Package ‘gep2pep’

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Type Package

Title Creation and Analysis of Pathway Expression Profiles (PEPs)

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Description Pathway Expression Profiles (PEPs) are based on the
expression of pathways (defined as sets of genes) as opposed to
individual genes. This package converts gene expression profiles
to PEPs and performs enrichment analysis of both pathways and
experimental conditions, such as "drug set enrichment analysis"
and "gene2drug" drug discovery analysis respectively.

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gep2pep-package

Description

Pathway Expression Profiles (PEPs) are based on the expression of pathways (or generic gene sets) belonging to a collection, as opposed to individual genes. gep2pep supports the conversion of gene expression profiles (GEPs) to PEPs and performs enrichment analysis of both pathways and conditions.

Details

gep2pep creates a local repository of gene sets, which can also be imported from the MSigDB [1] database. The local repository is in the repo format. When a GEP, defined as a ranked list of genes, is passed to buildPEPs, the stored database of pathways is used to convert the GEP to a PEP and permanently store the latter.

One type of analysis that can be performed on PEPs and that is directly supported by gep2pep is the Drug-Set Enrichment Analysis (DSEA [2]). It finds pathways that are consistently dysregulated by a set of drugs, as opposed to a background of other drugs. Of course PEPs may refer to non-pharmacological conditions (genetic perturbations, disease states, cell types, etc.) for analogous analyses. See CondSEA function.

A complementary approach is that of finding conditions that consistently dysregulate a set of pathways. This is the pathway-based version of the Gene Set Enrichment Analysis (GSEA). As an application example, this approach can be used to find drugs mimicking the dysregulation of a gene by looking for drugs dysregulating pathways involving the gene (this has been published as the gene2drug tool [3]). See PathSEA.
Both DSEA and gene2drug analyses can be performed using preprocessed data from [http://dsea.tigem.it/downloads.php](http://dsea.tigem.it/downloads.php). The data include Connectivity Map [4] GEPs (drug-induced gene expression profiles) converted to PEPs in the form of a gep2pep repository.

Naming conventions:

- **pathway**: any set of gene identifiers (not necessarily representing a molecular pathway).
- **pathway collection**: a set of pathways.
- **pathway database**: a set of pathway collections, like the MSigDB.
- **Gene Expression Profile (GEP)**: a named vector where names are gene identifiers of the same type as those in the pathway database and elements are ranks ranging from 1 to the number of genes.
- **Pathway Expression Profile (PEP)**: a ranked list of pathways, as converted from a GEP according to a pathway collection.
- **condition**: any transcriptomic-modelled biological state (drug treatment, gene knock-out, disease state, cell type, etc.) characterized by an induced GEP and therefore a PEP.
- **gep2pep repository**: a pathway database and possibly a related database of PEPs as created by the gep2pep package. It is implemented in repo format.

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**References**


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### addSingleGeneSets

Adding a single-gene psuedo-sets.

**Description**

This function can be used to add single-gene (as opposed to pathway) -based collections. Sets including a single gene don’t need to go through normal Kolmogorov-Smirnov statistic computation and are treated differently for performance.

**Usage**

```
addSingleGeneSets(rp, genes, organism = “Homo Sapiens")
```
Arguments

rp A repository created by `createRepository`.

genes a character vector containing the gene names. For each of them a single-gene `GeneSet` will be created.

organism Character vector used to annotate the created sets. "Homo Sapiens" by default.

Details

Enrichment Scores and p-values for sets including a single gene are computed with dedicated (fast) routines. Although a statistic based on a single gene is not efficient per se, it is useful to have data in the same format as pathway-based profiles. `buildPEPs` internally calls single gene dedicated routines whenever a gene set collection is tagged (see repo function tag) with "SGE" ("Single Gene Expression"), which is done automatically by `addSingleGeneSets`. In that case, the `min_size` parameter is ignored.

Value

Nothing, used for side effects.

See Also

`buildPEPs`

Examples

```r
db <- loadSamplePWS()
repo_path <- file.path(tempdir(), "gep2pepTemp")

rp <- createRepository(repo_path, db)

## The following will create PEPs in 2 separate files
geps <- loadSampleGEP()
addSingleGeneSets(rp, rownames(geps))

unlink(repo_path, TRUE)
```

---

## as.CategorizedCollection

**Converts GeneSetCollection objects to CategorizedCollection objects.**

**Description**

Converts GeneSetCollection objects to CategorizedCollection objects.

**Usage**

```r
as.CategorizedCollection(GScollection, category = "uncategorized",
subCategory = "uncategorized")
```
as.CategorizedCollection

Arguments

GScollection  An object of class GeneSetCollection.
category      The name of the category that all the gene sets will be assigned to (see details).
subCategory   The name of the subcategory that all the gene sets will be assigned to (see details).

Details

This function sets the CollectionType for each set in the collection to CategorizedCollection. If GScollection contains BroadCollection gene sets, their fields category and subcategory will be used. Otherwise the category and subcategory fields will be used.

Value

A CategorizedCollection object

Examples

## Not run:
## To run this example, first obtain the MSigDB database in XML format (see
## http://software.broadinstitute.org/gsea/downloads.jsp). It is
## assumed that the database is locally available as the file
## "msigdb_v6.0.xml".

The \code{importMSigDB.xml} function is just a shortcut to the following:

db <- getBroadSets("msigdb_v6.1.xml")
db <- as.CategorizedCollection(db)

## The database is now in an acceptable format to create a local
## repository using createRepository

## End(Not run)

## A small sample of the MSigDB as imported by importMSigDB.xml is
## included in gep2pep. The following creates (and deletes) a
## gep2pep repository.

db_sample <- loadSamplePWS()

## The function \code{as.CategorizedCollection} can also be used to
## create arbitrary gene set collections specifying the categories
## and subcategories once for all the sets:

library(GSEABase)
mysets <- as.CategorizedCollection(
  GeneSetCollection(
    list(GeneSet(c("g1", "g2"), setName="set1"),
         GeneSet(c("g3", "g4"), setName="set2"))
  ),
  category="mycategory",
  subCategory="mysubcategory"
newCollection <- GeneSetCollection(c(db_sample, mysets))
## The created repository will include both the sample gene sets 
## and the two sets just created:
repo_path <- file.path(tempdir(), "gep2pepTemp")
rp <- createRepository(repo_path, newCollection)
## removing temporary repository
unlink(repo_path, TRUE)

---

**buildPEPs**

*Build PEPs from GEPs and stores them in the repository.*

**Description**

Given a matrix of ranked lists of genes (GEPs) and a gep2pep repository, converts GEPs to PEPs and stores the latter in the repository.

**Usage**

```r
buildPEPs(rp, geps, min_size = 3, max_size = 500, parallel = FALSE,
collections = "all", replace_existing = FALSE, donotstore = FALSE,
progress_bar = TRUE, rawmode_id = NULL,
rawmode_outdir = file.path(rp$root(), "raw"))
```

**Arguments**

- **rp**
  A repository created by `createRepository`.

- **geps**
  A matrix of ranks where each row corresponds to a gene and each column to a condition. Each column must include all ranks from 1 to the number of rows. Row and column names must be defined. Row names will be matched against gene identifiers in the pathways collections, and unrecognized gene names will not be used.

- **min_size**
  An integer representing the minimum number of genes that must be included in a set before the KS statistic is computed. Smaller gene sets will get ES=NA and p=NA. Default is 3. Ignored for SGE mode (see `addSingleGeneSets`).

- **max_size**
  An integer representing the maximum number of genes that must be included in a set before the KS statistic is computed. Larger gene sets will get ES=NA and p=NA. Default is 500.

- **parallel**
  If TRUE, gene sets will be processed in parallel. Requires a parallel backend.

- **collections**
  A subset of the collection names returned by `getCollections`. If set to "all" (default), all the collections in rp will be used.

- **replace_existing**
  What to do if PEPs, identified by column names of geps are already present in the repository. If set to TRUE, they will be replaced, otherwise they will be skipped and only PEPs of new conditions will be computed and added. Either ways, will throw a warning.
buildPEPs

**donotstore**  Just compute and return the pathway-based profiles without storing them in the repository. The repository is still required to load pathway data, however it will not be modified.

**progress_bar**  If set to TRUE (default) will show a progress bar updated after conversion of each column of geps.

**rawmode_id**  An integer to be appended to files produced in raw mode (see details). If set to NULL (default), raw mode is turned off.

**rawmode_outdir**  A character vector specifying the destination path for files produced in raw mode (by the default it is ROOT/raw, where ROOT is the root of the repository). Ignored if rawmode_id is NULL.

**Details**

By default, output is written to the repository as new items named using the collection name. However, it is possible to avoid the repository and write the output to regular files turning 'raw mode' on through the rawmode_id and rawmode_outdir parameters. This is particularly useful when dealing with very large corpora of GEPs, and conversions are split into independent jobs submitted to a scheduler. At the end, the data will need to be reconstructed and put into the repository using importFromRawMode in order to perform CondSEA or PathSEA analysis.

**Value**

Nothing. The computed PEPs will be available in the repository.

**See Also**

buildPEPs

**Examples**

db <- loadSamplePWS()
repo_path <- file.path(tempdir(), "gep2pepTemp")

rp <- createRepository(repo_path, db)
## Repo root created.
## Repo created.
## [15:45:06] Storing pathway data for collection: c3_TFT
## [15:45:06] Storing pathway data for collection: c3_MIR
## [15:45:06] Storing pathway data for collection: c4_CGN

rp
## ID    Dims      Size
## c3_TFT_sets 10 18.16 kB
## c3_MIR_sets 10 17.25 kB
## c4_CGN_sets 10 6.9 kB

## Loading sample gene expression profiles
geps <- loadSampleGEP()

geps[1:3,1:3]
## (+)_chelidonine (+)_isoprenaline (+/_)_catechin
## AKT3  88  117  417
## MED6  357  410  34
## NR2E3 383  121  453
CategorizedCollection

Constructor method for objects of class CategorizedCollection.

Description

See CategorizedCollection-class.

Usage

CategorizedCollection(category = "uncategorized",
                      subCategory = "uncategorized")

Arguments

category A character defining the main category that the gene set belongs to.
subCategory A character defining the secondary category that the gene set belongs to.

Value

An object of class CategorizedCollection.

Examples

library(GSEABase)
gs1 <- GeneSet(setName="set1", setIdentifier="101")
collectionType(gs1) <- CategorizedCollection()
CategorizedCollection-class

A class to contain categorized gene set collection

Description

This class is a simple generalization of the BroadCollection function of GSEABase to store gene sets having assigned categories and subcategories that can be different from those of the MSigDB.

Slots

- category A character defining the main category that the gene set belongs to.
- subCategory A character defining the secondary category that the gene set belongs to.

checkRepository Check an existing repository for consistency

Description

Check both repository data consistency (see repo_check from the repo package) and specific gep2pep data consistency.

Usage

checkRepository(rp)

Arguments

- rp A repository created by createRepository.

Value

Nothing.

Examples

db <- loadSamplePWS()
repo_path <- file.path(tempdir(), "gep2pepTemp")

rp <- createRepository(repo_path, db)
checkRepository(rp)
unlink(repo_path, TRUE)
clearCache  

_Clear cached ranked matrices_

**Description**

Clear cached ranked matrices

**Usage**

```r
clearCache(rp_peps)
```

**Arguments**

- `rp_peps` A repository created with `createRepository`, and containing PEPs created with `buildPEPs`.

**Details**

This will clear everything in the repository tagged with "stashed", which by default includes only matrices ranked by some gep2pep functions such as `CondSEA`.

**Value**

Nothing, used for side effects

**See Also**

`CondSEA`

**Examples**

```r
db <- loadSamplePWS()
repo_path <- file.path(tempdir(), "gep2pepTemp")

rp <- createRepository(repo_path, db)
geps <- loadSampleGEP()
buildPEPs(rp, geps)

pgset <- c("(+)_chelidonine", "(+/-)_catechin")
psea <- CondSEA(rp, pgset, usecache=TRUE)
## the repository contains cached data
print(rp, all=TRUE)

clearCache(rp)

unlink(repo_path, TRUE)
```
Condition Set Enrichment Analysis (CondSEA) can be seen as a Gene-SEA performed over rows (as opposed to columns) of a matrix of GEPs. It tells how much a pathway is consistently dysregulated under a set of conditions (such as a set of drug treatments, disease states, cell types, etc.) when compared to a statistical background of other conditions.

Usage

CondSEA(rp_peps, pgset, bgset = "all", collections = "all", details = TRUE, rankingFun = rankPEPsByRows.ES, usecache = FALSE, sortoutput = TRUE)

Arguments

- rp_peps: A repository created with createRepository, and containing PEPs created with buildPEPs.
- pgset: A vector of names of conditions. Corresponding PEPs must exist in all the pathway collections currently in rp.
- bgset: The background against which to compare pgset. If set to "all" (default), all the remaining PEPs will be used. If provided, the corresponding PEPs must exist in all the pathway collections currently in rp.
- collections: A subset of the collection names returned by getCollections. If set to "all" (default), all the collections in rp will be used.
- details: If TRUE (default) rank details will be reported for each condition in pgset.
- rankingFun: The function used to rank PEPs column-wise. By default rankPEPsByRows.ES is used, which ranks using gene set enrichment scores (see details).
- usecache: If set to TRUE, the computed ranked matrix will be stored in the repository (see details). FALSE by default.
- sortoutput: If TRUE (default) the output gene sets will be sorted in order of increasing p-value.

Details

For each pathway, all conditions are ranked by how much they dysregulate it (from the most UP-regulating to the most DOWN-regulating). Then, a Kolmogorov-Smirnov (KS) test is performed to compare the ranks assigned to conditions in pgset against the ranks assigned to conditions in bgset. A positive (negative) Enrichment Score (ES) of the KS test indicates whether each pathway is UP- (DOWN-) regulated by pgset as compared to bgset. A p-value is associated to the ES.

When PEPs are obtained from drug-induced gene expression profiles, PathSEA is the Drug-Set Enrichment Analysis [1].

The rankingFun must take in input PEPs like those loaded from the repository and return a matrix of row-wise ranks. Each row must contains ranks from 1 to the number of PEPs minus the number of NAs in the row.
When `usecache=TRUE`, the ranked matrix is permanently stored in HDF5 format, and subsequent calls to `CondSEA` will load from the disk the necessary ranks (not the whole matrix). The correct cached data is identified by the alphabetically sorted union(pgset,bgset), by the collection name, and by the ranking function. Additional calls to `CondSEA` with variations of these inputs will create additional cache. Cached data is hidden in the repository by default and can be printed with `rp_peps$print(all=TRUE)`, and cleared with `clearCache(rp_peps)`.

**Value**

A list of 2, by names "CondSEA" and "details". The "CondSEA" entry is a 2-columns matrix including ESs and p-values (see details) for each pathway database and condition. The "details" entry reports the rank of each condition in `pgset` for each pathway.

**References**


**See Also**

getResults, getDetails, clearCache

**Examples**

db <- loadSamplePWS()
repo_path <- file.path(tempdir(), "gep2pepTemp")

rp <- createRepository(repo_path, db)
geps <- loadSampleGEP()
buildPEPs(rp, geps)

pgset <- c("(+)_chelidonine", "(+/-)_catechin")
psea <- CondSEA(rp, pgset)

res <- getResults(psea, "c3_TFT")

## getting the names of the top pathways

setId2setName(loadCollection(rp, "c3_TFT"), rownames(res))

unlink(repo_path, TRUE)

### createMergedRepository

*Merge multiple PEPs to build a repository of consensus PEPs*

**Description**

Merge multiple PEPs to build a repository of consensus PEPs
createMergedRepository

Usage

createMergedRepository(rpIn_path, rpOut_path, mergestr,
progressBar = TRUE, collections = "all")

Arguments

rpIn_path path to existing gep2pep repository
rpOut_path path where the new merged repository will be created
mergestr a named list of character vectors, each one including a set of PEP names. For each list entry, a consensus PEP will be created and assigned the entry name.
progressBar if TRUE, show a progress bar
collections A subset of the collection names returned by getCollections. If set to "all" (default), all the collections in rp will be used.

Details

The merging is performed as follows. Given N PEPs, the corresponding consensus PEP will get as enrichment score the average enrichment scores of the N PEPs, and as p-value the composition of the N PEP p-values by Fisher’s method.

Value

Nothing, used for side effects.

Examples

db <- loadSamplePWS()
repo_path <- file.path(tempdir(), "gep2pepTemp")
rp <- createRepository(repo_path, db)
geps <- loadSampleGEP()
buildPEPs(rp, geps)

mergestr <- list(
  che_iso = c("(+)_chelidonine", "(+)_isoprenaline"),
  cat_mk = c("(+/-)_catechin", "(_)_mk_801"
)

merged_path <- file.path(tempdir(), "gep2pepTempMerged")
createMergedRepository(repo_path, merged_path, mergestr)
unlink(repo_path, TRUE)
unlink(merged_path, TRUE)
createRepository  

*Creates a repository of pathway collections.*

**Description**

Given a database of collections, stores them in a local repository to be used by gep2pep functions.

**Usage**

```r
createRepository(path, sets, name = NULL, description = NULL)
```

**Arguments**

- `path`  
  Path to a non-existing directory where the repository will be created.
- `sets`  
  An object of class `CategorizedCollection`.
- `name`  
  Name of the repository. Defaults to `NULL` (a generic name will be given).
- `description`  
  Description of the repository. If `NULL` (default), a generic description will be given.

**Details**

`sets` can be created by `importMSigDB.xml` or using `GSEABase GeneSetCollection` class and then converting it to `CategorizedCollection`. See examples.

**Value**

An object of class `repo` that can be passed to `gep2pep` functions.

**See Also**

`buildPEPs`

**Examples**

```r
db <- loadSamplePWS()
repo_path <- file.path(tempdir(), "gep2pepTemp")

rp <- createRepository(repo_path, db)
## Repo root created.
## Repo created.
## [15:45:06] Storing pathway data for collection: c3_TFT
## [15:45:06] Storing pathway data for collection: c3_MIR
## [15:45:06] Storing pathway data for collection: c4_CGN

rp
## ID Dims Size
## c3_TFT_sets 10 18.16 kB
## c3_MIR_sets 10 17.25 kB
## c4_CGN_sets 10 6.9 kB

unlink(repo_path, TRUE)
```
exportSEA

Export CondSEA or PathSEA results to XLS format

Description

The XLS output includes the full CondSEA or PathSEA results, together with additional gene set information for the CondSEA. If the PathSEA or CondSEA analysis was performed with details=TRUE, details will be reported in the XLS file. This function requires the WriteXLS library.

Usage

exportSEA(rp, results, outname = NULL)

Arguments

rp A repository created by createRepository.
results The output of CondSEA or PathSEA.
outname Name of the XLS file to be created.

Value

Nothing.

See Also

CondSEA, PathSEA

Examples

db <- loadSamplePWS()
repo_path <- file.path(tempdir(), "gep2pepTemp")

rp <- createRepository(repo_path, db)
geps <- loadSampleGEP()
buildPEPs(rp, geps)

pgset <- c("(+)_chelidonine", "(+/-)_catechin")
psea <- CondSEA(rp, pgset)

## Not run:
exportSEA(rp, psea)

## End(Not run)
unlink(repo_path, TRUE)
gene2pathways  
Finds pathways including a given gene.

Description
Given a gene, find the set of pathways that involve it in each collection of the repository. This can be used to define a set of pathways for the PathSEA.

Usage

gene2pathways(rp, genes, and = TRUE)

Arguments
rp  A repository created by createRepository.
genes  A vector of gene identifiers of the same type as that used to create the repository.
and  If set to TRUE (default), will return sets containing all of genes. Otherwise will return the sets containing any of genes.

Value
A database of pathways suitable as input to PathSEA.

See Also
createRepository, PathSEA

Examples

db <- loadSamplePWS()
repo_path <- file.path(tempdir(), "gep2pepTemp")

rp <- createRepository(repo_path, db)

## Finding all pathways containing "FAM126A":
subpw <- gene2pathways(rp, "FAM126A")

print(names(subpw))

unlink(repo_path, TRUE)
**getCollections**

*Returns the names of the pathway collections in a repository.*

**Description**

Given a gep2pep repository, returns the names of the stored collections by looking at appropriate repository item names.

**Usage**

```
getCollections(rp)
```

**Arguments**

- `rp` A repository created by `createRepository`.

**Details**

Each collection in a database has a "category" and a "subcategory" assigned, which are used to build the collection identifier as "category_subcategory". This function obtains the identifiers by looking at data stored in the repository `rp` (entries that are tagged with "sets").

**Value**

Vector of collection names (see details).

**Examples**

```r
db <- loadSamplePWS()
repo_path <- file.path(tempdir(), "gep2pepTemp")

rp <- createRepository(repo_path, db)
## Repo root created.
## Repo created.
## [15:45:06] Storing pathway data for collection: c3_TFT
## [15:45:06] Storing pathway data for collection: c3_MIR
## [15:45:06] Storing pathway data for collection: c4_CGN

getcollections(rp)
## [1] "c3_TFT" "c3_MIR" "c4_CGN"

unlink(repo_path, TRUE)
```
getDetails

Extracts the details matrix from CondSEA or PathSEA output

Description

Extracts the details matrix from CondSEA or PathSEA output

Usage

getDetails(analysis, collection)

Arguments

- **analysis**: The output of either CondSEA or PathSEA.
- **collection**: One of the names returned by getCollections.

Value

A matrix including the ranks of each pathway (over rows) and each condition (over columns) used as input to CondSEA or PathSEA.

See Also

CondSEA, PathSEA

Examples

db <- loadSamplePWS()
repo_path <- file.path(tempdir(), "gep2pepTemp")

rp <- createRepository(repo_path, db)
geps <- loadSampleGEP()
buildPEPs(rp, geps)

pgset <- c("(+)_chelidonine", "(+/-)_catechin")
psea <- CondSEA(rp, pgset)

getDetails(psea, "c3_TFT")

unlink(repo_path, TRUE)
**getResults**

*Extracts the results matrix from CondSEA or PathSEA output*

---

**Description**

Extracts the results matrix from CondSEA or PathSEA output

**Usage**

```r
getResults(analysis, collection)
```

**Arguments**

- `analysis` The output of either CondSEA or PathSEA.
- `collection` One of the names returned by `getCollections`.

**Value**

A 2-columns matrix including ESs and p-values (see details) for each pathway database and condition.

**See Also**

CondSEA, PathSEA

**Examples**

```r
db <- loadSamplePWS()
repo_path <- file.path(tempdir(), "gep2pepTemp")

rp <- createRepository(repo_path, db)
geps <- loadSampleGEP()
buildPEPs(rp, geps)

pgset <- c("(+)_chelidonine", "(+/-)_catechin")
psea <- CondSEA(rp, pgset)
getResults(psea, "c3_TFT")
unlink(repo_path, TRUE)
```
Description

Raw mode is meant to deal with large collections of PEPs (like hundreds of thousands). In this case, problems may arise while trying to convert GEPs by loading all of them in memory at once. Raw mode is meant to be used with HDF5 format, which allows to load subsets of GEPs from the disk. buildPEPs, when used in raw mode, can create the corresponding subsets of PEPs, so that the job can be distributed on a computer cluster. importFromRawMode is meant to join the chunks into HDF5 matrices, which are then stored into the repository. The .loadPEPs function can seamlessly load PEPs stored in normal (RDS) or HDF5 format.

Usage

importFromRawMode(rp, path = file.path(rp$root(), "raw"),
  collections = "all")

Arguments

rp         A repository created by createRepository.
path       Path were raw PEPs are stored (default is a "raw" directory under the repository root folder).
collections        A subset of the collection names returned by getCollections. If set to "all" (default), all the collections in rp will be used.

Details

PEPs are expect to be found at the specified path and follow the naming convention as generated by buildPEPs. According to such convention, each file is named using the format category_subcategory#chunknumber.RDS. All non-alphanumeric characters from the original category and subcategory names are replace with an underscore (in rare cases this could create ambiguity that should be manually prevented). All chunks for the same subcategory are joined together following the chunk numbers into a single HDF5 matrix and stored in the repository as an "attachment" (see repo documentation).

Note that raw PEPs (by default everything at repository_root/raw) can be safely removed once they have been imported.

Value

Nothing, used for side effects.

See Also

buildPEPs
Examples

db <- loadSamplePWS()
repo_path <- file.path(tempdir(), "gep2pepTemp")

rp <- createRepository(repo_path, db)

## The following will create PEPs in 2 separate files
geps <- loadSampleGEP()
buildPEPs(rp, geps[,1:2], progress_bar=FALSE,
          rawmode_id=1)
buildPEPs(rp, geps[,3:5], progress_bar=FALSE,
          rawmode_id=2)

## The separate files are then merged into one (possibly big) file
## in HDF5 format
importFromRawMode(rp)

## Now most operations (excluding the addition of new PEPs to
## existing collections) will be available as usual.
unlink(repo_path, TRUE)

importMSigDB.xml

Imports pathways data from an MSigDB XML file.

Description

Creates a GeneSetCollection object using the XML distribution of the MSigDB (see references). The returned object can be passed to createRepository.

Usage

importMSigDB.xml(fname, organism = "Homo Sapiens")

Arguments

fname     Path to an XML file downloaded from MSigDB.
organism  Select only gene sets for a given organism. Default is "Homo Sapiens".

Details

This function now just calls getBroadSets(fname) from the GSEABase package. However, it is left for backward compatibility and as an entry point to package functionalities.

Value

A CategorizedCollection object

References

http://software.broadinstitute.org/gsea/downloads.jsp
Examples

## Not run:

## To run this example, first obtain the MSigDB database in XML
## format (see
## http://software.broadinstitute.org/gsea/downloads.jsp). It is
## assumed that the database is locally available as the file
## "msigdb_v6.0.xml".

db <- importMSigDB.xml("msigdb_v6.0.xml")

## The database is now in an acceptable format to create a local
## repository using createRepository

## End(Not run)

## A small excerpt from the MSigDB is included in gep2pep. The
## following creates (and then deletes) a gep2pep repository.

db_sample <- loadSamplePWS()

repo_path <- file.path(tempdir(), "gep2pepTemp")
rp <- createRepository(repo_path, db_sample)

## removing temporary repository
unlink(repo_path, TRUE)

loadCollection  Loads a collection of pathways from the repository

Description

Loads a collection of pathways from the repository

Usage

loadCollection(rp, collection)

Arguments

rp  A repository created by createRepository.

collection  One of the names returned by getCollections.

Value

a GeneSetCollection object loaded from the repository rp.

Examples

db <- loadSamplePWS()
repo_path <- file.path(tempdir(), "gep2pepTemp")
loadESmatrix

```
rp <- createRepository(repo_path, db)
geps <- loadSampleGEP()

loadCollection(rp, "c3_TFT")

unlink(repo_path, TRUE)
```

---

**loadESmatrix**  
**Loads the matrix of Enrichment Scores for a collection**

**Description**

Loads the matrix of Enrichment Scores for a collection.

**Usage**

```
loadESmatrix(rp, collection)
```

**Arguments**

- **rp**  
  A repository created by `createRepository`.

- **collection**  
  One of the names returned by `getCollections`.

**Value**

The matrix of Enrichment Scores (ES) of the Kolmogorov-Smirnov statistic for the pathway collection, if previously computed with `buildPEPs`. The entry $i,j$ reports the ES for the pathway $i$, condition $j$. If `buildPEPs` was not run, throws an error.

**Examples**

```
db <- loadSamplePWS()
repopath <- file.path(tempdir(), "gep2pepTemp")

rp <- createRepository(repopath, db)
geps <- loadSampleGEP()
buildPEPs(rp, geps)

loadESmatrix(rp, "c3_TFT")[1:5,1:2]

unlink(repopath, TRUE)
```
loadPVmatrix     Loads the matrix of p-values for a collection

Description
Loads the matrix of p-values for a collection

Usage
loadPVmatrix(rp, collection)

Arguments

rp   A repository created by createRepository.
collection One of the names returned by getCollections.

Value
The matrix of p-values (PV) of the Kolmogorov-Smirnov statistic for the pathway collection, if previously computed with buildPEPs. The entry \( i,j \) reports the PV for the pathway \( i \), condition\( j \). If buildPEPs was not run, throws an error.

Examples

```
db <- loadSamplePWS()
repo_path <- file.path(tempdir(), "gep2pepTemp")

rp <- createRepository(repo_path, db)
geps <- loadSampleGEP()
buildPEPs(rp, geps)

loadPVmatrix(rp, "c3_TFT")

unlink(repo_path, TRUE)
```

loadSampleGEP     Loads sample Gene Expression Profiles

Description
Loads sample Gene Expression Profiles

Usage
loadSampleGEP()

Value
Sample gene expression data
loadSamplePWS

Examples

geps <- loadSampleGEP()

loadSamplePWS  Loads sample pathway collections

Description

Loads sample pathway collections

Usage

loadSamplePWS()

Value

Sample pathway collections in GeneSetCollection format

Examples

geps <- loadSampleGEP()

makeCollectionIDs  Creates a collection label for each pathway.

Description

Given a database, uses "category" and "subcategory" entries to create a vector of collection identifiers. Useful to extract a collection from a database.

Usage

makeCollectionIDs(sets)

Arguments

sets  A pathway database in the same format as output by importMSigDB.xml.

Value

A vector of identifiers, one per pathway, with the format: "category_subcategory".

See Also

importMSigDB.xml
Examples

db <- loadSamplePWS()
ids <- makeCollectionIDs(db)

unique(ids)
## [1] "c3_TFT" "c3_MIR" "c4_CGN"

db <- db[ids=="c3_MIR"]

length(db)
## [1] 10

openRepository

Opens an existing repository of pathway collections.

Description

The repository must have been created by `createRepository`. Provides an R object to interact with the repository.

Usage

openRepository(path)

Arguments

path  
Path to a directory where the repository has been created with `createRepository`.

Details

This function only calls the `repo_open` function from the `repo` package on `path`. It is meant to allow users not to explicitly load the `repo` library, unless they want to access advanced features.

Value

An object of class `repo` that can be passed to `gep2pep` functions.

See Also

`createRepository`

Examples

db <- loadSamplePWS()
repo_path <- file.path(tempdir(), "gep2pepTemp")

rp <- createRepository(repo_path, db)
 rp2 <- openRepository(repo_path)

## rp and rp2 point to the same data:
identical(rp$entries(), rp2$entries())
### Description

PathSEA is analogous to the Gene Set Enrichment Analysis (GSEA), but for pathways instead of single genes. It can therefore be used to look for conditions under which a given set of pathways is consistently UP- or DOWN-regulated.

### Usage

```r
PathSEA(rp_peps, pathways, bgsets = "all", collections = "all", subset = "all", details = TRUE, rankingFun = rankPEPsByCols.SPV)
```

### Arguments

- **rp_peps**: A repository created with `createRepository`, and containing PEPs created with `buildPEPs`.
- **pathways**: A database of pathways in the same format as input to `createRepository`. PSEA will be performed for each database separately.
- **bgsets**: Another list like pathways, representing the statistical background for each database. If set to "all" (the default), all pathways that are in the repository and not in pathways will be used.
- **collections**: A subset of the collection names returned by `getCollections`. If set to "all" (default), all the collections in rp will be used.
- **subset**: Character vector including PEP names to be considered (all by default, which may take time).
- **details**: If TRUE (default) details will be reported for each condition in `pgset`.
- **rankingFun**: The function used to rank PEPs column-wise. By default `rankPEPsByCols.ES` is used, which uses gene set enrichment scores (see details).

### Details

For each condition, all pathways are ranked by how much they are dysregulated by it (from the most UP-regulated to the most DOWN-regulated, according to the corresponding p-values). Then, a Kolmogorov-Smirnov (KS) test is performed to compare the ranks assigned to pathways in `pathways` against the ranks assigned to pathways in `bgsets`. A positive (negative) Enrichment Score (ES) of the KS test indicates whether each pathway is UP- (DOWN-) regulated by `pgset` as compared to `bgset`. A p-value is associated to the ES.

When PEPs are obtained from drug-induced gene expression profiles, PathSEA can be used together with `gene2pathways` to perform gene2drug [1] analysis, which predicts which drugs may target a gene of interest (or mimick such effect).

The `rankingFun` must take in input PEPs like those loaded from the repository and return a matrix of column-wise ranks. Each column must contain ranks from 1 to the number of gene sets minus the number of NAs in the column.
Value

A list of 2, by names "PathSEA" and "details". The "PathSEA" entry is a 2-columns matrix including ESs and p-values for each collection and condition. The "details" entry reports the rank of each pathway in pathways for each condition.

References


See Also

getResults, getDetails

Examples

library(GSEABase)

db <- loadSamplePWS()
repo_path <- file.path(tempdir(), "gep2pepTemp")

rp <- createRepository(repo_path, db)
geps <- loadSampleGEP()
buildPEPs(rp, geps)


w <- sapply(db, setIdentifier) %in% pathways

psea <- PathSEA(rp, db[w])

getResults(psea, "c3_TFT")

unlink(repo_path, TRUE)
**setId2setName**

Converts gene set IDs to gene set names

**Description**

Converts gene set IDs to gene set names

**Usage**

```r
setId2setName(sets, ids)
```

**Arguments**

- `sets`: An object of class `GeneSetCollection`
- `ids`: character vector of gene set IDs to be converted to set names

**Value**

A vector of gene set names

**See Also**

`CondSEA`, `PathSEA`

**Examples**

```r
collection <- loadSamplePWS()
setId2setName(collection, c("M3128", "M11607"))
```
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