

# Package ‘paxtoolsr’

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**Type** Package

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

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**Imports** utils, httr, igraph, plyr, rjson, R.utils, jsonlite, readr

**Depends** R (>= 3.2), rJava (>= 0.9-8), XML

**Suggests** testthat, knitr, BiocStyle, rmarkdown, RColorBrewer, biomaRt, estrogen, affy, hgu95av2, hgu95av2cdf, limma, foreach, doSNOW, parallel, org.Hs.eg.db

**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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---

addAttributeList      *Add attributes using a list of vectors to an igraph object*

---

**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

**Examples**

```
library(igraph)
g <- barabasi.game(20)
g <- set_vertex_attr(g, "name", value=LETTERS[1:20])
g <- addAttributeList(g, "isProt", list(A=TRUE, B=FALSE, C=TRUE, D=TRUE, E=FALSE))
```

---

convertDataFrameListsToVectors

*Convert columns with list in data.frame to vector*

---

**Description**

Convert columns with list in data.frame to vector

**Usage**

```
convertDataFrameListsToVectors(df, delimiter = ";")
```

**Arguments**

|           |   |
|-----------|---|
| df        | a data.frame                            |
| delimiter | a delimiter to concatenate (DEFAULT: ;) |

**Value**

a data.frame without list columns

**Note**

Lists as columns are useful programmatically, but cause issue in writing output to text-based files

**Examples**

```
df <- data.frame(id = 1:2, name = c("Jon", "Mark"),
  children = I(list(c("Mary", "James"), c("Greta", "Sally"))))
df <- convertDataFrameListsToVectors(df)
```

---

 convertIds

*Covert IDs Using org.Hs.eg.db*


---

**Description**

Covert IDs Using org.Hs.eg.db

**Usage**

```
convertIds(ids, from = "UNIPROT", to = "SYMBOL")
```

**Arguments**

|      |                           |
|------|---------------------------|
| ids  | a vector of ids           |
| from | the original ID type      |
| to   | the ID type to convert to |

**Value**

a vector of converted IDs

**Examples**

```
convertIds("TP53", "SYMBOL", "ENTREZID")
```

---

 convertSifToGmt

*Convert SIF to GMT*


---

**Description**

Convert SIF to GMT

**Usage**

```
convertSifToGmt(sif, name = "gmt", returnSmallMolecules = FALSE)
```

**Arguments**

sif                    a data.frame representing a SIF (Simple Interaction Format)  
name                   the name of the gene set  
returnSmallMolecules                   a boolean whether to return genes or small molecules in the gene set

**Value**

a list with one entry being a vector

**Examples**

```
sif <- readSif(system.file("extdata", "test_sif.txt", package="paxtoolsr"))  
gmt <- convertSifToGmt(sif)
```

---

|              |                                      |
|--------------|--------------------------------------|
| downloadFile | <i>Check Cache and Download File</i> |
|--------------|--------------------------------------|

---

**Description**

Check Cache and Download File

**Usage**

```
downloadFile(baseUrl, fileName, destDir = NULL,  
              cacheEnv = "PAXTOOLS_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**

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

---

|             |   |
|-------------|---|
| downloadPc2 | <i>Download Pathway Commons files (uses menu and cache)</i> |
|-------------|---|

---

### Description

Download Pathway Commons files (uses menu and cache)

### Usage

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

### Arguments

|                  |  |
|------------------|--|
| selectedFileName | a string, a name of a file to skip the the interactive selection   |
| destDir          | a string, the destination directory for the file to be downloaded (Default: NULL).<br>If NULL, then file will be downloaded to cache directory file.path(Sys.getenv("HOME"),<br>".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<br>and above. Parameter set as version="8". Available versions " <a href="http://www.pathwaycommons.org/archi">http://www.pathwaycommons.org/archi</a> |
| verbose          | a flag to display debugging information (Default: FALSE)   |
| ...              | additional parameters to send to corresponding read* methods   |

### Value

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

### Examples

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

## End(Not run)
```

---

|                  |  |
|------------------|--|
| downloadSignedPC | <i>Download a SIF file containing only signed interactions</i> |
|------------------|--|

---

**Description**

Download a SIF file containing only signed interactions

**Usage**

```
downloadSignedPC(destDir = NULL, forceCache = FALSE)
```

**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") |
| forceCache | a boolean to force the use of a cached version (DEFAULT: FALSE); the current host of the file (GitHub) does not support the LAST-MODIFIED header   |

**Value**

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

**Examples**

```
# downloadSignedPC()
```

---

|       |  |
|-------|--|
| fetch | <i>Fetch a set of IDs from a BioPAX OWL file</i> |
|-------|--|

---

**Description**

This function will create a subsetting 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, ids = NULL, interactionTypes = NULL, dataSources = NULL,
          interactionPubmedIds = NULL, pathwayNames = NULL, mediatorIds = NULL,
          edgelist = NULL, idsBothParticipants = FALSE,
          edgelistCheckReverse = TRUE, verbose = FALSE)
```

**Arguments**

|                      |   |
|----------------------|---|
| sif                  | a binary SIF as a data.frame with three columns: "PARTICIPANT_A", "INTERACTION_TYPE", "PARTICIPANT_B"   |
| ids                  | a vector of IDs to be kept  |
| interactionTypes     | a vector of interaction types to be kept (List of interaction types: <a href="http://www.pathwaycommons.org/pc">http://www.pathwaycommons.org/pc</a> )                  |
| dataSources          | a vector of data sources to be kept. For Extended SIF.  |
| interactionPubmedIds | a vector of Pubmed IDs to be kept. For Extended SIF.  |
| pathwayNames         | a vector of pathway names to be kept. For Extended SIF.   |
| mediatorIds          | a vector of mediator IDs to be kept. For Extended SIF. Mediator IDs are the full BioPAX objects that were simplified to interaction given in the SIF. For Extended SIF. |
| 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)            |
| idsBothParticipants  | a boolean whether both interaction participants should be in a given interaction when using the ids parameter; TRUE if both (DEFAULT: TRUE)                             |
| edgelistCheckReverse | a boolean whether to check for edges in the reverse order (DEFAULT: TRUE)   |
| verbose              | Show debugging information (DEFAULT: FALSE)   |



**Value**

filtered interactions with three columns: "PARTICIPANT\_A", "INTERACTION\_TYPE", "PARTICIPANT\_B". The intersection of multiple filters is returned.

**Examples**

```
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$edges, ids=c("CHEBI:17640", "MCM3"))
results <- filterSif(tmp$edges, dataSources=c("INOH", "KEGG"))
results <- filterSif(tmp$edges, dataSources=c("IntAct"), ids=c("CHEBI:17640", "MCM3"))
results <- filterSif(tmp$edges, pathwayNames=c("Metabolic pathways"))
results <- filterSif(tmp$edges,
  mediatorIds=c("http://purl.org/pc2/8/MolecularInteraction_1452626895158"))
results <- filterSif(tmp$edges, interactionPubmedId="17654400")
```

```
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 | <i>Get Error Message for a Pathway Commons Error</i> |
|-----------------|--|

---

**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 | <i>Get the neighbors of a set of IDs in a BioPAX file</i> |
|--------------|---|

---

**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**

```
getPc(uri, format = "BIOPAX", verbose = FALSE, ...)
```

**Arguments**

|         |  |
|---------|--|
| uri     | a vector that includes valid/existing BioPAX element's URI (RDF ID; for utility classes that were "normalized", such as entity refereneces and controlled vocabularies, it is usually a Idntifiers.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 <a href="#">pcFormats</a>  |
| verbose | a boolean, display the command used to query Pathway Commons   |
| ...     | additional arguments to read* methods that handle data from 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>

**Value**

a XMLInternalDocument object

**See Also**

[pcFormats](#)

**Examples**

```
uri <- "http://identifiers.org/uniprot/014503"
#results <- getPc(uri)

uri <- c("http://identifiers.org/uniprot/014503", "http://identifiers.org/uniprot/Q9P2X7")
#results <- getPc(uri, verbose=TRUE)
```

---

getPcDatabaseNames      *Get a Pathway Commons Databases*

---

**Description**

Get a Pathway Commons Databases

**Usage**

```
getPcDatabaseNames(version)
```

**Arguments**

version                  PC2 version

**Value**

a names of databases that can be used as part of queries

**Examples**

```
getPcDatabaseNames(version=10)
```

---

getPcUrl                      *Get base Pathway Commons URL*

---

**Description**

Get base Pathway Commons URL

**Usage**

```
getPcUrl()
```

**Details**

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

**Value**

a string with base Pathway Commons URL

**Examples**

```
url <- getPcUrl()
```

---

getShortestPathSif      *Get the shortest between two IDs (HGNC or CHEBI)*

---

**Description**

Get the shortest between two IDs (HGNC or CHEBI)

**Usage**

```
getShortestPathSif(sif, idA, idB, mode = c("all", "out", "in"),  
  weights = NULL, verbose = FALSE, filterFun, ...)
```

**Arguments**

|           |  |
|-----------|--|
| sif       | a SIF network  |
| idA       | HGNC or CHEBI (CHEBI:XXXXX) ID                           |
| idB       | HGNC or CHEBI (CHEBI:XXXXX) ID                           |
| mode      | see <code>shortest_paths()</code> in <code>igraph</code> |
| weights   | see <code>shortest_paths()</code> in <code>igraph</code> |
| verbose   | a boolean whether to show debugging information          |
| filterFun | a function to filter multiple paths of the same length   |
| ...       | additional arguments passed on to <code>filterFun</code> |

**Value**

a data.frame representing a SIF network

**Examples**

```
idA <- "DAP3"  
idB <- "RPS16"  
sif <- readSif(system.file("extdata", "test_sif_shortestPath.txt", package="paxtoolsr"))  
filterFun <- function(vpaths) { idx <- sample(1:length(vpaths), 1); return(vpaths[[idx]] ) }  
m1 <- getShortestPathSif(sif, idA, idB, mode="all", weights=NULL, filterFun=filterFun, verbose=TRUE)
```

---

```
getSifInteractionCategories
```

*Get a list of categories of SIF interactions*

---

### Description

Get a list of categories of SIF interactions

### Usage

```
getSifInteractionCategories()
```

### 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

```
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 <a href="#">pcGraphQueries</a> 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: <a href="#">pcDirections</a> .   |
| limit      | graph query search distance limit (default: 1).  |
| format     | output format. Valid options: <a href="#">pcFormats</a>  |
| 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](#)

**Examples**

```
source <- "http://identifiers.org/uniprot/014503"
#results <- graphPc(source=source, kind="neighborhood", format="TXT")
```

---

|                 |  |
|-----------------|--|
| integrateBiopax | <i>Integrate two BioPAX OWL files (DEPRECATED)</i> |
|-----------------|--|

---

**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)
```



---

|               |   |
|---------------|---|
| mapAttributes | <i>Map Attributes from igraph to Cytoscape JSON</i> |
|---------------|---|

---

**Description**

Map Attributes from igraph to Cytoscape JSON

**Usage**

```
mapAttributes(attr.names, all.attr, i)
```

**Arguments**

|            |                     |
|------------|---------------------|
| attr.names | names of attributes |
| all.attr   | all attributes      |
| i          | index               |

**Value**

attributes

**Note**

From [https://github.com/idekerlab/cy-rest-R/blob/17f748426bb5e48ba4075b9d97318ad582b250da/utility/cytoscape\\_utility.R](https://github.com/idekerlab/cy-rest-R/blob/17f748426bb5e48ba4075b9d97318ad582b250da/utility/cytoscape_utility.R)

---

|           |  |
|-----------|--|
| mapValues | <i>Map values from One Vector to Another</i> |
|-----------|--|

---

**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 | <i>Acceptable Pathway Commons Directions</i> |
|--------------|--|

---

**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()
```

---

|           |   |
|-----------|---|
| pcFormats | <i>Acceptable Pathway Commons Formats</i> |
|-----------|---|

---

**Description**

A simple function to see valid options

**Usage**

```
pcFormats()
```

**Details**

See references.

**Value**

acceptable Pathway Commons formats

**References**

Output Formats Description: <http://www.pathwaycommons.org/pc2/help/formats.html>

**Examples**

```
pcFormats()
```

---

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  |
| ...     | other arguments passed to read* methods for reading different formats |

**Value**

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

**See Also**

[pcFormats](#)

**Examples**

```
fileName <- system.file("extdata", "test_biopax.owl", package="paxtoolsr")
content <- readChar(fileName, file.info(fileName)$size)
results <- processPcRequest(content, "BIOPAX")
```

---

|            |   |
|------------|---|
| readBiopax | <i>Read BioPAX files as XML documents</i> |
|------------|---|

---

**Description**

Read BioPAX files as XML documents

**Usage**

```
readBiopax(inputFile)
```

**Arguments**

inputFile      an inputFile

**Value**

an XMLInternalDocument

**Examples**

```
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

```
readGmt(inputFile, removePrefix = FALSE, returnInfo = FALSE)
```

### Arguments

|              |   |
|--------------|---|
| inputFile    | an inputFile  |
| removePrefix | Pathway Commons genesets are prefixed with a NCBI organism taxonomy number (e.g. 9606 for humans); this is a boolean whether to remove the prefix (default: FALSE)  |
| returnInfo   | a boolean whether to return information on genesets; these results are returned a list of two items: 1) basic GMT results and 2) datasource, organism, and id type information for each gene set (default: FALSE) |

### Value

a named list where each entry corresponds to a gene set or a list described in the returnInfo parameter

### Examples

```
results <- readGmt(system.file("extdata", "test_gsea.gmt", package="paxtoolsr"))
results <- readGmt(system.file("extdata", "test_gsea_1.gmt", package="paxtoolsr"))
results <- readGmt(system.file("extdata", "test_gsea.gmt", package="paxtoolsr"), removePrefix=TRUE)
results <- readGmt(system.file("extdata", "test_gsea.gmt", package="paxtoolsr"), returnInfo=TRUE)
```

---

readPcPathwaysInfo        *Read in Pathway Commons Pathways Information*

---

### Description

Read in Pathway Commons Pathways Information

### Usage

```
readPcPathwaysInfo(inputFile = NULL, version = NULL)
```

### Arguments

|           |   |
|-----------|---|
| inputFile | an inputFile; if NULL then retrieve the current pathways.txt; see details (default: NULL)   |
| version   | a version number for a previous version of Pathway Commons data; versions 3 and above. Parameter set as version="8". Available versions " <a href="http://www.pathwaycommons.org/archi">http://www.pathwaycommons.org/archi</a> |

**Details**

This file is generally found as pathways.txt.gz (e.g. <http://www.pathwaycommons.org/archives/PC2/current/pathways.txt>)

**Value**

a data.frame

**Examples**

```
file <- system.file("extdata", "pathways.txt.gz", package="paxtoolsr")
results <- readPcPathwaysInfo(file, version="8")
```

---

|          |   |
|----------|---|
| readSbgn | <i>Read SBGN files as XML documents</i> |
|----------|---|

---

**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 | <i>Read in a binary SIF file</i> |
|---------|----------------------------------|

---

**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

**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)
```

**Arguments**

inputFile      an inputFile

**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"))
```



---

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

```
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**

```
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>=0, 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, ecnnumber, 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**

```

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

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

```

---

splitSifnxByPathway     *Splits SIFNX entries into individual pathways*

---

**Description**

Splits SIFNX entries into individual pathways

**Usage**

```
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 semi-colon: ";". |
| 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 indices for a given pathway

---

summarize                     *Summarize a BioPAX file*

---

**Description**

This function provides a summary of BioPAX classes.

**Usage**

```
summarize(inputFile)
```

**Arguments**

|           |   |
|-----------|---|
| inputFile | a string of the name of the input BioPAX OWL file |
|-----------|---|

**Details**

BioPAX classes are defined by the BioPAX specification: <http://www.biopax.org/>

**Value**

list with BioPAX class counts

**Examples**

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

---

|              |                                |
|--------------|--------------------------------|
| summarizeSif | <i>Summarize a SIF Network</i> |
|--------------|--------------------------------|

---

**Description**

Summarize a SIF Network

**Usage**

```
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**

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

---

|             |   |
|-------------|---|
| toCytoscape | <i>Convert igraph to Cytoscape JSON</i> |
|-------------|---|

---

**Description**

Convert igraph to Cytoscape JSON

**Usage**

```
toCytoscape(igraphobj)
```

**Arguments**

igraphobj      an igraph object

**Value**

a JSON object

**Note**

From [https://github.com/idekerlab/cy-rest-R/blob/17f748426bb5e48ba4075b9d97318ad582b250da/utility/cytoscape\\_utility.R](https://github.com/idekerlab/cy-rest-R/blob/17f748426bb5e48ba4075b9d97318ad582b250da/utility/cytoscape_utility.R)

**Examples**

```
library(igraph)
g <- barabasi.game(20)
json <- toCytoscape(g)
```

---

|        |  |
|--------|--|
| toGSEA | <i>Converts a BioPAX OWL file to a GSEA GMT gene set</i> |
|--------|--|

---

**Description**

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

**Usage**

```
toGSEA(inputFile, outputFile = NULL, database = "uniprot",
        crossSpeciesCheckFlag = TRUE)
```

**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 | <i>Retrieve top pathways</i> |
|-------------|------------------------------|

---

### Description

This command returns all "top" pathways.

### Usage

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

### Arguments

|            |  |
|------------|--|
| q          | [Optional] a keyword, name, external identifier, or a Lucene query string, like in 'search', but the default is '*' (match all). |
| 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
- pathway URI ID for the pathway

### Examples

```
#results <- topPathways(q="TP53", datasource="panther")
```

---

`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**

<http://www.cs.bilkent.edu.tr/~ivis/layout/cose-animated-demo/cose.html>

**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)
```



**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/>

**Value**

see readSif()

**Examples**

```
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(), idType = "uniprot")
```

**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  
 idType          a string either "hgnc" or "uniprot" (DEFAULT: uniprot, more common)

**Details**

Information on SIF conversion is provided on the Pathway Commons site: <http://www.pathwaycommons.org/pc2/>. Also, this is a Java-based methods, it is best to use full paths.

**Value**

see readSifnx()

**Examples**

```
inputFile <- system.file("extdata", "raf_map_kinase_cascade_reactome.owl", package="paxtoolsr")
results <- toSifnx(inputFile=inputFile)
```

traverse

*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 | <i>Validate BioPAX files</i> |
|----------|------------------------------|

---

## 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

Rodchenkov I, Demir E, Sander C, Bader GD. The BioPAX Validator, <http://www.ncbi.nlm.nih.gov/pubmed/23918249>

## Examples

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

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