Package ‘cmapR’

May 14, 2024

Type Package
Title CMap Tools in R
Date 2023-04-03
Version 1.16.0
Description The Connectivity Map (CMap) is a massive resource of perturbational gene expression profiles built by researchers at the Broad Institute and funded by the NIH Library of Integrated Network-Based Cellular Signatures (LINCS) program. Please visit https://clue.io for more information. The cmapR package implements methods to parse, manipulate, and write common CMap data objects, such as annotated matrices and collections of gene sets.
License file LICENSE
Depends R (>= 4.0)
Imports methods, rhdf5, data.table, flowCore, SummarizedExperiment, matrixStats
Suggests knitr, testthat, BiocStyle, rmarkdown
VignetteBuilder knitr
biocViews DataImport, DataRepresentation, GeneExpression
URL https://github.com/cmap/cmapR
BugReports https://github.com/cmap/cmapR/issues
LazyData true
RoxygenNote 7.1.1
git_url https://git.bioconductor.org/packages/cmapR
git_branch RELEASE_3_19
git_last_commit eae06f8
git_last_commit_date 2024-04-30
Repository Bioconductor 3.19
Date/Publication 2024-05-14
Author Ted Natoli [aut, cre] (<https://orcid.org/0000-0002-0953-0206>)
Maintainer Ted Natoli <ted.e.natoli@gmail.com>
## Contents

align_matrices ........................................ 3  
annotate.gct ........................................ 4  
append.dim ........................................... 5  
cdesc_char ........................................... 6  
check_colnames ...................................... 6  
check_dups ........................................... 7  
distil .................................................. 7  
ds ...................................................... 8  
extract.gct .......................................... 8  
fix.datatypes ........................................ 10  
GCT ..................................................... 11  
GCT-class ............................................. 12  
gene_set ............................................. 12  
ids ...................................................... 13  
is.wholenumber ........................................ 14  
kd_gct .................................................. 14  
lxb2mat .................................................. 15  
mat ...................................................... 16  
melt.gct ............................................... 17  
merge.gct ............................................. 18  
merge_with_precedence ................................ 19  
meta ..................................................... 20  
na_pad_matrix ......................................... 21  
parse.gctx ............................................ 21  
parse.gmt ............................................. 22  
parse.gmx ............................................. 23  
parse.grp ............................................. 24  
process_ids .......................................... 25  
rank.gct ............................................... 26  
read.gctx.ids ........................................ 27  
read.gctx.meta ....................................... 28  
robust_zscore ......................................... 29  
subset.gct ............................................ 29  
subset_to_ids ......................................... 30  
threshold .............................................. 31  
transpose.gct ......................................... 31  
update.gctx .......................................... 32  
write.gct ............................................. 33  
write.gctx ............................................ 34  
write.gctx.meta ...................................... 35  
write.tbl .............................................. 36  
write_gmt .............................................. 37  
write_grp ............................................. 38

## Index 39
align_matrices

Align the rows and columns of two (or more) matrices

Description

Align the rows and columns of two (or more) matrices

Usage

align_matrices(m1, m2, ..., L = NULL, na.pad = TRUE, as.3D = TRUE)

Arguments

m1
a matrix with unique row and column names

m2
a matrix with unique row and column names

... additional matrices with unique row and column names

L a list of matrix objects. If this is given, m1, m2, and ... are ignored

na.pad boolean indicating whether to pad the combined matrix with NAs for rows/columns
that are not shared by m1 and m2.

as.3D boolean indicating whether to return the result as a 3D array. If FALSE, will
return a list.

Value

an object containing the aligned matrices. Will either be a list or a 3D array

Examples

# construct some example matrices
m1 <- matrix(rnorm(20), nrow=4)
rownames(m1) <- letters[1:4]
colnames(m1) <- LETTERS[1:5]
m2 <- matrix(rnorm(20), nrow=5)
rownames(m2) <- letters[1:5]
colnames(m2) <- LETTERS[1:4]

m1
m2

# align them, padding with NA and returning a 3D array
align_matrices(m1, m2)

# align them, not padding and returning a list
align_matrices(m1, m2, na.pad=FALSE, as.3D=FALSE)
**Description**

Given a GCT object and either a `data.frame` or a path to an annotation table, apply the annotations to the gct using the given keyfield.

**Usage**

```r
annotate.gct(...)  
annotate_gct(g, annot, dim = "row", keyfield = "id")
```

## S4 method for signature 'GCT'

```r
annotate_gct(g, annot, dim = "row", keyfield = "id")
```

**Arguments**

- `...`: arguments passed on to `annotate_gct`
- `g`: a GCT object
- `annot`: a `data.frame` or path to text table of annotations
- `dim`: either `'row'` or `'column'` indicating which dimension of `g` to annotate
- `keyfield`: the character name of the column in `annot` that matches the row or column identifiers in `g`

**Value**

A GCT object with annotations applied to the specified dimension

**See Also**

Other GCT utilities: `melt.gct()`, `merge.gct()`, `rank.gct()`, `subset.gct()`

**Examples**

```r
gct_path <- system.file("extdata", "modzs_n25x50.gctx", package="cmapR")
# read the GCT file, getting the matrix only
g <- parse_gctx(gct_path, matrix_only=TRUE)
# separately, read the column annotations and then apply them using
# annotate.gct
cdesc <- read_gctx_meta(gct_path, dim="col")
g <- annotate_gct(g, cdesc, dim="col", keyfield="id")
```
**append.dim**

Append matrix dimensions to filename

**Description**

Append matrix dimensions to filename

**Usage**

`append.dim(...)`

`append_dim(ofile, mat, extension = "gct")`

**Arguments**

- ...: arguments passed on to `append_dim`
- `ofile`: the file name
- `mat`: the matrix
- `extension`: the file extension

**Details**

This is a helper function that most users will not use directly

**Value**

a character string of the filename with matrix dimensions appended

**See Also**

Other GCTX parsing functions: `gct`, `fix.datatypes()`, `parse.gctx()`, `process_ids()`, `read.gctx.ids()`, `read.gctx.meta()`, `write.gctx.meta()`, `write.gctx()`, `write.gct()`

**Examples**

```r
(filename <- cmapR:::append_dim("my.gctx.filename",
    matrix(nrow=10, ncol=15)))
```
check_colnames

An example table of metadata, as would be parsed from or parse.gctx.
Initially all the columns are of type character.

**Description**

An example table of metadata, as would be parsed from or parse.gctx. Initially all the columns are of type character.

**Usage**

cdesc_char

**Format**

An object of class `data.frame` with 368 rows and 8 columns.

**check_colnames**

Check whether `test_names` are columns in the `data.frame` `df`

**Description**

Check whether `test_names` are columns in the `data.frame` `df`

**Usage**

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

**Arguments**

- `test_names` a vector of column names to test
- `df` the `data.frame` 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`

**Examples**

```r
check_colnames(c("pert_id", "pert_iname"), cdesc_char) # TRUE
check_colnames(c("pert_id", "foobar"),
               cdesc_char, throw_error=FALSE)# FALSE, suppress error
```
check_dups

Check for duplicates in a vector

Description
Check for duplicates in a vector

Usage
check_dups(x, name = "")

Arguments
x the vector
name the name of the object to print in an error message if duplicates are found

Value
silently returns NULL

Examples
# this will throw an error, let's catch it
tryCatch(
  check_dups(c("a", "b", "c", "a", "d")),
  error=function(e) print(e)
)

distil

Collapse the rows or columns of a matrix using weighted averaging

Description
This is equivalent to the 'modz' procedure used in collapsing replicates in traditional L1000 data processing. The weight for each replicate is computed as its normalized average correlation to the other replicates in the set.

Usage
distil(m, dimension = "col", method = "spearman")

Arguments
m a numeric matrix where the rows or columns are assumed to be replicates
dimension the dimension to collapse. either 'row' or 'col'
method the correlation method to use
Value

a list with the following elements

- **values** a vector of the collapsed values
- **correlations** a vector of the pairwise correlations
- **weights** a vector of the computed weights

Examples

```r
m <- matrix(rnorm(30), ncol=3)
distil(m)
```

ds

An example of a GCT object with row and column metadata and gene expression values in the matrix.

Description

An example of a GCT object with row and column metadata and gene expression values in the matrix.

Usage

d

Format

An object of class GCT of length 1.

---

```
extract.gct
```

Extract elements from a GCT matrix

Description

extract the elements from a GCT object where the values of row_field and col_field are the same. A concrete example is if g represents a matrix of signatures of genetic perturbations, and you want to extract all the values of the targeted genes.
Usage

extract.gct(...)

extract_gct(
  g,
  row_field,
  col_field,
  rdesc = NULL,
  cdesc = NULL,
  row_keyfield = "id",
  col_keyfield = "id"
)

Arguments

... arguments passed on to extract_gct
  g the GCT object
  row_field the column name in rdesc to search on
  col_field the column name in cdesc to search on
  rdesc a data.frame of row annotations
  cdesc a data.frame of column annotations
  row_keyfield the column name of rdesc to use for annotating the rows of g
  col_keyfield the column name of cdesc to use for annotating the rows of g

Value

a list of the following elements

  mask a logical matrix of the same dimensions as ds@mat indicating which matrix elements have been extracted
  idx an array index into ds@mat representing which elements have been extracted
  vals a vector of the extracted values

Examples

# get the values for all targeted genes from a
# dataset of knockdown experiments
res <- extract_gct(kd_gct, row_field="pr_gene_symbol",
  col_field="pert_mfc_desc")
str(res)
stats::quantile(res$vals)
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

```r
fix.datatypes(...)  # arguments passed on to fix_datatypes
fix_datatypes(meta)  # a data.frame
```

Arguments

- `...`: arguments passed on to `fix_datatypes`
- `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.

See Also

Other GCTX parsing functions: `GCT`, `append.dim()`, `parse.gctx()`, `process_ids()`, `read.gctx.ids()`, `read.gctx.meta()`, `write.gctx.meta()`, `write.gctx()`, `write.gct()`

Examples

```r
# meta data table with all character types
str(cdesc_char)  # note how some column classes have changed
```
GCT

Initialize an object of class GCT

Description

Initialize an object of class GCT

Usage

GCT(
  mat = NULL,
  rdesc = NULL,
  cdesc = NULL,
  src = NULL,
  rid = NULL,
  cid = NULL,
  matrix_only = FALSE
)

Arguments

  mat a matrix
  rdesc a data.frame of row metadata
  cdesc a data.frame of column metadata
  src path to a GCT file to read
  rid vector of character identifiers for rows
  cid vector of character identifiers for columns
  matrix_only logical indicating whether to read just the matrix data from src

Details

If mat is provided, rid and cid are treated as the row and column identifiers for the matrix and are assigned to the rid and cid slots of the GCT object.

If mat is not provided but src is provided, rid and cid are treated as filters. Data will be read from the file path provided to src and will then be restricted to the character ids or integer indices provided to rid and cid. In a similar manner, matrix_only controls whether the row and column metadata are also read from the src file path.

Value

a GCT object

See Also

Other GCTX parsing functions: append.dim(), fix.datatypes(), parse.gctx(), process_ids(), read.gctx.ids(), read.gctx.meta(), write.gctx.meta(), write.gctx(), write.gct()
Examples

# an empty object
(g <- GCT())
# with a matrix
# note we must specify row and column ids
(g <- GCT(mat=matrix(rnorm(100), nrow=10),
          rid=letters[1:10], cid=letters[1:10]))
# from file
gct_file <- system.file("extdata", "modzs_n25x50.gctx", package="cmapR")
(g <- GCT(src=gct_file))

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
cdesc a data.frame of column descriptors
src a character indicating the source (usually file path) of the data

See Also

parse_gctx, write_gctx, read_gctx_meta, read_gctx_ids

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

gene_set

An example collection of gene sets as used in the Lamb 2006 CMap paper.

Description

An example collection of gene sets as used in the Lamb 2006 CMap paper.

Usage

gene_set
ids

Format
An object of class list of length 8.

Source
Lamb et al 2006 doi:10.1126/science.1132939

Description
Extract the or set row or column ids of a GCT object

Usage
ids(g, dimension = "row")

## S4 method for signature 'GCT'
ids(g, dimension = "row")

ids(g, dimension = "row") <- value

## S4 replacement method for signature 'GCT'
ids(g, dimension = "row") <- value

Arguments
g          the GCT object
dimension   the dimension to extract/update ['row' or 'column']
value       a character vector

Value
a vector of row ids

See Also
Other GCT accessor methods: mat(), meta()
Examples

# extract rids
rids <- ids(ds)
# extract column ids
cids <- ids(ds, "column")
# set rids
ids(ds) <- as.character(1:length(rids))
# set cids
ids(ds, "column") <- as.character(1:length(cids))

---

is.wholenumber  Check if x is a whole number

Description

Check if x is a whole number

Usage

is.wholenumber(x, tol = .Machine$double.eps*0.5)

Arguments

x  number to test
tol  the allowed tolerance

Value

boolean indicating whether x is tol away from a whole number value

Examples

is.wholenumber(1)
is.wholenumber(0.5)

---

kd_gct  An example GCT object of knockdown experiments targeting a subset of landmark genes.

Description

An example GCT object of knockdown experiments targeting a subset of landmark genes.

Usage

kd_gct
Format

An object of class GCT of length 1.

Description

Read an LXB file and return a matrix

Usage

```r
lxb2mat(lxb_path, columns = c("RID", "RP1"), newnames = c("barcode_id", "FI"))
```

Arguments

- `lxb_path`: the path to the lxb file
- `columns`: which columns in the lxb file to retain
- `newnames`: what to name these columns in the returned matrix

Value

a matrix

See Also

Other CMap parsing functions: `parse.gmt()`, `parse.gmx()`, `parse.grp()`, `write_gmt()`, `write_grp()`

Examples

```r
lxb_path <- system.file("extdata", "example.lxb", package="cmapR")
lxb_data <- lxb2mat(lxb_path)
str(lxb_data)
```
Extract or set the matrix of GCT object

### Description

Extract or set the matrix of GCT object

### Usage

```r
mat(g)
```

```r
# S4 method for signature 'GCT'
mat(g)
```

```r
mat(g) <- value
```

```r
# S4 replacement method for signature 'GCT'
mat(g) <- value
```

### Arguments

- `g` the GCT object
- `value` a numeric matrix

### Value

a matrix

### See Also

Other GCT accessor methods: `ids()`, `meta()`

### Examples

```r
# get the matrix
m <- mat(ds)
# set the matrix
mat(ds) <- matrix(0, nrow=nrow(m), ncol=ncol(m))
```
melt.gct

Transform a GCT object into a long form `data.table` (aka 'melt')

Description

Utilizes the `melt.data.table` function to transform the matrix into long form. Optionally can include the row and column annotations in the transformed `data.table`.

Usage

melt.gct(...)

melt.gct(
  g,
  suffixes = NULL,
  remove_symmetries = FALSE,
  keep_rdesc = TRUE,
  keep_cdesc = TRUE,
  ...
)

## S4 method for signature 'GCT'

melt.gct(
  g,
  suffixes = NULL,
  remove_symmetries = FALSE,
  keep_rdesc = TRUE,
  keep_cdesc = TRUE,
  ...
)

Arguments

... further arguments passed along to `data.table::merge`
g the GCT object
suffixes the character suffixes to be applied if there are collisions between the names of the row and column descriptors
remove_symmetries boolean indicating whether to remove the lower triangle of the matrix (only applies if `g@mat` is symmetric)
keep_rdesc boolean indicating whether to keep the row descriptors in the final result
keep_cdesc boolean indicating whether to keep the column descriptors in the final result

Value

A `data.table` object with the row and column ids and the matrix values and (optionally) the row and column descriptors
merge.gct

Merge two GCT objects together

Description

Merge two GCT objects together

Usage

## S3 method for class 'gct'
merge(...)
merge_gct(g1, g2, dim = "row", matrix_only = FALSE)

## S4 method for signature 'GCT,GCT'
merge_gct(g1, g2, dim = "row", matrix_only = FALSE)

Arguments

... arguments passed on to merge_gct
g1 the first GCT object
g2 the second GCT object
dim the dimension on which to merge (row or column)
matrix_only boolean indicating whether to keep only the data matrices from g1 and g2 and ignore their row and column meta data

Value

a GCT object

See Also

Other GCT utilities: annotate.gct(), melt.gct(), rank.gct(), subset.gct()
Examples

# take the first 10 and last 10 rows of an object
# and merge them back together
(a <- subset_gct(ds, rid=1:10))
(b <- subset_gct(ds, rid=969:978))
(merged <- merge_gct(a, b, dim="row"))

merge_with_precedence  Merge two data.frames, but where there are common fields those in x are retained and those in y are dropped.

Description

Merge two data.frames, but where there are common fields those in x are retained and those in y are dropped.

Usage

merge_with_precedence(x, y, by, allow.cartesian = TRUE, as_data_frame = TRUE)

Arguments

x the data.frame whose columns take precedence
y another data.frame
by a vector of column names to merge on
allow.cartesian boolean indicating whether it’s ok for repeated values in either table to merge with each other over and over again.
as_data_frame boolean indicating whether to ensure the returned object is a data.frame instead of a data.table. This ensures compatibility with GCT object conventions, that is, the rdesc and cdesc slots must be strictly data.frame objects.

Value

a data.frame or data.table object

See Also
data.table::merge

Examples

(x <- data.table::data.table(foo=letters[1:10], bar=1:10))
(y <- data.table::data.table(foo=letters[1:10], bar=11:20, baz=LETTERS[1:10]))
# the 'bar' column from y will be dropped on merge
cmapR:::merge_with_precedence(x, y, by="foo")
Description

Extract the or set metadata of a GCT object

Usage

```
meta(g, dimension = "row")
```

## S4 method for signature 'GCT'

```
meta(g, dimension = "row")
```

```
meta(g, dimension = "row") <- value

## S4 replacement method for signature 'GCT'

```
meta(g, dimension = "row") <- value
```

Arguments

- `g` the GCT object
- `dimension` the dimension to extract/update ['row' or 'column']
- `value` a data.frame

Value

a data.frame

See Also

Other GCT accessor methods: `ids()`, `mat()`

Examples

```
# extract rdesc
rdesc <- meta(ds)

# extract cdesc
cdesc <- meta(ds, dim="column")

# set rdesc
meta(ds) <- data.frame(x=sample(letters, nrow(rdesc), replace=TRUE))

# set cdesc
meta(ds, dim="column") <- data.frame(x=sample(letters, nrow(cdesc), replace=TRUE))
```
na_pad_matrix  Pad a matrix with additional rows/columns of NA values

Description
Pad a matrix with additional rows/columns of NA values

Usage
na_pad_matrix(m, row_universe = NULL, col_universe = NULL)

Arguments
m a matrix with unique row and column names
row_universe a vector with the universe of possible row names
col_universe a vector with the universe of possible column names

Value
a matrix

Examples
m <- matrix(rnorm(10), nrow=2)ownames(m) <- c("A", "B")
colnames(m) <- letters[1:5]
na_pad_matrix(m, row_universe=LETTERS, col_universe=letters)

parse.gctx Parse a GCTX file into the workspace as a GCT object

Description
Parse a GCTX file into the workspace as a GCT object

Usage
parse.gctx(...)

parse_gctx(fname, rid = NULL, cid = NULL, matrix_only = FALSE)
parse.gmt

Arguments

... arguments passed on to parse_gctx
fname path to the GCTX file on disk
rid either a vector of character or integer row indices or a path to a grp file containing character row indices. Only these indicies will be parsed from the file.
cid either a vector of character or integer column indices or a path to a grp file containing character column indices. Only these indicies will be parsed from the file.
matrix_only boolean indicating whether to parse only the matrix (ignoring row and column annotations)

Details

parse_gctx also supports parsing of plain text GCT files, so this function can be used as a general GCT parser.

Value

a GCT object

See Also

Other GCTX parsing functions: GCT, append_dim(), fix.datatypes(), process_ids(), read.gctx.ids(), read.gctx.meta(), write.gctx.meta(), write.gctx(), write.gct()

Examples

```
gct_file <- system.file("extdata", "modzs_n25x50.gctx", package="cmapR")
(ds <- parse_gctx(gct_file))

# matrix only
(ds <- parse_gctx(gct_file, matrix_only=TRUE))

# only the first 10 rows and columns
(ds <- parse_gctx(gct_file, rid=1:10, cid=1:10))
```

Description

Read a GMT file and return a list
parse.gmx

Usage

parse.gmt(...)

parse.gmt(fname)

Arguments

... arguments passed on to parse.gmt
fname the file path to be parsed

Details

parse.gmt returns a nested list object. The top level contains one list per row in fname. Each of these is itself a list with the following fields:
- head: the name of the data (row in fname)
- desc: description of the corresponding data
- len: the number of data items
- entry: a vector of the data items

Value

a list of the contents of fname. See details.

See Also

Visit http://clue.io/help for details on the GMT file format
Other CMap parsing functions: lxb2mat(), parse.gmx(), parse.grp(), write_gmt(), write_grp()

Examples

gmt_path <- system.file("extdata", "query_up.gmt", package="cmapR")
gmt <- parse.gmt(gmt_path)
str(gmt)

parse.gmx Read a GMX file and return a list

Description

Read a GMX file and return a list

Usage

parse.gmx(...)

parse.gmx(fname)
parse.grp

Arguments

... arguments passed on to parse_gmx
fname the file path to be parsed

Details

parse_gmx returns a nested list object. The top level contains one list per column in fname. Each of these is itself a list with the following fields:
- head: the name of the data (column in fname)
- desc: description of the corresponding data
- len: the number of data items
- entry: a vector of the data items

Value

a list of the contents of fname. See details.

See Also

Visit http://clue.io/help for details on the GMX file format
Other CMap parsing functions: lxb2mat(), parse.gmt(), parse.grp(), write_gmt(), write_grp()

Examples

gmx_path <- system.file("extdata", "lm_probes.gmx", package="cmapR")
gmx <- parse_gmx(gmx_path)
str(gmx)

parse.grp  
Read a GRP file and return a vector of its contents

Description

Read a GRP file and return a vector of its contents

Usage

parse.grp(...)  
parse.grp(fname)

Arguments

... arguments passed on to parse.grp
fname the file path to be parsed

Value

a vector of the contents of fname
See Also

Visit [http://clue.io/help](http://clue.io/help) for details on the GRP file format

Other CMap parsing functions: `lxb2mat()`, `parse.gmt()`, `parse.gmx()`, `write_gmt()`, `write_grp()`

Examples

```r
grp_path <- system.file("extdata", "lm_epsilon_n978.grp", package="cmapR")
values <- parse_grp(grp_path)
str(values)
```

---

**process_ids**

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

### Description

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

### Usage

```
process_ids(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`

### See Also

Other GCTX parsing functions: `GCT`, `append.dim()`, `fix.datatypes()`, `parse.gctx()`, `read.gctx.ids()`, `read.gctx.meta()`, `write.gctx.meta()`, `write.gctx()`, `write.gct()`

### Examples

```r
gct_file <- system.file("extdata", "modzs_n25x50.gctx", package="cmapR")
ids <- read_gctx_ids(gct_file)
processed_ids <- cmapR:::process_ids(ids[1:10], ids)
str(processed_ids)
```
rank.gct

Convert a GCT object’s matrix to ranks

Description

Convert a GCT object’s matrix to ranks

Usage

rank.gct(...)

rank_gct(g, dim = "col", decreasing = TRUE)

## S4 method for signature 'GCT'
rank_gct(g, dim = "col", decreasing = TRUE)

Arguments

... arguments passed on to rank_gct
g the GCT object to rank
dim the dimension along which to rank (row or column)
decreasing boolean indicating whether higher values should get lower ranks

Value

a modified version of g, with the values in the matrix converted to ranks

See Also

Other GCT utilities: annotate.gct(), melt.gct(), merge.gct(), subset.gct()

Examples

(ranked <- rank_gct(ds, dim="column"))
# scatter rank vs. score for a few columns
m <- mat(ds)
m_ranked <- mat(ranked)
plot(m[, 1:3], m_ranked[, 1:3],
     xlab="score", ylab="rank")
**read.gctx.ids**

**Read GCTX row or column ids**

**Description**

Read GCTX row or column ids

**Usage**

```r
read.gctx.ids(...) read_gctx_ids(gctx_path, dim = "row")
```

**Arguments**

- `...`: arguments passed on to `read_gctx_ids`
- `gctx_path`: path to the GCTX file
- `dim`: which ids to read (row or column)

**Value**

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

**See Also**

Other GCTX parsing functions: `GCT`, `append.dim()`, `fix.datatypes()`, `parse.gctx()`, `process_ids()`, `read.gctx.meta()`, `write.gctx.meta()`, `write.gctx()`, `write.gct()`

**Examples**

```r
gct_file <- system.file("extdata", "modzs_n25x50.gctx", package="cmapR")
# row ids
rid <- read_gctx_ids(gct_file)
head(rid)
# column ids
cid <- read_gctx_ids(gct_file, dim="column")
head(cid)
```
read.gctx.meta

Parse row or column metadata from GCTX files

Description

Parse row or column metadata from GCTX files

Usage

read.gctx.meta(...)

read_gctx_meta(gctx_path, dim = "row", ids = NULL)

Arguments

... arguments passed on to read_gctx_meta
gctx_path the path to the GCTX file
dim which metadata to read (row or column)
ids a character vector of a subset of row/column ids for which to read the metadata

Value

a data.frame of metadata

See Also

Other GCTX parsing functions: GCT.append.dim(), fix.datatypes(), parse.gctx(), process_ids(), read.gctx.ids(), write.gctx.meta(), write.gctx(), write.gct()

Examples

gct_file <- system.file("extdata", "modzs_n25x50.gctx", package="cmapR")
# row meta
row_meta <- read_gctx_meta(gct_file)
str(row_meta)
# column meta
col_meta <- read_gctx_meta(gct_file, dim="column")
str(col_meta)
# now for only the first 10 ids
col_meta_first10 <- read_gctx_meta(gct_file, dim="column",
ids=col_meta$id[1:10])
str(col_meta_first10)
robust_zscore

Compute robust z-scores

Description

robust_zscore implementation takes in a 1D vector, returns 1D vector after computing robust zscores
\[ rZ = (x - \text{med}(x))/\text{mad}(x) \]

Usage

robust_zscore(x, min_mad = 1e-06, ...)

Arguments

x numeric vector to z-score
min_mad the minimum allowed MAD, useful for avoiding division by very small numbers
... further options to median, max functions

Value

transformed version of x

Examples

(x <- rnorm(25))
(robust_zscore(x))

# with min_mad
(robust_zscore(x, min_mad=1e-4))

subset.gct

Subset a gct object using the provided row and column ids

Description

Subset a gct object using the provided row and column ids

Usage

## S3 method for class 'gct'
subset(...)

subset_gct(g, rid = NULL, cid = NULL)

## S4 method for signature 'GCT'
subset_gct(g, rid = NULL, cid = NULL)
Arguments

... arguments passed on to subset_gct
g a gct object
rid a vector of character ids or integer indices for ROWS
cid a vector of character ids or integer indices for COLUMNS

Value

a GCT object

See Also

Other GCT utilities: annotate.gct(), melt.gct(), merge.gct(), rank.gct()

Examples

# first 10 rows and columns by index
(a <- subset_gct(ds, rid=1:10, cid=1:10))

# first 10 rows and columns using character ids
# use \code{ids} to extract the ids
rid <- ids(ds)
cid <- ids(ds, dimension="col")
(b <- subset_gct(ds, rid=rid[1:10], cid=cid[1:10]))

identical(a, b) # TRUE

subset_to_ids

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

Description

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

Usage

subset_to_ids(df, ids)

Arguments

df data.frame to subset
ids the ids to subset to

Value

a subset version of df
**threshold**

*Threshold a numeric vector*

**Description**

Threshold a numeric vector

**Usage**

threshold(x, minval, maxval)

**Arguments**

- **x**: the vector
- **minval**: minimum allowed value
- **maxval**: maximum allowed value

**Value**

a thresholded version of x

**Examples**

```r
x <- rnorm(20)
threshold(x, -0.1, -0.1)
```

---

**transpose.gct**

*Transpose a GCT object*

**Description**

Transpose a GCT object

**Usage**

```r
transpose.gct(...)
```

```r
transpose_gct(g)
```

```
## S4 method for signature 'GCT'
transpose_gct(g)
```

**Arguments**

- **...**: arguments passed on to transpose_gct
- **g**: the GCT object
Value

a modified version of the input GCT object where the matrix has been transposed and the row and column ids and annotations have been swapped.

Examples

transpose_gct(ds)

update.gctx

Update the matrix of an existing GCTX file

Description

Update the matrix of an existing GCTX file

Usage

## S3 method for class 'gctx'
update(...)

update_gctx(x, ofile, rid = NULL, cid = NULL)

Arguments

... arguments passed on to update_gctx
x an array of data
ofile the filename of the GCTX to update
rid integer indices or character ids of the rows to update
cid integer indices or character ids of the columns to update

Details

Overwrite the rows and columns of ofile as indicated by rid and cid respectively. rid and cid can either be integer indices or character ids corresponding to the row and column ids in ofile.

Value

silently returns NULL
Examples

```r
## Not run:
m <- matrix(rnorm(20), nrow=10)
# update by integer indices
update_gctx(m, ofile="my.gctx", rid=1:10, cid=1:2)
# update by character ids
row_ids <- letters[1:10]
col_ids <- LETTERS[1:2]
update_gctx(m, ofile="my.gctx", rid=row_ids, cid=col_ids)
## End(Not run)
```

write.gct

Write a GCT object to disk in GCT format

Description

Write a GCT object to disk in GCT format

Usage

```r
write.gct(...)
```

```r
write_gct(ds, ofile, precision = 4, appenddim = TRUE, ver = 3)
```

Arguments

- `...`: arguments passed on to `write_gct`
- `ds`: the GCT object
- `ofile`: the desired output filename
- `precision`: the numeric precision at which to save the matrix. See details.
- `appenddim`: boolean indicating whether to append matrix dimensions to filename
- `ver`: the GCT version to write. See details.

Details

Since GCT is text format, the higher precision you choose, the larger the file size. `ver` is assumed to be 3, aka GCT version 1.3, which supports embedded row and column metadata in the GCT file. Any other value passed to `ver` will result in a GCT version 1.2 file which contains only the matrix data and no annotations.

Value

silently returns NULL
See Also

Other GCTX parsing functions: GCT, append.dim(), fix.datatypes(), parse.gctx(), process_ids(), read.gctx.ids(), read.gctx.meta(), write.gctx.meta(), write.gctx()

Examples

# note this will create a GCT file in your current directory
write_gct(ds, "dataset", precision=2)

write.gctx   Write a GCT object to disk in GCTX format

Description

Write a GCT object to disk in GCTX format

Usage

write.gctx(...)

write_gctx(
  ds, ofile,
  appenddim = TRUE,
  compression_level = 0,
  matrix_only = FALSE,
  max_chunk_kb = 1024
)

Arguments

... arguments passed on to write.gctx
ds a GCT object
ofile the desired file path for writing
appenddim boolean indicating whether the resulting filename will have dimensions appended (e.g. my_file_n384x978.gctx)
compression_level integer between 1-9 indicating how much to compress data before writing. Higher values result in smaller files but slower read times.
matrix_only boolean indicating whether to write only the matrix data (and skip row, column annotations)
max_chunk_kb for chunking, the maximum number of KB a given chunk will occupy
**write.gctx.meta**

### Value

silently returns NULL

### See Also

Other GCTX parsing functions: `GCT.append.dim()`, `fix.datatypes()`, `parse.gctx()`, `process_ids()`, `read.gctx.ids()`, `read.gctx.meta()`, `write.gctx.meta()`, `write.gct()`

### Examples

```r
# note this will create a GCT file in your current directory
write_gctx(ds, "dataset")
```

---

**write.gctx.meta**  
*Write a data.frame of meta data to GCTX file*

### Description

Write a data.frame of meta data to GCTX file

### Usage

```r
write.gctx.meta(...)  
write_gctx_meta(ofile, df, dimension = "row")
```

### Arguments

- ... arguments passed on to `write_gctx_meta`
- `ofile` the desired file path for writing
- `df` the data.frame of annotations
- `dimension` the dimension to annotate (row or column)

### Value

silently returns NULL

### See Also

Other GCTX parsing functions: `GCT.append.dim()`, `fix.datatypes()`, `parse.gctx()`, `process_ids()`, `read.gctx.ids()`, `read.gctx.meta()`, `write.gctx()`, `write.gct()`
write.tbl

Write a data.frame to a tab-delimited text file

Description
Write a data.frame to a tab-delimited text file

Usage
write.tbl(...)

Arguments...
... additional arguments passed on to write.table
tbl the data.frame to be written
ofile the desired file name

Details
This method simply calls write.table with some preset arguments that generate a unquoted, tab-delimited file without row names.

Value
silently returns NULL

See Also
write.table

Examples
## Not run:
write_tbl(cdesc_char, "col_meta.txt")
## End(Not run)
write_gmt

Write a nested list to a GMT file

Description

Write a nested list to a GMT file

Usage

write_gmt(lst, fname)

Arguments

lst the nested list to write. See details.
fname the desired file name

Details

lst needs to be a nested list where each sub-list is itself a list with the following fields: - head: the name of the data - desc: description of the corresponding data - len: the number of data items - entry: a vector of the data items

Value

silently returns NULL

See Also

Visit http://clue.io/help for details on the GMT file format

Other CMap parsing functions: lxb2mat(), parse.gmt(), parse.gmx(), parse.grp(), write_grp()

Examples

## Not run:
write_gmt(gene_set, "gene_set.gmt")

## End(Not run)
**write_grp**

*Write a vector to a GRP file*

**Description**

Write a vector to a GRP file

**Usage**

\[ \text{write_grp(vals, fname)} \]

**Arguments**

- `vals`: the vector of values to be written
- `fname`: the desired file name

**Value**

silently returns NULL

**See Also**

Visit [http://clue.io/help](http://clue.io/help) for details on the GRP file format

Other CMap parsing functions: `lxb2mat()`, `parse.gmt()`, `parse.gmx()`, `parse.grp()`, `write_gmt()`

**Examples**

```
## Not run:
write_grp(letters, "letter.grp")

## End(Not run)
```
Index

* CMap parsing functions
  lxb2mat, 15
  parse.gmt, 22
  parse.gmx, 23
  parse.grp, 24
  write_gmt, 37
  write_grp, 38

* GCT accessor methods
  ids, 13
  mat, 16
  meta, 20

* GCT utilities
  annotate.gct, 4
  melt.gct, 17
  merge.gct, 18
  rank.gct, 26
  subset.gct, 29

* GCT utilities
  transpose.gct, 31

* GCTX parsing functions
  append.dim, 5
  fix.datatypes, 10
  GCT, 11
  parse.gctx, 21
  process_ids, 25
  read.gctx.ids, 27
  read.gctx.meta, 28
  write.gctx, 33
  write.gctx.meta, 35

* datasets
  cdesc_char, 6
  ds, 8
  gene_set, 12
  kd_gct, 14

* internal
  append.dim, 5
  fix.datatypes, 10
  merge_with_precedence, 19
  process_ids, 25
  subset_to_ids, 30
  write.gctx.meta, 35
  align_matrices, 3
  annotate.gct, 4, 18, 26, 30
  annotate_gct, GCT-method (annotate.gct), 4
  append_dim, 5, 10, 11, 22, 25, 27, 28, 34, 35
  distil, 7
  ds, 8
  extract.gct, 8
  extract_gct, extract.gct, 8
  fix.datatypes, 5, 10, 11, 22, 25, 27, 28, 34, 35
  fix_datatypes, fix.datatypes, 10
  GCT, 5, 10, 11, 22, 25, 27, 28, 34, 35
  GCT-class, 12
  gene_set, 12
  ids, 13, 16, 20
  ids, GCT-method (ids), 13
  ids<-(ids), 13
  ids<-, GCT-method (ids), 13
  is.wholenumber, 14
  kd_gct, 14
  lxb2mat, 15, 23–25, 37, 38