

# Package ‘GDSArray’

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**Title** Representing GDS files as array-like objects

**Version** 1.27.2

**Description** GDS files are widely used to represent genotyping or sequence data. The GDSArray package implements the ``GDSArray`` class to represent nodes in GDS files in a matrix-like representation that allows easy manipulation (e.g., subsetting, mathematical transformation) in `_R_`. The data remains on disk until needed, so that very large files can be processed.

**biocViews** Infrastructure, DataRepresentation, Sequencing, GenotypingArray

**Depends** R (>= 3.5), gdsfmt, methods, BiocGenerics, DelayedArray (>= 0.5.32)

**License** GPL-3

**Encoding** UTF-8

**URL** <https://github.com/Bioconductor/GDSArray>

**BugReports** <https://github.com/Bioconductor/GDSArray/issues>

**Imports** tools, S4Vectors (>= 0.17.34), SNPRelate, SeqArray

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acquireGDS	<i>Acquire the GDS file connection in R in the gds.class class.</i>
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### Description

Acquire a (possibly cached) `gds.class` object given it's path.

### Usage

```
acquireGDS(path, type = NULL, ...)
```

```
releaseGDS(path, type = NULL, ...)
```

### Arguments

<code>path</code>	String containing a path to a GDS file.
<code>type</code>	String containing the GDS file type. Case insensitive. Can be "seqgds" for a GDS file with sequencing data, or "snpgds" for a GDS file with SNP data. This argument was added for the <code>VariantExperiment</code> package for certain functionalities. By default is <code>NULL</code> , which returns a regular <code>gds.class</code> .
<code>...</code>	arguments to be passed to <code>openfn.gds()</code> inside <code>acquireGDS</code> .

### Details

`acquireConn` will cache the `gds.class` object in the current R session to avoid repeated initialization. This improves efficiency for repeated calls. The cached `gds.class` object for any given path can be deleted by calling `releaseGDS` for the same path.

### Value

For `acquireGDS`, by default returns a regular `gds.class` object, which are identical to that returned by `gdsfmt::openfn.gds(path)`. If `type` is not `NULL`, a `SeqVarGDSClass` that is identical to `SeqArray::seqOpen(path)`, or `SNPGDSFileClass` that is identical to `SNPRelate::snpgdsOpen(path)`. Both are inherited from `gds.class` but with additional checking and methods.

For `releaseGDS`, any existing `gds.class` object for the path is disconnected and cleared from cache, and `NULL` is invisibly returned. This is equivalent to that returned by `gdsfmt::closefn.gds()` except it take path as input. If `path=NULL`, all cached connections are removed.

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**Examples**

```
fn <- gdsExampleFileName()
gdscon <- acquireGDS(fn)
acquireGDS(fn) ## just re-uses the cache
acquireGDS(fn, type = "seqgds") ## construct a new GDS connection
releaseGDS(fn) ## clears the cache
```

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extract_array	<i>GDSArray constructor and coercion methods.</i>
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**Description**

extract\_array: the function to extract data from a GDS file, by taking GDSArraySeed as input. This function is required by the DelayedArray for the seed contract.

GDSArray: The function to convert a gds file into the GDSArray data structure.

GDSArray example data

**Usage**

```
## S4 method for signature 'GDSArraySeed'
extract_array(x, index)

GDSArray(gdsfile, varname)

gdsExampleFileName(type = c("seqgds", "snpgds"))
```

**Arguments**

x	the GDSArraySeed object
index	An unnamed list of subscripts as positive integer vectors, one vector per dimension in x. Empty and missing subscripts (represented by integer(0) and NULL list elements, respectively) are allowed. The subscripts can contain duplicated indices. They cannot contain NAs or non-positive values.
gdsfile	Can be a GDSArraySeed, a character string of gds file name, or an "gds.class" R object.
varname	A character string specifying the gds array node to be read into GDSArray.
type	the type of gds file, available are "seqgds" for SeqVarGDSClass and "snpgds" for SNPGDSFileClass.

**Value**

GDSArray class object.

**Examples**

```
fn <- gdsExampleFileName("snpgds")
allnodes <- gdsnodes(fn) ## print all available gds nodes in fn.
allnodes
GDSArray(fn, "genotype")
GDSArray(fn, "sample.annot/pop.group")

fn1 <- gdsExampleFileName("seqgds")
allnodes1 <- gdsnodes(fn1) ## print all available gds nodes in fn1.
allnodes1
## GDSArray(fn1, "genotype/data")
GDSArray(fn1, "variant.id")
GDSArray(fn1, "sample.annotation/family")
GDSArray(fn1, "annotation/format/DP/data")
GDSArray(fn1, "annotation/info/DP")
gdsExampleFileName("snpgds")
gdsExampleFileName("seqgds")
```

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GDSFile-class

*GDSFile constructor and methods.*

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**Description**

GDSFile: GDSFile is a light-weight class to represent a GDS file. It has the '\$' completion method to complete any possible gds nodes. If the slot of 'current\_path' in 'GDSFile' object represent a valid gds node, it will return the 'GDSArray' of that node directly. Otherwise, it will return the 'GDSFile' object with an updated 'current\_path'.

GDSFile: the GDSFile class constructor.

gdsfile: filename slot getter for GDSFile object.

gdsfile<-: filename slot setter for GDSFile object.

gdsnodes: to get the available gds nodes from a gds file name or a GDSFile object.

**Usage**

```
GDSFile(file, current_path = "")

## S4 method for signature 'GDSFile'
gdsfile(object)

gdsfile(object) <- value

## S4 method for signature 'GDSFile'
x$name
```

```
## S4 method for signature 'ANY'
gdsnodes(x, node)
```

### Arguments

file	the GDS file path.
current_path	the current path to the closest gds node.
object	GDSFile object.
value	the new gds file path
x	a character string for the GDS file name or a GDSFile object.
name	the name of gds node
node	the node name of a gds file or GDSFile object.

### Value

gdsfile: the file path of corresponding GDSfile object.

\$: a GDSFile with updated @current\_path, or GDSArray object if the current\_path is a valid gds node.

gdsnodes: a character vector of all available gds nodes within the related GDS file and the specified node.

### Examples

```
fn <- gdsExampleFileName("seqgds")
gf <- GDSFile(fn)
gdsfile(gf)
fn <- gdsExampleFileName("snpgds")
gdsnodes(fn)
gdsnodes(fn, "annotation/info")
fn1 <- gdsExampleFileName("snpgds")
gdsnodes(fn1)
gdsnodes(fn1, "sample.annot")
gf <- GDSFile(fn)
gdsnodes(gf)
gdsnodes(gf, "genotype")
gdsfile(gf)
```

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seed, GDSArray-method *GDSArraySeed or GDSArray related methods, slot getters and setters.*

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### Description

dim, dimnames: dimension and dimnames of object contained in the GDS file.

seed: the GDSArraySeed getter for GDSArray object.

seed<-: the GDSArraySeed setter for GDSArray object.

gdsfile: on-disk location of GDS file represented by this object.

**Usage**

```
## S4 method for signature 'GDSArray'  
seed(x)  
  
## S4 replacement method for signature 'GDSArray'  
seed(x) <- value  
  
gdsfile(object)  
  
## S4 method for signature 'GDSArraySeed'  
gdsfile(object)  
  
## S4 method for signature 'GDSArray'  
gdsfile(object)  
  
## S4 method for signature 'DelayedArray'  
gdsfile(object)
```

**Arguments**

x	the GDSArray and GDSArraySeed objects.
value	the new GDSArraySeed for the GDSArray object.
object	GDSArray, GDSMatrix, GDSArraySeed, GDSFile or SummarizedExperiment object.

**Value**

dim: the integer vector of dimensions for GDSArray or GDSArraySeed objects.  
dimnames: the unnamed list of dimension names for GDSArray and GDSArraySeed objects.  
seed: the GDSArraySeed of GDSArray object.  
gdsfile: the character string for the gds file path.

**Examples**

```
fn <- gdsExampleFileName("snpgds")  
ga <- GDSArray(fn, "sample.annot/pop.group")  
dim(ga)  
dimnames(ga)  
type(ga)  
seed(ga)  
dim(seed(ga))  
gdsfile(ga)
```

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