

# Package ‘GDSArray’

April 16, 2019

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

**Version** 1.2.0

**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

**RoxygenNote** 6.0.1

**VignetteBuilder** knitr

**Suggests** testthat, knitr, BiocStyle, BiocManager

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

**git\_branch** RELEASE\_3\_8

**git\_last\_commit** 0889e32

**git\_last\_commit\_date** 2018-10-30

**Date/Publication** 2019-04-15

**Author** Qian Liu [aut, cre],  
Martin Morgan [aut],  
Hervé Pagès [aut]

**Maintainer** Qian Liu <qliu7@buffalo.edu>

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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

```
file <- SNPRelate::snpgdsExampleFileName()
ga <- GDSArray(file, "sample.annot/pop.group")
dim(ga)
dimnames(ga)
type(ga)
seed(ga)
dim(seed(ga))
gdsfile(ga)
```

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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(file, name = NA)

example(pkg = "GDSArray")
```

### 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.
file	the gds file name.
name	the gds array node to be read into GDSArraySeed / GDSArray. For GDSArray, the default value for name is the genotype data.
pkg	the package name, which is "GDSArray" by default.

**Value**

GDSArray class object.

**Examples**

```
file <- SNPRelate::snpgdsExampleFileName()
allnodes <- gdsnodes(file) ## print all available gds nodes in file.
allnodes
GDSArray(file)
GDSArray(file, "sample.annot/pop.group")

file1 <- SeqArray::seqExampleFileName("gds")
allnodes1 <- gdsnodes(file1) ## print all available gds nodes in file1.
allnodes1
GDSArray(file1)
GDSArray(file1, "variant.id")
GDSArray(file1, "sample.annotation/family")
GDSArray(file1, "annotation/format/DP/data")
GDSArray(file1, "annotation/info/DP")
example("GDSArray")
```

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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:** file slot getter for GDSFile object.

**gdsfile<-:** file slot setter for GDSFile object.

**gdsnodes:** to get the available gds nodes from the GDSFile object or the file path with extension of ".gds".

**Usage**

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

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

## S4 replacement method for signature 'GDSFile'
gdsfile(object) <- value

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

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

**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 GDSFile object. or GDS file path (for gdsnodes()).
name	the name of gds node

**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 for the available gds nodes. When input is GDS file path, it returns all available gds nodes within the GDS file, no matter there is value or not. When input is GDSFile object, it returns only the gds nodes that could construct unique GDSArray objects, which means that the gds node has non-zero-dimensions, and is actually array, and all GDSArrays returned from these nodes are unique (by excluding the gds nodes that has 'code~ prefix).

**Examples**

```
file <- SeqArray::seqExampleFileName("gds")
gf <- GDSFile(file)
gdsfile(gf)

file <- SNPRelate::snpgdsExampleFileName()
gdsnodes(file)
file1 <- SeqArray::seqExampleFileName("gds")
gdsnodes(file1)
gf <- GDSFile(file)
gdsnodes(gf)
gdsfile(gf)
```

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