

# Package ‘SeqArray’

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**Description** Data management of large-scale whole-genome sequencing variant calls with thousands of individuals: genotypic data (e.g., SNVs, indels and structural variation calls) and annotations in SeqArray files are stored in an array-oriented and compressed manner, with efficient data access using the R programming language.

**License** GPL-3

**VignetteBuilder** knitr

**ByteCompile** TRUE

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**BugReports** <http://github.com/zhengxwen/SeqArray/issues>

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**R topics documented:**

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SeqArray-package

*Data Management of Large-scale Whole-Genome Sequence Variant Calls***Description**

Data management of large-scale whole-genome sequencing variants.

## Details

As the cost of DNA sequencing rapidly decreases, whole-genome sequencing (WGS) is generating data at an unprecedented rate. Scientists are being challenged to manage data sets that are terabyte-sized, contain diverse types of data and complex data relationships. Data analyses of WGS requires a general file format for storing genetic variants including single nucleotide variations (SNVs), insertions and deletions (indels) and structural variants. The variant call format (VCF) is a generic and flexible format for storing DNA polymorphisms developed for the 1000 Genomes Project that is the standard WGS format in use today. VCF is a textual format usually stored in compressed files that supports rich annotations and relatively efficient data retrieval. However, VCF files are large and the computational burden associated with all data retrieval from text files can be significant for a large WGS study with thousands of samples.

To provide an efficient alternative to VCF for WGS data, we developed a new data format and accompanying Bioconductor package, “SeqArray”. Key features of SeqArray are efficient storage including multiple high compression options, data retrieval by variant or sample subsets, support for parallel access and computing, and C++ integration in the R programming environment. The SeqArray package provides R functions for efficient block-wise computations, and enables scientists to develop custom R scripts for exploratory data analysis.

Webpage: <http://github.com/zhengxwen/SeqArray>, <http://www.bioconductor.org/packages/SeqArray/>

## Author(s)

Xiuwen Zheng <zhengxwen@gmail.com>

## Examples

```
# the file of VCF
vcf.fn <- seqExampleFileName("vcf")
vcf.fn
# or vcf.fn <- "C:/YourFolder/Your_VCF_File.vcf"

# parse the header
seqVCF_Header(vcf.fn)

# get sample id
seqVCF_SampID(vcf.fn)

# convert
seqVCF2GDS(vcf.fn, "tmp.gds", storage.option="ZIP_RA")
seqSummary("tmp.gds")

# list the structure of GDS variables
f <- seqOpen("tmp.gds")
f

seqClose(f)
unlink("tmp.gds")

#####

# the GDS file
(gds.fn <- seqExampleFileName("gds"))
```

```

# display
(f <- seqOpen(gds.fn))

# get 'sample.id'
(samp.id <- seqGetData(f, "sample.id"))
# "NA06984" "NA06985" "NA06986" ...

# get 'variant.id'
head(variant.id <- seqGetData(f, "variant.id"))

# get 'chromosome'
table(seqGetData(f, "chromosome"))

# get 'allele'
head(seqGetData(f, "allele"))
# "T,C" "G,A" "G,A" ...

# set sample and variant filters
seqSetFilter(f, sample.id=samp.id[c(2,4,6,8,10)])
set.seed(100)
seqSetFilter(f, variant.id=sample(variant.id, 10))

# get genotypic data
seqGetData(f, "genotype")

# get annotation/info/DP
seqGetData(f, "annotation/info/DP")

# get annotation/info/AA, a variable-length dataset
seqGetData(f, "annotation/info/AA")
# $length      <- indicating the length of each variable-length data
# [1] 1 1 1 1 1 1 ...
# $data        <- the data according to $length
# [1] "T" "C" "T" "C" "G" "C" ...

# get annotation/format/DP, a variable-length dataset
seqGetData(f, "annotation/format/DP")
# $length      <- indicating the length of each variable-length data
# [1] 1 1 1 1 1 1 ...
# $data        <- the data according to $length
#      variant
# sample [1] [2] [3] [4] [5] [6] ...
# [1,] 25 25 22 3 4 17 ...

# read multiple variables variant by variant
seqApply(f, c(geno="genotype", phase="phase", qual="annotation/id"),
  FUN=function(x) print(x), as.is="none")

# get the numbers of alleles per variant
head(seqApply(f, "allele",
  FUN=function(x) length(unlist(strsplit(x,","))), as.is="integer"))
# or
head(seqGetData(f, "$num_allele"))

```

```
#####

# remove the sample and variant filters
seqResetFilter(f)

# calculate the frequency of reference allele,
# a faster version could be obtained by C coding
af <- seqApply(f, "genotype", FUN=function(x) mean(x==0L, na.rm=TRUE),
  as.is="double")
length(af)
summary(af)

# close the GDS file
seqClose(f)
```

---

KG_P1_SampData	<i>Simulated sample data for 1000 Genomes Phase 1</i>
----------------	---

---

**Description**

An AnnotatedDataFrame with columns sample.id, sex, age, and phenotype, where the identifiers in sample.id match those in the SeqArray file.

**Usage**

```
KG_P1_SampData
```

**Value**

An AnnotatedDataFrame

---

seqAlleleFreq	<i>Get Allele Frequencies or Counts</i>
---------------	---

---

**Description**

Calculates the allele frequencies or counts.

**Usage**

```
seqAlleleFreq(gdsfile, ref.allele=0L, .progress=FALSE, parallel=seqGetParallel())
seqAlleleCount(gdsfile, ref.allele=0L, .progress=FALSE, parallel=seqGetParallel())
```

**Arguments**

gdsfile	a <a href="#">SeqVarGDSClass</a> object
ref.allele	NULL, a single numeric value, a numeric vector or a character vector; see Value
.progress	if TRUE, show progress information
parallel	FALSE (serial processing), TRUE (multicore processing), numeric value or other value; parallel is passed to the argument cl in <a href="#">seqParallel</a> , see <a href="#">seqParallel</a> for more details.

**Value**

If `ref.allele=NULL`, the function returns a list of allele frequencies/counts according to all allele per site. If `ref.allele` is a single numeric value (like `0L`), it returns a numeric/integer vector for the specified allele (`0L` for the reference allele, `1L` for the first alternative allele, etc). If `ref.allele` is a numeric vector, `ref.allele` specifies each allele per site. If `ref.allele` is a character vector, `ref.allele` specifies the desired allele for each site (e.g. ancestral allele for the derived allele frequency/count).

**Author(s)**

Xiuwen Zheng

**See Also**

[seqNumAllele](#), [seqMissing](#), [seqParallel](#), [seqGetParallel](#)

**Examples**

```
# the GDS file
(gds.fn <- seqExampleFileName("gds"))

# display
f <- seqOpen(gds.fn)

# return a list
head(seqAlleleFreq(f, NULL, .progress=TRUE))

# return a numeric vector
summary(seqAlleleFreq(f, 0L, .progress=TRUE))

# return a numeric vector, AA is ancestral allele
AA <- toupper(seqGetData(f, "annotation/info/AA")$data)
head(seqAlleleFreq(f, AA))

# allele counts
head(seqAlleleCount(f, NULL, .progress=TRUE))
head(seqAlleleCount(f, 0L, .progress=TRUE))
head(seqAlleleCount(f, AA, .progress=TRUE))

# close the GDS file
seqClose(f)
```

---

seqApply

*Apply Functions Over Array Margins*

---

**Description**

Returns a vector or list of values obtained by applying a function to margins of genotypes and annotations.

**Usage**

```
seqApply(gdsfile, var.name, FUN, margin=c("by.variant", "by.sample"),
  as.is=c("none", "list", "integer", "double", "character", "logical", "raw"),
  var.index=c("none", "relative", "absolute"), parallel=FALSE,
  .useraw=FALSE, .progress=FALSE, .list_dup=TRUE, ...)
```

**Arguments**

<code>gdsfile</code>	a <a href="#">SeqVarGDSClass</a> object
<code>var.name</code>	the variable name(s), see details
<code>FUN</code>	the function to be applied
<code>margin</code>	giving the dimension which the function will be applied over
<code>as.is</code>	returned value: a list, an integer vector, etc; <code>as.is</code> can be a <a href="#">connection</a> object, or a GDS node <a href="#">gdsn.class</a> object; if "unlist" is used, produces a vector which contains all the atomic components, via <code>unlist(..., recursive=FALSE)</code>
<code>var.index</code>	if "none", call <code>FUN(x, ...)</code> without variable index; if "relative" or "absolute", add an argument to the user-defined function <code>FUN</code> like <code>FUN(index, x, ...)</code> where <code>index</code> is an index of variant starting from 1 if <code>margin = "by.variant"</code> : "relative" for indexing in the selection defined by <a href="#">seqSetFilter</a> , "absolute" for indexing with respect to all data
<code>parallel</code>	FALSE (serial processing), TRUE (multicore processing), numeric value or other value; <code>parallel</code> is passed to the argument <code>cl</code> in <a href="#">seqParallel</a> , see <a href="#">seqParallel</a> for more details.
<code>.useraw</code>	TRUE, force to use RAW instead of INTEGER for genotypes and dosages; FALSE, use INTEGER; NA, use RAW for small numbers instead of INTEGER if possible, it is needed to detect data type (RAW or INTEGER) in the user-defined function; for genotypes, 0xFF is missing value if RAW is used
<code>.progress</code>	if TRUE, show progress information
<code>.list_dup</code>	internal use only
<code>...</code>	optional arguments to <code>FUN</code>

**Details**

The variable name should be "sample.id", "variant.id", "position", "chromosome", "allele", "genotype", "annotation/id", "annotation/qual", "annotation/filter", "annotation/info/VARIABLE\_NAME" or "annotation/format/VARIABLE\_NAME".

"@genotype", "annotation/info/@VARIABLE\_NAME" or "annotation/format/@VARIABLE\_NAME" are used to obtain the index associated with these variables.

"\$dosage" is also allowed for the dosages of reference allele (integer: 0, 1, 2 and NA for diploid genotypes).

"\$dosage\_alt" returns a RAW/INTEGER matrix for the dosages of alternative allele without distinguishing different alternative alleles.

"\$num\_allele" returns an integer vector with the numbers of distinct alleles.

"\$ref" returns a character vector of reference alleles

"\$alt" returns a character vector of alternative alleles (delimited by comma)

"\$chrom\_pos" returns characters with the combination of chromosome and position, e.g., "1:1272721".

"\$chrom\_pos\_allele" returns characters with the combination of chromosome, position and alleles, e.g., "1:1272721\_A\_G" (i.e., chr:position\_REF\_ALT).

The algorithm is highly optimized by blocking the computations to exploit the high-speed memory instead of disk.

### Value

A vector, a list of values or none.

### Author(s)

Xiuwen Zheng

### See Also

[seqBlockApply](#), [seqSetFilter](#), [seqGetData](#), [seqParallel](#), [seqGetParallel](#)

### Examples

```
# the GDS file
(gds.fn <- seqExampleFileName("gds"))

# display
(f <- seqOpen(gds.fn))

# get 'sample.id'
(samp.id <- seqGetData(f, "sample.id"))
# "NA06984" "NA06985" "NA06986" ...

# get 'variant.id'
head(variant.id <- seqGetData(f, "variant.id"))

# set sample and variant filters
set.seed(100)
seqSetFilter(f, sample.id=samp.id[c(2,4,6,8,10)],
             variant.id=sample(variant.id, 10))

# read
seqApply(f, "genotype", FUN=print, margin="by.variant")
seqApply(f, "genotype", FUN=print, margin="by.variant", .useraw=TRUE)

seqApply(f, "genotype", FUN=print, margin="by.sample")
seqApply(f, "genotype", FUN=print, margin="by.sample", .useraw=TRUE)

# read multiple variables variant by variant
seqApply(f, c(geno="genotype", phase="phase", rsid="annotation/id",
             DP="annotation/format/DP"), FUN=print, as.is="none")

# get the numbers of alleles per variant
seqApply(f, "allele",
         FUN=function(x) length(unlist(strsplit(x,","))), as.is="integer")

# output to a file
fl <- file("tmp.txt", "wt")
seqApply(f, "genotype", FUN=sum, na.rm=TRUE, as.is=fl)
close(fl)
readLines("tmp.txt")
```



```

seqApply(f, "genotype", FUN=sum, na.rm=TRUE, as.is=stdout())
seqApply(f, "genotype", FUN=sum, na.rm=TRUE, as.is="integer")
# should be identical

#####
# with an index of variant

seqApply(f, c(geno="genotype", phase="phase", rsid="annotation/id"),
  FUN=function(index, x) { print(index); print(x); index },
  as.is="integer", var.index="relative")
# it is as the same as
which(seqGetFilter(f)$variant.sel)

#####
# reset sample and variant filters
seqResetFilter(f)

# calculate the frequency of reference allele,
# a faster version could be obtained by C coding
af <- seqApply(f, "genotype", FUN=function(x) mean(x=="L", na.rm=TRUE),
  as.is="double")
length(af)
summary(af)

#####
# apply the user-defined function sample by sample

# reset sample and variant filters
seqResetFilter(f)
summary(seqApply(f, "genotype", FUN=function(x) { mean(is.na(x)) },
  margin="by.sample", as.is="double"))

# set sample and variant filters
set.seed(100)
seqSetFilter(f, sample.id=samp.id[c(2,4,6,8,10)],
  variant.id=sample(variant.id, 10))

seqApply(f, "genotype", FUN=print, margin="by.variant", as.is="none")

seqApply(f, "genotype", FUN=print, margin="by.sample", as.is="none")

seqApply(f, c(sample.id="sample.id", genotype="genotype"), FUN=print,
  margin="by.sample", as.is="none")

# close the GDS file
seqClose(f)

# delete the temporary file

```

```
unlink("tmp.txt")
```

---

seqAsVCF

*VariantAnnotation objects*

---

## Description

Create a [VCF-class](#) object

## Usage

```
seqAsVCF(x, chr.prefix="", info=NULL, geno=NULL)
```

## Arguments

x	a <a href="#">SeqVarGDSClass</a> object
chr.prefix	prefix to add to seqlevels
info	which INFO fields to return
geno	which GENO fields to return

## Details

Coerces a [SeqVarGDSClass](#) object to a [VCF-class](#) object. Row names correspond to the variant.id. info and geno specify the 'INFO' and 'GENO' (FORMAT) fields to return, respectively. If not specified, all fields are returned; if 'NA' no fields are returned. Use [seqSetFilter](#) prior to calling seqAsVCF to specify samples and variants to return.

The **VariantAnnotation** package should be loaded to explore this object.

## Value

A [CollapsedVCF](#) object.

## Author(s)

Stephanie Gogarten, Xiuwen Zheng

## See Also

[VCF-class](#)

## Examples

```
gds <- seqOpen(seqExampleFileName("gds"))

## Not run:
library(VariantAnnotation)
seqAsVCF(gds)

## End(Not run)

seqClose(gds)
```

seqBED2GDS

*Convert PLINK BED Format to SeqArray Format***Description**

Converts a PLINK BED file to a SeqArray GDS file.

**Usage**

```
seqBED2GDS(bed.fn, fam.fn, bim.fn, out.gdsfn,
           compress.geno="LZMA_RA", compress.annotation="LZMA_RA",
           optimize=TRUE, digest=TRUE, verbose=TRUE)
```

**Arguments**

bed.fn	the file name of binary file, genotype information
fam.fn	the file name of first six columns of ".ped"
bim.fn	the file name of extended MAP file: two extra columns = allele names
out.gdsfn	the file name, output a file of SeqArray format
compress.geno	the compression method for "genotype"; optional values are defined in the function add.gdsn
compress.annotation	the compression method for the GDS variables, except "genotype"; optional values are defined in the function add.gdsn
optimize	if TRUE, optimize the access efficiency by calling <a href="#">cleanup.gds</a>
digest	a logical value (TRUE/FALSE) or a character ("md5", "sha1", "sha256", "sha384" or "sha512"); add hash codes to the GDS file if TRUE or a digest algorithm is specified
verbose	if TRUE, show information

**Value**

Return the file name of SeqArray file with an absolute path.

**Author(s)**

Xiuwen Zheng

**See Also**

[seqSNP2GDS](#), [seqVCF2GDS](#)

**Examples**

```
library(SNPRelate)

# PLINK BED files
bed.fn <- system.file("extdata", "plinkhapmap.bed.gz", package="SNPRelate")
fam.fn <- system.file("extdata", "plinkhapmap.fam.gz", package="SNPRelate")
bim.fn <- system.file("extdata", "plinkhapmap.bim.gz", package="SNPRelate")
```

```
# convert
seqBED2GDS(bed.fn, fam.fn, bim.fn, "tmp.gds")

seqSummary("tmp.gds")

# remove the temporary file
unlink("tmp.gds", force=TRUE)
```

---

seqBlockApply

*Apply Functions Over Array Margins via Blocking*


---

### Description

Returns a vector or list of values obtained by applying a function to margins of genotypes and annotations via blocking.

### Usage

```
seqBlockApply(gdsfile, var.name, FUN, margin=c("by.variant"),
  as.is=c("none", "list", "unlist"), var.index=c("none", "relative", "absolute"),
  bsize=1024L, parallel=FALSE, .useraw=FALSE, .progress=FALSE, ...)
```

### Arguments

gdsfile	a <a href="#">SeqVarGDSClass</a> object
var.name	the variable name(s), see details
FUN	the function to be applied
margin	giving the dimension which the function will be applied over
as.is	returned value: a list, a vector or none; as.is can be a <a href="#">connection</a> object, or a GDS node <a href="#">gdsn.class</a> object; if "unlist" is used, produces a vector which contains all the atomic components, via <code>unlist(..., recursive=FALSE)</code>
var.index	if "none", call <code>FUN(x, ...)</code> without variable index; if "relative" or "absolute", add an argument to the user-defined function FUN like <code>FUN(index, x, ...)</code> where index is an index of variant starting from 1 if margin = "by.variant": "relative" for indexing in the selection defined by <a href="#">seqSetFilter</a> , "absolute" for indexing with respect to all data
bsize	block size
parallel	FALSE (serial processing), TRUE (multicore processing), numeric value or other value; parallel is passed to the argument <code>cl</code> in <a href="#">seqParallel</a> , see <a href="#">seqParallel</a> for more details.
.useraw	TRUE, force to use RAW instead of INTEGER for genotypes and dosages; FALSE, use INTEGER; NA, use RAW instead of INTEGER if possible; for genotypes, 0xFF is missing value if RAW is used
.progress	if TRUE, show progress information
...	optional arguments to FUN

**Details**

The variable name should be "sample.id", "variant.id", "position", "chromosome", "allele", "genotype", "annotation/id", "annotation/qual", "annotation/filter", "annotation/info/VARIABLE\_NAME" or "annotation/format/VARIABLE\_NAME".

"@genotype", "annotation/info/@VARIABLE\_NAME" or "annotation/format/@VARIABLE\_NAME" are used to obtain the index associated with these variables.

"\$dosage" is also allowed for the dosages of reference allele (integer: 0, 1, 2 and NA for diploid genotypes).

"\$dosage\_alt" returns a RAW/INTEGER matrix for the dosages of alternative allele without distinguishing different alternative alleles.

"\$num\_allele" returns an integer vector with the numbers of distinct alleles.

"\$ref" returns a character vector of reference alleles

"\$alt" returns a character vector of alternative alleles (delimited by comma)

"\$chrom\_pos" returns characters with the combination of chromosome and position, e.g., "1:1272721".

"\$chrom\_pos\_allele" returns characters with the combination of chromosome, position and alleles, e.g., "1:1272721\_A\_G" (i.e., chr:position\_REF\_ALT).

The algorithm is highly optimized by blocking the computations to exploit the high-speed memory instead of disk.

**Value**

A vector, a list of values or none.

**Author(s)**

Xiuwen Zheng

**See Also**

[seqApply](#), [seqSetFilter](#), [seqGetData](#), [seqParallel](#), [seqGetParallel](#)

**Examples**

```
# the GDS file
(gds.fn <- seqExampleFileName("gds"))

# display
(f <- seqOpen(gds.fn))

# get 'sample.id'
(samp.id <- seqGetData(f, "sample.id"))
# "NA06984" "NA06985" "NA06986" ...

# get 'variant.id'
head(variant.id <- seqGetData(f, "variant.id"))

# set sample and variant filters
set.seed(100)
seqSetFilter(f, sample.id=samp.id[c(2,4,6,8,10)],
            variant.id=sample(variant.id, 10))
```

```

# read
seqApply(f, "genotype", FUN=print, margin="by.variant")
seqApply(f, "genotype", FUN=print, margin="by.variant", .useraw=TRUE)

seqApply(f, "genotype", FUN=print, margin="by.sample")
seqApply(f, "genotype", FUN=print, margin="by.sample", .useraw=TRUE)

# read in block
seqGetData(f, "$dosage")
seqBlockApply(f, "$dosage", print, bsize=3)
seqBlockApply(f, "$dosage", function(x) x, as.is="list", bsize=3)
seqBlockApply(f, c(dos="$dosage", pos="position"), print, bsize=3)

# close the GDS file
seqClose(f)

```

---

seqCheck

*Data Integrity Checking*


---

### Description

Performs data integrity on a SeqArray GDS file.

### Usage

```
seqCheck(gdsfile, verbose=TRUE)
```

### Arguments

gdsfile	a <a href="#">SeqVarGDSClass</a> object, or a file name
verbose	if TRUE, display information

### Value

A list of the following components:

hash	a <code>data.frame</code> for hash checking, including algo for digest algorithms and ok for the checking states
dimension	a <code>data.frame</code> for checking the dimension of each variable, including ok for the checking states and info for the error messages

### Author(s)

Xiuwen Zheng

### Examples

```

# the GDS file
(gds.fn <- seqExampleFileName("gds"))

seqCheck(gds.fn)

```

---

seqClose-methods	<i>Close the SeqArray GDS File</i>
------------------	------------------------------------

---

**Description**

Closes a SeqArray GDS file which is open.

**Usage**

```
## S4 method for signature 'gds.class'  
seqClose(object)  
## S4 method for signature 'SeqVarGDSClass'  
seqClose(object)
```

**Arguments**

object            a SeqArray object

**Details**

If object is

- [gds.class](#), close a general GDS file
- [SeqVarGDSClass](#), close the sequence GDS file.

**Value**

None.

**Author(s)**

Xiuwen Zheng

**See Also**

[seqOpen](#)

---

seqDelete	<i>Delete GDS Variables</i>
-----------	-----------------------------

---

**Description**

Deletes variables in the SeqArray GDS file.

**Usage**

```
seqDelete(gdsfile, info.var=character(), fmt.var=character(),  
          samp.var=character(), verbose=TRUE)
```

**Arguments**

<code>gdsfile</code>	a <a href="#">SeqVarGDSClass</a> object
<code>info.var</code>	the variables in the INFO field, i.e., "annotation/info/VARIABLE_NAME"
<code>fmt.var</code>	the variables in the FORMAT field, i.e., "annotation/format/VARIABLE_NAME"
<code>samp.var</code>	the variables in the sample annotation field, i.e., "sample.annotation/VARIABLE_NAME"
<code>verbose</code>	if TRUE, show information

**Value**

None.

**Author(s)**

Xiuwen Zheng

**See Also**

[seqOpen](#), [seqClose](#)

**Examples**

```
# the file of GDS
gds.fn <- seqExampleFileName("gds")
file.copy(gds.fn, "tmp.gds")

# display
(f <- seqOpen("tmp.gds", FALSE))

seqDelete(f, info.var=c("HM2", "AA"), fmt.var="DP")
f

# close the GDS file
seqClose(f)

# clean up the fragments, reduce the file size
cleanup.gds("tmp.gds")

# remove the temporary file
unlink("tmp.gds", force=TRUE)
```

---

seqDigest

*Hash function digests*

---

**Description**

Create hash function digests for all or a subset of data

**Usage**

```
seqDigest(gdsfile, varname, algo=c("md5"), verbose=FALSE)
```



**Arguments**

<code>gdsfile</code>	a <a href="#">SeqVarGDSClass</a> object
<code>varname</code>	the variable name(s), see details
<code>algo</code>	the digest hash algorithm: "md5"
<code>verbose</code>	if TRUE, show progress information

**Details**

The variable name should be "sample.id", "variant.id", "position", "chromosome", "allele", "annotation/id", "annotation/qual", "annotation/filter", "annotation/info/VARIABLE\_NAME", or "annotation/format/VARIABLE\_NAME".

Users can define a subset of data via [seqSetFilter](#) and create a hash digest for the subset only.

**Value**

A hash character.

**Author(s)**

Xiuwen Zheng

**See Also**

[seqSetFilter](#), [seqApply](#)

**Examples**

```
# the GDS file
(gds.fn <- seqExampleFileName("gds"))

# display
f <- seqOpen(gds.fn)

seqDigest(f, "genotype")
seqDigest(f, "annotation/filter")
seqDigest(f, "annotation/format/DP")

# close the GDS file
seqClose(f)
```

---

`seqExampleFileName`     *Example files*

---

**Description**

The example files of VCF and GDS format.

**Usage**

```
seqExampleFileName(type=c("gds", "vcf", "KG_Phase1"))
```

**Arguments**

type                    either "gds" or "vcf"

**Details**

The SeqArray GDS file was created from a subset of VCF data of the 1000 Genomes Phase 1 Project.

**Value**

Return the file name of a VCF file shipped with the package if type = "vcf", or the file name of a GDS file if type = "gds".

**Author(s)**

Xiuwen Zheng

**Examples**

```
seqExampleFileName("gds")
seqExampleFileName("vcf")
seqExampleFileName("KG_Phase1")
```

---

seqExport	<i>Export to a GDS File</i>
-----------	-----------------------------

---

**Description**

Exports to a GDS file with selected samples and variants, which are defined by seqSetFilter().

**Usage**

```
seqExport(gdsfile, out.fn, info.var=NULL, fmt.var=NULL, samp.var=NULL,
          optimize=TRUE, digest=TRUE, verbose=TRUE)
```

**Arguments**

gdsfile	a <a href="#">SeqVarGDSClass</a> object
out.fn	the file name of output GDS file
info.var	characters, the variable name(s) in the INFO field for import; or NULL for all variables
fmt.var	characters, the variable name(s) in the FORMAT field for import; or NULL for all variables
samp.var	characters, the variable name(s) in the folder "sample.annotation"
optimize	if TRUE, optimize the access efficiency by calling <a href="#">cleanup.gds</a>
digest	a logical value (TRUE/FALSE) or a character ("md5", "sha1", "sha256", "sha384" or "sha512"); add md5 hash codes to the GDS file if TRUE or a digest algorithm is specified
verbose	if TRUE, show information

**Value**

Return the file name of GDS format with an absolute path.

**Author(s)**

Xiuwen Zheng

**See Also**

[seqVCF2GDS](#)

**Examples**

```
# open the GDS file
(gds.fn <- seqExampleFileName("gds"))
(f <- seqOpen(gds.fn))

# get 'sample.id'
head(samp.id <- seqGetData(f, "sample.id"))

# get 'variant.id'
head(variant.id <- seqGetData(f, "variant.id"))

set.seed(100)
# set sample and variant filters
seqSetFilter(f, sample.id=samp.id[c(2,4,6,8,10,12,14,16)])
seqSetFilter(f, variant.id=sample(variant.id, 100))

# export
seqExport(f, "tmp.gds")
seqExport(f, "tmp.gds", info.var=character())
seqExport(f, "tmp.gds", fmt.var=character())
seqExport(f, "tmp.gds", samp.var=character())

# show file
(f1 <- seqOpen("tmp.gds")); seqClose(f1)

# close
seqClose(f)

# delete the temporary file
unlink("tmp.gds")
```

---

seqGDS2SNP

*Convert to a SNP GDS File*

---

**Description**

Converts a SeqArray GDS file to a SNP GDS file.

**Usage**

```
seqGDS2SNP(gdsfile, out.gdsfn, dosage=FALSE, compress.geno="LZMA_RA",
           compress.annotation="LZMA_RA", ds.type=c("packedreal16", "float", "double"),
           optimize=TRUE, verbose=TRUE)
```

**Arguments**

<code>gdsfile</code>	character (GDS file name), or a <a href="#">SeqVarGDSClass</a> object
<code>out.gdsfn</code>	the file name, output a file of VCF format
<code>dosage</code>	a logical value, or characters for the variable name of dosage in the SeqArray file; if FALSE exports genotypes, otherwise exports dosages
<code>compress.geno</code>	the compression method for "genotype"; optional values are defined in the function <code>add.gdsn</code>
<code>compress.annotation</code>	the compression method for the GDS variables, except "genotype"; optional values are defined in the function <code>add.gdsn</code>
<code>ds.type</code>	applicable when import dosages, the data type for storing dosages; see <a href="#">add.gdsn</a>
<code>optimize</code>	if TRUE, optimize the access efficiency by calling <a href="#">cleanup.gds</a>
<code>verbose</code>	if TRUE, show information

**Details**

[seqSetFilter](#) can be used to define a subset of data for the conversion.

**Value**

Return the file name of VCF file with an absolute path.

**Author(s)**

Xiuwen Zheng

**See Also**

[seqSNP2GDS](#), [seqVCF2GDS](#), [seqGDS2VCF](#)

**Examples**

```
# the GDS file
gds.fn <- seqExampleFileName("gds")

seqGDS2SNP(gds.fn, "tmp.gds")

# delete the temporary file
unlink("tmp.gds")
```

---

`seqGDS2VCF`*Convert to a VCF File*

---

**Description**

Converts a SeqArray GDS file to a Variant Call Format (VCF) file.

**Usage**

```
seqGDS2VCF(gdsfile, vcf.fn, info.var=NULL, fmt.var=NULL, use_Rsamtools=TRUE,  
           verbose=TRUE)
```

**Arguments**

<code>gdsfile</code>	a <a href="#">SeqVarGDSClass</a> object
<code>vcf.fn</code>	the file name, output a file of VCF format; or a <a href="#">connection</a> object
<code>info.var</code>	a list of variable names in the INFO field, or NULL for using all variables; character ( <code>∅</code> ) for no variable in the INFO field
<code>fmt.var</code>	a list of variable names in the FORMAT field, or NULL for using all variables; character ( <code>∅</code> ) for no variable in the FORMAT field
<code>use_Rsamtools</code>	TRUE for loading the Rsamtools package, see details
<code>verbose</code>	if TRUE, show information

**Details**

[seqSetFilter](#) can be used to define a subset of data for the export.

If the filename extension is "gz", the gzip compression algorithm is used to compress the output data. When the Rsamtools package is installed, the exported file utilizes the bgzf format ([bgzip](#), a variant of gzip format) allowing for fast indexing.

**Value**

Return the file name of VCF file with an absolute path.

**Author(s)**

Xiuwen Zheng

**References**

Danecek, P., Auton, A., Abecasis, G., Albers, C.A., Banks, E., DePristo, M.A., Handsaker, R.E., Lunter, G., Marth, G.T., Sherry, S.T., et al. (2011). The variant call format and VCFtools. *Bioinformatics* 27, 2156-2158.

**See Also**

[seqVCF2GDS](#)

**Examples**

```

# the GDS file
(gds.fn <- seqExampleFileName("gds"))

# display
(f <- seqOpen(gds.fn))

# output the first 10 samples
samp.id <- seqGetData(f, "sample.id")
seqSetFilter(f, sample.id=samp.id[1:5])

# convert
seqGDS2VCF(f, "tmp.vcf.gz")

# no INFO and FORMAT
seqGDS2VCF(f, "tmp1.vcf.gz", info.var=character(), fmt.var=character())

# output BN,GP,AA,DP,HM2 in INFO (the variables are in this order), no FORMAT
seqGDS2VCF(f, "tmp2.vcf.gz", info.var=c("BN","GP","AA","DP","HM2"),
  fmt.var=character())

# read
(txt <- readLines("tmp.vcf.gz", n=20))
(txt <- readLines("tmp1.vcf.gz", n=20))
(txt <- readLines("tmp2.vcf.gz", n=20))

#####
# Users could compare the new VCF file with the original VCF file
# call "diff" in Unix (a command line tool comparing files line by line)

# using all samples and variants
seqResetFilter(f)

# convert
seqGDS2VCF(f, "tmp.vcf.gz")

# file.copy(seqExampleFileName("vcf"), "old.vcf.gz", overwrite=TRUE)
# system("diff <(gunzip -c old.vcf.gz) <(gunzip -c tmp.vcf.gz)")

# 1a2,3
# > ##fileDate=20130309
# > ##source=SeqArray_RPackage_v1.0

# LOOK GOOD!

# delete temporary files
unlink(c("tmp.vcf.gz", "tmp1.vcf.gz", "tmp2.vcf.gz"))

```

```
# close the GDS file
seqClose(f)
```

---

seqGetData

*Get Data*


---

### Description

Gets data from a SeqArray GDS file.

### Usage

```
seqGetData(gdsfile, var.name, .useraw=FALSE)
```

### Arguments

gdsfile	a <a href="#">SeqVarGDSClass</a> object
var.name	the variable name, see details
.useraw	TRUE, force to use RAW instead of INTEGER for genotypes and dosages; FALSE, use INTEGER; NA, use RAW for small numbers instead of INTEGER if possible; 0xFF is missing value if RAW is used

### Details

The variable name should be "sample.id", "variant.id", "position", "chromosome", "allele", "genotype", "annotation/id", "annotation/qual", "annotation/filter", "annotation/info/VARIABLE\_NAME" or "annotation/format/VARIABLE\_NAME".

"@genotype", "annotation/info/@VARIABLE\_NAME" or "annotation/format/@VARIABLE\_NAME" are used to obtain the index associated with these variables.

"\$dosage" is also allowed for the dosages of reference allele (integer: 0, 1, 2 and NA for diploid genotypes).

"\$dosage\_alt" returns a RAW/INTEGER matrix for the dosages of alternative allele without distinguishing different alternative alleles.

"\$num\_allele" returns an integer vector with the numbers of distinct alleles.

"\$ref" returns a character vector of reference alleles

"\$alt" returns a character vector of alternative alleles (delimited by comma)

"\$chrom\_pos" returns characters with the combination of chromosome and position, e.g., "1:1272721".

"\$chrom\_pos\_allele" returns characters with the combination of chromosome, position and alleles, e.g., "1:1272721\_A\_G" (i.e., chr:position\_REF\_ALT).

### Value

Return vectors or lists.

### Author(s)

Xiuwen Zheng

**See Also**

[seqSetFilter](#), [seqApply](#)

**Examples**

```
# the GDS file
(gds.fn <- seqExampleFileName("gds"))

# display
(f <- seqOpen(gds.fn))

# get 'sample.id'
(samp.id <- seqGetData(f, "sample.id"))
# "NA06984" "NA06985" "NA06986" ...

# get 'variant.id'
head(variant.id <- seqGetData(f, "variant.id"))

# get 'chromosome'
table(seqGetData(f, "chromosome"))

# get 'allele'
head(seqGetData(f, "allele"))
# "T,C" "G,A" "G,A" ...

# get '$chrom_pos'
head(seqGetData(f, "$chrom_pos"))

# get '$dosage'
seqGetData(f, "$dosage")[1:6, 1:10]

# get '$num_allele'
head(seqGetData(f, "$num_allele"))

# set sample and variant filters
seqSetFilter(f, sample.id=samp.id[c(2,4,6,8,10)])
set.seed(100)
seqSetFilter(f, variant.id=sample(variant.id, 10))

# get genotypic data
seqGetData(f, "genotype")

# get annotation/info/DP
seqGetData(f, "annotation/info/DP")

# get annotation/info/AA, a variable-length dataset
seqGetData(f, "annotation/info/AA")
# $length          <- indicating the length of each variable-length data
# [1] 1 1 1 1 1 1 ...
# $data            <- the data according to $length
# [1] "T" "C" "T" "C" "G" "C" ...

# get annotation/format/DP, a variable-length dataset
seqGetData(f, "annotation/format/DP")
# $length          <- indicating the length of each variable-length data
```



```

# [1] 1 1 1 1 1 1 ...
# $data          <- the data according to $length
#   variant
# sample [,1] [,2] [,3] [,4] [,5] [,6] ...
# [1,]    25    25    22     3     4    17 ...

# close the GDS file
seqClose(f)

```

---

seqGetFilter

*Get the Filter of GDS File*


---

## Description

Gets the filter of samples and variants.

## Usage

```
seqGetFilter(gdsfile, .useraw=FALSE)
```

## Arguments

gdsfile	a <a href="#">SeqVarGDSClass</a> object
.useraw	returns logical vectors if FALSE, and returns raw vectors if TRUE

## Value

Return a list:

sample.sel	a logical/raw vector indicating selected samples
variant.sel	a logical/raw vector indicating selected variants

## Author(s)

Xiuwen Zheng

## See Also

[seqSetFilter](#)

## Examples

```

# the GDS file
(gds.fn <- seqExampleFileName("gds"))

# display
(f <- seqOpen(gds.fn))

# get 'sample.id'
(samp.id <- seqGetData(f, "sample.id"))
# "NA06984" "NA06985" "NA06986" ...

# get 'variant.id'

```

```

head(variant.id <- seqGetData(f, "variant.id"))

# set sample and variant filters
seqSetFilter(f, sample.id=samp.id[c(2,4,6,8,10)])
set.seed(100)
seqSetFilter(f, variant.id=sample(variant.id, 10))

# get filter
z <- seqGetFilter(f)

# the number of selected samples
sum(z$sample.sel)
# the number of selected variants
sum(z$variant.sel)

z <- seqGetFilter(f, .useraw=TRUE)
head(z$sample.sel)
head(z$variant.sel)

# close the GDS file
seqClose(f)

```

seqMerge

*Merge Multiple SeqArray GDS Files***Description**

Merges multiple SeqArray GDS files.

**Usage**

```
seqMerge(gds.fn, out.fn, storage.option="LZMA_RA", info.var=NULL, fmt.var=NULL,
         samp.var=NULL, optimize=TRUE, digest=TRUE, geno.pad=TRUE, verbose=TRUE)
```

**Arguments**

gds.fn	the file names of multiple GDS files
out.fn	the output file name
storage.option	specify the storage and compression option, "ZIP_RA" ( <a href="#">seqStorageOption("ZIP_RA")</a> ); or "LZMA_RA" to use LZMA compression algorithm with higher compression ratio (by default)
info.var	characters, the variable name(s) in the INFO field; NULL for all variables, or <code>character()</code> excludes all INFO variables
fmt.var	characters, the variable name(s) in the FORMAT field; NULL for all variables, or <code>character()</code> excludes all FORMAT variables
samp.var	characters, the variable name(s) in 'sample.annotation'; or NULL for all variables
optimize	if TRUE, optimize the access efficiency by calling <a href="#">cleanup.gds</a>

digest	a logical value (TRUE/FALSE) or a character ("md5", "sha1", "sha256", "sha384" or "sha512"); add md5 hash codes to the GDS file if TRUE or a digest algorithm is specified
geno.pad	TRUE, pad a 2-bit genotype array in bytes to avoid recompressing genotypes if possible
verbose	if TRUE, show information

### Details

The function merges multiple SeqArray GDS files. Users can specify the compression method and level for the new GDS file. If `gds.fn` contains one file, users can change the storage type to create a new file.

WARNING: the functionality of `seqMerge()` is limited.

### Value

Return the file name of GDS format with an absolute path.

### Author(s)

Xiuwen Zheng

### See Also

[seqVCF2GDS](#), [seqExport](#)

### Examples

```
# the VCF file
vcf.fn <- seqExampleFileName("vcf")

# the number of variants
total.count <- seqVCF_Header(vcf.fn, getnum=TRUE)$num.variant

split.cnt <- 5
start <- integer(split.cnt)
count <- integer(split.cnt)

s <- (total.count+1) / split.cnt
st <- 1L
for (i in 1:split.cnt)
{
  z <- round(s * i)
  start[i] <- st
  count[i] <- z - st
  st <- z
}

fn <- paste0("tmp", 1:split.cnt, ".gds")

# convert to 5 gds files
for (i in 1:split.cnt)
{
  seqVCF2GDS(vcf.fn, fn[i], storage.option="ZIP_RA",
            start=start[i], count=count[i])
}
```

```

}

# merge
seqMerge(fn, "tmp.gds", storage.option="ZIP_RA")
seqSummary("tmp.gds")

####

vcf.fn <- seqExampleFileName("gds")
file.copy(vcf.fn, "test.gds", overwrite=TRUE)

# modify 'sample.id'
f <- openfn.gds("test.gds", FALSE)
sid <- read.gdsn(index.gdsn(f, "sample.id"))
add.gdsn(f, "sample.id", paste("S", 1:length(sid)), replace=TRUE)
closefn.gds(f)

# merging
seqMerge(c(vcf.fn, "test.gds"), "output.gds", storage.option="ZIP_RA")

# delete the temporary files
unlink(c("tmp.gds", "test.gds", "output.gds"), force=TRUE)
unlink(fn, force=TRUE)

```

---

seqMissing

*Missing genotype percentage*


---

### Description

Calculates the missing rates per variant or per sample.

### Usage

```
seqMissing(gdsfile, per.variant=TRUE, .progress=FALSE, parallel=seqGetParallel())
```

### Arguments

<code>gdsfile</code>	a <a href="#">SeqVarGDSClass</a> object
<code>per.variant</code>	missing rate per variant if TRUE, or missing rate per sample if FALSE
<code>.progress</code>	if TRUE, show progress information
<code>parallel</code>	FALSE (serial processing), TRUE (multicore processing), numeric value or other value; <code>parallel</code> is passed to the argument <code>cl</code> in <a href="#">seqParallel</a> , see <a href="#">seqParallel</a> for more details.

### Value

A vector of missing rates.

### Author(s)

Xiuwen Zheng

**See Also**

[seqAlleleFreq](#), [seqNumAllele](#), [seqParallel](#), [seqGetParallel](#)

**Examples**

```
# the GDS file
(gds.fn <- seqExampleFileName("gds"))

# display
(f <- seqOpen(gds.fn))

summary(seqMissing(f, TRUE, .progress=TRUE))

summary(seqMissing(f, FALSE, .progress=TRUE))

# close the GDS file
seqClose(f)
```

---

seqNumAllele	<i>Number of alleles</i>
--------------	--------------------------

---

**Description**

Returns the numbers of alleles for each site.

**Usage**

```
seqNumAllele(gdsfile)
```

**Arguments**

gdsfile            a [SeqVarGDSClass](#) object

**Value**

The numbers of alleles for each site.

**Author(s)**

Xiuwen Zheng

**See Also**

[seqAlleleFreq](#), [seqMissing](#)

## Examples

```
# the GDS file
(gds.fn <- seqExampleFileName("gds"))

# display
f <- seqOpen(gds.fn)

table(seqNumAllele(f))

# close the GDS file
seqClose(f)
```

---

seqOpen

*Open a SeqArray GDS File*

---

## Description

Opens a SeqArray GDS file.

## Usage

```
seqOpen(gds.fn, readonly=TRUE, allow.duplicate=FALSE)
```

## Arguments

<code>gds.fn</code>	the file name
<code>readonly</code>	whether read-only or not
<code>allow.duplicate</code>	if TRUE, it is allowed to open a GDS file with read-only mode when it has been opened in the same R session

## Details

It is strongly suggested to call `seqOpen` instead of `openfn.gds`, since `seqOpen` will perform internal checking for data integrity.

## Value

Return an object of class `gds.class`.

## Author(s)

Xiuwen Zheng

## See Also

[seqClose](#), [seqGetData](#), [seqApply](#)

**Examples**

```
# the GDS file
(gds.fn <- seqExampleFileName("gds"))

# open the GDS file
gdsfile <- seqOpen(gds.fn)

# display the contents of the GDS file in a hierarchical structure
gdsfile

# close the GDS file
seqClose(gdsfile)
```

---

seqOptimize	<i>Optimize the Storage of Data Array</i>
-------------	---

---

**Description**

Transpose data array or matrix for possibly higher-speed access.

**Usage**

```
seqOptimize(gdsfn, target=c("chromosome", "by.sample"), format.var=TRUE,
            cleanup=TRUE, verbose=TRUE)
```

**Arguments**

gdsfn	the file name of GDS
target	"chromosome", "by.sample"; see details
format.var	a character vector for selected variable names, or TRUE for all variables, according to "annotation/format"
cleanup	call <code>link{cleanup.gds}</code> if TRUE
verbose	if TRUE, show information

**Details**

"chromosome": adding or updating two additional nodes '@chrom\_rle\_val' and '@chrom\_rle\_len' for faster chromosome indexing, requiring SeqArray>=v1.20.0.

"by.sample": optimizing GDS file for `seqApply(..., margin="by.sample")`. Warning: optimizing GDS file for reading data by sample may increase file size by up to 2X as genotype data and all format data are duplicated.

**Value**

None.

**Author(s)**

Xiuwen Zheng

**See Also**

[seqGetData](#), [seqApply](#)

**Examples**

```
# the file name of VCF
(vcf.fn <- seqExampleFileName("vcf"))
# or vcf.fn <- "C:/YourFolder/Your_VCF_File.vcf"

# convert
seqVCF2GDS(vcf.fn, "tmp.gds", storage.option="ZIP_RA")

# prepare data for the SeqVarTools package
seqOptimize("tmp.gds", target="by.sample")

# list the structure of GDS variables
(f <- seqOpen("tmp.gds"))
# close
seqClose(f)

# delete the temporary file
unlink("tmp.gds")
```

---

seqParallel

*Apply Functions in Parallel*

---

**Description**

Applies a user-defined function in parallel.

**Usage**

```
seqParallel(cl=seqGetParallel(), gdsfile, FUN,
            split=c("by.variant", "by.sample", "none"), .combine="unlist",
            .selection.flag=FALSE, ...)
seqParApply(cl=seqGetParallel(), x, FUN, load.balancing=TRUE, ...)
```

**Arguments**

cl	NULL or FALSE: serial processing; TRUE: multicore processing (the maximum number of cores minor one); a numeric value: the number of cores to be used; a cluster object for parallel processing, created by the functions in the package <a href="#">parallel</a> , like <a href="#">makeCluster</a> ; a BiocParallelParam object from the BiocParallel package. See details
gdsfile	a <a href="#">SeqVarGDSClass</a> object, or NULL
FUN	the function to be applied, should be like FUN(gdsfile, ...) or FUN(...)
split	split the dataset by variant or sample according to multiple processes, or "none" for no split



.combine            define a function for combining results from different processes; by default, "unlist" is used, to produce a vector which contains all the atomic components, via `unlist(..., recursive=FALSE)`; "list", return a list of results created by child processes; "none", no return; or a function, like "+".

.selection.flag    TRUE – passes a logical vector of selection to the second argument of `FUN(gdsfile, selection, ...)`

x                    a vector (atomic or list), passed to `FUN`

load.balancing    if TRUE, call `clusterApplyLB` instead of `clusterApply`

...                 optional arguments to `FUN`

## Details

When `cl` is TRUE or a numeric value, forking techniques are used to create a new child process as a copy of the current R process, see `?parallel::mcfork`. However, forking is not available on Windows, and `makeCluster` is called to make a cluster which will be deallocated after calling `FUN`.

It is strongly suggested to use `seqParallel` together with `seqParallelSetup`. `seqParallelSetup` could work around the problem of forking on Windows, without allocating clusters frequently.

The user-defined function could use two predefined variables `SeqArray:::process_count` and `SeqArray:::process_index` to tell the total number of cluster nodes and which cluster node being used.

`seqParallel(, gdsfile=NULL, FUN=..., split="none")` could be used to setup multiple streams of pseudo-random numbers, and see `nextRNGStream` or `nextRNGSubStream` in the package `parallel`.

## Value

A vector or list of values.

## Author(s)

Xiuwen Zheng

## See Also

[seqSetFilter](#), [seqGetData](#), [seqApply](#), [seqParallelSetup](#), [seqGetParallel](#)

## Examples

```
library(parallel)

# choose an appropriate cluster size or number of cores
seqParallelSetup(2)

# the GDS file
(gds.fn <- seqExampleFileName("gds"))

# display
(gdsfile <- seqOpen(gds.fn))

# the uniprocessor version
afreq1 <- seqParallel(, gdsfile, FUN = function(f) {
  seqApply(f, "genotype", as.is="double",
```

```

        FUN=function(x) mean(x==0, na.rm=TRUE))
    }, split = "by.variant")

length(afreq1)
summary(afreq1)

# run in parallel
afreq2 <- seqParallel(, gdsfile, FUN = function(f) {
    seqApply(f, "genotype", as.is="double",
        FUN=function(x) mean(x==0, na.rm=TRUE))
    }, split = "by.variant")

length(afreq2)
summary(afreq2)

# check
length(afreq1) # 1348
all(afreq1 == afreq2)

#####
# check -- variant splits

seqParallel(, gdsfile, FUN = function(f) {
    v <- seqGetFilter(f)
    sum(v$variant.sel)
    }, split = "by.variant")
# [1] 674 674

#####

seqParallel(, NULL, FUN = function() {
    paste(SeqArray:::process_index, SeqArray:::process_count, sep=" / ")
    }, split = "none")

#####

# close the GDS file
seqClose(gdsfile)

seqParallelSetup(FALSE)

```

---

seqParallelSetup

*Setup/Get a Parallel Environment*


---

## Description

Sets up a parallel environment in R for the current session.

## Usage

```
seqParallelSetup(cluster=TRUE, verbose=TRUE)
seqGetParallel()
```

## Arguments

cluster	NULL or FALSE: serial processing; TRUE: parallel processing with the maximum number of cores minor one; a numeric value: the number of cores to be used; a cluster object for parallel processing, created by the functions in the package <a href="#">parallel</a> , like <a href="#">makeCluster</a> . See details
verbose	if TRUE, show information

## Details

When `cl` is TRUE or a numeric value, forking techniques are used to create a new child process as a copy of the current R process, see `?parallel::mcfork`. However, forking is not available on Windows, so multiple processes created by [makeCluster](#) are used instead. The R environment option `seqarray.parallel` will be set according to the value of `cluster`. Using `seqParallelSetup(FALSE)` removes the registered cluster, as does stopping the registered cluster.

## Value

`seqParallelSetup()` has no return, and `seqGetParallel()` returns `getOption("seqarray.parallel", FALSE)`.

## Author(s)

Xiuwen Zheng

## See Also

[seqParallel](#), [seqApply](#)

## Examples

```
library(parallel)

seqParallelSetup(2L)

# the GDS file
(gds.fn <- seqExampleFileName("gds"))

# display
(f <- seqOpen(gds.fn))

# run in parallel
summary(seqMissing(f))

# close the GDS file
seqClose(f)

seqParallelSetup(FALSE)
```

---

seqRecompress                      *Recompress the GDS file*

---

### Description

Recompress the SeqArray GDS file.

### Usage

```
seqRecompress(gds.fn, compress=c("ZIP", "LZ4", "LZMA", "Ultra", "UltraMax"),
              exclude=character(), optimize=TRUE, verbose=TRUE)
```

### Arguments

gds.fn	the file name of SeqArray file
compress	the compression method
exclude	excluded GDS nodes
optimize	if TRUE, optimize the access efficiency by calling <a href="#">cleanup.gds</a>
verbose	if TRUE, show information

### Details

This function requires gdsfmt ( $\geq$  v1.17.2). [seqVCF2GDS](#) usually takes lots of memory when the compression method "LZMA\_RA.max", "Ultra" or "UltraMax" is specified. So users could call `seqVCF2GDS(, storage.option="ZIP_RA")` first, and then recompress the GDS file with a higher compression option, e.g., "UltraMax". `seqRecompress()` takes much less memory, since it recompresses data in a GDS node each time.

### Value

None.

### Author(s)

Xiuwen Zheng

### See Also

[seqVCF2GDS](#), [seqStorageOption](#)

### Examples

```
gds.fn <- seqExampleFileName("gds")
file.copy(gds.fn, "tmp.gds")

seqRecompress(gds.fn, "LZMA")

unlink("tmp.gds")
```

---

seqSetFilter-methods *Set a Filter to Sample or Variant*


---

**Description**

Sets a filter to sample and/or variant.

**Usage**

```
## S4 method for signature 'SeqVarGDSCClass,ANY'
seqSetFilter(object, variant.sel,
             sample.sel=NULL, variant.id=NULL, sample.id=NULL,
             action=c("set", "intersect", "push", "push+set", "push+intersect", "pop"),
             verbose=TRUE)
## S4 method for signature 'SeqVarGDSCClass,GRanges'
seqSetFilter(object, variant.sel,
             rm.txt="chr", intersect=FALSE, verbose=TRUE)
## S4 method for signature 'SeqVarGDSCClass,GRangesList'
seqSetFilter(object, variant.sel,
             rm.txt="chr", intersect=FALSE, verbose=TRUE)
## S4 method for signature 'SeqVarGDSCClass,IRanges'
seqSetFilter(object, variant.sel,
             chr, intersect=FALSE, verbose=TRUE)
seqResetFilter(object, sample=TRUE, variant=TRUE, verbose=TRUE)
seqSetFilterChrom(object, include=NULL, is.num=NA, from.bp=NULL, to.bp=NULL,
                 intersect=FALSE, verbose=TRUE)
seqSetFilterPos(object, chr, pos, intersect=FALSE, multi.pos=FALSE,
                verbose=TRUE)
```

**Arguments**

object	a <a href="#">SeqVarGDSCClass</a> object
variant.sel	a logical/raw/index vector indicating the selected variants; <a href="#">GRanges</a> , a <a href="#">GRanges</a> object for the genomic locations; <a href="#">GRangesList</a> , a <a href="#">GRangesList</a> object for storing a collection of <a href="#">GRanges</a> objects; <a href="#">IRanges</a> , a <a href="#">IRanges</a> object for storing a collection of range objects
sample.sel	a logical/raw/index vector indicating the selected samples
variant.id	ID of selected variants
sample.id	ID of selected samples
action	"set" – set the current filter via <code>sample.id</code> , <code>variant.id</code> , <code>samp.sel</code> or <code>variant.sel</code> ; "intersect" – set the current filter to the intersection of selected samples and/or variants; "push" – push the current filter to the stack, and it could be recovered by "pop" later, no change on the current filter; "push+set" – push the current filter to the stack, and changes the current filter via <code>sample.id</code> , <code>variant.id</code> , <code>samp.sel</code> or <code>variant.sel</code> ; "push+intersect" – push the current filter to the stack, and set the current filter to the intersection of selected samples and/or variants; "pop" – pop up the last filter
rm.txt	a character, the characters will be removed from <code>seqnames(variant.sel)</code>
chr	a vector of character for chromosome coding

pos	a vector of numeric values for genome coordinate
sample	logical, if TRUE, include all samples
variant	logical, if TRUE, include all variants
include	NULL, or a vector of characters for specified chromosome(s)
is.num	a logical variable: TRUE, chromosome code is numeric; FALSE, chromosome is not numeric; is.num=TRUE is usually used to exclude non-autosomes
from.bp	NULL, no limit; a numeric vector, the lower bound of position
to.bp	NULL, no limit; a numeric vector, the upper bound of position
intersect	if FALSE, the candidate samples/variants for selection are all samples/variants (by default); if TRUE, the candidate samples/variants are from the selected samples/variants defined via the previous call
multi.pos	FALSE, use the first matched position; TRUE, allow multiple variants at the same position
verbose	if TRUE, show information

### Details

seqResetFilter(file) is equivalent to seqSetFilter(file), where the selection arguments in seqSetFilter are NULL.

If from.bp and to.bp has values, they should be equal-size as include. A trio of include, from.bp and to.bp indicates a region on human genomes. NA in from.bp is treated as 0, and NA in to.bp is treated as the maximum of integer ( $2^{31} - 1$ ).

### Value

None.

### Author(s)

Xiuwen Zheng

### See Also

[seqSetFilterChrom](#), [seqSetFilterCond](#), [seqGetFilter](#), [seqGetData](#), [seqApply](#)

### Examples

```
# the GDS file
(gds.fn <- seqExampleFileName("gds"))

# display
(f <- seqOpen(gds.fn))

# get 'sample.id'
(samp.id <- seqGetData(f, "sample.id"))
# "NA06984" "NA06985" "NA06986" ...

# get 'variant.id'
head(variant.id <- seqGetData(f, "variant.id"))

# get 'chromosome'
table(seqGetData(f, "chromosome"))
```

```
# get 'allele'
head(seqGetData(f, "allele"))
# "T,C" "G,A" "G,A" ...

# set sample and variant filters
seqSetFilter(f, sample.id=samp.id[c(2,4,6,8)])
set.seed(100)
seqSetFilter(f, variant.id=sample(variant.id, 5))

# get genotypic data
seqGetData(f, "genotype")

## OR
# set sample and variant filters
seqSetFilter(f, sample.sel=c(2,4,6,8))
set.seed(100)
seqSetFilter(f, variant.sel=sample.int(length(variant.id), 5))

# get genotypic data
seqGetData(f, "genotype")

## set the intersection

seqResetFilter(f)
seqSetFilterChrom(f, 10L)
seqSummary(f, "genotype", check="none")

AF <- seqAlleleFreq(f)
table(AF <= 0.9)

seqSetFilter(f, variant.sel=(AF<=0.9), action="intersect")
seqSummary(f, "genotype", check="none")

## chromosome

seqResetFilter(f)

seqSetFilterChrom(f, is.num=TRUE)
seqSummary(f, "genotype", check="none")

seqSetFilterChrom(f, is.num=FALSE)
seqSummary(f, "genotype", check="none")

seqSetFilterChrom(f, 1:4)
seqSummary(f, "genotype", check="none")
table(seqGetData(f, "chromosome"))

# HLA region
seqSetFilterChrom(f, 6, from.bp=29719561, to.bp=32883508)
seqSummary(f, "genotype", check="none")
```

```

# two regions
seqSetFilterChrom(f, c(1, 6), from.bp=c(1000000, 29719561),
  to.bp=c(90000000, 32883508))
seqSummary(f, "genotype", check="none")
seqGetData(f, "chromosome")

## intersection option

seqResetFilter(f)
seqSetFilterChrom(f, 6, from.bp=29719561, to.bp=32883508) # MHC
seqSetFilterChrom(f, include=6) # chromosome 6

seqResetFilter(f)
seqSetFilterChrom(f, 6, from.bp=29719561, to.bp=32883508) # MHC
seqSetFilterChrom(f, include=6, intersect=TRUE) # MHC region only

# close the GDS file
seqClose(f)

```

---

seqSetFilterCond      *Set a Filter to Variant with Allele Count/Freq*

---

## Description

Sets a filter to variant with specified allele count/frequency and missing rate.

## Usage

```
seqSetFilterCond(gdsfile, maf=NaN, mac=1L, missing.rate=NaN,
  parallel=seqGetParallel(), .progress=FALSE, verbose=TRUE)
```

## Arguments

gdsfile	a <a href="#">SeqVarGDSClass</a> object
maf	minimum minor reference allele frequency, or a range of MAF $\text{maf}[1] \leq \dots < \text{maf}[2]$
mac	minimum minor reference allele count, or a range of MAC $\text{mac}[1] \leq \dots < \text{mac}[2]$
missing.rate	maximum missing genotype rate
.progress	if TRUE, show progress information
parallel	FALSE (serial processing), TRUE (multicore processing), numeric value or other value; parallel is passed to the argument <code>cl</code> in <a href="#">seqParallel</a> , see <a href="#">seqParallel</a> for more details.
verbose	if TRUE, show information

## Value

None.



**Author(s)**

Xiuwen Zheng

**See Also**[seqSetFilter](#), [seqSetFilterChrom](#), [seqAlleleFreq](#), [seqAlleleCount](#), [seqMissing](#)**Examples**

```
# the GDS file
(gds.fn <- seqExampleFileName("gds"))

# display
(f <- seqOpen(gds.fn))

seqSetFilterChrom(f, c(1, 6))
seqSetFilterCond(f, maf=0.05, .progress=TRUE)

seqSetFilterChrom(f, c(1, 6))
seqSetFilterCond(f, maf=c(0.01, 0.05), .progress=TRUE)

# close the GDS file
seqClose(f)
```

seqSNP2GDS

*Convert SNPRelate Format to SeqArray Format***Description**

Converts a SNP GDS file to a SeqArray GDS file.

**Usage**

```
seqSNP2GDS(gds.fn, out.fn, storage.option="LZMA_RA", major.ref=TRUE,
           ds.type=c("packedreal16", "float", "double"), optimize=TRUE, digest=TRUE,
           verbose=TRUE)
```

**Arguments**

<code>gds.fn</code>	the file name of SNP format
<code>out.fn</code>	the file name, output a file of SeqArray format
<code>storage.option</code>	specify the storage and compression options, "LZMA_RA" to use LZMA compression algorithm with higher compression ratio compared to "ZIP_RA"
<code>major.ref</code>	if TRUE, use the major allele as a reference allele; otherwise, use A allele in SNP GDS file as a reference allele
<code>ds.type</code>	applicable when import dosages, the data type for storing dosages; see <a href="#">add.gdsn</a>
<code>optimize</code>	if TRUE, optimize the access efficiency by calling <a href="#">cleanup.gds</a>
<code>digest</code>	a logical value (TRUE/FALSE) or a character ("md5", "sha1", "sha256", "sha384" or "sha512"); add hash codes to the GDS file if TRUE or a digest algorithm is specified
<code>verbose</code>	if TRUE, show information

**Value**

Return the file name of SeqArray file with an absolute path. If the input file is genotype dosage, the dosage matrix is stored in the node annotation/format/DS with the estimated dosage of alternative alleles. Any value less than 0 or greater than 2 will be replaced by NaN.

**Author(s)**

Xiuwen Zheng

**See Also**

[seqGDS2SNP](#), [seqVCF2GDS](#), [seqGDS2VCF](#), [seqBED2GDS](#)

**Examples**

```
library(SNPRelate)

# the GDS file
gds.fn <- snpgdsExampleFileName()

seqSNP2GDS(gds.fn, "tmp.gds")

seqSummary("tmp.gds")

# remove the temporary file
unlink("tmp.gds", force=TRUE)
```

---

seqStorageOption

*Storage and Compression Options*

---

**Description**

Storage and compression options for GDS import and merging.

**Usage**

```
seqStorageOption(compression=c("ZIP_RA", "ZIP_RA.fast", "ZIP_RA.max",
  "LZ4_RA", "LZ4_RA.fast", "LZ4_RA.max", "LZMA_RA", "LZMA_RA.fast",
  "LZMA_RA.max", "Ultra", "UltraMax", "none"), mode=NULL, float.mode="float32",
  geno.compress=NULL, info.compress=NULL, format.compress=NULL,
  index.compress=NULL, ...)
```

**Arguments**

compression	the default compression level ("ZIP_RA"), see <a href="#">add.gdsn</a> for the description of compression methods
mode	a character vector, specifying storage type for corresponding variable, e.g., c('annotation/info/HM'='int', 'annotation/format/PL'='int')
float.mode	specify the storage mode for read numbers, e.g., "float32", "float64", "packedreal16"; the additional parameters can follow by colon, like "packedreal16:scale=0.0001"

geno.compress	NULL for the default value, or the compression method for genotypic data
info.compress	NULL for the default value, or the compression method for data sets stored in the INFO field (i.e., "annotation/info")
format.compress	NULL for the default value, or the compression method for data sets stored in the FORMAT field (i.e., "annotation/format")
index.compress	NULL for the default value, or the compression method for data index variables (e.g., "annotation/info/@HM")
...	other specified storage compression for corresponding variable, e.g., 'annotation/info/HM'="ZIP_MAX"

### Details

The compression modes "Ultra" and "UltraMax" attempt to maximize the compression ratio using gigabyte-sized or even terabyte-sized virtual memory, according to "LZMA\_RA.ultra" and "LZMA\_RA.ultra\_max" in [compression.gdsn](#). These features require gdsfmt ( $\geq v1.16.0$ ). "Ultra" and "UltraMax" may not increase the compression ratio much compared with "LZMA\_RA.max", and these options are designed for the users who want to exhaust the computational resources.

### Value

Return a list with a class name "SeqGDSSStorageClass", contains the compression algorithm for each data type.

### Author(s)

Xiuwen Zheng

### See Also

[seqVCF2GDS](#), [seqMerge](#)

### Examples

```
# the file of VCF
(vcf.fn <- seqExampleFileName("vcf"))

# convert
seqVCF2GDS(vcf.fn, "tmp1.gds", storage.option=seqStorageOption())
(f1 <- seqOpen("tmp1.gds"))

# convert (maximize the compression ratio)
seqVCF2GDS(vcf.fn, "tmp2.gds", storage.option=seqStorageOption("ZIP_RA.max"))
(f2 <- seqOpen("tmp2.gds"))

# does not compress the genotypic data
seqVCF2GDS(vcf.fn, "tmp3.gds", storage.option=
  seqStorageOption("ZIP_RA", geno.compress=""))
(f3 <- seqOpen("tmp3.gds"))

# compress with LZ4
seqVCF2GDS(vcf.fn, "tmp4.gds", storage.option=seqStorageOption("LZ4_RA"))
(f4 <- seqOpen("tmp4.gds"))
```

```
# close and remove the files
seqClose(f1)
seqClose(f2)
seqClose(f3)
seqClose(f4)

unlink(c("tmp1.gds", "tmp2.gds", "tmp3.gds", "tmp4.gds"))
```

---

seqSummary

*Summarize a SeqArray GDS File*


---

## Description

Gets the summary of SeqArray GDS file.

## Usage

```
seqSummary(gdsfile, varname=NULL, check=c("default", "none", "full"),
           verbose=TRUE)
```

## Arguments

gdsfile	a <a href="#">SeqVarGDSClass</a> object, or a file name
varname	if NULL, check the whole GDS file; or a character specifying variable name, and return a description of that variable. See details
check	should be one of "default", "none", "full"
verbose	if TRUE, display information

## Details

If check="default", the function performs regular checking, like variable dimensions. If check="full", it performs more checking, e.g., unique sample id, unique variant id, whether genotypic data are in a valid range or not.

## Value

If varname=NULL, the function returns a list:

filename	the file name
version	the version of SeqArray format
reference	genome reference, a character vector (0-length for undefined)
ploidy	the number of sets of chromosomes
num.sample	the total number of samples
num.variant	the total number of variants
allele	allele information, see seqSummary(gdsfile, "allele")
annot_qual	the total number of "annotation/qual" if check="none", or a summary object including min, max, median, mean
filter	filter information, see seqSummary(gdsfile, "annotation/filter")

info a data.frame of INFO field: ID, Number, Type, Description, Source and Version

format a data.frame of FORMAT field: ID, Number, Type and Description

sample.annot a data.frame of sample annotation with ID, Type and Description

— seqSummary(gdsfile, "genotype", check="none", verbose=FALSE) returns a list with components:

dim an integer vector: ploidy, # of samples, # of variants

seldim an integer vector: ploidy, # of selected samples, # of selected variants

— seqSummary(gdsfile, "allele") returns a data.frame with ID and descriptions (check="none"), or a list with components:

value a data.frame with ID and Description

table cross tabulation for the number of alleles per site

— seqSummary(gdsfile, "\$alt") returns a data.frame with ID and Description for describing the alternative alleles.

— seqSummary(gdsfile, "annotation/filter") or seqSummary(gdsfile, "\$filter") returns a data.frame with ID and description (check="none"), or a list with components:

value a data.frame with ID and Description

table cross tabulation for the variable 'filter'

— seqSummary(gdsfile, "annotation/info") or seqSummary(gdsfile, "\$info") returns a data.frame describing the variables in the folder "annotation/info" with ID, Number, Type, Description, Source and Version.

— seqSummary(gdsfile, "annotation/format") returns a data.frame describing the variables in the folder "annotation/format" with ID, Number, Type and Description.

— seqSummary(gdsfile, "sample.annotation") returns a data.frame describing sample annotation with ID, Type and Description.

— seqSummary(gdsfile, "\$reference") returns the genome reference if it is defined (a 0-length character vector if undefined).

— seqSummary(gdsfile, "\$contig") returns the contig information, a data.frame including ID.

— seqSummary(gdsfile, "\$format") returns a data.frame describing VCF FORMAT header with ID, Number, Type and Description. The first row is used for genotypes.

— seqSummary(gdsfile, "\$digest") returns a data.frame with the full names of GDS variables, digest codes and validation (FALSE/TRUE).

### Author(s)

Xiuwen Zheng

### See Also

[seqGetData](#), [seqApply](#)

**Examples**

```

# the GDS file
(gds.fn <- seqExampleFileName("gds"))

seqSummary(gds.fn)

ans <- seqSummary(gds.fn, check="full")
ans

seqSummary(gds.fn, "genotype")
seqSummary(gds.fn, "allele")
seqSummary(gds.fn, "annotation/filter")
seqSummary(gds.fn, "annotation/info")
seqSummary(gds.fn, "annotation/format")
seqSummary(gds.fn, "sample.annotation")

seqSummary(gds.fn, "$reference")
seqSummary(gds.fn, "$contig")
seqSummary(gds.fn, "$filter")
seqSummary(gds.fn, "$alt")
seqSummary(gds.fn, "$info")
seqSummary(gds.fn, "$format")
seqSummary(gds.fn, "$digest")

# open a GDS file
f <- seqOpen(gds.fn)

# get 'sample.id'
samp.id <- seqGetData(f, "sample.id")
# get 'variant.id'
variant.id <- seqGetData(f, "variant.id")

# set sample and variant filters
seqSetFilter(f, sample.id=samp.id[c(2,4,6,8,10)])
set.seed(100)
seqSetFilter(f, variant.id=sample(variant.id, 10))

seqSummary(f, "genotype")

# close a GDS file
seqClose(f)

```

---

seqSystem

*Get the parameters in the GDS system*


---

**Description**

Get a list of parameters in the GDS system

**Usage**

```
seqSystem()
```

**Value**

A list including

num.logical.core	the number of logical cores
compiler.flag	SIMD instructions supported by the compiler
options	list all options associated with SeqArray GDS format or packages

**Author(s)**

Xiuwen Zheng

**References**

<http://github.com/zhengxwen/SeqArray>

**Examples**

```
seqSystem()
```

---

seqTranspose	<i>Transpose Data Array</i>
--------------	-----------------------------

---

**Description**

Transpose data array or matrix for possibly higher-speed access.

**Usage**

```
seqTranspose(gdsfile, var.name, compress=NULL, verbose=TRUE)
```

**Arguments**

gdsfile	a <a href="#">SeqVarGDSClass</a> object
var.name	the variable name with '/' as a separator
compress	the compression option used in <a href="#">add.gdsn</a> ; or determine automatically if NULL
verbose	if TRUE, show information

**Details**

It is designed for possibly higher-speed access. More details will be provided in the future version.

**Value**

None.

**Author(s)**

Xiuwen Zheng

**See Also**

[seqGetData](#), [seqApply](#)

**Examples**

```
# the VCF file
(vcf.fn <- seqExampleFileName("vcf"))

# convert
seqVCF2GDS(vcf.fn, "tmp.gds", storage.option="ZIP_RA")

# list the structure of GDS variables
f <- seqOpen("tmp.gds", FALSE)
f

seqTranspose(f, "genotype/data")
f

# the original array
index.gdsn(f, "genotype/data")
# the transposed array
index.gdsn(f, "genotype/~data")

# close
seqClose(f)

# delete the temporary file
unlink("tmp.gds")
```

---

SeqVarGDSClass

*SeqVarGDSClass*

---

**Description**

A SeqVarGDSClass object provides access to a GDS file containing Variant Call Format (VCF) data. It extends [gds.class](#).

**Details**

A SeqArray GDS file is created from a VCF file with [seqVCF2GDS](#). This file can be opened with [seqOpen](#) to create a SeqVarGDSClass object.

**Accessors**

In the following code snippets *x* is a SeqVarGDSClass object.

`granges(x)`: Returns the chromosome and position of variants as a GRanges object. Names correspond to the variant.id.

`ref(x)`: Returns the reference alleles as a DNASTringSet.

`alt(x)`: Returns the alternate alleles as a DNASTringSetList.

`qual(x)`: Returns the quality scores.

`filt(x)`: Returns the filter data.



`fixed(x)`: Returns the fixed fields (ref, alt, qual, filt).  
`header(x)`: Returns the header as a [DataFramelist](#).  
`rowRanges(x)`: Returns a `GRanges` object with metadata.  
`colData(x)`: Returns a `DataFrame` with sample identifiers and any information in the 'sample.annotation' node.  
`info(x, info=NULL)`: Returns the info fields as a `DataFrame`. `info` is a character vector with the names of fields to return (default is to return all).  
`geno(x, geno=NULL)`: Returns the geno (format) fields as a `SimpleList`. `geno` is a character vector with the names of fields to return (default is to return all).

Other data can be accessed with [seqGetData](#).

### Coercion methods

In the following code snippets `x` is a `SeqVarGDSClass` object.

```
seqAsVCF(x, chr.prefix="", info=NULL, geno=NULL):
```

### Author(s)

Stephanie Gogarten, Xiuwen Zheng

### See Also

[gds.class](#), [seqOpen](#)

### Examples

```

gds <- seqOpen(seqExampleFileName("gds"))
gds

## sample ID
head(seqGetData(gds, "sample.id"))

## variants
granges(gds)

## Not run:
## alleles as comma-separated character strings
head(seqGetData(gds, "allele"))

## alleles as DNASTringSet or DNASTringSetList
ref(gds)
v <- alt(gds)

## genotype
geno <- seqGetData(gds, "genotype")
dim(geno)
## dimensions are: allele, sample, variant
geno[1,1:10,1:5]

## rsID
head(seqGetData(gds, "annotation/id"))

## alternate allele count

```

```

head(seqGetData(gds, "annotation/info/AC"))

## individual read depth
depth <- seqGetData(gds, "annotation/format/DP")
names(depth)
## VCF header defined DP as variable-length data
table(depth$length)
## all length 1, so depth$data should be a sample by variant matrix
dim(depth$data)
depth$data[1:10,1:5]

## End(Not run)

seqClose(gds)

```

seqVCF2GDS

*Reformat VCF Files***Description**

Reformats Variant Call Format (VCF) files.

**Usage**

```

seqVCF2GDS(vcf.fn, out.fn, header=NULL, storage.option="LZMA_RA",
  info.import=NULL, fmt.import=NULL, genotype.var.name="GT",
  ignore.chr.prefix="chr", scenario=c("general", "imputation"),
  reference=NULL, start=1L, count=-1L, optimize=TRUE, raise.error=TRUE,
  digest=TRUE, parallel=FALSE, verbose=TRUE)
seqBCF2GDS(bcf.fn, out.fn, header=NULL, storage.option="LZMA_RA",
  info.import=NULL, fmt.import=NULL, genotype.var.name="GT",
  ignore.chr.prefix="chr", scenario=c("general", "imputation"),
  reference=NULL, optimize=TRUE, raise.error=TRUE, digest=TRUE,
  bcftools="bcftools", verbose=TRUE)

```

**Arguments**

vcf.fn	the file name(s) of VCF format; or a <a href="#">connection</a> object
bcf.fn	a file name of binary VCF format (BCF)
out.fn	the file name of output GDS file
header	if NULL, header is set to be <a href="#">seqVCF_Header</a> (vcf.fn)
storage.option	specify the storage and compression option, "ZIP_RA" ( <a href="#">seqStorageOption</a> ("ZIP_RA")); or "LZMA_RA" to use LZMA compression algorithm with higher compression ratio by default; or "LZ4_RA" to use an extremely fast compression and decompression algorithm. "ZIP_RA.max", "LZMA_RA.max" and "LZ4_RA.max" correspond to the algorithms with a maximum compression level; the suffix "_RA" indicates that fine-level random access is available; see more details at <a href="#">seqStorageOption</a>
info.import	characters, the variable name(s) in the INFO field for import; or NULL for all variables

<code>fmt.import</code>	characters, the variable name(s) in the FORMAT field for import; or NULL for all variables
<code>genotype.var.name</code>	the ID for genotypic data in the FORMAT column; "GT" by default, VCFv4.0
<code>ignore.chr.prefix</code>	a vector of character, indicating the prefix of chromosome which should be ignored, like "chr"; it is not case-sensitive
<code>scenario</code>	"general": use float32 to store floating-point numbers (by default); "imputation": use packedreal16 to store DS and GP in the FORMAT field with four decimal place accuracy
<code>reference</code>	genome reference, like "hg19", "GRCh37"; if the genome reference is not available in VCF files, users could specify the reference here
<code>start</code>	the starting variant if importing part of VCF files
<code>count</code>	the maximum count of variant if importing part of VCF files, -1 indicates importing to the end
<code>optimize</code>	if TRUE, optimize the access efficiency by calling <code>cleanup.gds</code>
<code>raise.error</code>	TRUE: throw an error if numeric conversion fails; FALSE: get missing value if numeric conversion fails
<code>digest</code>	a logical value (TRUE/FALSE) or a character ("md5", "sha1", "sha256", "sha384" or "sha512"); add md5 hash codes to the GDS file if TRUE or a digest algorithm is specified
<code>parallel</code>	FALSE (serial processing), TRUE (parallel processing), a numeric value indicating the number of cores, or a cluster object for parallel processing; <code>parallel</code> is passed to the argument <code>c1</code> in <code>seqParallel</code> , see <code>seqParallel</code> for more details
<code>verbose</code>	if TRUE, show information
<code>bcftools</code>	the path of the program <code>bcftools</code>

## Details

If there are more than one files in `vcf.fn`, `seqVCF2GDS` will merge all VCF files together if they contain the same samples. It is useful to merge multiple VCF files if variant data are split by chromosomes.

The real numbers in the VCF file(s) are stored in 32-bit floating-point format by default. Users can set `storage.option=seqStorageOption(float.mode="float64")` to switch to 64-bit floating point format. Or packed real numbers can be adopted by setting `storage.option=seqStorageOption(float.mode="pa`

By default, the compression method is "ZIP\_RA" (zlib algorithm with default compression level + independent data blocks). Users can maximize the compression ratio by `storage.option="ZIP_RA.max"` or `storage.option=seqStorageOption("ZIP_RA.max")`. LZ4 (<http://cyan4973.github.io/lz4/>) is an option via `storage.option="LZ4_RA"` or `storage.option=seqStorageOption("LZ4_RA")`. LZMA (xz, <http://tukaani.org/xz/>) is another option via `storage.option="LZMA_RA"` or `storage.option=seqStorageOption("LZMA_RA")`, and it is known to have higher compression ratio than zlib.

If multiple cores/processes are specified in `parallel`, all VCF files are scanned to calculate the total number of variants before format conversion.

`storage.option="Ultra"` and `storage.option="UltraMax"` need much large memory. Users may consider using `seqRecompress` to recompress the GDS file after calling `seqVCF2GDS()`, since `seqRecompress()` takes much less memory when "Ultra" or "UltraMax" is used.

**Value**

Return the file name of GDS format with an absolute path.

**Author(s)**

Xiuwen Zheng

**References**

Danecek, P., Auton, A., Abecasis, G., Albers, C.A., Banks, E., DePristo, M.A., Handsaker, R.E., Lunter, G., Marth, G.T., Sherry, S.T., et al. (2011). The variant call format and VCFtools. *Bioinformatics* 27, 2156-2158.

**See Also**

[seqVCF\\_Header](#), [seqStorageOption](#), [seqMerge](#), [seqGDS2VCF](#), [seqRecompress](#)

**Examples**

```
# the VCF file
vcf.fn <- seqExampleFileName("vcf")

# conversion
seqVCF2GDS(vcf.fn, "tmp.gds", storage.option="ZIP_RA")

# conversion in parallel
seqVCF2GDS(vcf.fn, "tmp_p2.gds", storage.option="ZIP_RA", parallel=2L)

# display
(f <- seqOpen("tmp.gds"))
seqClose(f)

# convert without the INFO fields
seqVCF2GDS(vcf.fn, "tmp.gds", storage.option="ZIP_RA",
  info.import=character(0))

# display
(f <- seqOpen("tmp.gds"))
seqClose(f)

# convert without the INFO and FORMAT fields
seqVCF2GDS(vcf.fn, "tmp.gds", storage.option="ZIP_RA",
  info.import=character(0), fmt.import=character(0))

# display
(f <- seqOpen("tmp.gds"))
seqClose(f)

# delete the temporary file
unlink(c("tmp.gds", "tmp_p2.gds"), force=TRUE)
```

---

seqVCF\_Header                      *Parse the Header of a VCF/BCF File*

---

### Description

Parses the meta-information lines of a VCF or BCF file.

### Usage

```
seqVCF_Header(vcf.fn, getnum=FALSE)
```

### Arguments

vcf.fn	the file name of VCF or BCF format; or a <a href="#">connection</a> object for VCF format
getnum	if TRUE, return the total number of variants

### Details

The ID description contains four columns: ID – variable name; Number – the number of elements, see the webpage of the 1000 Genomes Project; Type – data type; Description – a variable description.

### Value

Return a list (with a class name "SeqVCFHeaderClass", S3 object):

fileformat	the file format
info	the ID description in the INFO field
filter	the ID description in the FILTER field
format	the ID description in the FORMAT field
alt	the ID description in the ALT field
contig	the description in the contig field
assembly	the link of assembly
reference	genome reference, or NULL if unknown
header	the other header lines
ploidy	ploidy, two for humans
num.sample	the number of samples
num.variant	the number of variants, applicable only if getnum=TRUE
sample.id	a vector of sample IDs in the VCF/BCF file

### Author(s)

Xiuwen Zheng

### References

Danecek, P., Auton, A., Abecasis, G., Albers, C.A., Banks, E., DePristo, M.A., Handsaker, R.E., Lunter, G., Marth, G.T., Sherry, S.T., et al. (2011). The variant call format and VCFtools. *Bioinformatics* 27, 2156-2158.

**See Also**

[seqVCF\\_SampID](#), [seqVCF2GDS](#)

**Examples**

```
# the VCF file
(vcf.fn <- seqExampleFileName("vcf"))
# or vcf.fn <- "C:/YourFolder/Your_VCF_File.vcf"

# get sample id
seqVCF_Header(vcf.fn, getnum=TRUE)

# use a connection object
f <- file(vcf.fn, "r")
seqVCF_Header(f, getnum=TRUE)
close(f)
```

---

seqVCF_SampID	<i>Get the Sample IDs</i>
---------------	---------------------------

---

**Description**

Returns the sample IDs of a VCF file.

**Usage**

```
seqVCF_SampID(vcf.fn)
```

**Arguments**

vcf.fn            the file name, output a file of VCF format; or a [connection](#) object

**Author(s)**

Xiuwen Zheng

**References**

Danecek, P., Auton, A., Abecasis, G., Albers, C.A., Banks, E., DePristo, M.A., Handsaker, R.E., Lunter, G., Marth, G.T., Sherry, S.T., et al. (2011). The variant call format and VCFtools. *Bioinformatics* 27, 2156-2158.

**See Also**

[seqVCF\\_Header](#), [seqVCF2GDS](#)

**Examples**

```
# the VCF file
(vcf.fn <- seqExampleFileName("vcf"))

# get sample id
seqVCF_SampID(vcf.fn)
```

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