA.

Examples

data <- c("A", "B", "C", "X", "Y", "Z")
oldValue <- LETTERS[1:20]
newValue <- letters[1:20]
results <- mapValues(data, oldValue, newValue)
mergeBiopax

Merges two BioPAX OWL files

Description

This function merges two BioPAX OWL files

Usage

mergeBiopax(inputFile1, inputFile2, outputFile = NULL)

Arguments

inputFile1 a string of the name of the input BioPAX OWL file
inputFile2 a string of the name of the input BioPAX OWL file
outputFile a string of the name of the output merged BioPAX OWL file (Optional)

Details

Only entities that share IDs will be merged. No additional merging occurs on cross-references. Merging may result in warning messages caused as a result of redundant actions being checked against by the Java library; these messages may be ignored.

Value

an XMLInternalDocument representing a BioPAX OWL file

Examples

outFile <- tempfile()
results <- mergeBiopax(system.file("extdata", "raf_map_kinase_cascade_reactome.owl",
package="paxtoolsr"),
system.file("extdata", "dna_replication.owl",
package="paxtoolsr"),
outFile)

pcDirections

Acceptable Pathway Commons Directions

Description

A simple function to see valid options

Usage

pcDirections()
Details

- BOTHSTREAM where the current entity can either be the source or target of an interaction
- DOWNSTREAM where the current entity can only be the source
- UPSTREAM where the current entity can only be the target

Value

acceptable Pathway Commons directions

Examples

pcDirections()
pcGraphQueries  Acceptable Pathway Commons Graph Queries

Description
A simple function to see valid options

Usage
pcGraphQueries()

Details
- COMMONSTREAM searches common downstream or common upstream of a specified set of entities based on the given directions within the boundaries of a specified length limit
- NEIGHBORHOOD searches the neighborhood of given source set of nodes
- PATHSBETWEEN finds the paths between specific source set of states or entities within the boundaries of a specified length limit
- PATHSFROMTO finds the paths from a specific source set of states or entities to a specific target set of states or entities within the boundaries of a specified length limit

Value
acceptable Pathway Commons graph queries

Examples
pcGraphQueries()

processPcRequest  Process Pathway Commons request in various formats

Description
Process Pathway Commons request in various formats

Usage
processPcRequest(content, format)

Arguments
- content  a string, content to be processed
- format  a string, the type of format

Value
an R object using one of the read* methods provided in this package corresponding to the format
**readBiopax**

*Read BioPAX files as XML documents*

**Description**

Read BioPAX files as XML documents

**Usage**

```r
readBiopax(inputFile)
```

**Arguments**

- `inputFile` an inputFile

**Value**

an XMLInternalDocument

**Examples**

```r
results <- readBiopax(system.file("extdata", "biopax3-short-metabolic-pathway.owl", package="paxtoolsr"))
```

---

**readGmt**

*Read in gene sets from GMT files*

**Description**

This function will read in gene sets in the GMT format into a named list.

**Usage**

```r
readGmt(inputFile)
```

**Arguments**

- `inputFile` an inputFile
Value
a named list where each entry corresponds to a gene set

Examples
results <- readGmt(system.file("extdata", "test_gsea.gmt", package="paxtoolsr"))

---

readSbgn
Read SBGN files as XML documents

Description
Read SBGN files as XML documents

Usage
readSbgn(inputFile)

Arguments
inputFile an inputFile

Value
an XMLInternalDocument

Examples
results <- readSbgn(system.file("extdata", "test_sbgn.xml", package="paxtoolsr"))

---

readSif
Read in a binary SIF file

Description
Read in a binary SIF file

Usage
readSif(inputFile)

Arguments
inputFile an inputFile

Value
a data.frame with the interactions in the binary SIF format
readSifnx

Examples
results <- readSif(system.file("extdata", "test_sif.txt", package="paxtoolsr"))

---

readSifnx  Read in a Extended SIF file

Description
Read in a Extended SIF file

Usage
readSifnx(inputFile, asDT = TRUE)

Arguments
- inputFile: an inputFile
- asDT: TODO

Details
SIFNX files from Pathway Commons commonly come a single file that includes a tab-delimited sections for nodes and another for edges. The sections are separated by an empty lines. These sections must be split before they are read.

Value
a list with nodes and edges entries

Examples
results <- readSifnx(system.file("extdata", "test_sifnx.txt", package="paxtoolsr"))
chebiIds <- lapply(results$nodesUniXref, function(x) { x[which(grepl("CHEBI", x))] })

searchListOfVectors  Search List of Vectors

Description
Search List of Vectors

Usage
searchListOfVectors(q, lst)

Arguments
- q: query vector
- lst: list of vectors to search
Details

Taken from: http://stackoverflow.com/questions/11002391/fast-way-of-getting-index-of-match-in-list

Value

A list of vectors with the same length as the query vector, each list entry will have indices for lst where there was a match with the query vector. Return NA if there were no matches.

Examples

```r
lst <- list(1:3, 3:5, 3:7)
q <- c(3, 5)
results <- searchListOfVectors(q, lst)
names(results) <- q

lst <- list(LETTERS[1:3], LETTERS[3:5], LETTERS[3:7])
q <- c("C", "E")
searchListOfVectors(q, lst)

lst <- list(LETTERS[3], LETTERS[4:6])
q <- "C"
searchListOfVectors(q, lst)

lst <- list(LETTERS[3], LETTERS[4:6])
q <- c("C")
searchListOfVectors(q, lst)

lst <- list(LETTERS[3], LETTERS[4:6])
q <- c("C", "E")
searchListOfVectors(q, lst)

lst <- list(LETTERS[3], LETTERS[4:6])
q <- "Z"
searchListOfVectors(q, lst)
```

searchPc

Search Pathway Commons

Description

This command provides a text search using the Lucene query syntax.

Usage

```r
searchPc(q, page = 0, datasource = NULL, organism = NULL, type = NULL, verbose = FALSE)
```
Arguments

- **q**: a keyword, name, external identifier, or a Lucene query string.
- **page**: an integer giving the search result page number (N\geq0, default: 0)
- **datasource**: a vector that is a filter by data source (use names or URIs of pathway data sources or of any existing Provenance object). If multiple data source values are specified, a union of hits from specified sources is returned. For example, datasource as c("reactome", "pid") returns hits associated with Reactome or PID.
- **organism**: a vector that is an organism filter. The organism can be specified either by official name, e.g. "homo sapiens" or by NCBI taxonomy id, e.g. "9606". Similar to data sources, if multiple organisms are declared a union of all hits from specified organisms is returned. For example organism as c("9606", "10016") returns results for both human and mice. Only humans, "9606" is officially supported.
- **type**: BioPAX class filter. See Details.
- **verbose**: a boolean, display the command used to query Pathway Commons

Details

Indexed fields were selected based on most common searches. Some of these fields are direct BioPAX properties, others are composite relationships. All index fields are (case-sensitive):comment, ecnumber, keyword, name, pathway, term, xrefdb, xrefid, dataSource, and organism. The pathway field maps to all participants of pathways that contain the keyword(s) in any of its text fields. This field is transitive in the sense that participants of all sub-pathways are also returned. Finally, keyword is a transitive aggregate field that includes all searchable keywords of that element and its child elements - e.g. a complex would be returned by a keyword search if one of its members has a match. Keyword is the default field type. All searches can also be filtered by data source and organism. It is also possible to restrict the domain class using the 'type' parameter. This query can be used standalone or to retrieve starting points for graph searches. Search strings are case insensitive unless put inside quotes.

BioPAX classes can be found at [http://www.pathwaycommons.org/pc2/#biopax_types](http://www.pathwaycommons.org/pc2/#biopax_types)

Value

an XMLInternalDocument with results

Examples

```r
query <- "Q06609"
#results <- searchPc(query)

query <- "glycolysis"
#results <- searchPc(query, type="Pathway")
```

Description

Extension on testthat code
Summary of BioPAX file

Usage

```r
skip_on_bioc()
```

Value

A boolean or NULL is returned

---

Split SIFNX entries into individual pathways

**Description**

Splits SIFNX entries into individual pathways

**Usage**

```r
splitSifnxByPathway(edges, parallel = FALSE)
```

**Arguments**

- `edges`: a data.frame with SIF content with the additional column "PATHWAY_NAMES". "PATHWAY_NAMES" should include pathway names delimited with a semicolon: ":;".
- `parallel`: a boolean that will parallelize the process; requires foreach/doSNOW/parallel packages

**Details**

This method can be slow; ~1.5 minutes for 150K+ rows. Has a parallelized method to speed things up.

**Value**

A list of where each entry is a vector of row indicies for a given pathway

---

Summarize a BioPAX file

**Description**

This function provides a summary of BioPAX classes.

**Usage**

```r
summarize(inputFile)
```

**Arguments**

- `inputFile`: a string of the name of the input BioPAX OWL file
summarizeSif

Details

BioPAX classes are defined by the BioPAX specification: [http://www.biopax.org/](http://www.biopax.org/)

Value

list with BioPAX class counts

Examples

```r
summary <- summarize(system.file("extdata", "raf_map_kinase_cascade_reactome.owl", package="paxtoolsr"))
```

summarizeSif  Summarize a SIF Network

Description

Summarize a SIF Network

Usage

```r
summarizeSif(sif)
```

Arguments

- `sif` a binary SIF as a data.frame with three columns: "PARTICIPANT_A", "INTERACTION_TYPE", "PARTICIPANT_B"

Value

a list containing a count of the unique genes in the SIF and counts for the interaction types in the network

Examples

```r
results <- readSif(system.file("extdata", "test_sif.txt", package="paxtoolsr"))
summarizeSif(results)
```
toGSEA

Converts a BioPAX OWL file to a GSEA GMT gene set

Description

This function converts pathway information stored as BioPAX files into the GSEA .gmt format.

Usage

toGSEA(inputFile, outputFile = NULL, database, crossSpeciesCheckFlag)

Arguments

inputFile a string of the name of the input OWL file
outputFile a string of the name of the output file
database a string of the name of the identifier type to be included (e.g. "HGNC Symbol")
crossSpeciesCheckFlag a boolean that ensures participant protein is from same species

Details

The GSEA GMT format is a tab-delimited format where each row represents a gene set. The first column is the gene set name. The second column is a brief description. Other columns for each row contain genes in the gene set; these rows may be of unequal lengths.

Value

see readGmt()

Examples

outFile <- tempfile()
results <- toGSEA(system.file("extdata", "biopax3-short-metabolic-pathway.owl", package="paxtoolsr"),
                   outFile,
                   "uniprot",
                   crossSpeciesCheckFlag=TRUE)

toLevel3

Convert a PSIMI or older BioPAX OWL file to BioPAX Level 3

Description

This file will convert PSIMI or older BioPAX objects to BioPAX Level 3

Usage

toLevel3(inputFile, outputFile = NULL)
Arguments

inputFile a string of the name of the input file
outputFile a string of the name of the output BioPAX OWL file

Value

an XMLInternalDocument representing a BioPAX OWL file

Examples

inputFile <- system.file("extdata", "raf_map_kinase_cascade_reactome.owl", package="paxtoolsr")
outFile <- tempfile()
results <- toLevel3(inputFile, outFile)

topPathways

Retrieve top pathways

Description

This command returns all "top" pathways.

Usage

topPathways(datasource = NULL, organism = NULL, verbose = FALSE)

Arguments

datasource filter by data source (same as for 'search').
organism organism filter (same as for 'search'),
verbose a boolean, display the command used to query Pathway Commons

Details

Pathways that are neither 'controlled' nor 'pathwayComponent' of another process.

Value

a data.frame with the following columns:

• uri URI ID for the pathway
• biopaxClass the type of BioPAX object
• name a human readable name
• dataSource the dataSource for the pathway
• organism an organism identifier
• pathwayURI ID for the pathway

Examples

datasource <- "panther"
#results <- topPathways(datasource=datasource)
toSBGN

Convert a BioPAX OWL file to SBGNML

Description

This function will convert a BioPAX OWL file into the Systems Biology Graphical Notation (SBGN) Markup Language (SBGNML) XML representation.

Usage

toSBGN(inputFile, outputFile = NULL)

Arguments

inputFile a string of the name of the input BioPAX OWL file
outputFile a string of the name of the output SBGNML file

Details

Objects in the SBGNML format are laid out using a Compound Spring Embedder (CoSE) layout.

Value

see readSbgn()

References


Examples

outFile <- tempfile()
results <- toSBGN(system.file("extdata", "biopax3-short-metabolic-pathway.owl", package="paxtoolsr"), outFile)

toSif

Convert a BioPAX OWL file to SIF

Description

Convert a BioPAX OWL file to a binary SIF file

Usage

toSif(inputFile, outputFile = NULL)
**toSifnx**

**Arguments**

- **inputFile** a string of the name of the input BioPAX OWL file
- **outputFile** a string of the name of the output SIF file (Optional)

**Details**

Information on SIF conversion is provided on the Pathway Commons site: [http://www.pathwaycommons.org.pc2/](http://www.pathwaycommons.org.pc2/)

**Value**

see readSif()

**Examples**

```r
outFile <- tempfile()
results <- toSif(system.file("extdata", "raf_map_kinase_cascade_reactome.owl", package="paxtoolsr"), outFile)
```

---

**toSifnx**

Converts BioPAX OWL file to extended binary SIF representation

**Description**

Converts BioPAX OWL file to extended binary SIF representation

**Usage**

`toSifnx(inputFile, outputFile = tempfile())`

**Arguments**

- **inputFile** a string with the name of the input BioPAX OWL file
- **outputFile** a string with the name of the output file for SIFNX information

**Details**

Information on SIF conversion is provided on the Pathway Commons site: [http://www.pathwaycommons.org.pc2/](http://www.pathwaycommons.org.pc2/)

**Value**

see readSifnx()

**Examples**

```r
inputFile <- system.file("extdata", "raf_map_kinase_cascade_reactome.owl", package="paxtoolsr")
results <- toSifnx(inputFile=inputFile)
```
Access Pathway Commons using XPath-type expressions

Description

This command provides XPath-like access to the Pathway Commons.

Usage

traverse(uri, path, verbose = FALSE)

Arguments

uri: a BioPAX element URI - specified similarly to the ’GET’ command above. Multiple IDs are allowed (uri=...&uri=...&uri=...).
path: a BioPAX property path in the form of property1[type1]/property2[type2]; see properties, inverse properties, Paxtools, org.biopax.paxtools.controller.PathAccessor.
verbose: a boolean, display the command used to query Pathway Commons

Details

With traverse users can explicitly state the paths they would like to access. The format of the path query is in the form: [Initial Class][property1][classRestriction(optional)][property2]... A "*" sign after the property instructs path accessor to transitively traverse that property. For example, the following path accessor will traverse through all physical entity components within a complex: "Complex/component*/entityReference/xref:UnificationXref" The following will list display names of all participants of interactions, which are components (pathwayComponent) of a pathway (note: pathwayOrder property, where same or other interactions can be reached, is not considered here): "Pathway/pathwayComponent:Interaction/participant*/displayName" The optional parameter classRestriction allows to restrict/filter the returned property values to a certain subclass of the range of that property. In the first example above, this is used to get only the Unification Xrefs. Path accessors can use all the official BioPAX properties as well as additional derived classes and parameters in paxtools such as inverse parameters and interfaces that represent anonymous union classes in OWL. (See Paxtools documentation for more details).

Value

an XMLInternalDocument with results

References

Paxtools Documentation: http://www.biopax.org/m2site/

Examples

uri <- "http://identifiers.org/uniprot/P38398"
#results <- traverse(uri=uri, path="ProteinReference/organism/displayName")
validate

Validate BioPAX files

Description

This function validates BioPAX files for errors.

Usage

```
validate(inputFile, outputFile = NULL, type = c("xml", "html", "biopax"),
         autoFix = FALSE, onlyErrors = FALSE, maxErrors = NULL,
         notStrict = FALSE)
```

Arguments

- `inputFile`: a string of the name of the input BioPAX OWL file
- `outputFile`: a string of the name of the output file containing validation results
- `type`: a string denoting the type of output: xml (default), html, biopax
- `autoFix`: a boolean that determines if the input file should be fixed automatically. Errors that can be automatically fixed include generating displayName properties from names, inferring organism, and inferring dataSource
- `onlyErrors`: a boolean of whether to only display errors
- `maxErrors`: a integer denoting the number of errors to return
- `notStrict`: a boolean of whether to be strict in validation (default: FALSE)

Details

See the publication by Rodchenkov, et al. for information on the BioPAX validator. See http://biopax.baderlab.org/validator for additional information on validator. See http://biopax.baderlab.org/validator/errorTypes.html for information on error types.

Value

an XMLInternalDocument is returned if type is set to "xml" otherwise the location of the outputfile is returned.

References


Examples

```
outFile <- tempfile()
rawDoc <- validate(system.file("extdata", "raf_map_kinase_cascade.reactome.owl",
                           package="paxtoolsr"), onlyErrors=TRUE)
```
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