

# Package ‘cmapR’

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**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.

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---

align_matrices	<i>Align the rows and columns of two (or more) matrices</i>
----------------	---

---

### 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)
```

---

annotate.gct	<i>Add annotations to a GCT object</i>
--------------	--

---

## 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

```
annotate.gct(...)  
  
annotate_gct(g, annot, dim = "row", keyfield = "id")  
  
## S4 method for signature 'GCT'  
annotate_gct(g, annot, dim = "row", keyfield = "id")
```

## Arguments

...	arguments passed on to <code>annotate_gct</code>
<code>g</code>	a GCT object
<code>annot</code>	a <a href="#">data.frame</a> or path to text table of annotations
<code>dim</code>	either 'row' or 'column' indicating which dimension of <code>g</code> to annotate
<code>keyfield</code>	the character name of the column in <code>annot</code> that matches the row or column identifiers in <code>g</code>

## 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

```
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	<i>Append matrix dimensions to filename</i>
------------	---

---

## Description

Append matrix dimensions to filename

## Usage

```
append.dim(...)  
append_dim(ofile, mat, extension = "gct")
```

## Arguments

...	arguments passed on to <code>append_dim</code>
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

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

---

cdesc_char	<i>An example table of metadata, as would be parsed from or parse.gctx. Initially all the columns are of type character.</i>
------------	--

---

**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	<i>Check whether test_names are columns in the <code>data.frame</code> df</i>
----------------	---

---

**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 <code>data.frame</code> 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**

```
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	<i>Check for duplicates in a vector</i>
------------	---

---

**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	<i>Collapse the rows or columns of a matrix using weighted averaging</i>
--------	--

---

**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**

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

---

ds	<i>An example of a GCT object with row and column metadata and gene expression values in the matrix.</i>
----	--

---

**Description**

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

**Usage**

```
ds
```

**Format**

An object of class GCT of length 1.

---

extract.gct	<i>Extract elements from a GCT matrix</i>
-------------	---

---

**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

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

```
fix_datatypes(meta)
```

### Arguments

<code>...</code>	arguments passed on to <code>fix_datatypes</code>
<code>meta</code>	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

```
# meta data table with all character types
str(cdesc_char)
fixed <- cmapR::fix_datatypes(cdesc_char)
# note how some column classes have changed
str(fixed)
```

---

GCT	<i>Initialize an object of class GCT</i>
-----	--

---

### 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
```

**Format**

An object of class `list` of length 8.

**Source**

Lamb et al 2006 doi:10.1126/science.1132939

---

ids	<i>Extract the or set row or column ids of a GCT object</i>
-----	---

---

**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**

<code>g</code>	the GCT object
<code>dimension</code>	the dimension to extract/update [ <code>'row'</code> or <code>'column'</code> ]
<code>value</code>	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	<i>Check if x is a whole number</i>
----------------	-------------------------------------

---

**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	<i>An example GCT object of knockdown experiments targeting a subset of landmark genes.</i>
--------	---

---

**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.

---

lxb2mat	<i>Read an LXB file and return a matrix</i>
---------	---

---

**Description**

Read an LXB file and return a matrix

**Usage**

```
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**

```
lxb_path <- system.file("extdata", "example.lxb", package="cmapR")
lxb_data <- lxb2mat(lxb_path)
str(lxb_data)
```

---

mat	<i>Extract or set the matrix of GCT object</i>
-----	--

---

**Description**

Extract or set the matrix of GCT object

**Usage**

```
mat(g)

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

mat(g) <- value

## 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**

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



---

melt.gct	<i>Transform a GCT object in to a long form <a href="#">data.table</a> (aka 'melt')</i>
----------	---

---

### 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 <code>data.table::merge</code>
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 <code>g@mat</code> 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

**See Also**

Other GCT utilities: [annotate.gct\(\)](#), [merge.gct\(\)](#), [rank.gct\(\)](#), [subset.gct\(\)](#)

**Examples**

```
# simple melt, keeping both row and column meta
head(melt_gct(ds))

# update row/column suffixes to indicate rows are genes, columns experiments
head(melt_gct(ds, suffixes = c("_gene", "_experiment")))

# ignore row/column meta
head(melt_gct(ds, keep_rdesc = FALSE, keep_cdesc = FALSE))
```

---

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 <code>data.frame</code> whose columns take precedence
y	another <code>data.frame</code>
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 <code>data.frame</code> instead of a <code>data.table</code> . This ensures compatibility with GCT object conventions, that is, the <code>rdesc</code> and <code>cdesc</code> slots must be strictly <code>data.frame</code> 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")
```

---

meta

*Extract the or set metadata of a GCT object*

---

### 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

<code>g</code>	the GCT object
<code>dimension</code>	the dimension to extract/update [ <code>'row'</code> or <code>'column'</code> ]
<code>value</code>	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	<i>Pad a matrix with additional rows/columns of NA values</i>
---------------	---

---

**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)
rownames(m) <- c("A", "B")
colnames(m) <- letters[1:5]
na_pad_matrix(m, row_universe=LETTERS, col_universe=letters)
```

---

parse.gctx	<i>Parse a GCTX file into the workspace as a GCT object</i>
------------	---

---

**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)
```

**Arguments**

...	arguments passed on to <code>parse_gctx</code>
<code>fname</code>	path to the GCTX file on disk
<code>rid</code>	either a vector of character or integer row indices or a path to a grp file containing character row indices. Only these indices will be parsed from the file.
<code>cid</code>	either a vector of character or integer column indices or a path to a grp file containing character column indices. Only these indices will be parsed from the file.
<code>matrix_only</code>	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))
```

---

parse.gmt

*Read a GMT file and return a list*

---

**Description**

Read a GMT file and return a list

**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)
```

**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", "1m_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> for details on the GRP file format

Other CMap parsing functions: [lxb2mat\(\)](#), [parse.gmt\(\)](#), [parse.gmx\(\)](#), [write.gmt\(\)](#), [write\\_grp\(\)](#)

**Examples**

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

---

process_ids	<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**

```
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**

```
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	<i>Convert a GCT object's matrix to ranks</i>
----------	---

---

### 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	<i>Read GCTX row or column ids</i>
---------------	------------------------------------

---

### Description

Read GCTX row or column ids

### Usage

```
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

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

---

## 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	<i>Compute robust z-scores</i>
---------------	--------------------------------

---

**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	<i>Subset a gct object using the provided row and column ids</i>
------------	--

---

**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	<i>Threshold a numeric vector</i>
-----------	-----------------------------------

---

**Description**

Threshold a numeric vector

**Usage**

```
threshold(x, minval, maxval)
```

**Arguments**

x	the vector
minval	minium allowed value
maxval	maximum allowed value

**Value**

a thresholded version of x

**Examples**

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

---

transpose.gct	<i>Transpose a GCT object</i>
---------------	-------------------------------

---

**Description**

Transpose a GCT object

**Usage**

```
transpose.gct(...)

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**

```
## 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**

```
write.gctx(...)
```

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

**Arguments**

...	arguments passed on to write_gctx
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	<i>Write a GCT object to disk in GCTX format</i>
------------	--

---

**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

**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**

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

---

write.gctx.meta	<i>Write a data.frame of meta data to GCTX file</i>
-----------------	---

---

**Description**

Write a data.frame of meta data to GCTX file

**Usage**

```
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\(\)](#)

## Examples

```
## Not run:  
# assume ds is a GCT object  
write_gctx_meta("/my/file/path", cdesc_char, dimension="col")  
  
## End(Not run)
```

---

write.tbl	<i>Write a data.frame to a tab-delimited text file</i>
-----------	--

---

## Description

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

## Usage

```
write.tbl(...)  
  
write_tbl(tbl, ofile, ...)
```

## 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	<i>Write a nested list to a GMT file</i>
-----------	--

---

### 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	<i>Write a vector to a GRP file</i>
-----------	-------------------------------------

---

**Description**

Write a vector to a GRP file

**Usage**

```
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> 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)
```

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