

# Package ‘SCArray’

October 14, 2021

**Type** Package

**Title** Large-scale single-cell RNA-seq data manipulation with GDS files

**Version** 1.0.0

**Date** 2021-04-30

**Depends** R (>= 3.5.0), gdsfmt (>= 1.27.4), methods, DelayedArray

**Imports** BiocGenerics, S4Vectors, IRanges, utils, SummarizedExperiment, SingleCellExperiment

**Suggests** Matrix, DelayedMatrixStats, scater, uwot, RUnit, knitr, markdown, rmarkdown

**Description** Provides large-scale single-cell RNA-seq 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

**VignetteBuilder** knitr

**ByteCompile** TRUE

**URL** <https://github.com/AbbVie-ComputationalGenomics/SCArray>

**biocViews** Infrastructure, DataRepresentation, DataImport, SingleCell, RNASeq

**git\_url** <https://git.bioconductor.org/packages/SCArray>

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SCArray-package	<i>Large-scale single-cell RNA-seq data manipulation with GDS files</i>
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**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", "LaMannoBrainData.gds", package="SCArray")

sce <- scExperiment(fn)
sce
```

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scArray	<i>Get an DelayedArray instance</i>
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**Description**

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

**Usage**

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

**Arguments**

gdsfile	character for a file name, or a single-cell GDS object with class <code>SCArrayFileClass</code>
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", "LaMannoBrainData.gds", package="SCArray")

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

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scClose	<i>Close the Single-cell GDS File</i>
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**Description**

Closes a single-cell GDS file which is open.

**Usage**

```
scClose(gdsfile)
```

**Arguments**

gdsfile	a single-cell GDS object with class <code>SCArrayFileClass</code>
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**Value**

None.

**Author(s)**

Xiuwen Zheng

**See Also**

[scOpen](#)

**Examples**

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

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

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

scClose(f)
```

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scConvGDS

*Create a GDS file*

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**Description**

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

**Usage**

```
scConvGDS(obj, outfn, 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
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 <a href="#">add.gdsn</a>
clean	TRUE
verbose	if TRUE, show information

**Value**

Return the path of the output file.

**Author(s)**

Xiuwen Zheng

**See Also**[scOpen](#), [scClose](#)**Examples**

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

scConvGDS(sce, "test.gds")

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

---

scExperiment

*Get a SummarizedExperiment*


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**Description**

Gets an instance of `SingleCellExperiment` or `SummarizedExperiment`.

**Usage**

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

**Arguments**

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

**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", "LaMannoBrainData.gds", package="SCArray")

sce <- scExperiment(fn)
sce
```

---

scOpen

*Open a Single-cell GDS File*

---

**Description**

Opens a single-cell GDS file.

**Usage**

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

**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

**Value**

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

**Author(s)**

Xiuwen Zheng

**See Also**

[scClose](#), [scArray](#)

**Examples**

```
# a GDS file for SingleCellExperiment
fn <- system.file("extdata", "LaMannoBrainData.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)
```

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