

# Package ‘cTRAP’

May 10, 2024

**Title** Identification of candidate causal perturbations from differential gene expression data

**Version** 1.22.0

**Description** Compare differential gene expression results with those from known cellular perturbations (such as gene knock-down, overexpression or small molecules) derived from the Connectivity Map. Such analyses allow not only to infer the molecular causes of the observed difference in gene expression but also to identify small molecules that could drive or revert specific transcriptomic alterations.

**Depends** R (>= 4.0)

**License** MIT + file LICENSE

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---

`.plotBubbles`      *Plot packed bubbles*

---

**Description**

Plot packed bubbles

**Usage**

```
.plotBubbles(data, title, colour = "orange")
```

**Arguments**

<code>data</code>	Data to plot
<code>title</code>	Character: plot title
<code>colour</code>	Character: bubble colour

**Value**

highchart object

---

`.prepareNavPage`      *Prepare Shiny page template*

---

**Description**

Prepare Shiny page template

**Usage**

```
.prepareNavPage(...)
```

**Value**

HTML elements

---

`.traceInList`      *Find an item in list of lists and return its coordinates*

---

**Description**

Find an item in list of lists and return its coordinates

**Usage**

```
.traceInList(ll, item)
```

---

```
analyseDrugSetEnrichment
    Analyse drug set enrichment
```

---

**Description**

Analyse drug set enrichment

**Usage**

```
analyseDrugSetEnrichment(
  sets,
  stats,
  col = NULL,
  nperm = 10000,
  maxSize = 500,
  ...,
  keyColSets = NULL,
  keyColStats = NULL
)
```

**Arguments**

sets	Named list of characters: named sets containing compound identifiers (obtain drug sets by running <code>prepareDrugSets()</code> )
stats	Named numeric vector or either a <code>similarPerturbations</code> or a <code>targetingDrugs</code> object (obtained after running <a href="#">rankSimilarPerturbations</a> or <a href="#">predictTargetingDrugs</a> , respectively)
col	Character: name of the column to use for statistics (only required if class of stats is either <code>similarPerturbations</code> or <code>targetingDrugs</code> )
nperm	Number of permutations to do. Minimal possible nominal p-value is about $1/nperm$
maxSize	Maximal size of a gene set to test. All pathways above the threshold are excluded.
...	Arguments passed on to <a href="#">fgsea::fgseaSimple</a>
minSize	Minimal size of a gene set to test. All pathways below the threshold are excluded.
scoreType	This parameter defines the GSEA score type. Possible options are ("std", "pos", "neg"). By default ("std") the enrichment score is computed as in the original GSEA. The "pos" and "neg" score types are intended to be used for one-tailed tests (i.e. when one is interested only in positive ("pos") or negative ("neg") enrichment).
nproc	If not equal to zero sets BPPARAM to use nproc workers (default = 0).
gseaParam	GSEA parameter value, all gene-level statis are raised to the power of 'gseaParam' before calculation of GSEA enrichment scores.

	BPPARAM Parallelization parameter used in bplapply. Can be used to specify cluster to run. If not initialized explicitly or by setting 'nproc' default value 'bpparam()' is used.
keyColSets	Character: column from sets to compare with column keyColStats from stats; automatically selected if NULL
keyColStats	Character: column from stats to compare with column keyColSets from sets; automatically selected if NULL

**Value**

Enrichment analysis based on GSEA

**See Also**

Other functions for drug set enrichment analysis: [loadDrugDescriptors\(\)](#), [plotDrugSetEnrichment\(\)](#), [prepareDrugSets\(\)](#)

**Examples**

```

descriptors <- loadDrugDescriptors()
drugSets <- prepareDrugSets(descriptors)

# Analyse drug set enrichment in ranked targeting drugs for a differential
# expression profile
data("diffExprStat")
gdsc <- loadExpressionDrugSensitivityAssociation("GDSC")
predicted <- predictTargetingDrugs(diffExprStat, gdsc)

analyseDrugSetEnrichment(drugSets, predicted)

```

---

as.table.referenceComparison

*Cross Tabulation and Table Creation*

---

**Description**

Cross Tabulation and Table Creation

**Usage**

```

## S3 method for class 'referenceComparison'
as.table(x, ..., clean = TRUE)

```

**Arguments**

x	referenceComparison object
...	Extra parameters not currently used
clean	Boolean: only show certain columns (to avoid redundancy)?

**Value**

Complete table with metadata based on a targetingDrugs object

**See Also**

Other functions related with the ranking of CMap perturbations: `filterCMapMetadata()`, `getCMapConditions()`, `getCMapPerturbationTypes()`, `loadCMapData()`, `loadCMapZscores()`, `parseCMapID()`, `plot.perturbationChanges()`, `plot.referenceComparison()`, `plotTargetingDrugsVSSimilarPerturbations()`, `prepareCMapPerturbations()`, `print.similarPerturbations()`, `rankSimilarPerturbations()`

Other functions related with the prediction of targeting drugs: `listExpressionDrugSensitivityAssociation()`, `loadExpressionDrugSensitivityAssociation()`, `plot.referenceComparison()`, `plotTargetingDrugsVSSimilarPerturbations()`, `predictTargetingDrugs()`

---

calculateCellLineMean *Calculate cell line mean*

---

**Description**

Calculate cell line mean

**Usage**

```
calculateCellLineMean(data, cellLine, metadata, rankPerCellLine)
```

**Arguments**

<code>data</code>	Data table: comparison against CMap data
<code>cellLine</code>	Character: perturbation identifiers as names and respective cell lines as values
<code>metadata</code>	Data table: data metadata
<code>rankPerCellLine</code>	Boolean: rank results based on both individual cell lines and mean scores across cell lines (TRUE) or based on mean scores alone (FALSE)? If <code>cellLineMean = FALSE</code> , individual cell line conditions are always ranked.

**Value**

A list with two items:

`data` input data with extra rows containing cell line average scores (if calculated)

`rankingInfo` data table with ranking information

`metadata` metadata associated with output data, including for identifiers regarding mean cell line scores

---

```
calculateEvenlyDistributedBins
```

*Calculate evenly-distributed bins*

---

### Description

Calculate evenly-distributed bins

### Usage

```
calculateEvenlyDistributedBins(
  numbers,
  maxBins = 15,
  k = 5,
  minPoints = NULL,
  ...,
  ids = NULL
)
```

### Arguments

numbers	Numeric
maxBins	Numeric: maximum number of bins for numeric columns
k	Numeric: constant; the higher the constant, the smaller the bin size (check minpts)
minPoints	Numeric: minimum number of points in a bin (if NULL, the minimum number of points is the number of non-missing values divided by maxBins divided by k)
...	Arguments passed on to <a href="#">binr::bins</a>
	max.breaks Used for initial cut. If exact.groups is FALSE, bins are merged until there's no bins with fewer than $\text{length}(x) / \text{max.breaks}$ points. In bins, one of max.breaks and minpts must be supplied.
	exact.groups if TRUE, the result will have exactly the number of target.bins; if FALSE, the result may contain fewer than target.bins bins
	verbose Indicates verbose output.
	errthresh If the error is below the provided value, stops after the first rough estimate of the bins.

### Value

Factor containing the respective group of each element in numbers



---

checkColnames      *Check whether test\_names are columns in the [data.frame](#)*

---

**Description**

Check whether test\_names are columns in the [data.frame](#)

**Usage**

```
checkColnames(test_names, df, throw_error = TRUE)
```

**Arguments**

test_names	a vector of column names to test
df	the <a href="#">data.frame</a> to test against
throw_error	boolean indicating whether to throw an error if any test_names are not found in df

**Value**

boolean indicating whether or not all test\_names are columns of df

**Source**

<https://github.com/cmap/cmapR>

---

chunkColumns      *Assign columns into chunks*

---

**Description**

Assign columns into chunks

**Usage**

```
chunkColumns(x, nrows, chunkGiB)
```

**Arguments**

x	Vector of elements
nrows	Numeric: number of rows
chunkGiB	Numeric: size (in gibibytes) of chunks to load reference file; only if argument reference is a file path

**Value**

List of chunks with equally distributed columns

---

closeOpenHandles	<i>Close open handles</i>
------------------	---------------------------

---

**Description**

Close open handles

**Usage**

```
closeOpenHandles()
```

**Value**

Closes all open identifiers

---

cmapMetadata	<i>CMap metadata</i>
--------------	----------------------

---

**Description**

CMap metadata obtained by running the following code:

```
cmapMetadata <- filterCMapMetadata("cmapMetadata.txt", cellLine = "HEPG2",  
                                  timepoint = "2 h")
```

---

cmapPerturbationsCompounds	<i>CMap perturbations sample for small molecules</i>
----------------------------	--

---

**Description**

CMap perturbations sample for small molecules obtained by running the following code:

```
cellLine <- c("HepG2", "HUH7")  
cmapMetadataCompounds <- filterCMapMetadata(  
  "cmapMetadata.txt", cellLine=cellLine, timepoint="24 h",  
  dosage="5 \u00B5M", perturbationType="Compound")  
  
cmapPerturbationsCompounds <- prepareCMapPerturbations(  
  cmapMetadataCompounds, "cmapZscores.gctx", "cmapGeneInfo.txt",  
  "cmapCompoundInfo_drugs.txt", loadZscores=TRUE)  
  
# Remove non-ASCII characters for portability reasons
```

```

metadata <- attr(cmapPerturbationsCompounds, "metadata")
metadata$pert_idose <- gsub("\u00B5", "micro", metadata$pert_idose)
metadata$pert_dose_unit <- gsub("\u00B5", "micro", metadata$pert_dose_unit)
attr(cmapPerturbationsCompounds, "metadata") <- metadata

```

---

cmapPerturbationsKD     *CMap perturbations sample for knockdown experiments*

---

## Description

CMap perturbations sample for knockdown experiments obtained by running the following code:

```

# Code for loading CMap gene KD HepG2 data
cellLine <- "HepG2"
cmapMetadataKD <- filterCMapMetadata(
  "cmapMetadata.txt", cellLine=cellLine,
  perturbationType="Consensus signature from shRNAs targeting the same gene")

cmapPerturbationsKD <- prepareCMapPerturbations(
  cmapMetadataKD, "cmapZscores.gctx", "cmapGeneInfo.txt",
  loadZscores=TRUE)

data("diffExprStat")
compareKD <- rankSimilarPerturbations(diffExprStat, cmapPerturbationsKD)

# Select only some perturbations (to reduce file size)
filter <- c(head(order(compareKD$spearman_rank)),
            tail(order(compareKD$spearman_rank)),
            head(order(compareKD$pearson_rank)),
            tail(order(compareKD$pearson_rank)),
            head(order(compareKD$gsea_rank)),
            tail(order(compareKD$gsea_rank)))
filter <- unique(compareKD[[1]][filter])
cmapPerturbationsKD <- cmapPerturbationsKD[ , filter]

# Remove non-ASCII characters for portability reasons
metadata <- attr(cmapPerturbationsKD, "metadata")
metadata$pert_idose <- gsub("\u00B5", "micro", metadata$pert_idose)
metadata$pert_dose_unit <- gsub("\u00B5", "micro", metadata$pert_dose_unit)
attr(cmapPerturbationsKD, "metadata") <- metadata

```

---

compareQuantile	<i>Compare vector against its quantile</i>
-----------------	--

---

**Description**

Check which elements of the vector are lower/greater than or equal to the quantile of a given vector.

**Usage**

```
compareQuantile(vec, prob, lte = FALSE)
```

**Arguments**

vec	Numeric vector
prob	Numeric: probability value between [0,1] to produce sample quantiles
lte	Boolean: check if values are <= quantile? If FALSE, checks if values are >= quantile

**Value**

Boolean vector regarding compared elements

---

compareWithAllMethods	<i>Compare reference using all methods</i>
-----------------------	--

---

**Description**

Compare reference using all methods

**Usage**

```
compareWithAllMethods(
  method,
  input,
  reference,
  geneSize = 150,
  cellLines = NULL,
  cellLineMean = "auto",
  rankPerCellLine = FALSE,
  threads = 1,
  chunkGiB = 1,
  verbose = FALSE
)
```

**Arguments**

method	Character: comparison method (spearman, pearson or gsea; multiple methods may be selected at once)
input	Named numeric vector of differentially expressed genes whose names are gene identifiers and respective values are a statistic that represents significance and magnitude of differentially expressed genes (e.g. t-statistics); or character of gene symbols composing a gene set that is tested for enrichment in reference data (only used if method includes gsea)
reference	Data matrix or character object with file path to CMap perturbations (see <a href="#">prepareCMapPerturbations()</a> ) or gene expression and drug sensitivity association (see <a href="#">loadExpressionDrugSensitivityAssociation()</a> )
geneSize	Numeric: number of top up-/down-regulated genes to use as gene sets to test for enrichment in reference data; if a 2-length numeric vector, the first index is the number of top up-regulated genes and the second index is the number of down-regulated genes used to create gene sets; only used if method includes gsea and if input is not a gene set
cellLines	Integer: number of unique cell lines
cellLineMean	Boolean: add rows with the mean of method across cell lines? If cellLineMean = "auto" (default), rows will be added when data for more than one cell line is available.
rankPerCellLine	Boolean: rank results based on both individual cell lines and mean scores across cell lines (TRUE) or based on mean scores alone (FALSE)? If cellLineMean = FALSE, individual cell line conditions are always ranked.
threads	Integer: number of parallel threads
chunkGiB	Numeric: size (in gibibytes) of chunks to load reference file; only if argument reference is a file path
verbose	Boolean: print additional details?
rankByAscending	Boolean: rank values based on their ascending (TRUE) or descending (FALSE) order?

**Value**

List of data tables with correlation and/or GSEA score results

**GSEA score**

When method = "gsea", weighted connectivity scores (WTCS) are calculated ([https://clue.io/connectopedia/cmap\\_algorithms](https://clue.io/connectopedia/cmap_algorithms)).

---

`convertENSEMBLtoGeneSymbols`*Convert ENSEMBL gene identifiers to gene symbols*

---

**Description**

Convert ENSEMBL gene identifiers to gene symbols

**Usage**

```
convertENSEMBLtoGeneSymbols(  
  genes,  
  dataset = "hsapiens_gene_ensembl",  
  mart = "ensembl"  
)
```

**Arguments**

<code>genes</code>	Character: ENSEMBL gene identifiers
<code>dataset</code>	Character: biomaRt dataset name
<code>mart</code>	Character: biomaRt database name

**Value**

Named character vector where names are the input ENSEMBL gene identifiers and the values are the matching gene symbols

---

`convertGeneIdentifiers`*Convert gene identifiers*

---

**Description**

Convert gene identifiers

**Usage**

```
convertGeneIdentifiers(  
  genes,  
  annotation = "Homo sapiens",  
  key = "ENSEMBL",  
  target = "SYMBOL",  
  ignoreDuplicatedTargets = TRUE  
)
```

**Arguments**

genes	Character: genes to be converted
annotation	OrgDb with genome wide annotation for an organism or character with species name to query OrgDb, e.g. "Homo sapiens"
key	Character: type of identifier used, e.g. ENSEMBL; read ?AnnotationDbi::columns
target	Character: type of identifier to convert to; read ?AnnotationDbi::columns
ignoreDuplicatedTargets	Boolean: if TRUE, identifiers that share targets with other identifiers will not be converted

**Value**

Character vector of the respective targets of gene identifiers. The previous identifiers remain other identifiers have the same target (in case `ignoreDuplicatedTargets = TRUE`) or if no target was found.

**Examples**

```
genes <- c("ENSG0000012048", "ENSG0000083093", "ENSG0000141510",
          "ENSG0000051180")
convertGeneIdentifiers(genes)
convertGeneIdentifiers(genes, key="ENSEMBL", target="UNIPROT")

# Explicit species name to automatically look for its OrgDb database
sp <- "Homo sapiens"
genes <- c("ENSG0000012048", "ENSG0000083093", "ENSG0000141510",
          "ENSG0000051180")
convertGeneIdentifiers(genes, sp)

# Alternatively, set the annotation database directly
ah <- AnnotationHub::AnnotationHub()
sp <- AnnotationHub::query(ah, c("OrgDb", "Homo sapiens"))[[1]]
columns(sp) # these attributes can be used to change the attributes

convertGeneIdentifiers(genes, sp)
```

---

counts

*Gene expression data sample*


---

**Description**

Gene expression data sample obtained by running the following code:

```
data("ENCODEmetadata")
ENCODEsamples <- loadENCODEsamples(ENCODEmetadata)[[1]]
counts <- prepareENCODEgeneExpression(ENCODEsamples)
```

```
# Remove low coverage (at least 10 counts shared across two samples)
minReads <- 10
minSamples <- 2
filter <- rowSums(counts[ , -c(1, 2)] >= minReads) >= minSamples
counts <- counts[filter, ]

# Convert ENSEMBL identifier to gene symbol
counts$gene_id <- convertGeneIdentifiers(counts$gene_id)
```

---

cTRAP

*cTRAP package*


---

## Description

Compare differential gene expression results with those from big datasets (e.g. CMap), allowing to infer which types of perturbations may explain the observed difference in gene expression.

Optimised to run in ShinyProxy with Celery/Flower backend with argument `shinyproxy = TRUE`.

## Usage

```
cTRAP(
  ...,
  commonPath = "data",
  expire = 14,
  fileSizeLimitMiB = 50,
  flowerURL = NULL,
  port = getOption("shiny.port"),
  host = getOption("shiny.host", "127.0.0.1")
)
```

## Arguments

...	Objects
commonPath	Character: path where to store data common to all sessions
expire	Character: days until a session expires (message purposes only)
fileSizeLimitMiB	Numeric: file size limit in MiB
flowerURL	Character: Flower REST API's URL (NULL to avoid using Celery/Flower backend)
port	The TCP port that the application should listen on. If the <code>port</code> is not specified, and the <code>shiny.port</code> option is set (with <code>options(shiny.port = XX)</code> ), then that port will be used. Otherwise, use a random port between 3000:8000, excluding ports that are blocked by Google Chrome for being considered unsafe: 3659, 4045, 5060, 5061, 6000, 6566, 6665:6669 and 6697. Up to twenty random ports will be tried.
host	The IPv4 address that the application should listen on. Defaults to the <code>shiny.host</code> option, if set, or "127.0.0.1" if not. See Details.



## Details

**Input:** To use this package, a named vector of differentially expressed gene metric is needed, where its values represent the significance and magnitude of the differentially expressed genes (e.g. t-statistic) and its names are gene symbols.

**Workflow:** The differentially expressed genes will be compared against selected perturbation conditions by:

- Spearman or Pearson correlation with z-scores of differentially expressed genes after perturbations from CMap. Use function `rankSimilarPerturbations` with `method = "spearman"` or `method = "pearson"`
- Gene set enrichment analysis (GSEA) using the (around) 12 000 genes from CMap. Use function `rankSimilarPerturbations` with `method = gsea`.

Available perturbation conditions for CMap include:

- Cell line(s).
- Perturbation type (gene knockdown, gene upregulation or drug intake).
- Drug concentration.
- Time points.

Values for each perturbation type can be listed with `getCMapPerturbationTypes()`

**Output:** The output includes a data frame of ranked perturbations based on the associated statistical values and respective p-values.

## Value

Launches result viewer and plotter (returns NULL)

## Author(s)

**Maintainer:** Nuno Saraiva-Agostinho <nunodanielagostinho@gmail.com>

Authors:

- Bernardo P. de Almeida
- Nuno L. Barbosa-Morais [lead]

## See Also

Useful links:

- <https://nuno-agostinho.github.io/cTRAP>
- <https://github.com/nuno-agostinho/cTRAP>
- Report bugs at <https://github.com/nuno-agostinho/cTRAP/issues>

Other visual interface functions: `launchCMapDataLoader()`, `launchDiffExprLoader()`, `launchDrugSetEnrichmentAnal`, `launchMetadataViewer()`, `launchResultPlotter()`

---

diffExprStat	<i>Differential expression's t-statistics sample</i>
--------------	--

---

**Description**

Differential expression's t-statistics sample obtained by running the following code:

```
data("counts")

# Perform differential gene expression analysis
diffExpr <- performDifferentialExpression(counts)

# Get t-statistics of differential expression with respective gene names
diffExprStat <- diffExpr$t
names(diffExprStat) <- diffExpr$Gene_symbol
```

---

dimnames.expressionDrugSensitivityAssociation	<i>Operations on expressionDrugSensitivityAssociation objects</i>
---	---

---

**Description**

Operations on expressionDrugSensitivityAssociation objects

**Usage**

```
## S3 method for class 'expressionDrugSensitivityAssociation'
dimnames(x)

## S3 method for class 'expressionDrugSensitivityAssociation'
dim(x)

## S3 method for class 'expressionDrugSensitivityAssociation'
x[i, j, drop = FALSE, ...]
```

**Arguments**

x	An expressionDrugSensitivityAssociation object
i, j	Character or numeric indexes specifying elements to extract
drop	Boolean: coerce result to the lowest possible dimension?
...	Extra arguments given to other methods

**Value**

Subset, dimension or dimension names

---

`downloadENCODEknockdownMetadata`*Download metadata for ENCODE knockdown experiments*

---

**Description**

Download metadata for ENCODE knockdown experiments

**Usage**

```
downloadENCODEknockdownMetadata(  
  cellLine = NULL,  
  gene = NULL,  
  file = "ENCODEmetadata.rds"  
)
```

**Arguments**

<code>cellLine</code>	Character: cell line
<code>gene</code>	Character: target gene
<code>file</code>	Character: RDS filepath with metadata (if file doesn't exist, it will be created)

**Value**

Data frame containing ENCODE knockdown experiment metadata

**See Also**

Other functions related with using ENCODE expression data: [loadENCODEsamples\(\)](#), [performDifferentialExpression\(\)](#), [prepareENCODEgeneExpression\(\)](#)

**Examples**

```
downloadENCODEknockdownMetadata("HepG2", "EIF4G1")
```

---

`downloadIfNotFound`*Download data if given file is not found*

---

**Description**

Download data if given file is not found

**Usage**

```
downloadIfNotFound(link, file, ask = FALSE, toExtract = NULL)
```

**Arguments**

link	Character: link to download file
file	Character: filepath
ask	Boolean: ask to download file?
toExtract	Character: files to extract (if NULL, extract all)

**Value**

Download file if file is not found

---

ENCODEmetadata	<i>ENCODE metadata sample</i>
----------------	-------------------------------

---

**Description**

ENCODE metadata sample obtained by running the following code:

```
gene <- "EIF4G1"
cellLine <- "HepG2"
ENCODEmetadata <- downloadENCODEknockdownMetadata(cellLine, gene)

table(ENCODEmetadata$`Experiment target`)
length(unique(ENCODEmetadata$`Experiment target`))
```

---

filterCMapMetadata	<i>Filter CMap metadata</i>
--------------------	-----------------------------

---

**Description**

Filter CMap metadata

**Usage**

```
filterCMapMetadata(
  metadata,
  cellLine = NULL,
  timepoint = NULL,
  dosage = NULL,
  perturbationType = NULL
)
```

**Arguments**

metadata	Data frame (CMap metadata) or character (respective filepath)
cellLine	Character: cell line (if NULL, all values are loaded)
timepoint	Character: timepoint (if NULL, all values are loaded)
dosage	Character: dosage (if NULL, all values are loaded)
perturbationType	Character: type of perturbation (if NULL, all perturbation types are loaded)

**Value**

Filtered CMap metadata

**See Also**

Other functions related with the ranking of CMap perturbations: [as.table.referenceComparison\(\)](#), [getCMapConditions\(\)](#), [getCMapPerturbationTypes\(\)](#), [loadCMapData\(\)](#), [loadCMapZscores\(\)](#), [parseCMapID\(\)](#), [plot.perturbationChanges\(\)](#), [plot.referenceComparison\(\)](#), [plot.TargetingDrugsVSSimilarPerturbations\(\)](#), [prepareCMapPerturbations\(\)](#), [print.similarPerturbations\(\)](#), [rankSimilarPerturbations\(\)](#)

**Examples**

```
cmapMetadata <- loadCMapData("cmapMetadata.txt", "metadata")
filterCMapMetadata(cmapMetadata, cellLine="HEPG2", timepoint="2 h",
                  dosage="25 ng/mL")
```

---

findIntersectingCompounds

*Check for intersecting compounds across specific columns on both datasets*

---

**Description**

Check for intersecting compounds across specific columns on both datasets

**Usage**

```
findIntersectingCompounds(data1, data2, keys1 = NULL, keys2 = NULL)
```

**Value**

List containing three elements: matching compounds `commonCompounds` between column key 1 and key 2 from the first and second datasets, respectively

---

`fix.datatypes`*Adjust the data types for columns of a meta data frame*

---

**Description**

GCT(X) parsing initially returns data frames of row and column descriptors where all columns are of type character. This is inconvenient for analysis, so the goal of this function is to try and guess the appropriate data type for each column.

**Usage**

```
fix.datatypes(meta)
```

**Arguments**

`meta` a data.frame

**Details**

This is a low-level helper function which most users will not need to access directly

**Value**

`meta` the same data frame with (potentially) adjusted column types

**Source**

<https://github.com/cmap/cmapR>

**See Also**

Other GCTX parsing functions: [processIds\(\)](#), [readGctxIds\(\)](#), [readGctxMeta\(\)](#)

---

`GCT-class`*An S4 class to represent a GCT object*

---

**Description**

The GCT class serves to represent annotated matrices. The `mat` slot contains said data and the `rdesc` and `cdesc` slots contain data frames with annotations about the rows and columns, respectively

**Slots**

mat a numeric matrix  
rid a character vector of row ids  
cid a character vector of column ids  
rdesc a data.frame of row descriptors  
rdesc a data.frame of column descriptors  
src a character indicating the source (usually file path) of the data

**Source**

<https://github.com/cmap/cmapR>

**See Also**

<http://clue.io/help> for more information on the GCT format

---

getCMapConditions      *List available conditions in CMap datasets*

---

**Description**

Downloads metadata if not available

**Usage**

```
getCMapConditions(  
  metadata,  
  cellline = NULL,  
  timepoint = NULL,  
  dosage = NULL,  
  perturbationType = NULL,  
  control = FALSE  
)
```

**Arguments**

metadata	Data frame (CMap metadata) or character (respective filepath)
cellline	Character: cell line (if NULL, all values are loaded)
timepoint	Character: timepoint (if NULL, all values are loaded)
dosage	Character: dosage (if NULL, all values are loaded)
perturbationType	Character: type of perturbation (if NULL, all perturbation types are loaded)
control	Boolean: show controls for perturbation types?

**Value**

List of conditions in CMap datasets

**See Also**

Other functions related with the ranking of CMap perturbations: [as.table.referenceComparison\(\)](#), [filterCMapMetadata\(\)](#), [getCMapPerturbationTypes\(\)](#), [loadCMapData\(\)](#), [loadCMapZscores\(\)](#), [parseCMapID\(\)](#), [plot.perturbationChanges\(\)](#), [plot.referenceComparison\(\)](#), [plot.TargetingDrugsVSsimilarPerturbations\(\)](#), [prepareCMapPerturbations\(\)](#), [print.similarPerturbations\(\)](#), [rankSimilarPerturbations\(\)](#)

**Examples**

```
## Not run:
cmapMetadata <- loadCMapData("cmapMetadata.txt", "metadata")

## End(Not run)
getCMapConditions(cmapMetadata)
```

---

getCMapPerturbationTypes

*Get CMap perturbation types*

---

**Description**

Get CMap perturbation types

**Usage**

```
getCMapPerturbationTypes(control = FALSE)
```

**Arguments**

control            Boolean: return perturbation types used as control?

**Value**

Perturbation types and respective codes as used by CMap datasets

**See Also**

Other functions related with the ranking of CMap perturbations: [as.table.referenceComparison\(\)](#), [filterCMapMetadata\(\)](#), [getCMapConditions\(\)](#), [loadCMapData\(\)](#), [loadCMapZscores\(\)](#), [parseCMapID\(\)](#), [plot.perturbationChanges\(\)](#), [plot.referenceComparison\(\)](#), [plot.TargetingDrugsVSsimilarPerturbations\(\)](#), [prepareCMapPerturbations\(\)](#), [print.similarPerturbations\(\)](#), [rankSimilarPerturbations\(\)](#)

**Examples**

```
getCMapPerturbationTypes()
```



---

getENCODEcontrols	<i>Get experiments files for a given control</i>
-------------------	--

---

**Description**

Get experiments files for a given control

**Usage**

```
getENCODEcontrols(control, table)
```

**Arguments**

control	Character: control identifier
table	Data frame

**Value**

Character vector with respective experiment identifiers

---

HTMLfast	<i>Faster version of shiny::HTML</i>
----------	--------------------------------------

---

**Description**

Faster version of shiny::HTML

**Usage**

```
HTMLfast(text)
```

**Arguments**

text	Character: text
------	-----------------

**Value**

HTML element

---

launchCMapDataLoader *Load CMap data via a visual interface*

---

## Description

Load CMap data via a visual interface

## Usage

```
launchCMapDataLoader(  
  metadata = "cmapMetadata.txt",  
  zscores = "cmapZscores.gctx",  
  geneInfo = "cmapGeneInfo.txt",  
  compoundInfo = "cmapCompoundInfo.txt",  
  cellline = NULL,  
  timepoint = NULL,  
  dosage = NULL,  
  perturbationType = NULL  
)
```

## Arguments

metadata	Data frame (CMap metadata) or character (respective filepath)
zscores	Data frame (GCTX z-scores) or character (respective filepath to load data from file)
geneInfo	Data frame (CMap gene info) or character (respective filepath to load data from file)
compoundInfo	Data frame (CMap compound info) or character (respective filepath to load data from file)
cellLine	Character: cell line (if NULL, all values are loaded)
timepoint	Character: timepoint (if NULL, all values are loaded)
dosage	Character: dosage (if NULL, all values are loaded)
perturbationType	Character: type of perturbation (if NULL, all perturbation types are loaded)

## Value

CMap data

## See Also

Other visual interface functions: [cTRAP\(\)](#), [launchDiffExprLoader\(\)](#), [launchDrugSetEnrichmentAnalyser\(\)](#), [launchMetadataViewer\(\)](#), [launchResultPlotter\(\)](#)

---

launchDiffExprLoader *Load differential expression data via a visual interface*

---

**Description**

Currently only supports loading data from ENCODE knockdown experiments

**Usage**

```
launchDiffExprLoader(  
  cellLine = NULL,  
  gene = NULL,  
  file = "ENCODEmetadata.rds",  
  path = "."  
)
```

**Arguments**

cellLine	Character: cell line
gene	Character: target gene
file	Character: RDS filepath with metadata (if file doesn't exist, it will be created)
path	Character: path where to download files

**Value**

Differential expression data

**See Also**

Other visual interface functions: [cTRAP\(\)](#), [launchCMapDataLoader\(\)](#), [launchDrugSetEnrichmentAnalyser\(\)](#), [launchMetadataViewer\(\)](#), [launchResultPlotter\(\)](#)

---

launchDrugSetEnrichmentAnalyser  
*View and plot results via a visual interface*

---

**Description**

View and plot results via a visual interface

**Usage**

```
launchDrugSetEnrichmentAnalyser(sets, ...)
```

**Arguments**

sets	Named list of characters: named sets containing compound identifiers (obtain drug sets by running prepareDrugSets())
...	Objects

**Value**

Launches result viewer and plotter (returns NULL)

**See Also**

Other visual interface functions: [cTRAP\(\)](#), [launchCMapDataLoader\(\)](#), [launchDiffExprLoader\(\)](#), [launchMetadataViewer\(\)](#), [launchResultPlotter\(\)](#)

---

launchMetadataViewer *View metadata via a visual interface*

---

**Description**

View metadata via a visual interface

**Usage**

```
launchMetadataViewer(...)
```

**Arguments**

...	Objects
-----	---------

**Value**

Metadata viewer (returns NULL)

**See Also**

Other visual interface functions: [cTRAP\(\)](#), [launchCMapDataLoader\(\)](#), [launchDiffExprLoader\(\)](#), [launchDrugSetEnrichmentAnalyser\(\)](#), [launchResultPlotter\(\)](#)

---

launchResultPlotter    *View and plot results via a visual interface*

---

**Description**

View and plot results via a visual interface

**Usage**

```
launchResultPlotter(...)
```

**Arguments**

...                    Objects

**Value**

Launches result viewer and plotter (returns NULL)

**See Also**

Other visual interface functions: [cTRAP\(\)](#), [launchCMapDataLoader\(\)](#), [launchDiffExprLoader\(\)](#), [launchDrugSetEnrichmentAnalyser\(\)](#), [launchMetadataViewer\(\)](#)

---

listExpressionDrugSensitivityAssociation

*List available gene expression and drug sensitivity correlation matrices*

---

**Description**

List available gene expression and drug sensitivity correlation matrices

**Usage**

```
listExpressionDrugSensitivityAssociation(url = FALSE)
```

**Arguments**

url                    Boolean: return download link?

**Value**

Character vector of available gene expression and drug sensitivity correlation matrices

**See Also**

Other functions related with the prediction of targeting drugs: [as.table.referenceComparison\(\)](#), [loadExpressionDrugSensitivityAssociation\(\)](#), [plot.referenceComparison\(\)](#), [plotTargetingDrugsVSSimilarPerturbations\(\)](#), [predictTargetingDrugs\(\)](#)

**Examples**

```
listExpressionDrugSensitivityAssociation()
```

---

loadCMapData

*Load CMap data*

---

**Description**

Load CMap data (if not found, file will be automatically downloaded)

**Usage**

```
loadCMapData(
  file,
  type = c("metadata", "geneInfo", "zscores", "compoundInfo"),
  zscoresID = NULL
)
```

**Arguments**

file	Character: path to file
type	Character: type of data to load (metadata, geneInfo, zscores or compoundInfo)
zscoresID	Character: identifiers to partially load z-scores file (for performance reasons; if NULL, all identifiers will be loaded)

**Value**

Metadata as a data table

**Note**

If type = "compoundInfo", two files from **The Drug Repurposing Hub** will be downloaded containing information about drugs and perturbations. The files will be named file with `_drugs` and `_samples` before their extension, respectively.

**See Also**

Other functions related with the ranking of CMap perturbations: [as.table.referenceComparison\(\)](#), [filterCMapMetadata\(\)](#), [getCMapConditions\(\)](#), [getCMapPerturbationTypes\(\)](#), [loadCMapZScores\(\)](#), [parseCMapID\(\)](#), [plot.perturbationChanges\(\)](#), [plot.referenceComparison\(\)](#), [plotTargetingDrugsVSSimilarPerturbations\(\)](#), [prepareCMapPerturbations\(\)](#), [print.similarPerturbations\(\)](#), [rankSimilarPerturbations\(\)](#)

**Examples**

```
# Load CMap metadata (data is automatically downloaded if not available)
cmapMetadata <- loadCMapData("cmapMetadata.txt", "metadata")

# Load CMap gene info
loadCMapData("cmapGeneInfo.txt", "geneInfo")
## Not run:
# Load CMap zscores based on filtered metadata
cmapMetadataKnockdown <- filterCMapMetadata(
  cmapMetadata, cellLine="HepG2",
  perturbationType="Consensus signature from shRNAs targeting the same gene")
loadCMapData("cmapZscores.gctx.gz", "zscores", cmapMetadataKnockdown$sig_id)

## End(Not run)
```

---

loadCMapZscores	<i>Load matrix of CMap perturbation's differential expression z-scores (optional)</i>
-----------------	---

---

**Description**

Load matrix of CMap perturbation's differential expression z-scores (optional)

**Usage**

```
loadCMapZscores(data, inheritAttrs = FALSE, verbose = TRUE)
```

**Arguments**

data	perturbationChanges object
inheritAttrs	Boolean: convert to perturbationChanges object and inherit attributes from data?
verbose	Boolean: print additional details?

**Value**

Matrix containing CMap perturbation z-scores (genes as rows, perturbations as columns)

**See Also**

Other functions related with the ranking of CMap perturbations: [as.table.referenceComparison\(\)](#), [filterCMapMetadata\(\)](#), [getCMapConditions\(\)](#), [getCMapPerturbationTypes\(\)](#), [loadCMapData\(\)](#), [parseCMapID\(\)](#), [plot.perturbationChanges\(\)](#), [plot.referenceComparison\(\)](#), [plotTargetingDrugsVSSimilarPerturbations\(\)](#), [prepareCMapPerturbations\(\)](#), [print.similarPerturbations\(\)](#), [rankSimilarPerturbations\(\)](#)

**Examples**

```

metadata <- loadCMapData("cmapMetadata.txt", "metadata")
metadata <- filterCMapMetadata(metadata, cellLine="HepG2")
## Not run:
perts <- prepareCMapPerturbations(metadata, "cmapZscores.gctx",
                                   "cmapGeneInfo.txt")
zscores <- loadCMapZscores(perts[ , 1:10])

## End(Not run)

```

---

```
loadCTRPgeneExpression
```

*Load CTRP data*

---

**Description**

If given paths direct to non-existing files, those files will be downloaded

**Usage**

```

loadCTRPgeneExpression(
  geneExpressionFile = "CTRP 2.1/geneExpr.txt",
  geneInfoFile = "CTRP 2.1/geneInfo.txt",
  cellLineInfoFile = "CTRP 2.1/cellLineInfo.txt"
)

loadCTRPdrugSensitivity(
  drugSensitivityFile = "CTRP 2.1/drugSensitivity.txt",
  experimentFile = "CTRP 2.1/experimentInfo.txt",
  compoundFile = "CTRP 2.1/compoundInfo.txt"
)

loadCTRPcompoundInfo(compoundFile = "CTRP 2.1/compoundInfo.txt")

loadNCI60geneExpression(
  file = "NCI60/geneExpr.xls",
  cellLineInfoFile = "cellLineInfo.xls"
)

loadGDSC7file(file, filename, type, ...)

loadGDSC7cellLineInfo(file = "GDSC_7/cellLineInfo.xlsx")

loadGDSC7compoundInfo(file = "GDSC_7/compoundInfo.xlsx")

loadGDSC7geneExpression(file = "GDSC_7/geneExpr.txt")

loadGDSC7drugSensitivity(file = "GDSC_7/drugs.xlsx")

```



**Arguments**

geneExpressionFile      Character: path to file with gene expression  
geneInfoFile      Character: path to file with gene information  
cellLineInfoFile      Character: path to file with cell line information  
drugSensitivityFile      Character: path to file with drug sensitivity  
experimentFile      Character: path to file with experiment information  
compoundFile      Character: path to file with compound information  
file      Character: file path

**Value**

Data frame

---

loadDrugDescriptors      *Load table with drug descriptors*

---

**Description**

Load table with drug descriptors

**Usage**

```
loadDrugDescriptors(  
  source = c("NCI60", "CMap"),  
  type = c("2D", "3D"),  
  file = NULL,  
  path = NULL  
)
```

**Arguments**

source      Character: source of compounds used to calculate molecular descriptors (NCI60 or CMap)  
type      Character: load 2D or 3D molecular descriptors  
file      Character: filepath to drug descriptors (automatically downloaded if file does not exist)  
path      Character: folder where to find files (optional; file may contain the full filepath if preferred)

**Value**

Data table with drug descriptors

**See Also**

Other functions for drug set enrichment analysis: [analyseDrugSetEnrichment\(\)](#), [plotDrugSetEnrichment\(\)](#), [prepareDrugSets\(\)](#)

**Examples**

```
loadDrugDescriptors()
```

---

loadENCODEsample	<i>Load ENCODE sample</i>
------------------	---------------------------

---

**Description**

Load ENCODE sample

**Usage**

```
loadENCODEsample(metadata, replicate, control = FALSE, path = ".")
```

**Arguments**

metadata	Data frame: ENCODE metadata
replicate	Number: replicate
control	Boolean: load control experiment?
path	Character: path where to download files

**Value**

Data table with ENCODE sample data

---

loadENCODEsamples	<i>Load ENCODE samples</i>
-------------------	----------------------------

---

**Description**

Samples are automatically downloaded if they are not found in the current working directory.

**Usage**

```
loadENCODEsamples(metadata, path = ".")
```

**Arguments**

metadata	Character: ENCODE metadata
path	Character: path where to download files

**Value**

List of loaded ENCODE samples

**See Also**

Other functions related with using ENCODE expression data: [downloadENCODEknockdownMetadata\(\)](#), [performDifferentialExpression\(\)](#), [prepareENCODEgeneExpression\(\)](#)

**Examples**

```
if (interactive()) {  
  # Load ENCODE metadata for a specific cell line and gene  
  cellLine <- "HepG2"  
  gene <- c("EIF4G1", "U2AF2")  
  ENCODEmetadata <- downloadENCODEknockdownMetadata(cellLine, gene)  
  
  # Load samples based on filtered ENCODE metadata  
  loadENCODEsamples(ENCODEmetadata)  
}
```

---

loadExpressionDrugSensitivityAssociation

*Load gene expression and drug sensitivity correlation matrix*

---

**Description**

Load gene expression and drug sensitivity correlation matrix

**Usage**

```
loadExpressionDrugSensitivityAssociation(  
  source,  
  file = NULL,  
  path = NULL,  
  rows = NULL,  
  cols = NULL,  
  loadValues = FALSE  
)
```

**Arguments**

source	Character: source of matrix to load; see <a href="#">listExpressionDrugSensitivityAssociation</a>
file	Character: filepath to gene expression and drug sensitivity association dataset (automatically downloaded if file does not exist)
path	Character: folder where to find files (optional; file may contain the full filepath if preferred)
rows	Character or integer: rows

cols	Character or integer: columns
loadValues	Boolean: load data values (if available)? If FALSE, downstream functions will load and process directly from the file chunk by chunk, resulting in a lower memory footprint

**Value**

Correlation matrix between gene expression (rows) and drug sensitivity (columns)

**See Also**

Other functions related with the prediction of targeting drugs: [as.table.referenceComparison\(\)](#), [listExpressionDrugSensitivityAssociation\(\)](#), [plot.referenceComparison\(\)](#), [plotTargetingDrugsVSsimilarPeptides\(\)](#), [predictTargetingDrugs\(\)](#)

**Examples**

```
gdsc <- listExpressionDrugSensitivityAssociation()[[1]]
loadExpressionDrugSensitivityAssociation(gdsc)
```

---

loadNCI60drugSensitivity  
*Load CTRP data*

---

**Description**

If given paths direct to non-existing files, those files will be downloaded

**Usage**

```
loadNCI60drugSensitivity(file = "NCI60/drugSensitivity.xls")
```

**Arguments**

file	Character: file path
------	----------------------

**Value**

Data frame

---

`matchStatsWithDrugSetsID`*Match identifiers between data and drug sets*

---

**Description**

Match identifiers between data and drug sets

**Usage**

```
matchStatsWithDrugSetsID(  
  sets,  
  stats,  
  col = "values",  
  keyColSets = NULL,  
  keyColStats = NULL  
)
```

**Arguments**

<code>sets</code>	Named list of characters: named sets containing compound identifiers (obtain drug sets by running <code>prepareDrugSets()</code> )
<code>stats</code>	Named numeric vector or either a <code>similarPerturbations</code> or a <code>targetingDrugs</code> object (obtained after running <a href="#">rankSimilarPerturbations</a> or <a href="#">predictTargetingDrugs</a> , respectively)
<code>col</code>	Character: name of the column to use for statistics (only required if class of <code>stats</code> is either <code>similarPerturbations</code> or <code>targetingDrugs</code> )
<code>keyColSets</code>	Character: column from <code>sets</code> to compare with column <code>keyColStats</code> from <code>stats</code> ; automatically selected if NULL
<code>keyColStats</code>	Character: column from <code>stats</code> to compare with column <code>keyColSets</code> from <code>sets</code> ; automatically selected if NULL

**Value**

Statistic values from input data and corresponding identifiers as names (if no match is found, the original identifier from argument `stats` is used)

---

parseCMapID *Parse CMap identifier*

---

**Description**

Parse CMap identifier

**Usage**

```
parseCMapID(id, cellLine = FALSE)
```

**Arguments**

id	Character: CMap identifier
cellLine	Boolean: if TRUE, return cell line information from CMap identifier; else, return the CMap identifier without the cell line

**Value**

Character vector with information from CMap identifiers

**See Also**

Other functions related with the ranking of CMap perturbations: [as.table.referenceComparison\(\)](#), [filterCMapMetadata\(\)](#), [getCMapConditions\(\)](#), [getCMapPerturbationTypes\(\)](#), [loadCMapData\(\)](#), [loadCMapZscores\(\)](#), [plot.perturbationChanges\(\)](#), [plot.referenceComparison\(\)](#), [plotTargetingDrugsVSsimilarP](#), [prepareCMapPerturbations\(\)](#), [print.similarPerturbations\(\)](#), [rankSimilarPerturbations\(\)](#)

**Examples**

```
id <- c("CVD001_HEPG2_24H:BRD-K94818765-001-01-0:4.8",
       "CVD001_HEPG2_24H:BRD-K96188950-001-04-5:4.3967",
       "CVD001_HUH7_24H:BRD-A14014306-001-01-1:4.1")
parseCMapID(id, cellLine=TRUE)
parseCMapID(id, cellLine=FALSE)
```

---

performDifferentialExpression  
*Perform differential gene expression based on ENCODE data*

---

**Description**

Perform differential gene expression based on ENCODE data

**Usage**

```
performDifferentialExpression(counts)
```

**Arguments**

counts            Data frame: gene expression

**Value**

Data frame with differential gene expression results between knockdown and control

**See Also**

Other functions related with using ENCODE expression data: [downloadENCODEknockdownMetadata\(\)](#), [loadENCODEsamples\(\)](#), [prepareENCODEgeneExpression\(\)](#)

**Examples**

```
if (interactive()) {
  # Download ENCODE metadata for a specific cell line and gene
  cellLine <- "HepG2"
  gene <- "EIF4G1"
  ENCODEmetadata <- downloadENCODEknockdownMetadata(cellLine, gene)

  # Download samples based on filtered ENCODE metadata
  ENCODEsamples <- loadENCODEsamples(ENCODEmetadata)[[1]]

  counts <- prepareENCODEgeneExpression(ENCODEsamples)

  # Remove low coverage (at least 10 counts shared across two samples)
  minReads <- 10
  minSamples <- 2
  filter <- rowSums(counts[ , -c(1, 2)] >= minReads) >= minSamples
  counts <- counts[filter, ]

  # Convert ENSEMBL identifier to gene symbol
  counts$gene_id <- convertGeneIdentifiers(counts$gene_id)

  # Perform differential gene expression analysis
  diffExpr <- performDifferentialExpression(counts)
}
```

---

performGSEA

*Perform GSEA*

---

**Description**

Perform GSEA

**Usage**

```
performGSEA(pathways, stats)
```

**Value**

List with results of running GSEA

---

plot.perturbationChanges

*Operations on a perturbationChanges object*

---

**Description**

Operations on a perturbationChanges object

**Usage**

```
## S3 method for class 'perturbationChanges'
plot(
  x,
  perturbation,
  input,
  method = c("spearman", "pearson", "gsea"),
  geneSize = 150,
  genes = c("both", "top", "bottom"),
  ...,
  title = NULL
)
```

```
## S3 method for class 'perturbationChanges'
x[i, j, drop = FALSE, ...]
```

```
## S3 method for class 'perturbationChanges'
dim(x)
```

```
## S3 method for class 'perturbationChanges'
dimnames(x)
```

**Arguments**

x	perturbationChanges object
perturbation	Character (perturbation identifier) or a similarPerturbations table (from which the respective perturbation identifiers are retrieved)
input	Named numeric vector of differentially expressed genes whose names are gene identifiers and respective values are a statistic that represents significance and magnitude of differentially expressed genes (e.g. t-statistics); or character of gene symbols composing a gene set that is tested for enrichment in reference data (only used if method includes gsea)
method	Character: comparison method (spearman, pearson or gsea; multiple methods may be selected at once)



geneSize	Numeric: number of top up-/down-regulated genes to use as gene sets to test for enrichment in reference data; if a 2-length numeric vector, the first index is the number of top up-regulated genes and the second index is the number of down-regulated genes used to create gene sets; only used if method includes gsea and if input is not a gene set
genes	Character: when plotting gene set enrichment analysis (GSEA), plot most up-regulated genes (genes = "top"), most down-regulated genes (genes = "bottom") or both (genes = "both"); only used if method = "gsea" and geneset = NULL
...	Extra arguments
title	Character: plot title (if NULL, the default title depends on the context; ignored when plotting multiple perturbations)
i, j	Character or numeric indexes specifying elements to extract
drop	Boolean: coerce result to the lowest possible dimension?

**Value**

Subset, plot or return dimensions or names of a perturbationChanges object

**See Also**

Other functions related with the ranking of CMap perturbations: [as.table.referenceComparison\(\)](#), [filterCMapMetadata\(\)](#), [getCMapConditions\(\)](#), [getCMapPerturbationTypes\(\)](#), [loadCMapData\(\)](#), [loadCMapZscores\(\)](#), [parseCMapID\(\)](#), [plot.referenceComparison\(\)](#), [plotTargetingDrugsVSSimilarPerturbations\(\)](#), [prepareCMapPerturbations\(\)](#), [print.similarPerturbations\(\)](#), [rankSimilarPerturbations\(\)](#)

**Examples**

```
data("diffExprStat")
data("cmapPerturbationsKD")

compareKD <- rankSimilarPerturbations(diffExprStat, cmapPerturbationsKD)
EIF4G1knockdown <- grep("EIF4G1", compareKD[[1]], value=TRUE)
plot(cmapPerturbationsKD, EIF4G1knockdown, diffExprStat, method="spearman")
plot(cmapPerturbationsKD, EIF4G1knockdown, diffExprStat, method="pearson")
plot(cmapPerturbationsKD, EIF4G1knockdown, diffExprStat, method="gsea")

data("cmapPerturbationsCompounds")
pert <- "CVD001_HEPG2_24H:BRD-A14014306-001-01-1:4.1"
plot(cmapPerturbationsCompounds, pert, diffExprStat, method="spearman")
plot(cmapPerturbationsCompounds, pert, diffExprStat, method="pearson")
plot(cmapPerturbationsCompounds, pert, diffExprStat, method="gsea")

# Multiple cell line perturbations
pert <- "CVD001_24H:BRD-A14014306-001-01-1:4.1"
plot(cmapPerturbationsCompounds, pert, diffExprStat, method="spearman")
plot(cmapPerturbationsCompounds, pert, diffExprStat, method="pearson")
plot(cmapPerturbationsCompounds, pert, diffExprStat, method="gsea")
```

---

```
plot.referenceComparison
```

*Plot data comparison*

---

### Description

If `element = NULL`, comparison is plotted based on all elements. Otherwise, show scatter or GSEA plots for a single element compared with previously given differential expression results.

### Usage

```
## S3 method for class 'referenceComparison'
plot(
  x,
  element = NULL,
  method = c("spearman", "pearson", "gsea", "rankProduct"),
  n = c(3, 3),
  showMetadata = TRUE,
  plotNonRankedPerturbations = FALSE,
  alpha = 0.3,
  genes = c("both", "top", "bottom"),
  ...,
  zscores = NULL,
  title = NULL
)
```

### Arguments

<code>x</code>	referenceComparison object: obtained after running <a href="#">rankSimilarPerturbations()</a> or <a href="#">predictTargetingDrugs()</a>
<code>element</code>	Character: identifier in the first column of <code>x</code>
<code>method</code>	Character: method to plot results; choose between <code>spearman</code> , <code>pearson</code> , <code>gsea</code> or <code>rankProduct</code> (the last one is only available if <code>element = NULL</code> )
<code>n</code>	Numeric: number of top and bottom genes to label (if a vector of two numbers is given, the first and second numbers will be used as the number of top and bottom genes to label, respectively); only used if <code>element = NULL</code>
<code>showMetadata</code>	Boolean: show available metadata information instead of identifiers (if available)? Only used if <code>element = NULL</code>
<code>plotNonRankedPerturbations</code>	Boolean: plot non-ranked data in grey? Only used if <code>element = NULL</code>
<code>alpha</code>	Numeric: transparency; only used if <code>element = NULL</code>
<code>genes</code>	Character: when plotting gene set enrichment analysis (GSEA), plot most up-regulated genes ( <code>genes = "top"</code> ), most down-regulated genes ( <code>genes = "bottom"</code> ) or both ( <code>genes = "both"</code> ); only used if <code>method = "gsea"</code> and <code>geneset = NULL</code>
<code>...</code>	Extra arguments currently not used

zscores	Data frame (GCTX z-scores) or character (respective filepath to load data from file)
title	Character: plot title (if NULL, the default title depends on the context; ignored when plotting multiple perturbations)

**Value**

Plot illustrating the reference comparison

**See Also**

Other functions related with the ranking of CMap perturbations: [as.table.referenceComparison\(\)](#), [filterCMapMetadata\(\)](#), [getCMapConditions\(\)](#), [getCMapPerturbationTypes\(\)](#), [loadCMapData\(\)](#), [loadCMapZscores\(\)](#), [parseCMapID\(\)](#), [plot.perturbationChanges\(\)](#), [plotTargetingDrugsVSsimilarPerturbations\(\)](#), [prepareCMapPerturbations\(\)](#), [print.similarPerturbations\(\)](#), [rankSimilarPerturbations\(\)](#)

Other functions related with the prediction of targeting drugs: [as.table.referenceComparison\(\)](#), [listExpressionDrugSensitivityAssociation\(\)](#), [loadExpressionDrugSensitivityAssociation\(\)](#), [plotTargetingDrugsVSsimilarPerturbations\(\)](#), [predictTargetingDrugs\(\)](#)

**Examples**

```
# Example of a differential expression profile
data("diffExprStat")

## Not run:
# Download and load CMap perturbations to compare with
cellLine <- "HepG2"
cmapMetadataKD <- filterCMapMetadata(
  "cmapMetadata.txt", cellLine=cellLine,
  perturbationType="Consensus signature from shRNAs targeting the same gene")

cmapPerturbationsKD <- prepareCMapPerturbations(
  cmapMetadataKD, "cmapZscores.gctx", "cmapGeneInfo.txt", loadZscores=TRUE)

## End(Not run)

# Rank similar CMap perturbations
compareKD <- rankSimilarPerturbations(diffExprStat, cmapPerturbationsKD)

# Plot ranked list of CMap perturbations
plot(compareKD, method="spearman")
plot(compareKD, method="spearman", n=c(7, 3))
plot(compareKD, method="pearson")
plot(compareKD, method="gsea")

# Plot results for a single perturbation
pert <- compareKD[[1, 1]]
plot(compareKD, pert, method="spearman", zscores=cmapPerturbationsKD)
plot(compareKD, pert, method="pearson", zscores=cmapPerturbationsKD)
plot(compareKD, pert, method="gsea", zscores=cmapPerturbationsKD)
```

```

# Predict targeting drugs based on a given differential expression profile
gdsc <- loadExpressionDrugSensitivityAssociation("GDSC 7")
predicted <- predictTargetingDrugs(diffExprStat, gdsc)

# Plot ranked list of targeting drugs
plot(predicted, method="spearman")
plot(predicted, method="spearman", n=c(7, 3))
plot(predicted, method="pearson")
plot(predicted, method="gsea")

# Plot results for a single targeting drug
drug <- predicted$compound[[4]]
plot(predicted, drug, method="spearman")
plot(predicted, drug, method="pearson")
plot(predicted, drug, method="gsea")

```

---

plotDrugSetEnrichment *Plot drug set enrichment*

---

## Description

Plot drug set enrichment

## Usage

```

plotDrugSetEnrichment(
  sets,
  stats,
  col = "rankProduct_rank",
  selectedSets = NULL,
  keyColSets = NULL,
  keyColStats = NULL
)

```

## Arguments

sets	Named list of characters: named sets containing compound identifiers (obtain drug sets by running <code>prepareDrugSets()</code> )
stats	Named numeric vector or either a <code>similarPerturbations</code> or a <code>targetingDrugs</code> object (obtained after running <a href="#">rankSimilarPerturbations</a> or <a href="#">predictTargetingDrugs</a> , respectively)
col	Character: name of the column to use for statistics (only required if class of stats is either <code>similarPerturbations</code> or <code>targetingDrugs</code> )
selectedSets	Character: drug sets to plot (if NULL, plot all)
keyColSets	Character: column from sets to compare with column <code>keyColStats</code> from stats; automatically selected if NULL
keyColStats	Character: column from stats to compare with column <code>keyColSets</code> from sets; automatically selected if NULL

**Value**

List of GSEA plots per drug set

**See Also**

Other functions for drug set enrichment analysis: [analyseDrugSetEnrichment\(\)](#), [loadDrugDescriptors\(\)](#), [prepareDrugSets\(\)](#)

**Examples**

```
descriptors <- loadDrugDescriptors()
drugSets <- prepareDrugSets(descriptors)

# Analyse drug set enrichment in ranked targeting drugs for a differential
# expression profile
data("diffExprStat")
gdsc <- loadExpressionDrugSensitivityAssociation("GDSC")
predicted <- predictTargetingDrugs(diffExprStat, gdsc)

plotDrugSetEnrichment(drugSets, predicted)
```

---

plotESplot

*Render GSEA enrichment plot*

---

**Description**

Render GSEA enrichment plot

**Usage**

```
plotESplot(enrichmentScore, gseaStat, compact = FALSE)
```

**Value**

GSEA enrichment plot

---

plotGSEA

*Plot gene set enrichment analysis (GSEA)*

---

**Description**

Plot gene set enrichment analysis (GSEA)

**Usage**

```
plotGSEA(
  stats,
  geneset,
  genes = c("both", "top", "bottom"),
  title = "GSEA plot",
  gseaParam = 1,
  compact = FALSE
)
```

**Arguments**

stats	Named numeric vector: statistics
genes	Character: when plotting gene set enrichment analysis (GSEA), plot most up-regulated genes (genes = "top"), most down-regulated genes (genes = "bottom") or both (genes = "both"); only used if method = "gsea" and geneset = NULL
title	Character: plot title (if NULL, the default title depends on the context; ignored when plotting multiple perturbations)
gseaParam	Numeric: GSEA-like parameter
compact	Boolean: render a compact version of the GSEA plot?

**Value**

Grid of plots illustrating a GSEA plot

---

plotMetricDistribution

*Plot metric distribution*

---

**Description**

Plot metric distribution

**Usage**

```
plotMetricDistribution(stat, compact = FALSE)
```

**Value**

Metric distribution plot

---

plotSingleCorr	<i>Render scatter plot to show a single relationship</i>
----------------	--

---

**Description**

Render scatter plot to show a single relationship

**Usage**

```
plotSingleCorr(perturbation, ylabel, diffExprGenes, title = NULL)
```

**Arguments**

perturbation	List of named numeric vectors containing the differential expression profile score per gene for a perturbation; each perturbation of the list will be rendered with a different colour
ylabel	Character: Y axis label
diffExprGenes	Named numeric vector
title	Character: plot title (if NULL, the default title depends on the context; ignored when plotting multiple perturbations)

**Value**

Scatter plot

---

plotTargetingDrugsVSSimilarPerturbations	<i>Plot similar perturbations against predicted targeting drugs</i>
--	---

---

**Description**

Plot similar perturbations against predicted targeting drugs

**Usage**

```
plotTargetingDrugsVSSimilarPerturbations(  
  targetingDrugs,  
  similarPerturbations,  
  column,  
  labelBy = "pert_iname",  
  quantileThreshold = 0.25,  
  showAllScores = FALSE,  
  keyColTargetingDrugs = NULL,  
  keyColSimilarPerturbations = NULL  
)
```





---

predictTargetingDrugs *Predict targeting drugs*

---

## Description

Identify compounds that may target the phenotype associated with a user-provided differential expression profile by comparing such against a correlation matrix of gene expression and drug sensitivity.

## Usage

```
predictTargetingDrugs(  
  input,  
  expressionDrugSensitivityCor,  
  method = c("spearman", "pearson", "gsea"),  
  geneSize = 150,  
  isDrugActivityDirectlyProportionalToSensitivity = NULL,  
  threads = 1,  
  chunkGiB = 1,  
  verbose = FALSE  
)
```

## Arguments

input	Named numeric vector of differentially expressed genes whose names are gene identifiers and respective values are a statistic that represents significance and magnitude of differentially expressed genes (e.g. t-statistics); or character of gene symbols composing a gene set that is tested for enrichment in reference data (only used if method includes gsea)
expressionDrugSensitivityCor	Matrix or character: correlation matrix of gene expression (rows) and drug sensitivity (columns) across cell lines or path to file containing such data; see <a href="#">loadExpressionDrugSensitivityAssociation()</a> .
method	Character: comparison method (spearman, pearson or gsea; multiple methods may be selected at once)
geneSize	Numeric: number of top up-/down-regulated genes to use as gene sets to test for enrichment in reference data; if a 2-length numeric vector, the first index is the number of top up-regulated genes and the second index is the number of down-regulated genes used to create gene sets; only used if method includes gsea and if input is not a gene set
isDrugActivityDirectlyProportionalToSensitivity	Boolean: are the values used for drug activity directly proportional to drug sensitivity? If NULL, the argument expressionDrugSensitivityCor must have a non-NULL value for attribute isDrugActivityDirectlyProportionalToSensitivity.
threads	Integer: number of parallel threads

chunkGiB	Numeric: if second argument is a path to an HDF5 file (.h5 extension), that file is loaded and processed in chunks of a given size in gibibytes (GiB); lower values decrease peak RAM usage (see details below)
verbose	Boolean: print additional details?

**Value**

Data table with correlation and/or GSEA score results

**Process data by chunks**

If a file path to a valid HDF5 (.h5) file is provided instead of a data matrix, that file can be loaded and processed in chunks of size chunkGiB, resulting in decreased peak memory usage.

The default value of 1 GiB (1 GiB =  $1024^3$  bytes) allows loading chunks of ~10000 columns and 14000 rows ( $10000 * 14000 * 8 \text{ bytes} / 1024^3 = 1.04 \text{ GiB}$ ).

**GSEA score**

When method = "gsea", weighted connectivity scores (WTCS) are calculated ([https://clue.io/connectopedia/cmap\\_algorithms](https://clue.io/connectopedia/cmap_algorithms)).

**See Also**

Other functions related with the prediction of targeting drugs: [as.table.referenceComparison\(\)](#), [listExpressionDrugSensitivityAssociation\(\)](#), [loadExpressionDrugSensitivityAssociation\(\)](#), [plot.referenceComparison\(\)](#), [plotTargetingDrugsVSimilarPerturbations\(\)](#)

**Examples**

```
# Example of a differential expression profile
data("diffExprStat")

# Load expression and drug sensitivity association derived from GDSC data
gdsc <- loadExpressionDrugSensitivityAssociation("GDSC 7")

# Predict targeting drugs on a differential expression profile
predictTargetingDrugs(diffExprStat, gdsc)
```

---

```
prepareCMapPerturbations
  Prepare CMap perturbation data
```

---

**Description**

Prepare CMap perturbation data

**Usage**

```
prepareCMapPerturbations(
  metadata,
  zscores,
  geneInfo,
  compoundInfo = NULL,
  ...,
  loadZscores = FALSE
)
```

**Arguments**

metadata	Data frame (CMap metadata) or character (respective filepath to load data from file)
zscores	Data frame (GCTX z-scores) or character (respective filepath to load data from file)
geneInfo	Data frame (CMap gene info) or character (respective filepath to load data from file)
compoundInfo	Data frame (CMap compound info) or character (respective filepath to load data from file)
...	Arguments passed on to <a href="#">filterCMapMetadata</a>
cellLine	Character: cell line (if NULL, all values are loaded)
timepoint	Character: timepoint (if NULL, all values are loaded)
dosage	Character: dosage (if NULL, all values are loaded)
perturbationType	Character: type of perturbation (if NULL, all perturbation types are loaded)
loadZscores	Boolean: load matrix of perturbation z-scores? Not recommended in systems with less than 30GB of RAM; if FALSE, downstream functions will load and process the file directly chunk by chunk, resulting in a lower memory footprint

**Value**

CMap perturbation data attributes and filename

**See Also**

Other functions related with the ranking of CMap perturbations: [as.table.referenceComparison\(\)](#), [filterCMapMetadata\(\)](#), [getCMapConditions\(\)](#), [getCMapPerturbationTypes\(\)](#), [loadCMapData\(\)](#), [loadCMapZscores\(\)](#), [parseCMapID\(\)](#), [plot.perturbationChanges\(\)](#), [plot.referenceComparison\(\)](#), [plotTargetingDrugsVSSimilarPerturbations\(\)](#), [print.similarPerturbations\(\)](#), [rankSimilarPerturbations\(\)](#)

**Examples**

```
metadata <- loadCMapData("cmapMetadata.txt", "metadata")
metadata <- filterCMapMetadata(metadata, cellLine="HepG2")
## Not run:
prepareCMapPerturbations(metadata, "cmapZscores.gctx", "cmapGeneInfo.txt")
```

```
## End(Not run)
```

---

```
prepareDrugSets
```

*Prepare drug sets from a table with compound descriptors*

---

## Description

Create a list of drug sets for each character and numeric column. For each character column, drugs are split across that column's unique values (see argument `maxUniqueElems`). For each numeric column, drugs are split across evenly-distributed bins.

## Usage

```
prepareDrugSets(  
  table,  
  id = 1,  
  maxUniqueElems = 15,  
  maxBins = 15,  
  k = 5,  
  minPoints = NULL  
)
```

## Arguments

<code>table</code>	Data frame: drug descriptors
<code>id</code>	Integer or character: index or name of the identifier column
<code>maxUniqueElems</code>	Numeric: ignore character columns with more unique elements than <code>maxUniqueElems</code>
<code>maxBins</code>	Numeric: maximum number of bins for numeric columns
<code>k</code>	Numeric: constant; the higher the constant, the smaller the bin size (check <code>minpts</code> )
<code>minPoints</code>	Numeric: minimum number of points in a bin (if <code>NULL</code> , the minimum number of points is the number of non-missing values divided by <code>maxBins</code> divided by <code>k</code> )

## Value

Named list of characters: named drug sets with respective compound identifiers as list elements

## See Also

Other functions for drug set enrichment analysis: [analyseDrugSetEnrichment\(\)](#), [loadDrugDescriptors\(\)](#), [plotDrugSetEnrichment\(\)](#)

## Examples

```
descriptors <- loadDrugDescriptors("NCI60")  
prepareDrugSets(descriptors)
```

---

```
prepareENCODEgeneExpression
      Load ENCODE gene expression data
```

---

**Description**

Load ENCODE gene expression data

**Usage**

```
prepareENCODEgeneExpression(samples)
```

**Arguments**

`samples`          List of loaded ENCODE samples

**Value**

Data frame containing gene read counts

**See Also**

[convertGeneIdentifiers\(\)](#)

Other functions related with using ENCODE expression data: [downloadENCODEknockdownMetadata\(\)](#), [loadENCODEsamples\(\)](#), [performDifferentialExpression\(\)](#)

**Examples**

```
if (interactive()) {
  # Load ENCODE metadata for a specific cell line and gene
  cellLine <- "HepG2"
  gene <- "EIF4G1"
  ENCODEmetadata <- downloadENCODEknockdownMetadata(cellLine, gene)

  # Load samples based on filtered ENCODE metadata
  ENCODEsamples <- loadENCODEsamples(ENCODEmetadata[[1]])

  prepareENCODEgeneExpression(ENCODEsamples)
}
```

---

`prepareExpressionDrugSensitivityAssociation`*Prepare gene expression and drug sensitivity correlation matrix*

---

**Description**

Prepare gene expression and drug sensitivity correlation matrix

**Usage**

```
prepareExpressionDrugSensitivityAssociation(  
  dataset = c("GDSC 7", "CTRP 2.1", "NCI60"),  
  method = "spearman"  
)
```

**Arguments**

dataset	Character: dataset to use (CTRP, GDSC or NCI60)
method	Character: correlation method to use between gene expression and drug sensitivity

**Details**

If path directs to non-existing files, data will be downloaded.

**Value**

Correlation matrix between gene expression and drug sensitivity

---

`prepareGSEAgeneSets`     *Prepare GSEA gene sets*

---

**Description**

Prepare GSEA gene sets

**Usage**

```
prepareGSEAgeneSets(input, geneSize)
```

**Arguments**

input	Named numeric vector of differentially expressed genes whose names are gene identifiers and respective values are a statistic that represents significance and magnitude of differentially expressed genes (e.g. t-statistics); or character of gene symbols composing a gene set that is tested for enrichment in reference data (only used if method includes gsea)
geneSize	Numeric: number of top up-/down-regulated genes to use as gene sets to test for enrichment in reference data; if a 2-length numeric vector, the first index is the number of top up-regulated genes and the second index is the number of down-regulated genes used to create gene sets; only used if method includes gsea and if input is not a gene set

**Value**

List of gene sets

---

prepareSetsCompoundInfo

*Get drug sets' compound info*

---

**Description**

Get drug sets' compound info

**Usage**

```
prepareSetsCompoundInfo(sets)
```

**Arguments**

sets	Named list of characters: named sets containing compound identifiers (obtain drug sets by running prepareDrugSets())
------	--

**Value**

List containing drug sets' compound info

---

```
prepareStatsCompoundInfo
```

*Prepare stats' compound information*

---

### Description

Prepare stats' compound information

### Usage

```
prepareStatsCompoundInfo(stats)
```

### Arguments

stats	Named numeric vector or either a <code>similarPerturbations</code> or a <code>targetingDrugs</code> object (obtained after running <code>rankSimilarPerturbations</code> or <code>predictTargetingDrugs</code> , respectively)
-------	--

### Value

List containing stats' compound info

---

```
prepareWordBreak
```

*Create word break opportunities (for HTML) using given characters*

---

### Description

Create word break opportunities (for HTML) using given characters

### Usage

```
prepareWordBreak(
  str,
  pattern = c(".", "-", "\\", "/", "_", ",", " ", "+", "="),
  html = TRUE
)
```

### Arguments

str	Character: text
pattern	Character: pattern(s) of interest to be used as word break opportunities
html	Boolean: convert to HTML?

### Value

String containing HTML elements



---

```
print.similarPerturbations
    Print a similarPerturbations object
```

---

**Description**

Print a similarPerturbations object

**Usage**

```
## S3 method for class 'similarPerturbations'
print(x, perturbation = NULL, ...)
```

**Arguments**

x	similarPerturbations object
perturbation	Character (perturbation identifier) or numeric (perturbation index)
...	Extra parameters passed to print

**Value**

Information on perturbationChanges object or on specific perturbations

**See Also**

Other functions related with the ranking of CMap perturbations: [as.table.referenceComparison\(\)](#), [filterCMapMetadata\(\)](#), [getCMapConditions\(\)](#), [getCMapPerturbationTypes\(\)](#), [loadCMapData\(\)](#), [loadCMapZscores\(\)](#), [parseCMapID\(\)](#), [plot.perturbationChanges\(\)](#), [plot.referenceComparison\(\)](#), [plotTargetingDrugsVSSimilarPerturbations\(\)](#), [prepareCMapPerturbations\(\)](#), [rankSimilarPerturbations\(\)](#)

---

```
processByChunks    Process data by chunks
```

---

**Description**

Process data by chunks

**Usage**

```
processByChunks(
  data,
  FUN,
  num,
  ...,
  threads = 1,
  chunkGiB = 1,
  verbose = FALSE
)
```

**Arguments**

data	Character containing a HDF5 file path (allowing partial loading) or data matrix (processed as single chunk if data matrix)
FUN	Function: function to run for each chunk
num	Numeric: numbers of methods to run per chunk
...	Arguments passed to FUN
threads	Integer: number of parallel threads
chunkGiB	Numeric: size (in gibibytes) of chunks to load reference file; only if argument reference is a file path
verbose	Boolean: print additional details?

**Value**

Results of running FUN

**Note**

All rows from file are currently loaded when processing chunks.

---

processIds	<i>Return a subset of requested GCTX row/column ids out of the universe of all ids</i>
------------	--

---

**Description**

Return a subset of requested GCTX row/column ids out of the universe of all ids

**Usage**

```
processIds(ids, all_ids, type = "rid")
```

**Arguments**

ids	vector of requested ids. If NULL, no subsetting is performed
all_ids	vector of universe of ids
type	flag indicating the type of ids being processed

**Details**

This is a low-level helper function which most users will not need to access directly

**Value**

a list with the following elements `ids`: a character vector of the processed ids `idx`: an integer list of their corresponding indices in `all_ids`

**Source**

<https://github.com/cmap/cmapR>

**See Also**

Other GCTX parsing functions: `fix.datatypes()`, `readGctxIds()`, `readGctxMeta()`

---

rankAgainstReference *Compare multiple methods and rank against reference accordingly*

---

**Description**

Compare multiple methods and rank against reference accordingly

**Usage**

```
rankAgainstReference(
  input,
  reference,
  method = c("spearman", "pearson", "gsea"),
  geneSize = 150,
  celllines = NULL,
  celllineMean = "auto",
  rankByAscending = TRUE,
  rankPerCellLine = FALSE,
  threads = 1,
  chunkGiB = 1,
  verbose = FALSE
)
```

**Arguments**

input	Named numeric vector of differentially expressed genes whose names are gene identifiers and respective values are a statistic that represents significance and magnitude of differentially expressed genes (e.g. t-statistics); or character of gene symbols composing a gene set that is tested for enrichment in reference data (only used if method includes gsea)
reference	Data matrix or character object with file path to CMap perturbations (see <code>prepareCMapPerturbations()</code> ) or gene expression and drug sensitivity association (see <code>loadExpressionDrugSensitivityAssociation()</code> )
method	Character: comparison method (spearman, pearson or gsea; multiple methods may be selected at once)
geneSize	Numeric: number of top up-/down-regulated genes to use as gene sets to test for enrichment in reference data; if a 2-length numeric vector, the first index is the number of top up-regulated genes and the second index is the number of down-regulated genes used to create gene sets; only used if method includes gsea and if input is not a gene set

cellLines	Integer: number of unique cell lines
cellLineMean	Boolean: add rows with the mean of method across cell lines? If cellLineMean = "auto" (default), rows will be added when data for more than one cell line is available.
rankByAscending	Boolean: rank values based on their ascending (TRUE) or descending (FALSE) order?
rankPerCellLine	Boolean: rank results based on both individual cell lines and mean scores across cell lines (TRUE) or based on mean scores alone (FALSE)? If cellLineMean = FALSE, individual cell line conditions are always ranked.
threads	Integer: number of parallel threads
chunkGiB	Numeric: if second argument is a path to an HDF5 file (.h5 extension), that file is loaded and processed in chunks of a given size in gibibytes (GiB); lower values decrease peak RAM usage (see details below)
verbose	Boolean: print additional details?

**Value**

Data table with correlation and/or GSEA score results

**Process data by chunks**

If a file path to a valid HDF5 (.h5) file is provided instead of a data matrix, that file can be loaded and processed in chunks of size chunkGiB, resulting in decreased peak memory usage.

The default value of 1 GiB (1 GiB =  $1024^3$  bytes) allows loading chunks of ~10000 columns and 14000 rows ( $10000 * 14000 * 8 \text{ bytes} / 1024^3 = 1.04 \text{ GiB}$ ).

**GSEA score**

When method = "gsea", weighted connectivity scores (WTCS) are calculated ([https://clue.io/connectopedia/cmap\\_algorithms](https://clue.io/connectopedia/cmap_algorithms)).

---

rankColumns

*Rank columns in a dataset*

---

**Description**

Rank columns in a dataset

**Usage**

```
rankColumns(table, rankingInfo, rankByAscending = TRUE, sort = FALSE)
```

**Arguments**

table	Data table: data; first column must be identifiers
rankingInfo	Data table: boolean values of which rows to rank based on columns (column names to be ranked must exactly match those available in argument table); first column must be identifiers
rankByAscending	Boolean: rank values based on their ascending (TRUE) or descending (FALSE) order?
sort	Boolean: sort data based on rank product's rank (if multiple methods are available) or by available ranks

**Details**

The rank product's rank is calculated if more than one method is ranked.

**Value**

Data table with the contents of table and extra columns with respective rankings

**Note**

The first column of data and rankingInfo must contain common identifiers.

---

rankSimilarPerturbations

*Rank differential expression profile against CMap perturbations by similarity*

---

**Description**

Compare differential expression results against CMap perturbations.

**Usage**

```
rankSimilarPerturbations(
  input,
  perturbations,
  method = c("spearman", "pearson", "gsea"),
  geneSize = 150,
  cellLineMean = "auto",
  rankPerCellLine = FALSE,
  threads = 1,
  chunkGiB = 1,
  verbose = FALSE
)
```

**Arguments**

input	Named numeric vector of differentially expressed genes whose names are gene identifiers and respective values are a statistic that represents significance and magnitude of differentially expressed genes (e.g. t-statistics); or character of gene symbols composing a gene set that is tested for enrichment in reference data (only used if method includes gsea)
perturbations	perturbationChanges object: CMap perturbations (check <a href="#">prepareCMapPerturbations()</a> )
method	Character: comparison method (spearman, pearson or gsea; multiple methods may be selected at once)
geneSize	Numeric: number of top up-/down-regulated genes to use as gene sets to test for enrichment in reference data; if a 2-length numeric vector, the first index is the number of top up-regulated genes and the second index is the number of down-regulated genes used to create gene sets; only used if method includes gsea and if input is not a gene set
cellLineMean	Boolean: add rows with the mean of method across cell lines? If cellLineMean = "auto" (default), rows will be added when data for more than one cell line is available.
rankPerCellLine	Boolean: rank results based on both individual cell lines and mean scores across cell lines (TRUE) or based on mean scores alone (FALSE)? If cellLineMean = FALSE, individual cell line conditions are always ranked.
threads	Integer: number of parallel threads
chunkGiB	Numeric: if second argument is a path to an HDF5 file (.h5 extension), that file is loaded and processed in chunks of a given size in gibibytes (GiB); lower values decrease peak RAM usage (see details below)
verbose	Boolean: print additional details?

**Value**

Data table with correlation and/or GSEA score results

**Process data by chunks**

If a file path to a valid HDF5 (.h5) file is provided instead of a data matrix, that file can be loaded and processed in chunks of size chunkGiB, resulting in decreased peak memory usage.

The default value of 1 GiB (1 GiB =  $1024^3$  bytes) allows loading chunks of ~10000 columns and 14000 rows ( $10000 * 14000 * 8 \text{ bytes} / 1024^3 = 1.04 \text{ GiB}$ ).

**GSEA score**

When method = "gsea", weighted connectivity scores (WTCS) are calculated ([https://clue.io/connectopedia/cmap\\_algorithms](https://clue.io/connectopedia/cmap_algorithms)).

**See Also**

Other functions related with the ranking of CMap perturbations: [as.table.referenceComparison\(\)](#), [filterCMapMetadata\(\)](#), [getCMapConditions\(\)](#), [getCMapPerturbationTypes\(\)](#), [loadCMapData\(\)](#), [loadCMapZscores\(\)](#), [parseCMapID\(\)](#), [plot.perturbationChanges\(\)](#), [plot.referenceComparison\(\)](#), [plotTargetingDrugsVSsimilarPerturbations\(\)](#), [prepareCMapPerturbations\(\)](#), [print.similarPerturbations\(\)](#)

**Examples**

```
# Example of a differential expression profile
data("diffExprStat")

## Not run:
# Download and load CMap perturbations to compare with
cellLine <- c("HepG2", "HUH7")
cmapMetadataCompounds <- filterCMapMetadata(
  "cmapMetadata.txt", cellLine=cellLine, timepoint="24 h",
  dosage="5 \u00B5M", perturbationType="Compound")

cmapPerturbationsCompounds <- prepareCMapPerturbations(
  cmapMetadataCompounds, "cmapZscores.gctx", "cmapGeneInfo.txt",
  "cmapCompoundInfo_drugs.txt", loadZscores=TRUE)

## End(Not run)
perturbations <- cmapPerturbationsCompounds

# Rank similar CMap perturbations (by default, Spearman's and Pearson's
# correlation are used, as well as GSEA with the top and bottom 150 genes of
# the differential expression profile used as reference)
rankSimilarPerturbations(diffExprStat, perturbations)

# Rank similar CMap perturbations using only Spearman's correlation
rankSimilarPerturbations(diffExprStat, perturbations, method="spearman")
```

---

readGctxIds

*Read GCTX row or column ids*


---

**Description**

Read GCTX row or column ids

**Usage**

```
readGctxIds(gctx_path, dimension = "row")
```

**Arguments**

gctx_path	path to the GCTX file
dimension	which ids to read (row or column)

**Value**

a character vector of row or column ids from the provided file

**Source**

<https://github.com/cmap/cmapR>

**See Also**

Other GCTX parsing functions: [fix.datatypes\(\)](#), [processIds\(\)](#), [readGctxMeta\(\)](#)

---

readGctxMeta	<i>Parse row or column metadata from GCTX files</i>
--------------	---

---

**Description**

Parse row or column metadata from GCTX files

**Usage**

```
readGctxMeta(  
  gctx_path,  
  dimension = "row",  
  ids = NULL,  
  set_annot_rownames = TRUE  
)
```

**Arguments**

<code>gctx_path</code>	the path to the GCTX file
<code>dimension</code>	which metadata to read (row or column)
<code>ids</code>	a character vector of a subset of row/column ids for which to read the metadata
<code>set_annot_rownames</code>	a boolean indicating whether to set the rownames attribute of the returned data.frame to the corresponding row/column ids.

**Value**

a data.frame of metadata

**Source**

<https://github.com/cmap/cmapR>

**See Also**

Other GCTX parsing functions: [fix.datatypes\(\)](#), [processIds\(\)](#), [readGctxIds\(\)](#)



---

stripStr	<i>Strip non-alpha-numeric characters from a string</i>
----------	---

---

**Description**

Strip non-alpha-numeric characters from a string

**Usage**

```
stripStr(str)
```

**Arguments**

str	Character
-----	-----------

**Value**

Character without non-alphanumeric values

---

subsetData	<i>Subset data by rows and/or columns</i>
------------	---

---

**Description**

Subset data by rows and/or columns

**Usage**

```
subsetData(x, i, j, rowAttr, colAttr, nargs, ...)
```

**Value**

Subset data

---

subsetDim	<i>Subset rows or columns based on a given index</i>
-----------	--

---

**Description**

Subset rows or columns based on a given index

**Usage**

```
subsetDim(k, dims, nargs, areCols = TRUE)
```

**Value**

Subset rows/columns

---

subsetToIds	<i>Do a robust <code>data.frame</code> subset to a set of ids</i>
-------------	---

---

**Description**

Do a robust `data.frame` subset to a set of ids

**Usage**

```
subsetToIds(df, ids)
```

**Arguments**

df	<code>data.frame</code> to subset
ids	the ids to subset to

**Value**

a subset version of df

**Source**

<https://github.com/cmap/cmapR>

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