Package 'SCArray'

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Title Large-scale single-cell omics data manipulation with GDS files

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Description Provides large-scale single-cell omics data manipulation using Genomic Data Structure (GDS) files. It combines dense and sparse matrices stored in GDS files and the Bioconductor infrastructure framework (SingleCellExperiment and DelayedArray) to provide out-of-memory data storage and large-scale manipulation using the R programming language.

License GPL-3

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`SCArray-package` *Large-scale single-cell omics data manipulation with GDS files*

Description

The package combines dense/sparse matrices stored in GDS files and the Bioconductor infrastructure framework to provide out-of-memory data storage and manipulation using the R programming language.

Details

Package:	SCArray
Type:	Package
License:	GPL version 3

Author(s)

Xiuwen Zheng <xiuwen.zheng@abbvie.com>

Examples

```
# a GDS file for SingleCellExperiment
fn <- system.file("extdata", "example.gds", package="SCArray")

sce <- scExperiment(fn)
sce

rm(sce)
```

`row_nnzero` *Numbers of Non-zeros*

Description

Calculates the numbers of non-zeros for each row or column of a matrix-like object.

Usage

```
row_nnzero(x, na.counted=NA, ...)
col_nnzero(x, na.counted=NA, ...)

## S4 method for signature 'matrix'
row_nnzero(x, na.counted=NA, ...)
## S4 method for signature 'Matrix'
row_nnzero(x, na.counted=NA, ...)
## S4 method for signature 'DelayedMatrix'
row_nnzero(x, na.counted=NA, ...)
## S4 method for signature 'SC_GDSMatrix'
row_nnzero(x, na.counted=NA, ...)

## S4 method for signature 'matrix'
col_nnzero(x, na.counted=NA, ...)
## S4 method for signature 'Matrix'
col_nnzero(x, na.counted=NA, ...)
## S4 method for signature 'DelayedMatrix'
col_nnzero(x, na.counted=NA, ...)
## S4 method for signature 'SC_GDSMatrix'
col_nnzero(x, na.counted=NA, ...)
```

Arguments

`x`	a matrix-like object
`na.counted`	a logical: TRUE for counting NA/NaN as non-zero, FALSE for counting NA/NaN as zero, NA (default) for return NA when encountering NA/NaN
`...`	additional arguments passed to specific methods

Value

Return an integer vector object for the numbers of non-zeros.

Author(s)

Xiuwen Zheng

Examples

```
# a GDS file for SingleCellExperiment
fn <- system.file("extdata", "example.gds", package="SCArray")

cnt <- scArray(fn, "counts")
cnt

row_nnzero(cnt, na.counted=TRUE)
col_nnzero(cnt, na.counted=TRUE)


rm(cnt)
```

`scArray` *Get an DelayedArray instance*

Description

Gets an DelayedArray instance from a single-cell omics GDS file.

Usage

```
scArray(gdsfile, varname)
```

Arguments

`gdsfile`	character for a file name, or a single-cell GDS object with class `SCArrayFileClass`
`varname`	character for the node name in the GDS file

Value

Return an object of class `DelayedArray`.

Author(s)

Xiuwen Zheng

See Also

`scOpen`, `scExperiment`

Examples

```
# a GDS file for SingleCellExperiment
fn <- system.file("extdata", "example.gds", package="SCArray")

cnt <- scArray(fn, "counts")
cnt

rm(cnt)
```

SCArray-classes *Class list defined in SCArray*

Description

SCArrayFileClass is a class directly inheriting from gds.class. SC_GDSArray is a DelayedArray with a SCArraySeed. SC_GDSMatrix is 2-dim SC_GDSArray.

The package combines dense/sparse matrices stored in GDS files and the Bioconductor infrastructure framework to provide out-of-memory data storage and manipulation using the R programming language.

Author(s)

Xiuwen Zheng <xiuwen.zheng@abbvie.com>

SCArray-stats *SC_GDSMatrix row/column summarization*

Description

The row/column summarization methods for the SC_GDSMatrix matrix, extending the S4 methods in the **DelayedArray** and **DelayedMatrixStats** packages.

Usage

```
## S4 method for signature 'SC_GDSMatrix'
rowSums(x, na.rm=FALSE, dims=1)
## S4 method for signature 'SC_GDSMatrix'
colSums(x, na.rm=FALSE, dims=1)
## S4 method for signature 'SC_GDSMatrix'
rowSums2(x, rows=NULL, cols=NULL, na.rm=FALSE, ..., useNames=NA)
## S4 method for signature 'SC_GDSMatrix'
colSums2(x, rows=NULL, cols=NULL, na.rm=FALSE, ..., useNames=NA)

## S4 method for signature 'SC_GDSMatrix'
rowLogSumExps(lx, rows=NULL, cols=NULL, na.rm=FALSE, ..., useNames=NA)
## S4 method for signature 'SC_GDSMatrix'
colLogSumExps(lx, rows=NULL, cols=NULL, na.rm=FALSE, ..., useNames=NA)

## S4 method for signature 'SC_GDSMatrix'
rowProds(x, rows=NULL, cols=NULL, na.rm=FALSE,
    method=c("direct", "expSumLog"), ..., useNames=NA)
## S4 method for signature 'SC_GDSMatrix'
colProds(x, rows=NULL, cols=NULL, na.rm=FALSE,
    method=c("direct", "expSumLog"), ..., useNames=NA)

## S4 method for signature 'SC_GDSMatrix'
rowMeans(x, na.rm=FALSE, dims=1)
## S4 method for signature 'SC_GDSMatrix'
```

```
colMeans(x, na.rm=FALSE, dims=1)
## S4 method for signature 'SC_GDSMatrix'
rowMeans2(x, rows=NULL, cols=NULL, na.rm=FALSE, ..., useNames=NA)
## S4 method for signature 'SC_GDSMatrix'
colMeans2(x, rows=NULL, cols=NULL, na.rm=FALSE, ..., useNames=NA)
## S4 method for signature 'SC_GDSMatrix'
rowWeightedMeans(x, w=NULL, rows=NULL, cols=NULL, na.rm=FALSE, ..., useNames=NA)
## S4 method for signature 'SC_GDSMatrix'
colWeightedMeans(x, w=NULL, rows=NULL, cols=NULL, na.rm=FALSE, ..., useNames=NA)

## S4 method for signature 'SC_GDSMatrix'
rowVars(x, rows=NULL, cols=NULL, na.rm=FALSE, center=NULL, ..., useNames=NA)
## S4 method for signature 'SC_GDSMatrix'
colVars(x, rows=NULL, cols=NULL, na.rm=FALSE, center=NULL, ..., useNames=NA)
## S4 method for signature 'SC_GDSMatrix'
rowWeightedVars(x, w=NULL, rows=NULL, cols=NULL, na.rm=FALSE, ..., useNames=NA)
## S4 method for signature 'SC_GDSMatrix'
colWeightedVars(x, w=NULL, rows=NULL, cols=NULL, na.rm=FALSE, ..., useNames=NA)

## S4 method for signature 'SC_GDSMatrix'
rowSds(x, rows=NULL, cols=NULL, na.rm=FALSE, center=NULL, ..., useNames=NA)
## S4 method for signature 'SC_GDSMatrix'
colSds(x, rows=NULL, cols=NULL, na.rm=FALSE, center=NULL, ..., useNames=NA)
## S4 method for signature 'SC_GDSMatrix'
rowWeightedSds(x, w=NULL, rows=NULL, cols=NULL, na.rm=FALSE, ..., useNames=NA)
## S4 method for signature 'SC_GDSMatrix'
colWeightedSds(x, w=NULL, rows=NULL, cols=NULL, na.rm=FALSE, ..., useNames=NA)

## S4 method for signature 'SC_GDSMatrix'
rowMins(x, rows=NULL, cols=NULL, na.rm=FALSE)
## S4 method for signature 'SC_GDSMatrix'
colMins(x, rows=NULL, cols=NULL, na.rm=FALSE)
## S4 method for signature 'SC_GDSMatrix'
rowMaxs(x, rows=NULL, cols=NULL, na.rm=FALSE)
## S4 method for signature 'SC_GDSMatrix'
colMaxs(x, rows=NULL, cols=NULL, na.rm=FALSE)
## S4 method for signature 'SC_GDSMatrix'
rowRanges(x, rows=NULL, cols=NULL, na.rm=FALSE)
## S4 method for signature 'SC_GDSMatrix'
colRanges(x, rows=NULL, cols=NULL, na.rm=FALSE)

# Get means and variances together for each row or column,
#     return a matrix with two columns for mean and variance
scRowMeanVar(x, na.rm=FALSE, useNames=FALSE, ...)
scColMeanVar(x, na.rm=FALSE, useNames=FALSE, ...)
## S4 method for signature 'SC_GDSMatrix'
scRowMeanVar(x, na.rm=FALSE, useNames=FALSE, ...)
## S4 method for signature 'SC_GDSMatrix'
scColMeanVar(x, na.rm=FALSE, useNames=FALSE, ...)

# Compute column sums across rows
## S4 method for signature 'SC_GDSMatrix'
```

```
rowsum(x, group, reorder=TRUE, na.rm=FALSE, ...)
# Compute row sums across columns
## S4 method for signature 'SC_GDSMatrix'
colsum(x, group, reorder=TRUE, na.rm=FALSE, ...)

## S4 method for signature 'SC_GDSMatrix'
rowAnyNAs(x, rows=NULL, cols=NULL, ..., useNames=NA)
## S4 method for signature 'SC_GDSMatrix'
colAnyNAs(x, rows=NULL, cols=NULL, ..., useNames=NA)

## S4 method for signature 'SC_GDSMatrix'
rowCollapse(x, idxs, rows=NULL, ..., useNames=NA)
## S4 method for signature 'SC_GDSMatrix'
colCollapse(x, idxs, cols=NULL, ..., useNames=NA)

## S4 method for signature 'SC_GDSMatrix'
rowDiffs(x, rows=NULL, cols=NULL, lag=1L,
    differences=1L, ..., useNames=NA)
## S4 method for signature 'SC_GDSMatrix'
colDiffs(x, rows=NULL, cols=NULL, lag=1L,
    differences=1L, ..., useNames=NA)

## S4 method for signature 'SC_GDSMatrix'
rowSdDiffs(x, rows=NULL, cols=NULL, na.rm=FALSE,
    diff=1L, trim=0, ..., useNames=NA)
## S4 method for signature 'SC_GDSMatrix'
colSdDiffs(x, rows=NULL, cols=NULL, na.rm=FALSE,
    diff=1L, trim=0, ..., useNames=NA)

## S4 method for signature 'SC_GDSMatrix'
rowVarDiffs(x, rows=NULL, cols=NULL, na.rm=FALSE,
    diff=1L, trim=0, ..., useNames=NA)
## S4 method for signature 'SC_GDSMatrix'
colVarDiffs(x, rows=NULL, cols=NULL, na.rm=FALSE,
    diff=1L, trim=0, ..., useNames=NA)

## S4 method for signature 'SC_GDSMatrix'
rowAvgsPerColSet(X, W=NULL, rows=NULL, S, FUN=rowMeans, ...,
    na.rm=NA, tFUN=FALSE)
## S4 method for signature 'SC_GDSMatrix'
colAvgsPerRowSet(X, W=NULL, cols=NULL, S, FUN=colMeans, ...,
    na.rm=NA, tFUN=FALSE)
```

Arguments

x, lx, X	A SC_GDSMatrix object (inherited from DelayedMatrix)
dims	not used, it should be 1
rows, cols	specify the subset of rows (and/or columns) to operate over; if NULL, no subsetting
na.rm	if TRUE, missing values (NaN and NA) will be removed
w	NULL or a numeric vector for weights

W	NULL or a matrix for weights
center	NULL, or a vector of pre-calculated row (column) means
useNames	if TRUE, the name attributes of result are set
method	"direct" (by default) or "expSumLog" (calculates the product via the logarithmic transform)
group	a vector for grouping the rows or columns
reorder	if TRUE, order the resulting matrix as sort(unique(group)); otherwise, it will be in the order that groups were encountered
idxs	An index vector specifying the columns (rows) to be extracted; the vector will be reused if the length is less than the number of columns or rows
lag	the lag, an integer
differences, diff	the order of difference, an integer
trim	fraction of observations to be trimmed
S	an integer matrix specifying the subsets, see rowAvgsPerColSet
FUN	summary statistic function, see rowAvgsPerColSet
tFUN	If TRUE, X is transposed before it is passed to FUN, see rowAvgsPerColSet
...	additional arguments passed to specific methods: BPPARAM can be specified (if not specified, getAutoBPPARAM() is used instead)

Details

All these operations are block-processed according to the data stored in the GDS file.

Author(s)

Xiuwen Zheng

See Also

- The **DelayedMatrixStats** package for more row/column summarization methods for DelayedMatrix objects.
- DelayedArray-utils for other common operations on DelayedMatrix objects.
- DelayedMatrix objects.
- matrix objects in base R.
- getAutoBPPARAM, BiocParallelParam for parallel processing,
- The **MatrixGenerics** package for more row/column summarization methods.

SCArray-utils *SC_GDSArray subsetting, Ops, Math*

Description

Subsetting, Arith, Compare, Logic and Math operations on the SC_GDSArray object.

Usage

```
# x[i, j, ... , drop = TRUE]
## S4 method for signature 'SC_GDSArray'
i[j, ... , drop=TRUE]
# x[[i, j, ...]]
## S4 method for signature 'SC_GDSArray'
i[[j, ...]]

## S4 method for signature 'SC_GDSArray'
Ops(e1, e2)
## S4 method for signature 'SC_GDSArray'
Math(x)

# names(x) <- value
# dimnames(x) <- value

# Centers and/or scales the columns of a matrix
## S4 method for signature 'SC_GDSMatrix'
scale(x, center=TRUE, scale=TRUE)

## S4 method for signature 'SC_GDSArray,SC_GDSArray'
pmin2(e1, e2)
## S4 method for signature 'SC_GDSArray,vector'
pmin2(e1, e2)
## S4 method for signature 'vector,SC_GDSArray'
pmin2(e1, e2)
## S4 method for signature 'SC_GDSArray,SC_GDSArray'
pmax2(e1, e2)
## S4 method for signature 'SC_GDSArray,vector'
pmax2(e1, e2)
## S4 method for signature 'vector,SC_GDSArray'
pmax2(e1, e2)
```

Arguments

x	A SC_GDSArray or SC_GDSMatrix object
i, j, ...	indices specifying elements to extract
drop	if TRUE the result will be coerced to the lowest possible dimension
e1, e2	objects
value	NULL, a character vector for names<- or a list of character vectors for dimnames<-
center	either a logical value or a numeric vector (e.g., FALSE or 0 for no centering)
scale	either a logical value or a numeric vector (e.g., TRUE or 1 for no scaling)

Details

All these operations return a SC_GDSArray or SC_GDSMatrix object.

`Arith`: "+", "-", "*", "^", "%%", "%/%", "/"

`Compare`: "==", ">", "<", "!=", "<=", ">="

`Logic`: "&", "|".

`Ops`: "Arith", "Compare", "Logic"

`Math`: "abs", "sign", "sqrt", "ceiling", "floor", "trunc", "cummax", "cummin", "cumprod", "cumsum", "log", "log10", "log2", "log1p", "acos", "acosh", "asin", "asinh", "atan", "atanh", "exp", "expm1", "cos", "cosh", "cospi", "sin", "sinh", "sinpi", "tan", "tanh", "tanpi", "gamma", "lgamma", "digamma", "trigamma"

Value

All these operations return a SC_GDSArray or SC_GDSMatrix object.

Author(s)

Xiuwen Zheng

See Also

Ops, Math, SCArray-stats

Examples

```
fn <- system.file("extdata", "example.gds", package="SCArray")

x <- scArray(fn, "counts")

x[1:8, 1:32]
x > 0
pmin2(x, 1)
log1p(x)
scale(x)

rm(x)
```

---

scConvGDS *Create a GDS file*

Description

Creates a single-cell GDS file from an R object.

Usage

```
scConvGDS(obj, outfn, assay.name=NULL, save.sp=TRUE,
   type=c("float32", "float64", "int32"), compress="LZMA_RA", clean=TRUE, verbose=TRUE)
```

Arguments

obj	a dense/sparse matrix, DelayedMatrix, SummarizedExperiment or SingleCellExperiment
outfn	the output file name in GDS format
assay.name	a character vector for assay names or NULL; if NULL, to include all available assays, otherwise only include the assays in assay.name
save.sp	if TRUE, save it to a sparse matrix in GDS; otherwise, store dense matrix
type	numeric data type in the output file
compress	the compression method, see add.gdsn; or "" for no data compression
clean	TRUE
verbose	if TRUE, show information

Value

Return the path of the output file.

Author(s)

Xiuwen Zheng

See Also

scOpen, scClose, scMEX2GDS, scHDF2GDS

Examples

```
# load a SingleCellExperiment object
fn <- system.file("extdata", "example.rds", package="SCArray")
sce <- readRDS(fn)
sce

scConvGDS(sce, "test.gds")

# remove the temporary file
unlink("test.gds")
```

---

scExperiment *Get a SummarizedExperiment*

Description

Gets an instance of SingleCellExperiment or SummarizedExperiment.

Usage

```
scExperiment(gdsfile, sce=TRUE, use.names=TRUE, load.row=TRUE, load.col=TRUE)
```

Arguments

gdsfile	character for a file name, or a single-cell GDS object with class SCArrayFileClass
sce	if TRUE, return an instance of SingleCellExperiment, otherwise an instance of SummarizedExperiment
use.names	if TRUE, load dimnames from 'feature.id' and 'sample.id'
load.row	TRUE for loading rowData from the gds node "feature.data" in gdsfile
load.col	TRUE for loading colData from the gds node "sample.data" in gdsfile

Value

Return an instance of SingleCellExperiment or SummarizedExperiment.

Author(s)

Xiuwen Zheng

See Also

scOpen, scClose

Examples

```
# a GDS file for SingleCellExperiment
fn <- system.file("extdata", "example.gds", package="SCArray")

sce <- scExperiment(fn)
sce

remove(sce)
```

---

scGetFiles *File names for on-disk backend*

Description

Get a list of file names for DelayedArray with an on-disk backend.

Usage

```
scGetFiles(object, ...)
## S4 method for signature 'SC_GDSArray'
scGetFiles(object, ...)
## S4 method for signature 'SummarizedExperiment'
scGetFiles(object, ...)
```

Arguments

object	input R object (e.g., a GDS-specific DelayedArray)
...	additional arguments passed to specific methods

Value

Return a character vector storing file names.

Author(s)

Xiuwen Zheng

See Also

path

---

scHDF2GDS *Convert HDF5 files to GDS*

Description

Creates a single-cell GDS file from Cell Ranger HDF5 files.

Usage

```
scHDF2GDS(h5_fn, outfn, group=c("matrix", "mm10"), feature_path=character(),
    type=c("float32", "float64", "int32"), compress="LZMA_RA", clean=TRUE,
    verbose=TRUE)
```

Arguments

h5_fn	the input HDF5 file name
outfn	the output file name in GDS format
group	the name of the group in the HDF5 file where the sparse matrix is stored; if there are more than one group names, the first existing group in the HDF5 file is used; "mm10" is usually used for 10x Genomics datasets
feature_path	a character vector for feature variables, otherwise detecting automatically using "genes", "gene_names" and "features/*" when available
type	numeric data type in the output file
compress	the compression method, see add.gdsn
clean	TRUE
verbose	if TRUE, show information

Details

The packages **rhdf5** and **HDF5Array** should be installed.

Value

Return the path of the output file.

Author(s)

Xiuwen Zheng

See Also

scConvGDS, scMEX2GDS

---

scMemory *Load Data to Memory*

Description

Loads the internal data to memory for any on-disk object.

Usage

```
scMemory(x, ...)
## S4 method for signature 'DelayedArray'
scMemory(x, ...)
## S4 method for signature 'SummarizedExperiment'
scMemory(x, ...)
```

Arguments

x	input R object (e.g., a DelayedArray)
...	additional arguments passed to specific methods

Value

Return an object (it maybe a different type compared with x).

Author(s)

Xiuwen Zheng

Examples

```
suppressPackageStartupMessages(library(DelayedArray))

m <- matrix(1:12, nrow=3)
(mat <- DelayedArray(m))

str(scMemory(mat))
```

scMEX2GDS *Convert MEX files to GDS*

Description

Creates a single-cell GDS file from Cell Ranger MEX files.

Usage

```
scMEX2GDS(feature_fn, barcode_fn, mtx_fn, outfn,
    feature_colnm=c("id", "gene", "feature_type"),
    type=c("float32", "float64", "int32"), compress="LZMA_RA", clean=TRUE,
    verbose=TRUE)
```

Arguments

feature_fn	the input file name for features
barcode_fn	the input file name for barcodes
mtx_fn	the input count matrix in MEX format
outfn	the output file name in GDS format
feature_colnm	the column names used in feature_fn
type	numeric data type in the output file
compress	the compression method, see add.gdsn
clean	TRUE
verbose	if TRUE, show information

Value

Return the path of the output file.

Author(s)

Xiuwen Zheng

See Also

scConvGDS, scHDF2GDS

scNumSplit *Split a number*

Description

Splits a number into multiple groups with equal size.

Usage

```
scNumSplit(num, BPPARAM=getAutoBPPARAM())
```

Arguments

num	a length-one number (the total count) for splitting (must be >= 0)
BPPARAM	NULL, a number for the number of groups, or a BiocParallelParam object; if not specified, call getAutoBPPARAM()

Value

Return a list of length-two numeric vectors for the start and end positions. BPPARAM=NULL is as the same as BPPARAM=1, if it is a BiocParallelParam object, call bpnworkers() to get the number of groups.

Author(s)

Xiuwen Zheng

See Also

getAutoBPPARAM, BiocParallelParam, bpnworkers

Examples

```
scNumSplit(100, NULL)
scNumSplit(100, 0)
scNumSplit(100, 1)
scNumSplit(100, 3)
scNumSplit(100)

scNumSplit(0)  # zero-length
```

scObj *DelayedArray Object in GDS*

Description

Convert to SC_GDSArray/SC_GDSMatrix for utilizing GDS specific functions.

Usage

```
scObj(obj, verbose=FALSE)
```

Arguments

obj	a SummarizedExperiment, SingleCellExperiment or DelayedArray object
verbose	if TRUE, show information

Value

Return the object obj with the object class DelayedArray replaced by the class SC_GDSMatrix or SC_GDSArray.

Author(s)

Xiuwen Zheng

See Also

scArray, scExperiment

scOpen *Open/Close a Single-cell GDS File*

Description

Opens or closes a single-cell GDS file.

Usage

```
scOpen(gdsfn, readonly=TRUE, allow.duplicate=TRUE)
scClose(gdsfile)
```

Arguments

gdsfn	the input file name
readonly	whether read-only or not
allow.duplicate	if TRUE, it is allowed to open a GDS file with read-only mode when it has been opened in the same R session
gdsfile	a single-cell GDS object with class SCArrayFileClass

Value

Return an object of class SCArrayFileClass inherited from gds.class.

Author(s)

Xiuwen Zheng

See Also

scArray

Examples

```
# a GDS file for SingleCellExperiment
fn <- system.file("extdata", "example.gds", package="SCArray")

# open the GDS file
(f <- scOpen(fn))

# read a GDS file
cell.id <- read.gdsn(index.gdsn(f, "feature.id"))
samp.id <- read.gdsn(index.gdsn(f, "sample.id"))

# get a DelayedArray object
(cnt <- scArray(f, "counts"))

scClose(f)
```

---

scReplaceNA *Replacement*

Description

Replace NA/NaN in a GDS-specific DelayedArray by a specified value.

Usage

```
scReplaceNA(x, v=0L)
```

Arguments

x	a SC_GDSArray object
v	a length-one double or integer value

Value

Return an object with the class SC_GDSMatrix or SC_GDSArray.

Author(s)

Xiuwen Zheng

See Also

scSetMin, scSetMax, scSetBounds

Examples

```
suppressPackageStartupMessages(library(DelayedArray))

m <- matrix(1:12, nrow=3)
m[2, c(1,3)] <- NA
(mat <- DelayedArray(m))

new_m <-  scObj(mat)  # wrap a in-memory DelayedMatrix
class(new_m)  # SC_GDSMatrix

scReplaceNA(new_m,  999)
```

---

scRowAutoGrid *Automatic grids for matrix-like objects*

Description

Create automatic grids (RegularArrayGrid or ArbitraryArrayGrid for sparse matrices) to use for block processing of matrix-like objects, where the blocks are made of full rows or full columns.

Usage

```
scRowAutoGrid(x, force=FALSE, nnzero=NULL)
scColAutoGrid(x, force=FALSE, nnzero=NULL)
```

Arguments

x	a matrix-like object (e.g., a SC_GDSMatrix object)
force	a logical, only applicable when x is a sparse in-memory matrix or a sparse SC_GDSMatrix object, see details
nnzero	a numeric vector for the numbers of non-zeros for rows or columns, NULL (default) for calling row_nnzero() or col_nnzero() when needed

Details

The functions return regular RegularArrayGrid (calling rowAutoGrid() or colAutoGrid), when x is neither a sparse in-memory matrix nor a sparse SC_GDSMatrix object; otherwise, make use of the information of the numbers of non-zeros to create ArbitraryArrayGrid for more efficient grids. When force is applicable and force=TRUE, the functions return ArbitraryArrayGrid which needs the nnzero values. For force=FALSE, scRowAutoGrid() returns ArbitraryArrayGrid when x is not transposed, and scColAutoGrid() returns ArbitraryArrayGrid when x is transposed. If nnzero=NULL and it is needed, the numbers of non-zeros for rows or columns will be calculated internally. For a large matrix, it is more efficient when nnzero is pre-defined. The internal block size can be controlled by setAutoBlockSize(). If the number of blocks in ArbitraryArrayGrid is more than RegularArrayGrid, the functions return RegularArrayGrid instead when force is not TRUE.

Usually, gd <- scRowAutoGrid() or gd <- scColAutoGrid() is used together with blockApply(, grid=gd, as.sparse=attr(gd, "as.sparse")) or blockReduce(, grid=gd, as.sparse=attr(gd, "as.sparse")) to take advantage of sparse matrices.

Value

Return an object of RegularArrayGrid or ArbitraryArrayGrid. attr(, "as.sparse") is a suggested logical value for as.sparse in blockApply() or blockReduce().

Author(s)

Xiuwen Zheng

See Also

rowAutoGrid, colAutoGrid, setAutoBlockSize, blockApply, blockReduce

Examples

```
# a GDS file for SingleCellExperiment
fn <- system.file("extdata", "example.gds", package="SCArray")

cnt <- scArray(fn, "counts")
cnt

setAutoBlockSize(1048576)  # use 1MB

scRowAutoGrid(cnt)  # it returns RegularArrayGrid since cnt is not very sparse
rowAutoGrid(cnt)
scRowAutoGrid(cnt, force=TRUE)  # ArbitraryArrayGrid


library(Matrix)
cnt2 <- Diagonal(1e5)  # a very sparse matrix

scRowAutoGrid(cnt2)    # 5 blocks
length(rowAutoGrid(cnt2))    # 100000

scColAutoGrid(cnt2)          # 5 blocks
length(colAutoGrid(cnt2))    # 100000 blocks


setAutoBlockSize()  # reset

rm(cnt)
```

---

scRunPCA *Perform PCA on SC_GDSMatrix and expression data*

Description

Perform a Principal Components Analysis (PCA) on cells in the SingleCellExperiment object.

Usage

```
scRunPCA(sce, ncomponents=50, ntop=500, subset_row=NULL, scale=FALSE,
    altexp=NULL, name="PCA", exprs_values="logcounts", dimred=NULL,
    n_dimred=NULL, BSPARAM=NULL, BPPARAM=SerialParam(), verbose=TRUE)

## S4 method for signature 'SC_GDSMatrix'
runPCA(x, rank, center=TRUE, scale=FALSE, get.rotation=TRUE,
    get.pcs=TRUE, ...)
```

Arguments

sce	a SingleCellExperiment or SummarizedExperiment object
x	a SC_GDSMatrix object
ncomponents, rank	# of calculated principal components
ntop	# of features with the highest variances to use for PCA
subset_row	specifying the subset of features to use
center	if TRUE, expression values will be be centered
scale	if TRUE, expression values will be be standardized
altexp	String or integer scalar specifying an alternative experiment containing the input data
name	the name to be used to store the result in reducedDims
exprs_values	the assay name containing the expression values
dimred	String or integer scalar specifying the existing dimensionality reduction results to use
n_dimred	Integer scalar or vector specifying the dimensions to use if dimred is specified
BSPARAM	A BiocSingularParam object specifying which algorithm to be used in runPCA in the BiocSingular package
BPPARAM	A BiocParallelParam object for parallelized calculation
get.rotation	if TRUE, return rotation vectors
get.pcs	if TRUE, return principal component scores
verbose	if TRUE, show information
...	For runPCA, this contains further arguments to pass to runSVD, including BSPARAM to specify the algorithm that should be used, and BPPARAM to control parallelization.

Details

The function runPCA() simply calls runSVD and converts the results into a format similar to that returned by prcomp.

BSPARAM can be one of

ExactParam(): exact SVD with runExactSVD.

IrlbaParam(): approximate SVD with **irlba** via runIrlbaSVD.

RandomParam(): approximate SVD with **rsvd** via runRandomSVD.

FastAutoParam(): fast approximate SVD, chosen based on the matrix representation.

`fold=1` in BiocSingularParam is used for the situation that the covariance matrix is relatively small, and running SVD on the small covariance matrix can be more effecient. When `fold=Inf`, running SVD on the matrix directly and will read the matrix multiple times. If it is a file-based matrix, `fold=Inf` could be slow.

Value

Returns a SingleCellExperiment object containing the PC coordinate matrix in `reducedDims(..., name)`. The attributes of the PC coordinate matrix have "percentVar", "varExplained" and "rotation" (see `scater::runPCA` for more details).

Author(s)

Xiuwen Zheng

See Also

`runSVD` for the underlying SVD function.

?`BiocSingularParam` for the SVD algorithm choices.

`runPCA`.

Examples

```
library(BiocSingular)

# a GDS file for SingleCellExperiment
fn <- system.file("extdata", "example.gds", package="SCArray")

x <- scArray(fn, "counts")
x <- x[1:200, ]
x

pc <- runPCA(x, BSPARAM=ExactParam(fold=1))  # using covariance matrix
str(pc)

rm(x)
```

---

scSetBounds *Set the bounds*

Description

Set the maximum and/or minimum on a GDS-specific DelayedArray.

Usage

```
scSetMax(x, vmax)
scSetMin(x, vmin)
scSetBounds(x, vmin=NaN, vmax=NaN)
```

Arguments

x	a SC_GDSArray object
vmax	maximum, length-one
vmin	minimum, length-one

Value

Return an object with the class SC_GDSMatrix or SC_GDSArray.

Author(s)

Xiuwen Zheng

See Also

scReplaceNA

Examples

```
suppressPackageStartupMessages(library(DelayedArray))

m <- matrix(1:12, nrow=3)
(mat <- DelayedArray(m))

new_m <-  scObj(mat)  # wrap a in-memory DelayedMatrix
class(new_m)  # SC_GDSMatrix

scSetMax(new_m, 5)
scSetMin(new_m, 5)
scSetBounds(new_m, 4, 9)
```

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