

# Package ‘GBScleanR’

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**Type** Package

**Title** Error correction tool for noisy genotyping by sequencing (GBS) data

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**Description** GBScleanR is a package for quality check, filtering, and error correction of genotype data derived from next generation sequencer (NGS) based genotyping platforms. GBScleanR takes Variant Call Format (VCF) file as input. The main function of this package is `estGeno()` which estimates the true genotypes of samples from given read counts for genotype markers using a hidden Markov model with incorporating uneven observation ratio of allelic reads. This implementation gives robust genotype estimation even in noisy genotype data usually observed in Genotyping-By-Sequencing (GBS) and similar methods, e.g. RADseq. The current implementation accepts genotype data of a diploid population at any generation of multi-parental cross, e.g. biparental F2 from inbred parents, biparental F2 from outbred parents, and 8-way recombinant inbred lines (8-way RILs) which can be referred to as MAGIC population.

**License** GPL-3 + file LICENSE

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```
addScheme          #' Build a GbsrScheme object
```

---

**Description**

**GBScleanR** uses breeding scheme information to set the expected number of cross overs in a chromosome which is a required parameter for the genotype error correction with the Hidden Markov model implemented in the `estGeno()` function. This function build the object storing type crosses performed at each generation of breeding and population sizes.

**Usage**

```
addScheme(object, crosstype, mating, ...)

## S4 method for signature 'GbsrGenotypeData'
addScheme(object, crosstype, mating)
```

```
## S4 method for signature 'GbsrScheme'
addScheme(object, crosstype, mating)
```

### Arguments

|           |  |
|-----------|--|
| object    | A <a href="#">GbsrGenotypeData</a> object.   |
| crosstype | A string to indicate the type of cross conducted with a given generation.  |
| mating    | An integer matrix to indicate mating combinations. The each element should match with member IDs of the last generation. |
| ...       | Unused.  |

### Details

A scheme object is just a data.frame indicating a population size and a type of cross applied to each generation of the breeding process to generate the population which you are going to subject to the [estGeno\(\)](#) function. The crosstype can take either of "selfing", "sibling", "pairing", and "random". When you set crosstype = "random", you need to specify pop\_size to indicate how many individuals were crossed in the random mating. You also need to specify a matrix indicating combinations of mating, in which each column shows a pair of member IDs indicating parental samples of the cross. Member IDs are serial numbers starts from 1 and automatically assigned by [initScheme\(\)](#) and [addScheme\(\)](#). To check the member IDs, run [showScheme\(\)](#). Please see the examples section for more details of specifying a mating matrix. The created [GbsrScheme](#) object is set in the scheme slot of the [GbsrGenotypeData](#) object.

### Value

A [GbsrGenotypeData](#) object storing a [GbsrScheme](#) object in the "scheme" slot.

### See Also

[addScheme\(\)](#) and [showScheme\(\)](#)

### Examples

```
# Load data in the GDS file and instantiate a [GbsrGenotypeData] object.
gds_fn <- system.file("extdata", "sample.gds", package = "GBScleanR")
gds <- loadGDS(gds_fn)

# Biparental F2 population.
gds <- setParents(gds, parents = c("Founder1", "Founder2"))

# setParents gave member ID 1 and 2 to Founder1 and Founder2, respectively.
gds <- initScheme(gds, mating = cbind(c(1:2)))

# Now the progenies of the cross above have member ID 3.
# If `crosstype = "selfing"` or `"sibling"`, you can omit a `mating` matrix.
gds <- addScheme(gds, crosstype = "self")

#####
# Now you can execute `estGeno()` which requires a [GbsrScheme] object.

# Close the connection to the GDS file
closeGDS(gds)
```

---

|              |                                     |
|--------------|-------------------------------------|
| assignScheme | <i>Assign member IDs to samples</i> |
|--------------|-------------------------------------|

---

## Description

[GBScleanR](#) uses breeding scheme information to set the expected number of cross overs in a chromosome which is a required parameter for the genotype error correction with the Hidden Markov model implemented in the `estGeno()` function. This function assign member IDs to indicate which samples were derived from which pedigree that recorded in the [GbsrScheme](#) object.

## Usage

```
assignScheme(object, id, ...)  
  
## S4 method for signature 'GbsrGenotypeData'  
assignScheme(object, id)  
  
## S4 method for signature 'GbsrScheme'  
assignScheme(object, id)
```

## Arguments

|        |  |
|--------|--|
| object | A <a href="#">GbsrGenotypeData</a> object.                   |
| id     | A numeric vector indicating member IDs to assign to samples. |
| ...    | Unused.  |

## Details

Member IDs can be shown by [showScheme\(\)](#). Only the member IDs assigned to progenies (not parents) are available to assign to samples. If the last generation recorded in the [GbsrScheme](#) object has only one member ID that should be assigned to all samples in your population, you can omit assigning IDs by [assignScheme\(\)](#). In that case, [estGeno\(\)](#) automatically assign the only one member ID to all samples.

## Value

A [GbsrGenotypeData](#) object storing a [GbsrScheme](#) object in the "scheme" slot.

## See Also

[addScheme\(\)](#) and [showScheme\(\)](#)

## Examples

```
# Load data in the GDS file and instantiate a [GbsrGenotypeData] object.  
gds_fn <- system.file("extdata", "sample.gds", package = "GBScleanR")  
gds <- loadGDS(gds_fn)  
  
# Biparental F2 population.  
gds <- setParents(gds, parents = c("Founder1", "Founder2"))  
  
# setParents gave member ID 1 and 2 to Founder1 and Founder2, respectively.
```

```

gds <- initScheme(gds, mating = cbind(c(1:2)))

# Now the progeny of the cross above have member ID 3.
# If `crosstype = "selfing"` or `"sibling"`, you can omit a `mating` matrix.
gds <- addScheme(gds, crosstype = "self")

# The progeny of the selfing above has member ID 4.
# To execute genotype estimation for your samples, you need to assign a member
# ID to each of the samples.

# Check IDs of samples to be assigned member IDs if necessary.
getSamID(gds)

# The assignScheme() assign member IDs `id` to the samples in order.
# Please confirm the order of the member IDs in `id` and the order of the
# sample IDs shown by getSamID(gds).
gds <- assignScheme(gds, rep(4, nsam(gds)))

# If your population has samples all of which belong to only one pedigree,
# you can omit assignScheme() and let estGeno() automatically assign the
# last member ID to all samples.

#####
# Now you can execute `estGeno()` which requires a [GbsrScheme] object.

# Close the connection to the GDS file
closeGDS(gds)

```

---

boxplotGBSR

*Draw boxplots of specified statistics*


---

## Description

Draw boxplots of specified statistics

## Usage

```

boxplotGBSR(
  x,
  stats = "missing",
  target = c("marker", "sample"),
  color = c(Marker = "darkblue", Sample = "darkblue"),
  fill = c(Marker = "skyblue", Sample = "skyblue")
)

```

## Arguments

|        |  |
|--------|--|
| x      | A <a href="#">GbsrGenotypeData</a> object.   |
| stats  | A string to specify statistics to be drawn.  |
| target | Either or both of "marker" and "sample", e.g. target = "marker" to draw a histogram only for SNPs. |
| color  | A named vector "Marker" and "Sample" to specify border color of bins in the histograms.            |

**fill** A named vector "Marker" and "Sample" to specify fill color of bins in the histograms.

## Details

You can draw boxplots of several summary statistics of genotype counts and read counts per sample and per marker. The "stats" argument can take the following values:

**missing** Proportion of missing genotype calls.  
**het** Proportion of heterozygote calls.  
**raf** Reference allele frequency.  
**dp** Total read counts.  
**ad\_ref** Reference allele read counts.  
**ad\_alt** Alternative allele read counts.  
**rrf** Reference allele read frequency.  
**mean\_ref** Mean of reference allele read counts.  
**sd\_ref** Standard deviation of reference allele read counts.  
**median\_ref** Quantile of reference allele read counts.  
**mean\_alt** Mean of alternative allele read counts.  
**sd\_alt** Standard deviation of alternative allele read counts.  
**median\_alt** Quantile of alternative allele read counts.  
**mq** Mapping quality.  
**fs** Phred-scaled p-value (strand bias)  
**qd** Variant Quality by Depth  
**sor** Symmetric Odds Ratio (strand bias)  
**mqranks** Alt vs. Ref read mapping qualities  
**readposranks** Alt vs. Ref read position bias  
**baseqranks** Alt Vs. Ref base qualities

To draw boxplots for "missing", "het", "raf", you need to run `countGenotype()` first to obtain statistics. Similarly, "dp", "ad\_ref", "ad\_alt", "rrf" requires values obtained via `countRead()`. "mq", "fs", "qd", "sor", "mqranks", "readposranks", and "baseqranks" only work with `target = "marker"`, if your data contains those values supplied via SNP calling tools like [GATK](#).

## Value

A ggplot object.

## Examples

```
# Load data in the GDS file and instantiate a [GbsrGenotypeData] object.
gds_fn <- system.file("extdata", "sample.gds", package = "GBScleanR")
gds <- loadGDS(gds_fn)

# Summarize genotype count information to be used in `boxplotGBSR()`
gds <- countGenotype(gds)

boxplotGBSR(gds, stats = "missing")
```

```
# Close the connection to the GDS file
closeGDS(gds)
```

---

closeGDS

*Close the connection to the GDS file*

---

### Description

Close the connection to the GDS file linked to the given [GbsrGenotypeData](#) object.

### Usage

```
closeGDS(object, save_filter = FALSE, verbose = TRUE, ...)
```

```
## S4 method for signature 'GbsrGenotypeData'
closeGDS(object, save_filter, verbose)
```

### Arguments

|             |   |
|-------------|---|
| object      | A <a href="#">GbsrGenotypeData</a> object.  |
| save_filter | A logical whether to save the filtering information made via <a href="#">setSamFilter()</a> and <a href="#">setMarFilter()</a> in the GDS file. The saved filter information can be reused if set <code>load_filter = TRUE</code> for <a href="#">loadGDS()</a> . |
| verbose     | if TRUE, show information.  |
| ...         | Unused.   |

### Value

NULL.

### Examples

```
# Load data in the GDS file and instantiate a [GbsrGenotypeData] object.
gds_fn <- system.file("extdata", "sample.gds", package = "GBScleanR")
gds <- loadGDS(gds_fn)

# Close the connection to the GDS file
closeGDS(gds)
```



---

|               |  |
|---------------|--|
| countGenotype | <i>Count genotype calls and alleles per sample and per marker.</i> |
|---------------|--|

---

## Description

This function calculates several summary statistics of genotype calls and alleles per marker and per sample. Those values will be stored in the `SnprAnnotaionDataFrame` slot and the `sample` slot and obtained via getter functions, e.g.s `getCountGenoRef()`, `getCountAlleleRef()`, and `getMAF()`.

## Usage

```
countGenotype(object, target = "both", node = "raw", ...)

## S4 method for signature 'GbsrGenotypeData'
countGenotype(object, target, node)
```

## Arguments

|        |  |
|--------|--|
| object | A <a href="#">GbsrGenotypeData</a> object.       |
| target | Either of "marker" and "sample".                 |
| node   | Either of "raw", "filt", and "cor". See details. |
| ...    | Unused.  |

## Details

# Genotype call data can be obtained from the "genotype" node, the "filt.genotype" node, or the "corrected.genotype" node of the GDS file with `node = "raw"`, `node = "filt"`, or `node = "raw"`, respectively. The `setCallFilter()` function generate filtered genotype call data in the "filt.genotype" node which can be accessed as mentioned above. On the other hand, the "corrected.genotype" node can be generated via the `estGeno()` function.

## Value

A [GbsrGenotypeData](#) object with genotype count information.

## Examples

```
# Load data in the GDS file and instantiate a [GbsrGenotypeData] object.
gds_fn <- system.file("extdata", "sample.gds", package = "GBScleanR")
gds <- loadGDS(gds_fn)

# Summarize the genotype count information and store them in the
# [marker] and [sample] slots of the [GbsrGenotypeData] object.
gds <- countGenotype(gds)

# Get the proportion of missing genotype per sample.
sample_missing_rate <- getCountGenoMissing(gds,
                                           target = "sample",
                                           prop = TRUE)

# Get the minor allele frequency per marker.
marker_minor_allele_freq <- getMAF(gds, target = "marker")
```

```
# Draw histograms of the missing rate per sample and marker.
histGBSR(gds, stats = "missing")

# Close the connection to the GDS file.
closeGDS(gds)
```

---

countRead

*Count reads per sample and per marker.*


---

### Description

This function calculates several summary statistics of read counts per marker and per sample. Those values will be stored in the `SnprAnnotaionDataFrame` slot and the `sample` slot and obtained via getter functions, e.g. `getCountReadRef()` and `getCountReadAlt()`. This function first calculates normalized allele read counts by dividing allele read counts at each marker in each sample by the total allele read of the sample followed by multiplication by  $10^6$ . In other words, it calculates reads per million (rpm). Then, the function calculates mean, standard deviation, quantile values of rpm per marker and per sample. The results will be stored in the `SnprAnnotaionDataFrame` slot and the `sample` slot and obtained via getter functions, e.g. `getMeanReadRef()` and `getMedianReadAlt()`.

### Usage

```
countRead(object, target = "both", node = "raw", ...)

## S4 method for signature 'GbsrGenotypeData'
countRead(object, target, node)
```

### Arguments

|        |  |
|--------|--|
| object | A <a href="#">GbsrGenotypeData</a> object. |
| target | Either of "marker" and "sample".           |
| node   | Either of "raw" and "filt". See details.   |
| ...    | Unused.                                    |

### Details

Read count data can be obtained from the "annotation/format/AD/data" node or the "annotation/format/AD/filt.data" node of the GDS file with `node = "raw"` or `node = "filt"`, respectively. The `setCallFilter()` function generate filtered read count data in the "annotation/format/AD/filt.data" node which can be accessed as mentioned above.

### Value

A [GbsrGenotypeData](#) object with read count information.

**Examples**

```

# Load data in the GDS file and instantiate a [GbsrGenotypeData] object.
gds_fn <- system.file("extdata", "sample.gds", package = "GBScleanR")
gds <- loadGDS(gds_fn)

# Summarize the read count information and store them in the
# [marker] and [sample] slots of the [GbsrGenotypeData] object.
gds <- countRead(gds)

# Get the total read counts per marker
read_depth_per_marker <- getCountRead(gds, target = "marker")

# Get the proportion of reference allele reads per marker.
reference_read_freq <- getCountReadRef(gds, target = "marker", prop = TRUE)

# Draw histograms of reference allele read counts per sample and marker.
histGBSR(gds, stats = "ad_ref")

# Close the connection to the GDS file.
closeGDS(gds)

```

---

estGeno

*Genotype estimation using a hidden Markov model*


---

**Description**

Clean up genotype data by error correction based on genotype estimation using a hidden Markov model.

**Usage**

```

estGeno(
  object,
  node = "raw",
  recomb_rate = 0.04,
  error_rate = 0.0025,
  call_threshold = 0.9,
  het_parent = FALSE,
  optim = TRUE,
  iter = 2,
  n_threads = 1,
  dummy_reads = 5,
  ...
)

## S4 method for signature 'GbsrGenotypeData'
estGeno(
  object,
  node,
  recomb_rate,
  error_rate,

```

```

    call_threshold,
    het_parent,
    optim,
    iter,
    n_threads,
    dummy_reads
)

```

### Arguments

|                |   |
|----------------|---|
| object         | A <a href="#">GbsrGenotypeData</a> object.  |
| node           | Either "raw" or "filt" to indicate whether raw or filtered read counts are used for genotype estimation. See <a href="#">setCallFilter()</a> for the details of filtered read counts.         |
| recomb_rate    | A numeric value to indicate the expected recombination frequency per chromosome per megabase pairs.   |
| error_rate     | A numeric value of the expected sequence error rate.  |
| call_threshold | A numeric value of the probability threshold to accept estimated genotype calls.  |
| het_parent     | A logical value to indicate whether parental samples are outbred or inbred. If FALSE, this function assume all true genotype of markers in parents are homozygotes.                           |
| optim          | A logical value to specify whether to conduct parameter optimization for error correction.  |
| iter           | An integer value to specify the number of iterative parameter updates.  |
| n_threads      | An integer value to specify the number of threads used for the calculation. The default is 1 and if n_threads = NULL, automatically set half the number of available threads on the computer. |
| dummy_reads    | An integer to specify the number of dummy reads to assign to dummy parental samples for genotype estimation. See details.   |
| ...            | Unused.   |

### Details

If you have not set parental samples by [setParents\(\)](#) and initialized the scheme object using [initScheme\(\)](#), you have the scheme object without explicit parental information that is assumed to be a bi-parental population. In this case, [estGeno\(\)](#) will run in the parentless mode. In the parentless mode, the algorithm assumes that the given population is a bi-parental population. The number of reference allele reads and the number of alternative allele reads of the dummy parents are set based on `dummy_reads`, respectively. Dummy parent 1 has `dummy_reads` of the reference allele reads and 0 alternative allele reads at all markers, while dummy parent 2 has 0 and `dummy_reads` of reference and alternative allele reads at all markers. If the parents of your population were outbred lines or you cannot assume one of the parents has completely reference homozygotes and another has laternative homozygotes at all markers, Set `dummy_reads = 0` to leave uncertainty to estimate parental genotypes based on the offspring genotypes. Nevertheless, the parentless mode is less accurate and has more chance to get a genotype estimate randomly selected from the equally likely genotype estimates.

### Value

A [GbsrGenotypeData](#) object in which the "estimated.haplotype", "corrected.genotype" and "parents.genotype" nodes were added.

**Examples**

```

# Load data in the GDS file and instantiate a [GbsrGenotypeData] object.
gds_fn <- system.file("extdata", "sample.gds", package = "GBScleanR")
gds <- loadGDS(gds_fn)

# Find the IDs of parental samples.
parents <- grep("Founder", getSamID(gds), value = TRUE)

# Set the parents and flip allele information
# if the reference sample (Founder1 in our case) has homozygous
# alternative genotype at some markers of which alleles will
# be swapped to make the reference sample have homozygous
# reference genotype.
gds <- setParents(gds, parents = parents)

# Initialize a scheme object stored in the slot of the GbsrGenotypeData.
# We chose `crosstype = "pair"` because two inbred founders were mated
# in our breeding scheme.
# We also need to specify the mating matrix which has two rows and
# one column with integers 1 and 2 indicating a sample (founder)
# with the memberID 1 and a sample (founder) with the memberID 2
# were mated.
gds <- initScheme(gds, mating = cbind(c(1:2)))

# Add information of the next cross conducted in our scheme.
# We chose 'crosstype = "selfing"', which do not require a
# mating matrix.
gds <- addScheme(gds, crosstype = "selfing")

# Execute error correction by estimating genotype and haplotype of
# founders and offspring.
gds <- estGeno(gds)

# Close the connection to the GDS file.
closeGDS(gds)

```

---

GBScleanR

*GBScleanR: A package to conduct error correction for noisy genotyping by sequencing (reduced representation sequencing based genotyping) data.*

---

**Description**

GBScleanR is a package for quality check, filtering, and error correction of genotype data derived from next generation sequencer (NGS) based genotyping platforms. GBScleanR takes Variant Call Format (VCF) file as input. The main function of this package is "clean.geno" which estimates the true genotypes of samples from given read counts for genotype markers using a hidden Markov model with incorporating uneven observation ratio of allelic reads. This implementation gives robust genotype estimation even in noisy genotype data usually observed in Genotyping-By-Sequencing (GBS) and similar methods, e.g. RADseq. GBScleanR currently only supports genotype data of biparental populations.

**Author(s)**

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**See Also**

Useful links:

- <https://github.com/tomoyukif/GBScleanR>
- Report bugs at <https://github.com/tomoyukif/GBScleanR/issues>

---

gbsrGDS2CSV

*Write a CSV file based on data in a GDS file*


---

**Description**

Write out a CSV file with raw, filtered, corrected genotype data or estimated haplotype data stored in a GDS file.

**Usage**

```
gbsrGDS2CSV(
  object,
  out_fn,
  node = "raw",
  incl_parents = TRUE,
  bp2cm = NULL,
  format = "",
  read = FALSE,
  ...
)

## S4 method for signature 'GbsrGenotypeData'
gbsrGDS2CSV(object, out_fn, node, incl_parents, bp2cm, format, read)
```

**Arguments**

|              |   |
|--------------|---|
| object       | A <a href="#">GbsrGenotypeData</a> object.  |
| out_fn       | A string to specify the path to an output VCF file.   |
| node         | Either one of "raw", "filt", "cor", "hap", "dosage" to output raw genotype data, filtered genotype data, corrected genotype data, estimated haplotype data, and estimated allele dosage data, respectively.   |
| incl_parents | A logical value to specify whether parental samples should be included in an output VCF file or not.  |
| bp2cm        | A numeric value to convert positions in basepairs (bp) to centiMorgan (cm). The specified here is used to multiply position values. The default is NULL and then internally sets $bp2cm = 4e-06$ when <code>format = "qt1"</code> . If not <code>format = "qt1"</code> , 1 is set to <code>bp2cm</code> as default. |
| format       | A string to indicate the output format. See details.  |
| read         | A logical value to indicate whether read counts should be output with genotype data or not. See details.  |
| ...          | Unused.   |

## Details

Create a CSV file at location specified by `out_fn`. The setting `format = "qt1"` makes the function export the data in the r/ql format that can be loaded using `read.cross` as `format = "csvs"` with a phenotype data. If you have executed `estGeno()` and your population is a biparental population, set `'node = "dosage"` to export a r/ql format CSV in which homozygotes of the alleles of Parent 1 and 2, which have been specified by `setParents()`, are represented by A and B, respectively. If `'node = "raw"`, `'node = "fill"`, and `'node = "cor"`, A and B in the r/ql format CSV indicate homozygotes of reference and alternative alleles shown in a given VCF file. This means that if Parent 1 has the alternative allele homozygote at Marker 1 and Offspring 1 has the same genotype with Parent 1, the genotype of Offspring 1 at Marker 1 will be B in the r/ql format CSV. On the other hand, if you set `'node = "dosage"`, the genotype of Offspring 1 at Marker 1 will be A in the r/ql format CSV. The output CSV file has the rows indicating chromosome ID and positions of markers followed by the rows indicating genotype or haplotype data of samples. If `read = TRUE`, the output of each genotype call would be in the form of `GT:ADR,ADA` where GT, ADR, and ADA represent genotype, reference read count, and alternative read count, respectively. If `format = "qt1"`, `read = TRUE` will be ignored.

## Value

The path to the CSV file.

## Examples

```
# Load data in the GDS file and instantiate a [GbsrGenotypeData] object.
gds_fn <- system.file("extdata", "sample.gds", package = "GBScleanR")
gds <- loadGDS(gds_fn)

# Create a CSV file with data from the GDS file
# connected to the [GbsrGenotypeData] object.
out_fn <- tempfile("sample_out", fileext = ".csv")
gbsrGDS2CSV(gds, out_fn)

# Close the connection to the GDS file.
closeGDS(gds)
```

---

gbsrGDS2VCF

---

*Write a VCF file based on data in a GDS file*


---

## Description

Write out a VCF file with raw, filtered, or corrected genotype data stored in a GDS file. The output VCF file contains the GT, AD, and DP fields.

## Usage

```
gbsrGDS2VCF(
  object,
  out_fn,
  node = "raw",
  info.export = NULL,
  fmt.export = NULL,
```

```

    parents = TRUE,
    ...
)

## S4 method for signature 'GbsrGenotypeData'
gbsrGDS2VCF(object, out_fn, node, info.export, fmt.export, parents)

```

### Arguments

|             |   |
|-------------|---|
| object      | A <a href="#">GbsrGenotypeData</a> object.  |
| out_fn      | A string to specify the path to an output VCF file.   |
| node        | Either one of "raw" or "cor" to output raw genotype data or corrected genotype data, respectively.  |
| info.export | characters, the variable name(s) in the INFO node for export; or NULL for all variables. If you specify character(0), nothing will be exported from the INFO node.                    |
| fmt.export  | characters, the variable name(s) in the FORMAT node for import; or NULL for all variables. If you specify character(0), nothing will be exported from the FORMAT node, except for GT. |
| parents     | A logical value to specify whether parental samples should be included in an output VCF file or not.  |
| ...         | Unused.   |

### Details

Create a VCF file at location specified by `out_fn`. The connection to the GDS file of the input [GbsrGenotypeData](#) object will be automatically closed for internal file handling in this function. Please use [reopenGDS\(\)](#) to open the connection again. If you use [loadGDS\(\)](#), summary statistics and filtering information will be discarded.

### Value

The path to the VCF file.

### Examples

```

# Load data in the GDS file and instantiate a [GbsrGenotypeData] object.
gds_fn <- system.file("extdata", "sample.gds", package = "GBScleanR")
gds <- loadGDS(gds_fn)

# Create a VCF file with data from the GDS file
# connected to the [GbsrGenotypeData] oobject.
out_fn <- tempfile("sample_out", fileext = ".vcf.gz")
# gbsrGDS2VCF(gds, out_fn)

# Close the connection to the GDS file.
closeGDS(gds)

```



---

 GbsrGenotypeData-class

*Class* GbsrGenotypeData
 

---

### Description

The GbsrGenotypeData class is the main class of [GBScleanR](#) and user work with this class object.

### Details

The GbsrGenotypeData class is an extension of SeqVarGDSCClass in the [SeqArray](#) package to store summary data of genotypes and reads and a [GbsrScheme](#) object that contains mating scheme information of the given population.. The slots marker and sample store a [data.frame](#) object for variant-wise and sample-wise summary information, respectively. The scheme slot holds a [GbsrScheme](#) object. The function [loadGDS\(\)](#) initialize the GbsrGenotypeData class.

### Slots

marker A [data.frame](#) object.

sample A [data.frame](#) object.

scheme A [GbsrScheme](#) object.

### Examples

```
# `loadGDS()` initialize the `GbsrGenotypeData` object.

# Load a GDS file and instantiate a `GbsrGenotypeData` object.
gds_fn <- system.file("extdata", "sample.gds", package = "GBScleanR")
gds <- loadGDS(gds_fn)

# Close connection to the GDS file.
closeGDS(gds)
```

---

 GbsrScheme-class

*Class* GbsrScheme
 

---

### Description

[GBScleanR](#) uses breeding scheme information to set the expected number of cross overs in a chromosome which is a required parameter for the genotype error correction with the hidden Markov model implemented in the [estGeno\(\)](#) function. This class stores those information including ID of parental samples, type crosses performed at each generation of breeding and population sizes of each generation. This class is not exported.

**Slots**

crosstype A vector of strings indicating the type of crossing done at each generation.  
 mating A list of matrices showing combinations member IDs of samples mated.  
 parents A vector of member IDs of parents.  
 progenies A vector of member IDs of progenies produced at each generation.  
 samples A vector of member IDs of samples indicating which samples are derived from which pedigrees.

**See Also**

[GbsrGenotypeData](#) and [loadGDS\(\)](#).

**Examples**

```

# `loadGDS()` initialize a `GbsrScheme` object internally and
# attache it to the shceme slot of a [GbsrGenotypeData] object.

# Load data in the GDS file and instantiate
# a [GbsrGenotypeData] object.
gds_fn <- system.file("extdata", "sample.gds", package = "GBScleanR")
gds <- loadGDS(gds_fn)

# Print the information stored in the `GbsrScheme` object.
showScheme(gds)

# Close the connection to the GDS file.
closeGDS(gds)

```

---

gbsrVCF2GDS

---

*Convert a VCF file to a GDS file*


---

**Description**

This function converts a variant call data in the VCF format. The current implementation only accepts biallelic single nucleotide polymorphisms. Please filter out variants which are insertions and deletions or multiallelic. You may use "bcftools" or "vcftools" for filtering.

**Usage**

```

gbsrVCF2GDS(
  vcf_fn,
  out_fn,
  gt = "GT",
  info.import = NULL,
  fmt.import = NULL,
  force = FALSE,
  verbose = TRUE
)

```

**Arguments**

|             |  |
|-------------|--|
| vcf_fn      | A string to indicate path to an input VCF file.  |
| out_fn      | A string to indicate path to an output GDS file.   |
| gt          | the ID for genotypic data in the FORMAT column; "GT" by default, VCFv4.0.  |
| info.import | characters, the variable name(s) in the INFO field for import; or NULL for all variables. If you specify character(0), nothing will be retrieved from the INFO field.                    |
| fmt.import  | characters, the variable name(s) in the FORMAT field for import; or NULL for all variables. If you specify character(0), nothing will be retrieved from the FORMAT field, except for GT. |
| force       | A logical value to overwrite a GDS file even if the file specified in "out_fn" exists.   |
| verbose     | if TRUE, show information.   |

**Details**

gbsrVCF2GDS converts a VCF file to a GDS file. The data structure of the GDS file created via this function is same with those created by seqVCF2GDS() of SeqArray.

**Value**

The output GDS file path.

**Examples**

```
# Create a GDS file from a sample VCF file.
vcf_fn <- system.file("extdata", "sample.vcf", package = "GBScleanR")
gds_fn <- tempfile("sample", fileext = ".gds")
gbsrVCF2GDS(vcf_fn = vcf_fn, out_fn = gds_fn, force = TRUE)

# Load data in the GDS file and instantiate a `GbsrGenotypeData` object.
gds <- loadGDS(gds_fn)

# Close the connection to the GDS file.
closeGDS(gds)
```

---

getAllele

*Obtain reference allele information of markers*


---

**Description**

This function returns the reference allele and alternative allele(s).

**Usage**

```
getAllele(object, valid = TRUE, chr = NULL, ...)

## S4 method for signature 'GbsrGenotypeData'
getAllele(object, valid, chr)
```

**Arguments**

|        |   |
|--------|---|
| object | A <a href="#">GbsrGenotypeData</a> object.        |
| valid  | A logical value. See details.                     |
| chr    | A index to specify chromosome to get information. |
| ...    | Unused.   |

**Details**

If `valid = TRUE`, the alleles of markers which are labeled TRUE in the "valid" column of the "marker" slot will be returned. If you need the number of over all markers, set `valid = FALSE`. `validMar()` tells you which markers are valid.

**Value**

A vector of strings each of which is a "/" separated string and indicates the reference allele and the alternative allele(s) at a marker.

**Examples**

```
# Load data in the GDS file and instantiate a [GbsrGenotypeData] object.
gds_fn <- system.file("extdata", "sample.gds", package = "GBScleanR")
gds <- loadGDS(gds_fn)

getAllele(gds)

# Close the connection to the GDS file.
closeGDS(gds)
```

---

|               |   |
|---------------|---|
| getChromosome | <i>Obtain chromosome IDs of markers</i> |
|---------------|---|

---

**Description**

This function returns chromosome IDs of markers.

**Usage**

```
getChromosome(object, valid = TRUE, ...)

## S4 method for signature 'GbsrGenotypeData'
getChromosome(object, valid)
```

**Arguments**

|        |  |
|--------|--|
| object | A <a href="#">GbsrGenotypeData</a> object. |
| valid  | A logical value. See details.              |
| ...    | Unused.                                    |

**Details**

If `valid = TRUE`, the chromosome IDs of the markers which are labeled TRUE in the "valid" column of the "marker" slot will be returned. If you need the number of over all markers, set `valid = FALSE`. `validMar()` tells you which markers are valid.

**Value**

A vector of factors indicating chromosome IDs.

**Examples**

```
# Load data in the GDS file and instantiate a [GbsrGenotypeData] object.
gds_fn <- system.file("extdata", "sample.gds", package = "GBScleanR")
gds <- loadGDS(gds_fn)

getChromosome(gds)

# Close the connection to the GDS file.
closeGDS(gds)
```

---

|                                |   |
|--------------------------------|---|
| <code>getCountAlleleAlt</code> | <i>Obtain total alternative allele counts per SNP or per sample</i> |
|--------------------------------|---|

---

**Description**

Obtain total alternative allele counts per SNP or per sample

**Usage**

```
getCountAlleleAlt(object, target = "marker", valid = TRUE, prop = FALSE, ...)

## S4 method for signature 'GbsrGenotypeData'
getCountAlleleAlt(object, target, valid, prop)
```

**Arguments**

|                     |   |
|---------------------|---|
| <code>object</code> | A <a href="#">GbsrGenotypeData</a> object.  |
| <code>target</code> | Either of "marker" and "sample".  |
| <code>valid</code>  | A logical value. See details.   |
| <code>prop</code>   | A logical value whether to return values as proportions of total alternative allele counts to total non missing allele counts or not. |
| <code>...</code>    | Unused.   |

**Details**

You need to execute `countGenotype()` to calculate summary statistics to be obtained via this function. If `valid = TRUE`, the chromosome information of markers which are labeled TRUE in the `sample` slot will be returned. `validMar()` tells you which samples are valid.

**Value**

A numeric vector of (proportion of) alternative alleles per marker.

**Examples**

```
gds_fn <- system.file("extdata", "sample.gds", package = "GBScleanR")
gds <- loadGDS(gds_fn)
gds <- countGenotype(gds)
getCountAlleleAlt(gds)
closeGDS(gds) # Close the connection to the GDS file
```

---

getCountAlleleMissing *Obtain total missing allele counts per SNP or per sample*

---

**Description**

Obtain total missing allele counts per SNP or per sample

**Usage**

```
getCountAlleleMissing(
  object,
  target = "marker",
  valid = TRUE,
  prop = FALSE,
  ...
)

## S4 method for signature 'GbsrGenotypeData'
getCountAlleleMissing(object, target, valid, prop)
```

**Arguments**

|        |   |
|--------|---|
| object | A <a href="#">GbsrGenotypeData</a> object.  |
| target | Either of "marker" and "sample".  |
| valid  | A logical value. See details.   |
| prop   | A logical value whether to return values as proportions of total missing allele counts to the total allele number or not. |
| ...    | Unused.   |

**Details**

You need to execute [countGenotype\(\)](#) to calculate summary statistics to be obtained via this function. If `valid = TRUE`, the chromosome information of markers which are labeled TRUE in the [sample](#) slot will be returned. [validMar\(\)](#) tells you which samples are valid.

**Value**

A numeric vector of (proportion of) missing alleles per marker.

**Examples**

```
# Load data in the GDS file and instantiate a [GbsrGenotypeData] object.
gds_fn <- system.file("extdata", "sample.gds", package = "GBScleanR")
gds <- loadGDS(gds_fn)

# Summarize the genotype count information and store them in the
# [marker] and [sample] slots of the [GbsrGenotypeData] object.
gds <- countGenotype(gds)

getCountAlleleMissing(gds)

# Close the connection to the GDS file.
closeGDS(gds)
```

---

|                   |   |
|-------------------|---|
| getCountAlleleRef | <i>Obtain total reference allele counts per SNP or per sample</i> |
|-------------------|---|

---

**Description**

Obtain total reference allele counts per SNP or per sample

**Usage**

```
getCountAlleleRef(object, target = "marker", valid = TRUE, prop = FALSE, ...)

## S4 method for signature 'GbsrGenotypeData'
getCountAlleleRef(object, target, valid, prop)
```

**Arguments**

|        |   |
|--------|---|
| object | A <a href="#">GbsrGenotypeData</a> object.  |
| target | Either of "marker" and "sample".  |
| valid  | A logical value. See details.   |
| prop   | A logical value whether to return values as proportions of total reference allele counts to total non missing allele counts or not. |
| ...    | Unused.   |

**Details**

You need to execute [countGenotype\(\)](#) to calculate summary statistics to be obtained via this function. If `valid = TRUE`, the chromosome information of markers which are labeled TRUE in the [sample](#) slot will be returned. [validMar\(\)](#) tells you which samples are valid.

**Value**

A numeric vector of (proportion of) reference alleles per marker.

**Examples**

```
# Load data in the GDS file and instantiate a [GbsrGenotypeData] object.
gds_fn <- system.file("extdata", "sample.gds", package = "GBScleanR")
gds <- loadGDS(gds_fn)

# Summarize the genotype count information and store them in the
# [marker] and [sample] slots of the [GbsrGenotypeData] object.
gds <- countGenotype(gds)

getCountAlleleRef(gds)

# Close the connection to the GDS file.
closeGDS(gds)
```

---

|                 |   |
|-----------------|---|
| getCountGenoAlt | <i>Obtain total alternative genotype counts per SNP or per sample</i> |
|-----------------|---|

---

**Description**

Obtain total alternative genotype counts per SNP or per sample

**Usage**

```
getCountGenoAlt(object, target = "marker", valid = TRUE, prop = FALSE, ...)

## S4 method for signature 'GbsrGenotypeData'
getCountGenoAlt(object, target, valid, prop)
```

**Arguments**

|        |   |
|--------|---|
| object | A <a href="#">GbsrGenotypeData</a> object.  |
| target | Either of "marker" and "sample".  |
| valid  | A logical value. See details.   |
| prop   | A logical value whether to return values as proportions of total alternative genotype counts to total non missing genotype counts or not. |
| ...    | Unused.   |

**Details**

You need to execute [countGenotype\(\)](#) to calculate summary statistics to be obtained via this function. If `valid = TRUE`, the chromosome information of markers which are labeled TRUE in the [sample](#) slot will be returned. [validMar\(\)](#) tells you which samples are valid.

**Value**

A numeric vector of (proportion of) homozygous alternative genotype calls per marker.



**Examples**

```
# Load data in the GDS file and instantiate a [GbsrGenotypeData] object.
gds_fn <- system.file("extdata", "sample.gds", package = "GBScleanR")
gds <- loadGDS(gds_fn)

# Summarize the genotype count information and store them in the
# [marker] and [sample] slots of the [GbsrGenotypeData] object.
gds <- countGenotype(gds)

getCountGenoAlt(gds)

# Close the connection to the GDS file
closeGDS(gds)
```

---

|                 |   |
|-----------------|---|
| getCountGenoHet | <i>Obtain total heterozygote counts per SNP or per sample</i> |
|-----------------|---|

---

**Description**

Obtain total heterozygote counts per SNP or per sample

**Usage**

```
getCountGenoHet(object, target = "marker", valid = TRUE, prop = FALSE, ...)

## S4 method for signature 'GbsrGenotypeData'
getCountGenoHet(object, target, valid, prop)
```

**Arguments**

|        |   |
|--------|---|
| object | A <a href="#">GbsrGenotypeData</a> object.  |
| target | Either of "marker" and "sample".  |
| valid  | A logical value. See details.   |
| prop   | A logical value whether to return values as proportions of total heterozygote counts to total non missing genotype counts or not. |
| ...    | Unused.   |

**Details**

You need to execute [countGenotype\(\)](#) to calculate summary statistics to be obtained via this function. If `valid = TRUE`, the chromosome information of markers which are labeled TRUE in the [sample](#) slot will be returned. [validMar\(\)](#) tells you which samples are valid.

**Value**

A numeric vector of (proportion of) heterozygous genotype calls per marker.

**Examples**

```
# Load data in the GDS file and instantiate a [GbsrGenotypeData] object.
gds_fn <- system.file("extdata", "sample.gds", package = "GBScleanR")
gds <- loadGDS(gds_fn)

# Summarize the genotype count information and store them in the
# [marker] and [sample] slots of the [GbsrGenotypeData] object.
gds <- countGenotype(gds)

getCountGenoHet(gds)

# Close the connection to the GDS file.
closeGDS(gds)
```

---

getCountGenoMissing     *Obtain total missing genotype counts per SNP or per sample*

---

**Description**

Obtain total missing genotype counts per SNP or per sample

**Usage**

```
getCountGenoMissing(object, target = "marker", valid = TRUE, prop = FALSE, ...)

## S4 method for signature 'GbsrGenotypeData'
getCountGenoMissing(object, target, valid, prop)
```

**Arguments**

|        |  |
|--------|--|
| object | A <a href="#">GbsrGenotypeData</a> object.   |
| target | Either of "marker" and "sample".   |
| valid  | A logical value. See details.  |
| prop   | A logical value whether to return values as proportions of total missing genotype counts to the total genotype calls or not. |
| ...    | Unused.  |

**Details**

You need to execute [countGenotype\(\)](#) to calculate summary statistics to be obtained via this function. If `valid = TRUE`, the chromosome information of markers which are labeled TRUE in the [sample](#) slot will be returned. [validMar\(\)](#) tells you which samples are valid.

**Value**

A numeric vector of (proportion of) missing genotype calls per marker.

**Examples**

```
gds_fn <- system.file("extdata", "sample.gds", package = "GBScleanR")
gds <- loadGDS(gds_fn)
gds <- countGenotype(gds)
getCountGenoMissing(gds)
closeGDS(gds) # Close the connection to the GDS file
```

---

|                 |   |
|-----------------|---|
| getCountGenoRef | <i>Obtain total reference genotype counts per SNP or per sample</i> |
|-----------------|---|

---

**Description**

Obtain total reference genotype counts per SNP or per sample

**Usage**

```
getCountGenoRef(object, target = "marker", valid = TRUE, prop = FALSE, ...)

## S4 method for signature 'GbsrGenotypeData'
getCountGenoRef(object, target, valid, prop)
```

**Arguments**

|        |   |
|--------|---|
| object | A <a href="#">GbsrGenotypeData</a> object.  |
| target | Either of "marker" and "sample".  |
| valid  | A logical value. See details.   |
| prop   | A logical value whether to return values as proportions of total reference genotype counts to total non missing genotype counts or not. |
| ...    | Unused.   |

**Details**

You need to execute [countGenotype\(\)](#) to calculate summary statistics to be obtained via this function. If `valid = TRUE`, the chromosome information of markers which are labeled TRUE in the `sample` slot will be returned. [validMar\(\)](#) tells you which samples are valid.

**Value**

A numeric vector of (proportion of) homozygous reference genotype calls per marker.

**Examples**

```
# Load data in the GDS file and instantiate a [GbsrGenotypeData] object.
gds_fn <- system.file("extdata", "sample.gds", package = "GBScleanR")
gds <- loadGDS(gds_fn)

# Summarize the genotype count information and store them in the
# [marker] and [sample] slots of the [GbsrGenotypeData] object.
gds <- countGenotype(gds)
```

```

getCountGenoRef(gds)

# Close the connection to the GDS file.
closeGDS(gds)

```

---

|              |   |
|--------------|---|
| getCountRead | <i>Obtain total read counts per SNP or per sample</i> |
|--------------|---|

---

### Description

Obtain total read counts per SNP or per sample

### Usage

```

getCountRead(object, target = "marker", valid = TRUE, ...)

## S4 method for signature 'GbsrGenotypeData'
getCountRead(object, target, valid)

```

### Arguments

|        |  |
|--------|--|
| object | A <a href="#">GbsrGenotypeData</a> object. |
| target | Either of "marker" and "sample".           |
| valid  | A logical value. See details.              |
| ...    | Unused.                                    |

### Details

You need to execute [countRead\(\)](#) to calculate summary statistics to be obtained via this function. If `valid = TRUE`, the chromosome information of markers which are labeled TRUE in the [sample](#) slot will be returned. [validMar\(\)](#) tells you which samples are valid.

### Value

A integer vector of total read counts (reference allele reads + alternative allele reads) per marker.

### Examples

```

# Load data in the GDS file and instantiate a [GbsrGenotypeData] object.
gds_fn <- system.file("extdata", "sample.gds", package = "GBScleanR")
gds <- loadGDS(gds_fn)
gds <- countRead(gds)

getCountRead(gds)

# Close the connection to the GDS file.
closeGDS(gds)

```

---

|                 |   |
|-----------------|---|
| getCountReadAlt | <i>Obtain total alternative read counts per SNP or per sample</i> |
|-----------------|---|

---

### Description

Obtain total alternative read counts per SNP or per sample

### Usage

```
getCountReadAlt(object, target = "marker", valid = TRUE, prop = FALSE, ...)  
  
## S4 method for signature 'GbsrGenotypeData'  
getCountReadAlt(object, target, valid, prop)
```

### Arguments

|        |   |
|--------|---|
| object | A <a href="#">GbsrGenotypeData</a> object.  |
| target | Either of "marker" and "sample".  |
| valid  | A logical value. See details.   |
| prop   | A logical value whether to return values as proportions of total alternative read counts in total read counts per SNP or not. |
| ...    | Unused.   |

### Details

You need to execute [countRead\(\)](#) to calculate summary statistics to be obtained via this function. If `valid = TRUE`, the chromosome information of markers which are labeled TRUE in the [sample](#) slot will be returned. [validMar\(\)](#) tells you which samples are valid.

### Value

A numeric vector of (proportion of) alternative allele read counts per marker.

### Examples

```
# Load data in the GDS file and instantiate a [GbsrGenotypeData] object.  
gds_fn <- system.file("extdata", "sample.gds", package = "GBScleanR")  
gds <- loadGDS(gds_fn)  
gds <- countRead(gds)  
  
getCountReadAlt(gds)  
  
# Close the connection to the GDS file.  
closeGDS(gds)
```

---

getCountReadRef      *Obtain total reference read counts per SNP or per sample*

---

### Description

Obtain total reference read counts per SNP or per sample

### Usage

```
getCountReadRef(object, target = "marker", valid = TRUE, prop = FALSE, ...)

## S4 method for signature 'GbsrGenotypeData'
getCountReadRef(object, target, valid, prop)
```

### Arguments

|        |   |
|--------|---|
| object | A <a href="#">GbsrGenotypeData</a> object.  |
| target | Either of "marker" and "sample".  |
| valid  | A logical value. See details.   |
| prop   | A logical value whether to return values as proportions of total reference read counts in total read counts per SNP or not. |
| ...    | Unused.   |

### Details

You need to execute [countRead\(\)](#) to calculate summary statistics to be obtained via this function. If `valid = TRUE`, the chromosome information of markers which are labeled TRUE in the [sample](#) slot will be returned. [validMar\(\)](#) tells you which samples are valid.

### Value

A numeric vector of (proportion of) reference read counts per marker.

### Examples

```
# Load data in the GDS file and instantiate a [GbsrGenotypeData] object.
gds_fn <- system.file("extdata", "sample.gds", package = "GBScleanR")
gds <- loadGDS(gds_fn)
gds <- countRead(gds)

getCountReadRef(gds)

# Close the connection to the GDS file.
closeGDS(gds)
```

---

|              |                                     |
|--------------|-------------------------------------|
| getFixedBias | <i>Get fixed allele read biases</i> |
|--------------|-------------------------------------|

---

## Description

Get fixed allele read biases of markers

## Usage

```
getFixedBias(object, valid = TRUE, chr = NULL, ...)
```

```
## S4 method for signature 'GbsrGenotypeData'
getFixedBias(object, valid, chr)
```

## Arguments

|        |   |
|--------|---|
| object | A <a href="#">GbsrGenotypeData</a> object.                    |
| valid  | A logical value. See details.                                 |
| chr    | A integer or string to specify chromosome to get information. |
| ...    | Unused.   |

## Details

If `valid = TRUE`, A logical vector for the markers which are labeled TRUE in the "valid" column of the "marker" slot will be returned. If you need check the dominant markers in all markers, set `valid = FALSE`. [validMar\(\)](#) tells you which markers are valid.

## Value

A numeric vector of fixed allele read biases.

A [GbsrGenotypeData](#) object after adding dominant marker information

## See Also

[setFixedBias\(\)](#)

## Examples

```
# Create a GDS file from a sample VCF file.
vcf_fn <- system.file("extdata", "sample.vcf", package = "GBScleanR")
gds_fn <- tempfile("sample", fileext = ".gds")
gbsrVCF2GDS(vcf_fn = vcf_fn, out_fn = gds_fn, force = TRUE)

# Load data in the GDS file and instantiate a [GbsrGenotypeData] object.
gds <- loadGDS(gds_fn)

# Set fixed allele read biases.
# Initialize the bias vector to be assigned.
bias <- rep(NA, nmar(gds))

# As an example, select 20 markers randomly and assign 0 or 1 to them.
# Since the bias set by setFixedBias() function is the reference allele read
```

```

# bias. Thus, the values 0 and 1 means that the marker only gives alternative
# and reference allele reads, respectively.
# Set these fixed biases if some of your markers are dominant markers.
bias[sample(seq_along(bias), 20)] <- sample(c(0, 1), 20, replace = TRUE)

gds <- setFixedBias(gds, bias = bias)

fixed_bias <- getFixedBias(gds)

# Close the connection to the GDS file
closeGDS(gds)

```

---

getGenotype

*Get genotype call data.*


---

### Description

Genotype calls are retrieved from the GDS file linked to the given [GbsrGenotypeData](#) object.

### Usage

```

getGenotype(
  object,
  node = "raw",
  parents = FALSE,
  valid = TRUE,
  chr = NULL,
  phased = FALSE,
  ...
)

## S4 method for signature 'GbsrGenotypeData'
getGenotype(object, node, parents, valid, chr, phased)

```

### Arguments

|         |   |
|---------|---|
| object  | A <a href="#">GbsrGenotypeData</a> object.  |
| node    | Either of "raw", "filt", "cor", and "parents". See details.   |
| parents | A logical value or "only" whether to include data for parents or not or to get data only for parents. Ignored if node = "parents".                                    |
| valid   | A logical value. See details.   |
| chr     | A integer vector of indexes indicating chromosomes to get read count data.  |
| phased  | If set TRUE to phased, the function will return phased genotype data in a P x N x M array where P, N, and M are the ploidy, number of samples, and number of markers. |
| ...     | Unused.   |



**Details**

When `node = "raw"`, the raw genotype data stored in the "genotype/data" node will be returned, while `node = "filt"` make the function to return the filtered genotype data stored in the "annotation/format/FGT/data" that can be generated via the `setCallFilter()` function. `node = "cor"` indicates to get the corrected genotype data stored in the "annotation/format/CGT/data" that can be generated via the `estGeno()` function. The estimated parental genotypes, which also can be generated via the `estGeno()` function and stored in the "annotation/info/PGT" node, can be obtained with `node = "parents"`. If `valid = TRUE`, genotype calls for only valid marker and valid samples will be obtained.

**Value**

An integer matrix of genotype data which is represented by the number of reference alleles at each marker of each sample.

**See Also**

`setCallFilter()` and `estGeno()`

**Examples**

```
# Load data in the GDS file and instantiate a [GbsrGenotypeData] object.
gds_fn <- system.file("extdata", "sample.gds", package = "GBScleanR")
gds <- loadGDS(gds_fn)

geno <- getGenotype(gds)

# Close the connection to the GDS file.
closeGDS(gds)
```

---

getHaplotype

*Get haplotype call data.*


---

**Description**

Haplotype calls are retrieved from the GDS file linked to the given `GbsrGenotypeData` object.

**Usage**

```
getHaplotype(object, parents = FALSE, valid = TRUE, chr = NULL, ...)
```

```
## S4 method for signature 'GbsrGenotypeData'
getHaplotype(object, parents, valid, chr)
```

**Arguments**

`object` A `GbsrGenotypeData` object.

`parents` A logical value or "only" to include data for parents or to get data only for parents.

|       |  |
|-------|--|
| valid | A logical value. See details.  |
| chr   | A integer vector of indexes indicating chromosomes to get read count data. |
| ...   | Unused.  |

### Details

Haplotype call data can be obtained from the "estimated.haplotype" node of the GDS file which can be generated via the `estGeno()` function. Thus, this function is valid only after having executed `estGeno()`. If `valid = TRUE`, read counts for only valid marker and valid samples will be obtained.

### Value

An integer array of haplotype data. The array have  $2 \times M \times N$  dimensions, where  $M$  is the number of markers and  $N$  is the number of samples. Each integer values represent the origin of the haplotype. For example, in the population with two inbred founders, values take either 1 or 2 indicating the hapotype descent from founder 1 and 2. If two outbred founders, values take 1, 2, 3, or 4 indicating the first and second haplotype in founder 1 and the first and second haplotype in founder 2.

### See Also

[estGeno\(\)](#)

### Examples

```
# Load data in the GDS file and instantiate a [GbsrGenotypeData] object.
gds_fn <- system.file("extdata", "sample.gds", package = "GBScleanR")
gds <- loadGDS(gds_fn)

# Find the IDs of parental samples.
parents <- grep("Founder", getSamID(gds), value = TRUE)

# Set the parents and flip allele information
# if the reference sample (Founder1 in our case) has homozygous
# alternative genotype at some markers of which alleles will
# be swapped to make the reference sample have homozygous
# reference genotype.
gds <- setParents(gds, parents = parents)

# Initialize a scheme object stored in the slot of the GbsrGenotypeData.
# We chose `crosstype = "pair"` because two inbred founders were mated
# in our breeding scheme.
# We also need to specify the mating matrix which has two rows and
# one column with integers 1 and 2 indicating a sample (founder)
# with the memberID 1 and a sample (founder) with the memberID 2
# were mated.
gds <- initScheme(gds, mating = cbind(c(1:2)))

# Add information of the next cross conducted in our scheme.
# We chose 'crosstype = "selfing"', which do not require a
# mating matrix.
gds <- addScheme(gds, crosstype = "selfing")

# Execute error correction by estimating genotype and haplotype of
# founders and offspring.
gds <- estGeno(gds)
```

```
hap <- getHaplotype(gds)

# Close the connection to the GDS file.
closeGDS(gds)
```

---

getInfo *Obtain information stored in the "annotation/info" node*

---

### Description

The "annotation/info" node stores annotation information of markers obtained via SNP calling tools like bcftools and GATK.

### Usage

```
getInfo(object, var, valid = TRUE, chr = NULL, ...)

## S4 method for signature 'GbsrGenotypeData'
getInfo(object, var, valid, chr)
```

### Arguments

|        |   |
|--------|---|
| object | A <a href="#">GbsrGenotypeData</a> object.                      |
| var    | A string to indicate which annotation info should be retrieved. |
| valid  | A logical value. See details.                                   |
| chr    | A index to specify chromosome to get information.               |
| ...    | Unused.   |

### Details

If `valid = TRUE`, the information of the markers which are labeled TRUE in the "valid" column of the "marker" slot will be returned. If you need the number of over all markers, set `valid = FALSE`. [validMar\(\)](#) tells you which markers are valid.

### Value

A numeric vector of data stored in INFO node of the GDS file.

### Examples

```
# Load data in the GDS file and instantiate a [GbsrGenotypeData] object.
gds_fn <- system.file("extdata", "sample.gds", package = "GBScleanR")
gds <- loadGDS(gds_fn)

# Get mapping qualities (MQ) of markers.
mq <- getInfo(gds, "MQ")

# Close the connection to the GDS file.
closeGDS(gds)
```

---

|        |   |
|--------|---|
| getMAC | <i>Obtain minor allele counts per SNP or per sample</i> |
|--------|---|

---

### Description

Obtain minor allele counts per SNP or per sample

### Usage

```
getMAC(object, target = "marker", valid = TRUE, ...)  
  
## S4 method for signature 'GbsrGenotypeData'  
getMAC(object, target, valid)
```

### Arguments

|        |  |
|--------|--|
| object | A <a href="#">GbsrGenotypeData</a> object. |
| target | Either of "marker" and "sample".           |
| valid  | A logical value. See details.              |
| ...    | Unused.                                    |

### Details

You need to execute [countGenotype\(\)](#) to calculate summary statistics to be obtained via this function. If `valid = TRUE`, the chromosome information of markers which are labeled TRUE in the [sample](#) slot will be returned. [validMar\(\)](#) tells you which samples are valid.

### Value

A numeric vector of the minor allele counts per marker.

### Examples

```
# Load data in the GDS file and instantiate a [GbsrGenotypeData] object.  
gds_fn <- system.file("extdata", "sample.gds", package = "GBScleanR")  
gds <- loadGDS(gds_fn)  
  
# Summarize the genotype count information and store them in the  
# [marker] and [sample] slots of the [GbsrGenotypeData] object.  
gds <- countGenotype(gds)  
  
getMAC(gds)  
  
# Close the connection to the GDS file.  
closeGDS(gds)
```

---

|        |  |
|--------|--|
| getMAF | <i>Obtain minor allele frequencies per SNP or per sample</i> |
|--------|--|

---

### Description

Obtain minor allele frequencies per SNP or per sample

### Usage

```
getMAF(object, target = "marker", valid = TRUE, ...)  
  
## S4 method for signature 'GbsrGenotypeData'  
getMAF(object, target, valid)
```

### Arguments

|        |  |
|--------|--|
| object | A <a href="#">GbsrGenotypeData</a> object. |
| target | Either of "marker" and "sample".           |
| valid  | A logical value. See details.              |
| ...    | Unused.                                    |

### Details

You need to execute [countGenotype\(\)](#) to calculate summary statistics to be obtained via this function. If `valid = TRUE`, the chromosome information of markers which are labeled TRUE in the [sample](#) slot will be returned. [validMar\(\)](#) tells you which samples are valid.

### Value

A numeric vector of the minor allele frequencies per marker.

### Examples

```
# Load data in the GDS file and instantiate a [GbsrGenotypeData] object.  
gds_fn <- system.file("extdata", "sample.gds", package = "GBScleanR")  
gds <- loadGDS(gds_fn)  
  
# Summarize the genotype count information and store them in the  
# [marker] and [sample] slots of the [GbsrGenotypeData] object.  
gds <- countGenotype(gds)  
  
getMAF(gds)  
  
# Close the connection to the GDS file  
closeGDS(gds)
```

---

|          |                              |
|----------|------------------------------|
| getMarID | <i>Obtain the marker IDs</i> |
|----------|------------------------------|

---

### Description

Obtain the marker IDs

### Usage

```
getMarID(object, valid = TRUE, chr = NULL, ...)
```

```
## S4 method for signature 'GbsrGenotypeData'  
getMarID(object, valid, chr)
```

### Arguments

|        |   |
|--------|---|
| object | A <a href="#">GbsrGenotypeData</a> object.        |
| valid  | A logical value. See details.                     |
| chr    | A index to specify chromosome to get information. |
| ...    | Unused.   |

### Details

If `valid = TRUE`, the IDs of markers which are labeled TRUE in the "valid" column of the "marker" slot will be returned. If you need the number of over all markers, set `valid = FALSE`. [validMar\(\)](#) tells you which markers are valid.

### Value

A integer vector of marker IDs.

### Examples

```
# Load data in the GDS file and instantiate a [GbsrGenotypeData] object.  
gds_fn <- system.file("extdata", "sample.gds", package = "GBScleanR")  
gds <- loadGDS(gds_fn)  
  
getMarID(gds)  
  
# Close the connection to the GDS file.  
closeGDS(gds)
```

---

|                |  |
|----------------|--|
| getMeanReadAlt | <i>Obtain mean values of total alternative read counts per SNP or per sample</i> |
|----------------|--|

---

### Description

Obtain mean values of total alternative read counts per SNP or per sample

### Usage

```
getMeanReadAlt(object, target = "marker", valid = TRUE, ...)  
  
## S4 method for signature 'GbsrGenotypeData'  
getMeanReadAlt(object, target, valid)
```

### Arguments

|        |  |
|--------|--|
| object | A <a href="#">GbsrGenotypeData</a> object. |
| target | Either of "marker" and "sample".           |
| valid  | A logical value. See details.              |
| ...    | Unused.                                    |

### Details

You need to execute [countRead\(\)](#) to calculate summary statistics to be obtained via this function. If `valid = TRUE`, the chromosome information of markers which are labeled TRUE in the [sample](#) slot will be returned. [validMar\(\)](#) tells you which samples are valid.

### Value

A numeric vector of the mean values of alternative allele reads per marker.

### Examples

```
# Load data in the GDS file and instantiate a [GbsrGenotypeData] object.  
gds_fn <- system.file("extdata", "sample.gds", package = "GBScleanR")  
gds <- loadGDS(gds_fn)  
  
# Calculate means, standard deviations, quantiles of read counts  
# per marker and per sample with or without standardization of  
# the counts and store them in the [marker] and [sample] slots  
# of the [GbsrGenotypeData] object.  
gds <- countRead(gds)  
  
getMeanReadAlt(gds)  
  
# Close the connection to the GDS file.  
closeGDS(gds)
```

---

|                |  |
|----------------|--|
| getMeanReadRef | <i>Obtain mean values of total reference read counts per SNP or per sample</i> |
|----------------|--|

---

### Description

Obtain mean values of total reference read counts per SNP or per sample

### Usage

```
getMeanReadRef(object, target = "marker", valid = TRUE, ...)
```

```
## S4 method for signature 'GbsrGenotypeData'  
getMeanReadRef(object, target, valid)
```

### Arguments

|        |  |
|--------|--|
| object | A <a href="#">GbsrGenotypeData</a> object. |
| target | Either of "marker" and "sample".           |
| valid  | A logical value. See details.              |
| ...    | Unused.                                    |

### Details

You need to execute [countRead\(\)](#) to calculate summary statistics to be obtained via this function. If `valid = TRUE`, the chromosome information of markers which are labeled TRUE in the [sample](#) slot will be returned. [validMar\(\)](#) tells you which samples are valid.

### Value

A numeric vector of the mean values of reference allele reads per marker.

### Examples

```
gds_fn <- system.file("extdata", "sample.gds", package = "GBScleanR")  
gds <- loadGDS(gds_fn)  
gds <- countRead(gds)  
getMeanReadRef(gds)  
closeGDS(gds) # Close the connection to the GDS file
```



---

|                  |  |
|------------------|--|
| getMedianReadAlt | <i>Obtain quantile values of total alternative read counts per SNP or per sample</i> |
|------------------|--|

---

### Description

Obtain quantile values of total alternative read counts per SNP or per sample

### Usage

```
getMedianReadAlt(object, target = "marker", valid = TRUE, ...)
```

```
## S4 method for signature 'GbsrGenotypeData'
getMedianReadAlt(object, target, valid)
```

### Arguments

|        |  |
|--------|--|
| object | A <a href="#">GbsrGenotypeData</a> object. |
| target | Either of "marker" and "sample".           |
| valid  | A logical value. See details.              |
| ...    | Unused.                                    |

### Details

You need to execute [countRead\(\)](#) to calculate summary statistics to be obtained via this function. If `valid = TRUE`, the chromosome information of markers which are labeled TRUE in the [sample](#) slot will be returned. [validMar\(\)](#) tells you which samples are valid.

### Value

A numeric vector of the quantile values of alternative allele reads per marker.

### Examples

```
# Load data in the GDS file and instantiate a [GbsrGenotypeData] object.
gds_fn <- system.file("extdata", "sample.gds", package = "GBScleanR")
gds <- loadGDS(gds_fn)

# Calculate means, standard deviations, quantiles of read counts
# per marker and per sample with or without standardization of
# the counts and store them in the [marker] and [sample] slots
# of the [GbsrGenotypeData] object.
gds <- countRead(gds)

getMedianReadAlt(gds)

# Close the connection to the GDS file.
closeGDS(gds)
```

---

|                  |  |
|------------------|--|
| getMedianReadRef | <i>Obtain quantile values of total reference read counts per SNP or per sample</i> |
|------------------|--|

---

### Description

Obtain quantile values of total reference read counts per SNP or per sample

### Usage

```
getMedianReadRef(object, target = "marker", valid = TRUE, ...)
```

```
## S4 method for signature 'GbsrGenotypeData'
getMedianReadRef(object, target, valid)
```

### Arguments

|        |  |
|--------|--|
| object | A <a href="#">GbsrGenotypeData</a> object. |
| target | Either of "marker" and "sample".           |
| valid  | A logical value. See details.              |
| ...    | Unused.                                    |

### Details

You need to execute [countRead\(\)](#) to calculate summary statistics to be obtained via this function. If `valid = TRUE`, the chromosome information of markers which are labeled TRUE in the [sample](#) slot will be returned. [validMar\(\)](#) tells you which samples are valid.

### Value

A numeric vector of the quantile values of alternative allele reads per marker.

### Examples

```
# Load data in the GDS file and instantiate a [GbsrGenotypeData] object.
gds_fn <- system.file("extdata", "sample.gds", package = "GBScleanR")
gds <- loadGDS(gds_fn)

# Calculate means, standard deviations, quantiles of read counts
# per marker and per sample with or without standardization of
# the counts and store them in the [marker] and [sample] slots
# of the [GbsrGenotypeData] object.
gds <- countRead(gds)

getMedianReadRef(gds)

# Close the connection to the GDS file.
closeGDS(gds)
```

---

|            |  |
|------------|--|
| getParents | <i>Get parental sample information</i> |
|------------|--|

---

### Description

This function returns sample IDs, member IDs and indexes of parental samples set via `setParents()`. Sample IDs are IDs given by user or obtained from the original VCF file. Member IDs are serial numbers assigned by `setParents()`.

### Usage

```
getParents(object, bool = FALSE, verbose = TRUE, ...)
```

```
## S4 method for signature 'GbsrGenotypeData'  
getParents(object, bool, verbose = TRUE)
```

### Arguments

|         |  |
|---------|--|
| object  | A <code>GbsrGenotypeData</code> object.  |
| bool    | If TRUE, the function returns a logical vector indicating which samples have been set as parents.  |
| verbose | If FALSE, the function does not print a warning message even when parents were not specified in the given <code>GbsrGenotypeData</code> object. The setting <code>verbose = FALSE</code> is used in the other functions to call <code>getParents()</code> without evoking unnecessary warnings to users. |
| ...     | Unused.  |

### Value

A data frame of parents information indicating sampleIDs, memberIDs and indexes of parental lines assigned via `setParents()`.

### Examples

```
# Load data in the GDS file and instantiate a [GbsrGenotypeData] object.  
gds_fn <- system.file("extdata", "sample.gds", package = "GBScleanR")  
gds <- loadGDS(gds_fn)  
  
# Find the IDs of parental samples.  
parents <- grep("Founder", getSamID(gds), value = TRUE)  
  
# Set the parents.  
gds <- setParents(gds, parents = parents)  
  
# Get the information of parents.  
getParents(gds)  
  
# Close the connection to the GDS file.  
closeGDS(gds)
```

---

|             |                                |
|-------------|--------------------------------|
| getPosition | <i>Obtain marker positions</i> |
|-------------|--------------------------------|

---

### Description

This function returns physical positions of markers.

### Usage

```
getPosition(object, valid = TRUE, chr = NULL, ...)
```

```
## S4 method for signature 'GbsrGenotypeData'  
getPosition(object, valid, chr)
```

### Arguments

|        |   |
|--------|---|
| object | A <a href="#">GbsrGenotypeData</a> object.                    |
| valid  | A logical value. See details.                                 |
| chr    | A integer or string to specify chromosome to get information. |
| ...    | Unused.   |

### Details

If `valid = TRUE`, the positions of the markers which are labeled TRUE in the "valid" column of the "marker" slot will be returned. If you need the positions of over all markers, set `valid = FALSE`. [validMar\(\)](#) tells you which markers are valid.

### Value

An integer vector indicating the physical positions of markers.

### Examples

```
# Load data in the GDS file and instantiate a [GbsrGenotypeData] object.  
gds_fn <- system.file("extdata", "sample.gds", package = "GBScleanR")  
gds <- loadGDS(gds_fn)  
  
getPosition(gds)  
  
# Close the connection to the GDS file.  
closeGDS(gds)
```

---

|         |                             |
|---------|-----------------------------|
| getRead | <i>Get read count data.</i> |
|---------|-----------------------------|

---

### Description

Read counts for reference allele and alternative allele are retrieved from the GDS file linked to the given [GbsrGenotypeData](#) object.

### Usage

```
getRead(object, node = "raw", parents = FALSE, valid = TRUE, chr = NULL, ...)
```

```
## S4 method for signature 'GbsrGenotypeData'
getRead(object, node, parents, valid, chr)
```

### Arguments

|         |   |
|---------|---|
| object  | A <a href="#">GbsrGenotypeData</a> object.  |
| node    | Either of "raw" and "filt". See details.  |
| parents | A logical value or "only" whether to include data for parents or not or to get data only for parents. |
| valid   | A logical value. See details.   |
| chr     | An integer vector of indexes indicating chromosomes to get read count data.                           |
| ...     | Unused.   |

### Details

When `node = "raw"`, the raw read counts stored in the "annotation/format/AD/data" node will be returned, while `node = "filt"` make the function to return the filtered read counts stored in the "annotation/format/FAD/data" that can be generated via the [setCallFilter\(\)](#) function. If `valid = TRUE`, read counts for only valid marker and valid samples will be obtained.

### Value

A named list with two elements "ref" and "alt" storing a matrix of reference allele read counts and a matrix of alternative read counts for all markers in all samples.

### See Also

[setCallFilter\(\)](#)

### Examples

```
# Load data in the GDS file and instantiate a [GbsrGenotypeData] object.
gds_fn <- system.file("extdata", "sample.gds", package = "GBScleanR")
gds <- loadGDS(gds_fn)

read <- getRead(gds)

# Close the connection to the GDS file.
closeGDS(gds)
```

---

|               |   |
|---------------|---|
| getReplicates | <i>Get identifiers to indicates which samples are replicates.</i> |
|---------------|---|

---

### Description

Not implemented yet. This function assign identifiers that indicates which samples are replicates those which should have the same genotypes at all markers.

### Usage

```
getReplicates(object, parents = FALSE, ...)

## S4 method for signature 'GbsrGenotypeData'
getReplicates(object, parents)
```

### Arguments

|         |  |
|---------|--|
| object  | A <a href="#">GbsrGenotypeData</a> object.   |
| parents | A logical value to indicate whether to include replicate IDs for parental samples in the output. If you specify parents = "only", this function returns replicate IDs only for parental samples. |
| ...     | Unused.  |

### Details

The replicates of samples specified in [setReplicates\(\)](#) will have the same genotypes at all markers in the estimated genotypes obtained via [estGeno\(\)](#). In the genotype estimation by [estGeno\(\)](#), the Viterbi scores for each possible genotype (haplotype) at each marker for the replicates will be replaced with the average score for the replicates.

### Value

A [GbsrGenotypeData](#) object with genotype count information.

### See Also

[setReplicates\(\)](#)

### Examples

```
# Load data in the GDS file and instantiate a [GbsrGenotypeData] object.
gds_fn <- system.file("extdata", "sample.gds", package = "GBScleanR")
gds <- loadGDS(gds_fn)

gds <- setParents(gds, parents = c("Founder1", "Founder2"))

# When your data has 100 samples, two replicates for each offspring,
# and the samples are ordered as the 1st replicate followed by the 2nd
# replicate, you can specify replicates as below.
# gds <- setReplicates(gds, replicates = rep(1:50, each = 2))

# If you need to confirm the order of samples, run the following code.
```

```
# id <- getSamID(gds)

# Replicate IDs should be set also to parents. Therefore, please include

# getReplicates(gds)

# Close the connection to the GDS file.
closeGDS(gds)
```

---

getSamID

*Obtain the sample IDs*

---

### Description

This function returns sample IDs.

### Usage

```
getSamID(object, valid = TRUE, parents = FALSE, ...)

## S4 method for signature 'GbsrGenotypeData'
getSamID(object, valid, parents)
```

### Arguments

|         |   |
|---------|---|
| object  | A <a href="#">GbsrGenotypeData</a> object.                  |
| valid   | A logical value. See details.                               |
| parents | A logical value whether to include data for parents or not. |
| ...     | Unused.   |

### Details

If `valid = TRUE`, the IDs of samples which are labeled TRUE in the "valid" column of the "sample" slot will be returned. If you need the number of over all samples, set `valid = FALSE`. [validSam\(\)](#) tells you which samples are valid.

### Value

A character vector of sample IDs.

### Examples

```
# Load data in the GDS file and instantiate a [GbsrGenotypeData] object.
gds_fn <- system.file("extdata", "sample.gds", package = "GBScleanR")
gds <- loadGDS(gds_fn)

getSamID(gds)

# Close the connection to the GDS file.
closeGDS(gds)
```

---

|              |  |
|--------------|--|
| getSDReadAlt | <i>Obtain standard deviations of total alternative read counts per SNP or per sample</i> |
|--------------|--|

---

### Description

Obtain standard deviations of total alternative read counts per SNP or per sample

### Usage

```
getSDReadAlt(object, target = "marker", valid = TRUE, ...)
```

```
## S4 method for signature 'GbsrGenotypeData'
getSDReadAlt(object, target, valid)
```

### Arguments

|        |  |
|--------|--|
| object | A <a href="#">GbsrGenotypeData</a> object. |
| target | Either of "marker" and "sample".           |
| valid  | A logical value. See details.              |
| ...    | Unused.                                    |

### Details

You need to execute [countRead\(\)](#) to calculate summary statistics to be obtained via this function. If `valid = TRUE`, the chromosome information of markers which are labeled TRUE in the [sample](#) slot will be returned. [validMar\(\)](#) tells you which samples are valid.

### Value

A numeric vector of the standard deviations of alternative allele reads per marker.

### Examples

```
# Load data in the GDS file and instantiate a [GbsrGenotypeData] object.
gds_fn <- system.file("extdata", "sample.gds", package = "GBScleanR")
gds <- loadGDS(gds_fn)

# Calculate means, standard deviations, quantiles of read counts
# per marker and per sample with or without standardization of
# the counts and store them in the [marker] and [sample] slots
# of the [GbsrGenotypeData] object.
gds <- countRead(gds)

getSDReadAlt(gds)

# Close the connection to the GDS file.
closeGDS(gds)
```



---

|              |  |
|--------------|--|
| getSDReadRef | <i>Obtain standard deviations of total reference read counts per SNP or per sample</i> |
|--------------|--|

---

### Description

Obtain standard deviations of total reference read counts per SNP or per sample

### Usage

```
getSDReadRef(object, target = "marker", valid = TRUE, ...)
```

```
## S4 method for signature 'GbsrGenotypeData'  
getSDReadRef(object, target, valid)
```

### Arguments

|        |  |
|--------|--|
| object | A <a href="#">GbsrGenotypeData</a> object. |
| target | Either of "marker" and "sample".           |
| valid  | A logical value. See details.              |
| ...    | Unused.                                    |

### Details

You need to execute [countRead\(\)](#) to calculate summary statistics to be obtained via this function. If `valid = TRUE`, the chromosome information of markers which are labeled TRUE in the [sample](#) slot will be returned. [validMar\(\)](#) tells you which samples are valid.

### Value

A numeric vector of the standard deviations of reference allele reads per marker.

### Examples

```
# Load data in the GDS file and instantiate a [GbsrGenotypeData] object.  
gds_fn <- system.file("extdata", "sample.gds", package = "GBScleanR")  
gds <- loadGDS(gds_fn)  
  
# Calculate means, standard deviations, quantiles of read counts  
# per marker and per sample with or without standardization of  
# the counts and store them in the [marker] and [sample] slots  
# of the [GbsrGenotypeData] object.  
gds <- countRead(gds)  
  
getSDReadRef(gds)  
  
# Close the connection to the GDS file.  
closeGDS(gds)
```

histGBSR

*Draw histograms of specified statistics***Description**

Draw histograms of specified statistics

**Usage**

```
histGBSR(
  x,
  stats = c("dp", "missing", "het"),
  target = c("marker", "sample"),
  binwidth = NULL,
  color = c(Marker = "darkblue", Sample = "darkblue"),
  fill = c(Marker = "skyblue", Sample = "skyblue")
)
```

**Arguments**

|                       |   |
|-----------------------|---|
| <code>x</code>        | A <a href="#">GbsrGenotypeData</a> object.  |
| <code>stats</code>    | A string to specify statistics to be drawn.   |
| <code>target</code>   | Either or both of "marker" and "sample", e.g. <code>target = "marker"</code> to draw a histogram only for SNPs. |
| <code>binwidth</code> | An integer to specify bin width of the histogram. This value is passed to the <code>ggplot</code> function.     |
| <code>color</code>    | A named vector "Marker" and "Sample" to specify border color of bins in the histograms.                         |
| <code>fill</code>     | A named vector "Marker" and "Sample" to specify fill color of bins in the histograms.                           |

**Details**

You can draw histograms of several summary statistics of genotype counts and read counts per sample and per marker. The "stats" argument can take the following values:

**missing** Proportion of missing genotype calls.

**het** Proportion of heterozygote calls.

**raf** Reference allele frequency.

**dp** Total read counts.

**ad\_ref** Reference allele read counts.

**ad\_alt** Alternative allele read counts.

**rrf** Reference allele read frequency.

**mean\_ref** Mean of reference allele read counts.

**sd\_ref** Standard deviation of reference allele read counts.

**median\_ref** Quantile of reference allele read counts.

**mean\_alt** Mean of alternative allele read counts.

**sd\_alt** Standard deviation of alternative allele read counts.

**median\_alt** Quantile of alternative allele read counts.

**mq** Mapping quality.

**fs** Phred-scaled p-value (strand bias)

**qd** Variant Quality by Depth

**sor** Symmetric Odds Ratio (strand bias)

**mqranksom** Alt vs. Ref read mapping qualities

**readposranksom** Alt vs. Ref read position bias

**baseqranksom** Alt Vs. Ref base qualities

To draw histograms for "missing", "het", "raf", you need to run `countGenotype()` first to obtain statistics. Similarly, "dp", "ad\_ref", "ad\_alt", "rfr" requires values obtained via `countRead()`. "mq", "fs", "qd", "sor", "mqranksom", "readposranksom", and "baseqranksom" only work with `target = "marker"`, if your data contains those values supplied via SNP calling tools like [GATK](#).

### Value

A ggplot object.

### Examples

```
# Load data in the GDS file and instantiate a [GbsrGenotypeData] object.
gds_fn <- system.file("extdata", "sample.gds", package = "GBScleanR")
gds <- loadGDS(gds_fn)

# Summarize genotype count information to be used in `histGBSR()`
gds <- countGenotype(gds)

# Draw histograms of missing rate, heterozygosity, and reference
# allele frequency per SNP and per sample.
histGBSR(gds, stats = "missing")

# Close the connection to the GDS file
closeGDS(gds)
```

---

initScheme

*Build a [GbsrScheme](#) object*

---

### Description

[GBScleanR](#) uses breeding scheme information to set the expected number of cross overs in a chromosome which is a required parameter for the genotype error correction with the hidden Markov model implemented in the `estGeno()` function. This function build the object storing type crosses performed at each generation of breeding and population sizes.

**Usage**

```

initScheme(object, mating, ...)

## S4 method for signature 'GbsrGenotypeData'
initScheme(object, mating)

## S4 method for signature 'GbsrScheme'
initScheme(object, mating, parents)

```

**Arguments**

|         |  |
|---------|--|
| object  | A <a href="#">GbsrGenotypeData</a> object.   |
| mating  | An integer matrix to indicate mating combinations. The each element should match with IDs of parental samples which are 1 to N. see Details. |
| ...     | Unused.  |
| parents | Indices of parental lines.   |

**Details**

A [GbsrScheme](#) object stores information of a population size, mating combinations and a type of cross applied to each generation of the breeding process to generate the population which you are going to subject to the [estGeno\(\)](#) function. The first generation should be parents of the population. It is supposed that [setParents\(\)](#) has been already executed and parents are labeled in the [GbsrGenotypeData](#) object. The number of parents are automatically recognized. The "crosstype" of the first generation can be "pairing" or "random" with `pop_size = N`, where N is the number of parents. You need to specify a matrix indicating combinations of mating, in which each column shows a pair of parental samples. For example, if you have only two parents, the mating matrix is `mating = cbind(c(1:2))`. The indices used in the matrix should match with the IDs labeled to parental samples by [setParents\(\)](#). The created [GbsrScheme](#) object is set in the scheme slot of the [GbsrGenotypeData](#) object.

**Value**

A [GbsrGenotypeData](#) object storing a [GbsrScheme](#) object in the "scheme" slot.

**See Also**

[addScheme\(\)](#) and [showScheme\(\)](#)

**Examples**

```

# Load data in the GDS file and instantiate a [GbsrGenotypeData] object.
gds_fn <- system.file("extdata", "sample.gds", package = "GBScleanR")
gds <- loadGDS(gds_fn)

# Biparental F2 population.
gds <- setParents(gds, parents = c("Founder1", "Founder2"))

# setParents gave member ID 1 and 2 to Founder1 and Founder2, respectively.
gds <- initScheme(gds, mating = cbind(c(1:2)))

# Now the progenies of the cross above have member ID 3.
# If `crosstype = "selfing"` or `"sibling"`, you can omit a `mating` matrix.

```

```
gds <- addScheme(gds, crosstype = "self")

# Now you can execute `estGeno()` which requires a [GbsrScheme] object.

# Close the connection to the GDS file
closeGDS(gds)
```

---

isOpenGDS

*Check if a GDS file has been opened or not.*

---

### Description

Check if a GDS file has been opened or not.

### Usage

```
isOpenGDS(object, ...)

## S4 method for signature 'GbsrGenotypeData'
isOpenGDS(object)
```

### Arguments

object           A [GbsrGenotypeData](#) object.  
...               Unused.

### Value

TRUE if the GDS file linked to the input [GbsrGenotypeData](#) object has been opened, while FALSE if closed.

### Examples

```
# Use a GDS file of example data.
gds_fn <- system.file("extdata", "sample.gds", package = "GBScleanR")

# Instantiation of [GbsrGenotypeData]
gds <- loadGDS(gds_fn)

# Check connection to the GDS file
isOpenGDS(gds)

# Close the connection to the GDS file
closeGDS(gds)
```

---

|         |   |
|---------|---|
| loadGDS | <i>Load a GDS file and construct a GbsrGenotypeData object.</i> |
|---------|---|

---

### Description

Load data stored in an input GDS file to R environment and create a GbsrGenotypeData instance. GBScleanR handles only one class GbsrGenotypeData and conducts all data manipulation via class methods for it.

### Usage

```
loadGDS(x, load_filter = FALSE, ploidy = 2, verbose = TRUE)
```

### Arguments

|             |   |
|-------------|---|
| x           | A string of the path to an input GDS file or a GbsrGenotypeData object to reload.   |
| load_filter | A logical whether to load the filtering information made via <code>setSamFilter()</code> and <code>setMarFilter()</code> and saved in the GDS file via <code>closeGDS()</code> with <code>save_filter = TRUE</code> . |
| ploidy      | Set the ploidy of the population.   |
| verbose     | if TRUE, show information.  |

### Details

The first time to load a newly produced GDS file will take long time due to data reformatting for quick access. The GbsrGenotypeData object returned from `loadGDS()` can be also handled as SeqVarGDSClass of the [SeqArray](#) package.

### Value

A GbsrGenotypeData object.

### Examples

```
# Create a GDS file from a sample VCF file.
vcf_fn <- system.file("extdata", "sample.vcf", package = "GBScleanR")
gds_fn <- tempfile("sample", fileext = ".gds")
gbsrVCF2GDS(vcf_fn = vcf_fn, out_fn = gds_fn, force = TRUE)

# Load data in the GDS file and instantiate a `GbsrGenotypeData` object.
gds <- loadGDS(gds_fn)

# Reload data from the GDS file.
gds <- loadGDS(gds)

# Close the connection to the GDS file.
closeGDS(gds)
```

---

|            |   |
|------------|---|
| makeScheme | <i>Automate a <a href="#">GbsrScheme</a> object building.</i> |
|------------|---|

---

### Description

[GBScleanR](#) uses breeding scheme information to set the expected number of cross overs in a chromosome which is a required parameter for the genotype error correction with the Hidden Markov model implemented in the `estGeno()` function. This function automates the building of a [GbsrScheme](#) object.

### Usage

```
makeScheme(object, generation, crosstype, ...)
```

```
## S4 method for signature 'GbsrGenotypeData'
makeScheme(object, generation, crosstype)
```

### Arguments

|            |  |
|------------|--|
| object     | A <a href="#">GbsrGenotypeData</a> object.   |
| generation | An integer to indicate which generation of selfing or sibling-crossing your population is. |
| crosstype  | A string to indicate the type of cross conducted with a given generation.                  |
| ...        | Unused.  |

### Details

A scheme object is just a data.frame indicating a population size and a type of cross applied to each generation of the breeding process to generate the population which you are going to subject to the `estGeno()` function. The `crosstype` specified to `makeScheme()` can take "selfing" and "sibling". When your population has  $2^n$  parents specified by `setParents()`, `makeScheme()` assumes those parents were crossed in the "funnel" design in which  $2^n$  parents are crossed to obtain  $2^{n/2}$  F1 hybrids followed by successive intercrossings (pairings) of the hybrids to combine the genomes of all parents in one family of siblings. The `makeScheme()` function assumes that the parents that were assigned an odd number member ID (N) in `setParents()` had been crossed with the parent that were assigned an even number (N+1). For example, if you set parents as shown below. The `makeScheme()` function prepare a scheme information that indicates the intercrossings of "p1 x p2", "p3 x p4", "p5 x p6", and "p7 x p8" followed by crossing of "p1xp2\_F1 x p3xp4\_F1" and "p5xp6\_F1 x p7xp8\_F1" and then crossing of the two 4-way crossed liens to produce 8-way crossed hybrid lines. If, for example, `generation = 5` indicating an F5 generation was specified to `makeScheme()`, the function adds 4 successive selfing or sibling crossings in the scheme. The created [GbsrScheme](#) object will be set in the scheme slot of the [GbsrGenotypeData](#) object.

### Value

A [GbsrGenotypeData](#) object storing a [GbsrScheme](#) object in the "scheme" slot.

### See Also

[initScheme\(\)](#), [addScheme\(\)](#), and [showScheme\(\)](#)

**Examples**

```
# Load data in the GDS file and instantiate a [GbsrGenotypeData] object.
gds_fn <- system.file("extdata", "sample.gds", package = "GBScleanR")
gds <- loadGDS(gds_fn)

# Biparental F2 population.
gds <- setParents(gds, parents = c("Founder1", "Founder2"))

gds <- makeScheme(gds, generation = 2, crosstype = "self")

#####
# Now you can execute `estGeno()` which requires a [GbsrScheme] object.

# Close the connection to the GDS file
closeGDS(gds)
```

---

nmar

*Return the number of SNPs.*


---

**Description**

This function returns the number of SNPs recorded in the GDS file connected to the given [GbsrGenotypeData](#) object.

**Usage**

```
nmar(object, valid = TRUE, chr = NULL, ...)

## S4 method for signature 'GbsrGenotypeData'
nmar(object, valid, chr)
```

**Arguments**

|        |   |
|--------|---|
| object | A <a href="#">GbsrGenotypeData</a> object.        |
| valid  | A logical value. See details.                     |
| chr    | A index to specify chromosome to get information. |
| ...    | Unused.   |

**Details**

If `valid = TRUE`, the number of markers which are labeled TRUE in the "valid" column of the "marker" slot will be returned. If you need the number of over all markers, set `valid = FALSE`. [validMar\(\)](#) tells you which markers are valid.

**Value**

An integer value to indicate the number of SNP markers.

**See Also**

[validMar\(\)](#)



**Examples**

```
# Load data in the GDS file and instantiate a [GbsrGenotypeData] object.
gds_fn <- system.file("extdata", "sample.gds", package = "GBScleanR")
gds <- loadGDS(gds_fn)

nmar(gds)

# Close the connection to the GDS file.
closeGDS(gds)
```

---

|      |                                      |
|------|--------------------------------------|
| nsam | <i>Return the number of samples.</i> |
|------|--------------------------------------|

---

**Description**

This function returns the number of samples recorded in the GDS file connected to the given [GbsrGenotypeData](#) object.

**Usage**

```
nsam(object, valid = TRUE, parents = FALSE, ...)

## S4 method for signature 'GbsrGenotypeData'
nsam(object, valid, parents)
```

**Arguments**

|         |  |
|---------|--|
| object  | A <a href="#">GbsrGenotypeData</a> object.                     |
| valid   | A logical value. See details.                                  |
| parents | A logical value whether to include to parental samples or not. |
| ...     | Unused.  |

**Details**

If `valid = TRUE`, the number of the samples which are labeled TRUE in the "valid" column of the "sample" slot will be returned. If you need the number of over all samples, set `valid = FALSE`. [validSam\(\)](#) tells you which samples are valid.

**Value**

An integer value to indicate the number of samples.

**See Also**

[validSam\(\)](#)

**Examples**

```
# Load data in the GDS file and instantiate a [GbsrGenotypeData] object.
gds_fn <- system.file("extdata", "sample.gds", package = "GBScleanR")
gds <- loadGDS(gds_fn)

nsam(gds)

# Close the connection to the GDS file.
closeGDS(gds)
```

pairsGBSR

*Draw a scatter plot of a pair of specified statistics***Description**

Draw a scatter plot of a pair of specified statistics

**Usage**

```
pairsGBSR(
  x,
  stats1 = "dp",
  stats2 = "missing",
  target = "marker",
  size = 0.5,
  alpha = 0.8,
  color = c(Marker = "darkblue", Sample = "darkblue"),
  fill = c(Marker = "skyblue", Sample = "skyblue"),
  smooth = FALSE
)
```

**Arguments**

|        |  |
|--------|--|
| x      | A <a href="#">GbsrGenotypeData</a> object.   |
| stats1 | A string to specify statistics to be drawn.  |
| stats2 | A string to specify statistics to be drawn.  |
| target | Either or both of "marker" and "sample", e.g. target = "marker" to draw a histogram only for SNPs.   |
| size   | A numeric value to specify the dot size of a scatter plot.   |
| alpha  | A numeric value [0-1] to specify the transparency of dots in a scatter plot.   |
| color  | A named vector "Marker" and "Sample" to specify border color of bins in the histograms.  |
| fill   | A named vector "Marker" and "Sample" to specify fill color of bins in the histograms. stats = "geno" only requires "Ref", "Het" and "Alt", while others uses the value named "Marker". |
| smooth | A logical value to indicate whether draw a smooth line for data points. See also <a href="#">ggplot2::stat_smooth()</a> .  |

## Details

You can draw a scatter plot of per-marker and/or per-sample summary statistics specified at `stats1` and `stats2`. The "stats1" and "stats2" arguments can take the following values:

**missing** Proportion of missing genotype calls.  
**het** Proportion of heterozygote calls.  
**raf** Reference allele frequency.  
**dp** Total read counts.  
**ad\_ref** Reference allele read counts.  
**ad\_alt** Alternative allele read counts.  
**rrf** Reference allele read frequency.  
**mean\_ref** Mean of reference allele read counts.  
**sd\_ref** Standard deviation of reference allele read counts.  
**median\_ref** Quantile of reference allele read counts.  
**mean\_alt** Mean of alternative allele read counts.  
**sd\_alt** Standard deviation of alternative allele read counts.  
**median\_alt** Quantile of alternative allele read counts.  
**mq** Mapping quality.  
**fs** Phred-scaled p-value (strand bias)  
**qd** Variant Quality by Depth  
**sor** Symmetric Odds Ratio (strand bias)  
**mqranks** Alt vs. Ref read mapping qualities  
**readposranks** Alt vs. Ref read position bias  
**baseqranks** Alt Vs. Ref base qualities

To draw scatter plots for "missing", "het", "raf", you need to run `countGenotype()` first to obtain statistics. Similarly, "dp", "ad\_ref", "ad\_alt", "rrf" requires values obtained via `countRead()`. "mq", "fs", "qd", "sor", "mqranks", "readposranks", and "baseqranks" only work with `target = "marker"`, if your data contains those values supplied via SNP calling tools like [GATK](#).

## Value

A ggplot object.

## Examples

```
# Load data in the GDS file and instantiate a [GbsrGenotypeData] object.
gds_fn <- system.file("extdata", "sample.gds", package = "GBScleanR")
gds <- loadGDS(gds_fn)

# Summarize genotype count information to be used in `pairsGBSR()`
gds <- countGenotype(gds)

# Draw scatter plots of missing rate vs heterozygosity.
pairsGBSR(gds, stats1 = "missing", stats2 = "het")

# Close the connection to the GDS file
closeGDS(gds)
```

---

plotDosage

*Draw line plots of allele dosage per marker per sample.*


---

### Description

This function counts a reference allele dosage per marker per sample and draw line plots of them in facets for each chromosome for each sample.

### Usage

```
plotDosage(
  x,
  coord = NULL,
  chr = NULL,
  ind = 1,
  node = "raw",
  showratio = TRUE,
  dot_fill = c("green", "darkblue"),
  size = 0.8,
  alpha = 0.8,
  line_color = "magenta"
)
```

### Arguments

|            |   |
|------------|---|
| x          | A <a href="#">GbsrGenotypeData</a> object.  |
| coord      | A vector with two integer specifying the number of rows and columns to draw faceted line plots for chromosomes.   |
| chr        | A vector of indexes to specify chromosomes to be drawn.   |
| ind        | An index to specify samples to be drawn.  |
| node       | Either one of "raw" or "filt" to output raw read data, or filtered read data, respectively.   |
| showratio  | If TRUE, draw dots indicating read ratio.   |
| dot_fill   | A vector of two strings to indicate the dot colors in the plot. The first and second elements of the vector are set as the colors for the lowest and highest values in the gradient coloring of the dots indicating total read counts par marker. |
| size       | A positive number to indicate the dot size in a plot.   |
| alpha      | A positive number in 0-1 to indicate the dot opacity in a plot.   |
| line_color | A string to indicate the line color in the plot.  |

### Value

A ggplot object.

**Examples**

```
# Load data in the GDS file and instantiate a [GbsrGenotypeData] object.
gds_fn <- system.file("extdata", "sample.gds", package = "GBScleanR")
gds <- loadGDS(gds_fn)

plotDosage(gds, ind = 1)

# Close the connection to the GDS file
closeGDS(gds)
```

plotGBSR

*Draw line plots of specified statistics***Description**

Draw line plots of specified statistics

**Usage**

```
plotGBSR(
  x,
  stats = c("dp", "missing", "het"),
  coord = NULL,
  lwd = 0.5,
  binwidth = NULL,
  color = c(Marker = "darkblue", Ref = "darkgreen", Het = "magenta", Alt = "blue")
)
```

**Arguments**

|                       |  |
|-----------------------|--|
| <code>x</code>        | A <a href="#">GbsrGenotypeData</a> object.   |
| <code>stats</code>    | A string to specify statistics to be drawn.  |
| <code>coord</code>    | A vector with two integer specifying the number of rows and columns to draw faceted line plots for chromosomes.  |
| <code>lwd</code>      | A numeric value to specify the line width in plots.  |
| <code>binwidth</code> | An integer to specify bin width of the histogram. This argument only work with <code>stats = "marker"</code> and is passed to the <code>ggplot</code> function.                            |
| <code>color</code>    | A strings vector named "Marker", "Ref", "Het", "Alt" to specify line colors. <code>stats = "geno"</code> only requires "Ref", "Het" and "Alt", while others uses the value named "Marker". |

**Details**

You can draw line plots of several summary statistics of genotype counts and read counts per sample and per marker. The "stats" argument can take the following values:

**marker** Marker density.

**geno** Proportion of missing genotype calls.

**missing** Proportion of missing genotype calls.

**het** Proportion of heterozygote calls.  
**raf** Reference allele frequency.  
**dp** Total read counts.  
**ad\_ref** Reference allele read counts.  
**ad\_alt** Alternative allele read counts.  
**rrf** Reference allele read frequency.  
**mean\_ref** Mean of reference allele read counts.  
**sd\_ref** Standard deviation of reference allele read counts.  
**median\_ref** Quantile of reference allele read counts.  
**mean\_alt** Mean of alternative allele read counts.  
**sd\_alt** Standard deviation of alternative allele read counts.  
**median\_alt** Quantile of alternative allele read counts.  
**mq** Mapping quality.  
**fs** Phred-scaled p-value (strand bias)  
**qd** Variant Quality by Depth  
**sor** Symmetric Odds Ratio (strand bias)  
**mqranks** Alt vs. Ref read mapping qualities  
**readposranks** Alt vs. Ref read position bias  
**baseqranks** Alt Vs. Ref base qualities

To draw line plots for "missing", "het", "raf", you need to run `countGenotype()` first to obtain statistics. Similarly, "dp", "ad\_ref", "ad\_alt", "rrf" requires values obtained via `countRead()`. "mq", "fs", "qd", "sor", "mqranks", "readposranks", "#", and "baseqranks" only work with target = "marker", if your data contains those values supplied via SNP calling tools like **GATK**.

## Value

A ggplot object.

## Examples

```
# Load data in the GDS file and instantiate a [GbsrGenotypeData] object.
gds_fn <- system.file("extdata", "sample.gds", package = "GBScleanR")
gds <- loadGDS(gds_fn)

# Summarize genotype count information to be used in `plotGBSR()`
gds <- countGenotype(gds)

# Draw line plots of missing rate, heterozygosity, proportion of genotype
# calls per SNP.
plotGBSR(gds, stats = "missing")

# Close the connection to the GDS file
closeGDS(gds)
```

---

|               |   |
|---------------|---|
| plotReadRatio | <i>Draw line plots of proportion of reference allele read counts per marker per sample.</i> |
|---------------|---|

---

### Description

This function calculate a proportion of reference allele read counts per marker per sample and draw line plots of them in facets for each chromosome for each sample.

### Usage

```
plotReadRatio(
  x,
  coord = NULL,
  chr = NULL,
  ind = 1,
  node = "raw",
  dot_fill = c("green", "darkblue"),
  size = 0.8,
  alpha = 0.8
)
```

### Arguments

|          |   |
|----------|---|
| x        | A <a href="#">GbsrGenotypeData</a> object.  |
| coord    | A vector with two integer specifying the number of rows and columns to draw faceted line plots for chromosomes.   |
| chr      | A vector of indexes to specify chromosomes to be drawn.   |
| ind      | A string of sample id or an index to specify the sample to be drawn.  |
| node     | Either one of "raw" or "filt" to output raw read data, or filtered read data, respectively.   |
| dot_fill | A vector of two strings to indicate the dot colors in the plot. The first and second elements of the vector are set as the colors for the lowest and highest values in the gradient coloring of the dots indicating total read counts par marker. |
| size     | A positive number to indicate the dot size in the plot.   |
| alpha    | A positive number in 0-1 to indicate the dot opacity in the plot.   |

### Value

A ggplot object.

### Examples

```
# Load data in the GDS file and instantiate a [GbsrGenotypeData] object.
gds_fn <- system.file("extdata", "sample.gds", package = "GBScleanR")
gds <- loadGDS(gds_fn)

plotReadRatio(gds, ind = 1)

# Close the connection to the GDS file
```

```
closeGDS(gds)
```

---

```
reopenGDS
```

```
Reopen the connection to the GDS file.
```

---

## Description

Reopen the connection to the GDS file.

## Usage

```
reopenGDS(object, ...)
```

```
## S4 method for signature 'GbsrGenotypeData'  
reopenGDS(object)
```

## Arguments

|        |  |
|--------|--|
| object | A <a href="#">GbsrGenotypeData</a> object. |
| ...    | Unused.                                    |

## Details

The `GbsrGenotypeData` object stores the file path of the GDS file even after closing the connection to the file. This function opens again the connection to the GDS file at the file path stored in the `GbsrGenotypeData` object. If the `GbsrGenotypeData` object already has an open connection to the GDS file, this function will reopen the connection. The data stored in the marker and sample slots will not be changed. Thus, you can open a connection with the GDS file while keeping information of filtering and summary statistics.

## Value

A [GbsrGenotypeData](#) object.

## Examples

```
# Use a GDS file of example data.  
gds_fn <- system.file("extdata", "sample.gds", package = "GBScanR")  
  
# Instantiation of [GbsrGenotypeData]  
gds <- loadGDS(gds_fn)  
  
# Close the connection to the GDS file  
closeGDS(gds)  
  
gds <- reopenGDS(gds)  
  
# Close the connection to the GDS file  
closeGDS(gds)
```



---

|                 |  |
|-----------------|--|
| resetCallFilter | <i>Set the original data to be used in GBScleanR's functions</i> |
|-----------------|--|

---

## Description

Set the "genotype" node and the "data" node as primary nodes for genotype data and read count data. The data stored in the primary nodes are used in the functions of GBScleanR.

## Usage

```
resetCallFilter(object, ...)

## S4 method for signature 'GbsrGenotypeData'
resetCallFilter(object)
```

## Arguments

|        |  |
|--------|--|
| object | A <a href="#">GbsrGenotypeData</a> object. |
| ...    | Unused.                                    |

## Details

A [GbsrGenotypeData](#) object storing information of the primary node of genotype data and read count data. All of the functions implemented in [GBScleanR](#) check the primary nodes and use data stored in those nodes. [setCallFilter\(\)](#) create new nodes storing filtered genotype calls and read counts in a GDS file and change the primary nodes to "filt.genotype" and "filt.data" for genotype and read count data, respectively. [resetCallFilter\(\)](#) set back the nodes to the original, those are "genotype" and "data" for genotype and read count data, respectively.

## Value

A [GbsrGenotypeData](#) object.

## Examples

```
# Create a GDS file from a sample VCF file.
vcf_fn <- system.file("extdata", "sample.vcf", package = "GBScleanR")
gds_fn <- tempfile("sample", fileext = ".gds")
gbsrVCF2GDS(vcf_fn = vcf_fn, out_fn = gds_fn, force = TRUE)

# Load data in the GDS file and instantiate a [GbsrGenotypeData] object.
gds <- loadGDS(gds_fn)

# Filter out set zero to read counts and
# missing to genotype calls of which meet the criteria.
gds <- setCallFilter(gds, dp_count = c(5, Inf))

# Now any functions of [GBScleanR] reference the genotype data
# stored in the "filt.genotype" node of the GDS file.

# If you need to set the "genotype" node, where store the raw genotype data
# as genotype to be referenced by the functions of GBScleanR,
# run the following.
```

```

gds <- resetCallFilter(gds)

# Reopening the connection to the GDS file also set the raw genotype again.
gds <- loadGDS(gds)

# Close the connection to the GDS file
closeGDS(gds)

```

---

|             |   |
|-------------|---|
| resetFilter | <i>Reset all filters made by <a href="#">setSamFilter()</a>, <a href="#">setMarFilter()</a>, and <a href="#">setCallFilter()</a>.</i> |
|-------------|---|

---

### Description

Return all data intact.

### Usage

```

resetFilter(object, ...)

## S4 method for signature 'GbsrGenotypeData'
resetFilter(object)

```

### Arguments

|        |  |
|--------|--|
| object | A <a href="#">GbsrGenotypeData</a> object. |
| ...    | Unused.                                    |

### Value

A [GbsrGenotypeData](#) object after removing all filters.  
A [GbsrGenotypeData](#) object after removing all filters on markers.

### Examples

```

# Create a GDS file from a sample VCF file.
vcf_fn <- system.file("extdata", "sample.vcf", package = "GBScleanR")
gds_fn <- tempfile("sample", fileext = ".gds")
gbsrVCF2GDS(vcf_fn = vcf_fn, out_fn = gds_fn, force = TRUE)

# Load data in the GDS file and instantiate a [GbsrGenotypeData] object.
gds <- loadGDS(gds_fn)

# `setCallFilter()` do not require summarized information of
# genotype counts and read counts.
gds <- setCallFilter(gds, dp_count = c(5, Inf))

# `setSamFilter()` and `setMarFilter()` needs information of
# the genotype count summary and the read count summary.
gds <- countGenotype(gds)
gds <- countRead(gds)

gds <- setSamFilter(gds,

```

```

        id = getSamID(gds)[1:10],
        missing = 0.2,
        dp = c(5, Inf))

gds <- setMarFilter(gds,
                  id = getMarID(gds)[1:100],
                  missing = 0.2,
                  dp = c(5, Inf))

gds <- setInfoFilter(gds, mq = 40, qd = 20)

# Reset all filters applied above.
gds <- resetFilter(gds)

# Close the connection to the GDS file.
closeGDS(gds)

```

---

|                |  |
|----------------|--|
| resetMarFilter | <i>Reset the filter made by <a href="#">setMarFilter()</a></i> |
|----------------|--|

---

## Description

Remove "invalid" labels put on markers and make all markers valid.

## Usage

```

resetMarFilter(object, ...)

## S4 method for signature 'GbsrGenotypeData'
resetMarFilter(object)

```

## Arguments

|        |  |
|--------|--|
| object | A <a href="#">GbsrGenotypeData</a> object. |
| ...    | Unused.                                    |

## Value

A [GbsrGenotypeData](#) object after removing all filters on markers.

## Examples

```

# Load data in the GDS file and instantiate a [GbsrGenotypeData] object.
gds_fn <- system.file("extdata", "sample.gds", package = "GBScleanR")
gds <- loadGDS(gds_fn)

# Check the number of markers.
nmar(gds)

# Summarize the information needed for filtering.
gds <- countGenotype(gds)
gds <- countRead(gds)

```

```

# filter out some markers meeting the criteria.
gds <- setMarFilter(gds,
                   id = getMarID(gds)[1:100],
                   missing = 0.2,
                   dp = c(5, Inf))

# Check the number of the retained markers.
nmar(gds)

# Reset all filters applied above.
gds <- resetMarFilter(gds)

# Check the number of the markers again.
nmar(gds)

# Close the connection to the GDS file.
closeGDS(gds)

```

---

|                |  |
|----------------|--|
| resetSamFilter | <i>Reset the filter made by <a href="#">setSamFilter()</a></i> |
|----------------|--|

---

## Description

Remove "invalid" labels put on samples and make all samples valid.

## Usage

```

resetSamFilter(object, ...)

## S4 method for signature 'GbsrGenotypeData'
resetSamFilter(object)

```

## Arguments

|        |  |
|--------|--|
| object | A <a href="#">GbsrGenotypeData</a> object. |
| ...    | Unused.                                    |

## Value

A [GbsrGenotypeData](#) object after removing all filters on samples.

## Examples

```

# Create a GDS file from a sample VCF file.
vcf_fn <- system.file("extdata", "sample.vcf", package = "GBScleanR")
gds_fn <- tempfile("sample", fileext = ".gds")
gbsrVCF2GDS(vcf_fn = vcf_fn, out_fn = gds_fn, force = TRUE)

# Load data in the GDS file and instantiate a [GbsrGenotypeData] object.
gds <- loadGDS(gds_fn)

# Summarize the information needed for filtering.
gds <- countGenotype(gds)

```

```

gds <- countRead(gds)

gds <- setSamFilter(gds,
                   id = getSamID(gds)[1:10],
                   missing = 0.2,
                   dp = c(5, Inf))

# Reset all filters applied above.
gds <- resetSamFilter(gds)

# Close the connection to the GDS file
closeGDS(gds)

```

---

|               |   |
|---------------|---|
| setCallFilter | <i>Filter out each genotype call meeting criteria</i> |
|---------------|---|

---

### Description

Perform filtering of each genotype call, neither markers nor samples. Each genotype call is supported by its read counts for the reference allele and the alternative allele of a marker of a sample. `setCallFilter()` set missing to the genotype calls which are not reliable enough and set zero to reference and alternative read counts of the genotype calls.

### Usage

```

setCallFilter(
  object,
  dp_count = c(0, Inf),
  ref_count = c(0, Inf),
  alt_count = c(0, Inf),
  dp_qtile = c(0, 1),
  ref_qtile = c(0, 1),
  alt_qtile = c(0, 1),
  ...
)

## S4 method for signature 'GbsrGenotypeData'
setCallFilter(
  object,
  dp_count,
  ref_count,
  alt_count,
  dp_qtile,
  ref_qtile,
  alt_qtile
)

```

### Arguments

`object` A [GbsrGenotypeData](#) object.

|           |   |
|-----------|---|
| dp_count  | A numeric vector with length two specifying lower and upper limit of total read counts (reference reads + alternative reads). |
| ref_count | A numeric vector with length two specifying lower and upper limit of reference read counts.                                   |
| alt_count | A numeric vector with length two specifying lower and upper limit of alternative read counts.                                 |
| dp_qtile  | A numeric vector with length two specifying lower and upper limit of quantile of total read counts in each sample.            |
| ref_qtile | A numeric vector with length two specifying lower and upper limit of quantile of reference read counts in each sample.        |
| alt_qtile | A numeric vector with length two specifying lower and upper limit of quantile of alternative read counts in each sample.      |
| ...       | Unused.   |

### Details

dp\_qtile, ref\_qtile, and alt\_qtile use quantile values of read counts of each sample to decide the lower and upper limit of read counts. This function generate two new nodes in the GDS file linked with the given [GbsrGenotypeData](#) object. The filtered read counts and genotype calls will be stored in the data node in the "FAD" folder and the data node in the "FGT" folder, while the data node in the "CFT" stores call filtering informatin. To reset the filter applied by setCallFilter(), run [resetCallFilter\(\)](#).

### Value

A [GbsrGenotypeData](#) object with filters on genotype calls.

### Examples

```
# Create a GDS file from a sample VCF file.
vcf_fn <- system.file("extdata", "sample.vcf", package = "GBScleanR")
gds_fn <- tempfile("sample", fileext = ".gds")
gbsrVCF2GDS(vcf_fn = vcf_fn, out_fn = gds_fn, force = TRUE)

# Load data in the GDS file and instantiate a [GbsrGenotypeData] object.
gds <- loadGDS(gds_fn)

# Filter out genotype calls supported by less than 5 reads.
gds <- setCallFilter(gds, dp_count = c(5, Inf))

# Filter out genotype calls supported by reads less than
# the 20 percentile of read counts per marker in each sample.
gds <- setCallFilter(gds, dp_qtile = c(0.2, 1))

# Reset the filter
gds <- resetCallFilter(gds)

# Close the connection to the GDS file.
closeGDS(gds)
```

---

|              |                                     |
|--------------|-------------------------------------|
| setFixedBias | <i>Set fixed allele read biases</i> |
|--------------|-------------------------------------|

---

### Description

Set fixed allele read biases of valid markers

### Usage

```
setFixedBias(object, bias, ...)

## S4 method for signature 'GbsrGenotypeData'
setFixedBias(object, bias)
```

### Arguments

|        |  |
|--------|--|
| object | A <a href="#">GbsrGenotypeData</a> object.   |
| bias   | A numeric vector of fixed allele read biases to be assigned to valid markers. The length of bias vector should match the number of valid markers. The values in the bias vector are assigned to the valid markers according to their order. NAs in the bias vector indicates non-fixed biases. |
| ...    | Unused.  |

### Details

Since the bias set by `setFixedBias()` function is the reference allele read bias. Thus, the values 0 and 1 mean that the marker only gives alternative and reference allele reads, respectively. Set these fixed biases if some of your markers are dominant markers.

### Value

A [GbsrGenotypeData](#) object after adding dominant marker information

### Examples

```
# Create a GDS file from a sample VCF file.
vcf_fn <- system.file("extdata", "sample.vcf", package = "GBScleanR")
gds_fn <- tempfile("sample", fileext = ".gds")
gbsrVCF2GDS(vcf_fn = vcf_fn, out_fn = gds_fn, force = TRUE)

# Load data in the GDS file and instantiate a [GbsrGenotypeData] object.
gds <- loadGDS(gds_fn)

# Set fixed allele read biases.
# Initialize the bias vector to be assigned.
bias <- rep(NA, nmar(gds))

# As an example, select 20 markers randomly and assign 0 or 1 to them.
# Since the bias set by setFixedBias() function is the reference allele read
# bias. Thus, the values 0 and 1 means that the marker only gives alternative
# and reference allele reads, respectively.
# Set these fixed biases if some of your markers are dominant markers.
```

```

bias[sample(seq_along(bias), 20)] <- sample(c(0, 1), 20, replace = TRUE)

gds <- setFixedBias(gds, bias = bias)

# Close the connection to the GDS file
closeGDS(gds)

```

---

setInfoFilter

*Filter out markers based on marker quality metrics*


---

### Description

A VCF file usually has marker quality metrics in the INFO field and those are stored in a GDS file created via [GBScleanR](#). This function filters out markers based on those marker quality metrics.

### Usage

```

setInfoFilter(
  object,
  mq = 0,
  fs = Inf,
  qd = 0,
  sor = Inf,
  mqranks = c(-Inf, Inf),
  readposranks = c(-Inf, Inf),
  baseqranks = c(-Inf, Inf),
  ...
)

## S4 method for signature 'GbsrGenotypeData'
setInfoFilter(object, mq, fs, qd, sor, mqranks, readposranks, baseqranks)

```

### Arguments

|              |  |
|--------------|--|
| object       | A <a href="#">GbsrGenotypeData</a> object.   |
| mq           | A numeric value to specify minimum mapping quality (shown as MQ in the VCF format).  |
| fs           | A numeric value to specify maximum Phred-scaled p-value (strand bias) (shown as FS in the VCF format).                               |
| qd           | A numeric value to specify minimum Variant Quality by Depth (shown as QD in the VCF format).   |
| sor          | A numeric value to specify maximum Symmetric Odds Ratio (strand bias) (shown as SOR in the VCF format).                              |
| mqranks      | A numeric values to specify the lower and upper limit of Alt vs. Ref read mapping qualities (shown as MQRankSum in the VCF format).  |
| readposranks | A numeric values to specify the lower and upper limit of Alt vs. Ref read position bias (shown as ReadPosRankSum in the VCF format). |
| baseqranks   | A numeric values to specify the lower and upper limit of Alt Vs. Ref base qualities (shown as BaseQRankSum in the VCF format).       |
| ...          | Unused.  |



**Details**

Detailed explanation of each metric can be found in [GATK's web site](#).

**Value**

A [GbsrGenotypeData](#) object with filters on markers.

**Examples**

```
# Load data in the GDS file and instantiate a [GbsrGenotypeData] object.
gds_fn <- system.file("extdata", "sample.gds", package = "GBScleanR")
gds <- loadGDS(gds_fn)

gds <- setInfoFilter(gds, mq = 40, qd = 20)

# Close the connection to the GDS file.
closeGDS(gds)
```

---

setMarFilter

*Filter out markers*


---

**Description**

Search markers which do not meet the criteria and label them as "invalid".

**Usage**

```
setMarFilter(
  object,
  id = NA_integer_,
  missing = 1,
  het = c(0, 1),
  mac = 0,
  maf = 0,
  ad_ref = c(0, Inf),
  ad_alt = c(0, Inf),
  dp = c(0, Inf),
  mean_ref = c(0, Inf),
  mean_alt = c(0, Inf),
  sd_ref = Inf,
  sd_alt = Inf,
  ...
)

## S4 method for signature 'GbsrGenotypeData'
setMarFilter(
  object,
  id,
  missing,
  het,
  mac,
  maf,
```

```

    ad_ref,
    ad_alt,
    dp,
    mean_ref,
    mean_alt,
    sd_ref,
    sd_alt
  )

```

### Arguments

|          |   |
|----------|---|
| object   | A <a href="#">GbsrGenotypeData</a> object.  |
| id       | A vector of integers matching with snp ID which can be retrieve by <code>getMarID()</code> . The markers with the specified IDs will be filtered out. |
| missing  | A numeric value [0-1] to specify the maximum missing genotype call rate per marker  |
| het      | A numeric vector with length two [0-1] to specify the minimum and maximum heterozygous genotype call rate per marker                                  |
| mac      | A integer value to specify the minimum minor allele count per marker  |
| maf      | A numeric value to specify the minimum minor allele frequency per marker.   |
| ad_ref   | A numeric vector with length two specifying lower and upper limit of reference read counts per marker.  |
| ad_alt   | A numeric vector with length two specifying lower and upper limit of alternative read counts per marker.  |
| dp       | A numeric vector with length two specifying lower and upper limit of total read counts per marker.  |
| mean_ref | A numeric vector with length two specifying lower and upper limit of mean of reference read counts per marker.  |
| mean_alt | A numeric vector with length two specifying lower and upper limit of mean of alternative read counts per marker.                                      |
| sd_ref   | A numeric value specifying the upper limit of standard deviation of reference read counts per marker.   |
| sd_alt   | A numeric value specifying the upper limit of standard deviation of alternative read counts per marker.   |
| ...      | Unused.   |

### Details

For `mean_ref`, `mean_alt`, `sd_ref`, and `sd_alt`, this function calculate mean and standard deviation of reads obtained for samples at each SNP marker. If a mean read counts of a marker was smaller than the specified lower limit or larger than the upper limit, this function labels the marker as "invalid". In the case of `sd_ref` and `sd_alt`, standard deviations of read counts of each marker are checked and the markers having a larger standard deviation will be labeled as "invalid". To check valid and invalid markers, run `validMar()`.

### Value

A [GbsrGenotypeData](#) object with filters on markers.

**Examples**

```
# Load data in the GDS file and instantiate a [GbsrGenotypeData] object.
gds_fn <- system.file("extdata", "sample.gds", package = "GBScleanR")
gds <- loadGDS(gds_fn)

# Summarize the information needed for filtering.
gds <- countGenotype(gds)
gds <- countRead(gds)

gds <- setMarFilter(gds,
                   id = getMarID(gds)[1:100],
                   missing = 0.2,
                   dp = c(5, Inf))

# Close the connection to the GDS file.
closeGDS(gds)
```

---

setParents

*Set labels to samples which should be recognized as parents of the population to be subjected to error correction.*

---

**Description**

Specify two or more samples in the dataset as parents of the population. Markers will be filtered out up on your specification.

**Usage**

```
setParents(object, parents, nonmiss = FALSE, mono = FALSE, bi = FALSE, ...)

## S4 method for signature 'GbsrGenotypeData'
setParents(object, parents, nonmiss, mono, bi)
```

**Arguments**

|         |   |
|---------|---|
| object  | A <a href="#">GbsrGenotypeData</a> object.  |
| parents | A vector of strings with at least length two. The specified strings should match with the samples ID available via <a href="#">getSamID()</a> . |
| nonmiss | A logical value whether to filter out markers which are missing in parents.   |
| mono    | A logical value whether to filter out markers which are not monomorphic in parents.   |
| bi      | A logical value whether to filter out markers which are not biallelic between parents.  |
| ...     | Unused.   |

## Details

The clean function of [GBScleanR](#) uses read count information of samples and their parents separately to estimate most probable genotype calls of them. Therefore, you must specify proper samples as parents via this function. If you would like to remove SNP markers which are not biallelic and/or not monomorphic in each parent, set `mono = TRUE` and `bi = TRUE`. The replicates of parental samples specified to the `repliate` argument of `setParents()` will have the same genotypes at all markers in the estimated genotypes obtained via `estGeno()`. In the genotype estimation by `estGeno()`, the Viterbi scores for each possible genotype at each marker for the replicates will be replaced with the average score for the replicates.

## Value

A [GbsrGenotypeData](#) object with parents information.

## Examples

```
# Load data in the GDS file and instantiate a [GbsrGenotypeData] object.
gds_fn <- system.file("extdata", "sample.gds", package = "GBScleanR")
gds <- loadGDS(gds_fn)

# Find the IDs of parental samples.
parents <- grep("Founder", getSamID(gds), value = TRUE)

# Set the parents and flip allele information
# if the reference sample (Founder1 in our case) has homozygous
# alternative genotype at some markers of which alleles will
# be swapped to make the reference sample have homozygous
# reference genotype.
gds <- setParents(gds, parents = parents)

# Initialize a scheme object stored in the slot of the GbsrGenotypeData.
# We chose `crosstype = "pair"` because two inbred founders were mated
# in our breeding scheme.
# We also need to specify the mating matrix which has two rows and
# one column with integers 1 and 2 indicating a sample (founder)
# with the memberID 1 and a sample (founder) with the memberID 2
# were mated.
gds <- initScheme(gds, mating = cbind(c(1:2)))

# Add information of the next cross conducted in our scheme.
# We chose 'crosstype = "selfing"', which do not require a
# mating matrix.
gds <- addScheme(gds, crosstype = "selfing")

# Execute error correction by estimating genotype and haplotype of
# founders and offspring.
gds <- estGeno(gds)

# Close the connection to the GDS file.
closeGDS(gds)
```

---

|               |   |
|---------------|---|
| setReplicates | <i>Set identifiers to indicates which samples are replicates.</i> |
|---------------|---|

---

### Description

Not implemented yet. This function assign identifiers that indicates which samples are replicates those which should have the same genotypes at all markers.

### Usage

```
setReplicates(object, replicates, ...)

## S4 method for signature 'GbsrGenotypeData'
setReplicates(object, replicates)
```

### Arguments

|            |   |
|------------|---|
| object     | A <a href="#">GbsrGenotypeData</a> object.  |
| replicates | A vector of integers, numbers, or characters to indicate grouping of samples as replicates. |
| ...        | Unused.   |

### Details

The replicates of samples specified in [setReplicates\(\)](#) will have the same genotypes at all markers in the estimated genotypes obtained via [estGeno\(\)](#). In the genotype estimation by [estGeno\(\)](#), the Viterbi scores for each possible genotype (haplotype) at each marker for the replicates will be replaced with the average score for the replicates.

### Value

A [GbsrGenotypeData](#) object with genotype count information.

### Examples

```
# Load data in the GDS file and instantiate a [GbsrGenotypeData] object.
gds_fn <- system.file("extdata", "sample.gds", package = "GBScleanR")
gds <- loadGDS(gds_fn)

gds <- setParents(gds, parents = c("Founder1", "Founder2"))

# When your data has 100 samples, two replicates for each offspring,
# and the samples are ordered as the 1st replicate followed by the 2nd
# replicate, you can specify replicates as below.
# gds <- setReplicates(gds, replicates = rep(1:50, each = 2))

# If you need to confirm the order of samples, run the following code.
# id <- getSamID(gds)

# Replicate IDs should be set also to parents. Therefore, please include

# Close the connection to the GDS file.
```

```
closeGDS(gds)
```

---

```
setSamFilter          Filter out samples
```

---

### Description

Search samples which do not meet the criteria and label them as "invalid".

### Usage

```
setSamFilter(
  object,
  id = NA_character_,
  missing = 1,
  het = c(0, 1),
  mac = 0,
  maf = 0,
  ad_ref = c(0, Inf),
  ad_alt = c(0, Inf),
  dp = c(0, Inf),
  mean_ref = c(0, Inf),
  mean_alt = c(0, Inf),
  sd_ref = Inf,
  sd_alt = Inf,
  ...
)

## S4 method for signature 'GbsrGenotypeData'
setSamFilter(
  object,
  id,
  missing,
  het,
  mac,
  maf,
  ad_ref,
  ad_alt,
  dp,
  mean_ref,
  mean_alt,
  sd_ref,
  sd_alt
)
```

### Arguments

|        |   |
|--------|---|
| object | A <a href="#">GbsrGenotypeData</a> object.  |
| id     | A vector of strings matching with sample ID which can be retrieve by <code>getSamID()</code> . The samples with the specified IDs will be filtered out. |

|          |   |
|----------|---|
| missing  | A numeric value [0-1] to specify the maximum missing genotype call rate per sample.                                 |
| het      | A vector of two numeric values [0-1] to specify the minimum and maximum heterozygous genotype call rate per sample. |
| mac      | A integer value to specify the minimum minor allele count per sample.   |
| maf      | A numeric value to specify the minimum minor allele frequency per sample.   |
| ad_ref   | A numeric vector with length two specifying lower and upper limit of reference read counts per sample.              |
| ad_alt   | A numeric vector with length two specifying lower and upper limit of alternative read counts per sample.            |
| dp       | A numeric vector with length two specifying lower and upper limit of total read counts per sample.                  |
| mean_ref | A numeric vector with length two specifying lower and upper limit of mean of reference read counts per sample.      |
| mean_alt | A numeric vector with length two specifying lower and upper limit of mean of alternative read counts per sample.    |
| sd_ref   | A numeric value specifying the upper limit of standard deviation of reference read counts per sample.               |
| sd_alt   | A numeric value specifying the upper limit of standard deviation of alternative read counts per sample.             |
| ...      | Unused.   |

### Details

For `mean_ref`, `mean_alt`, `sd_ref`, and `sd_alt`, this function calculate mean and standard deviation of reads obtained at SNP markers of each sample. If a mean read counts of a sample was smaller than the specified lower limit or larger than the upper limit, this function labels the sample as "invalid". In the case of `sd_ref` and `sd_alt`, standard deviations of read counts of each sample are checked and the samples having a larger standard deviation will be labeled as "invalid". To check valid and invalid samples, run `validSam()`.

### Value

A `GbsrGenotypeData` object with filters on samples.

### Examples

```
# Load data in the GDS file and instantiate a [GbsrGenotypeData] object.
gds_fn <- system.file("extdata", "sample.gds", package = "GBScleanR")
gds <- loadGDS(gds_fn)

# Summarize the information needed for filtering.
gds <- countGenotype(gds)
gds <- countRead(gds)

gds <- setSamFilter(gds,
  id = getSamID(gds)[1:10],
  missing = 0.2,
  dp = c(5, Inf))

# Close the connection to the GDS file.
```

```
closeGDS(gds)
```

---

```
showScheme          Show the information stored in a GbsrScheme object
```

---

## Description

Print the information of each generation in a [GbsrScheme](#) object in the scheme slot of a [GbsrGenotypeData](#) object. A [GbsrScheme](#) object stores information of a population size, mating combinations and a type of cross applied to each generation of the breeding process to generate the population which you are going to subject to the `estGeno()` function.

## Usage

```
showScheme(object, ...)

## S4 method for signature 'GbsrGenotypeData'
showScheme(object)

## S4 method for signature 'GbsrScheme'
showScheme(object, parents_name, pedigree)
```

## Arguments

|                           |  |
|---------------------------|--|
| <code>object</code>       | A <a href="#">GbsrGenotypeData</a> object.   |
| <code>...</code>          | Unused.  |
| <code>parents_name</code> | A vector of strings to indicate names of parental samples. This argument is used internally by <code>showScheme()</code> for the <code>gbsrGenotypeData</code> object.       |
| <code>pedigree</code>     | A integer vector indicating the member ID assignment to samples. This argument is used internally by <code>showScheme()</code> for the <code>gbsrGenotypeData</code> object. |

## Value

NULL. Print the scheme information on the R console.

## See Also

[initScheme\(\)](#) and [addScheme\(\)](#)

## Examples

```
# Load data in the GDS file and instantiate a [GbsrGenotypeData] object.
gds_fn <- system.file("extdata", "sample.gds", package = "GBScleanR")
gds <- loadGDS(gds_fn)

# Biparental F2 population.
gds <- setParents(gds, parents = c("Founder1", "Founder2"))

# setParents gave member ID 1 and 2 to Founder1 and Founder2, respectively.
gds <- initScheme(gds, mating = cbind(c(1:2)))
```



```

# Now the progenies of the cross above have member ID 3.
# If `crosstype = "selfing"` or `"sibling"`, you can omit a `mating` matrix.
gds <- addScheme(gds, crosstype = "self")

# Now you can execute `estGeno()` which requires a [GbsrScheme] object.

# Close the connection to the GDS file
closeGDS(gds)

```

---

|            |   |
|------------|---|
| thinMarker | <i>Remove markers potentially having redundant information.</i> |
|------------|---|

---

## Description

Markers within the length of the sequenced reads (usually ~ 150 bp, up to your sequencer) potentially have redundant information and those will cause unexpected errors in error correction which assumes independency of markers each other. This function only retains the first marker or the least missing rate marker from the markers locating within the specified stretch.

## Usage

```

thinMarker(object, range = 150, ...)

## S4 method for signature 'GbsrGenotypeData'
thinMarker(object, range)

```

## Arguments

|        |  |
|--------|--|
| object | A <a href="#">GbsrGenotypeData</a> object.                 |
| range  | A integer value to indicate the stretch to search markers. |
| ...    | Unused.  |

## Details

This function search valid markers from the first marker of each chromosome and compare its physical position with a neighbor marker. If the distance between those markers are equal or less than range, one of them which has a larger missing rate will be removed (labeled as invalid marker). When the first marker was retained and the second marker was removed as invalid marker, next the distance between the first marker and the third marker will be checked and this cycle is repeated until reaching the end of each chromosome. Run [validMar\(\)](#) to check the valid SNP markers.

## Value

A [GbsrGenotypeData](#) object with filters on markers.

**Examples**

```
# Load data in the GDS file and instantiate a [GbsrGenotypeData] object.
gds_fn <- system.file("extdata", "sample.gds", package = "GBScleanR")
gds <- loadGDS(gds_fn)

# Summarize genotype count information to be used in thinMarker().
gds <- countGenotype(gds)
gds <- thinMarker(gds, range = 150)

closeGDS(gds) # Close the connection to the GDS file
```

---

validMar

*Return a logical vector indicating which are valid SNP markers.*


---

**Description**

Return a logical vector indicating which are valid SNP markers.

**Usage**

```
validMar(object, chr = NULL, ...)

validMar(object) <- value

## S4 method for signature 'GbsrGenotypeData'
validMar(object, chr)

## S4 replacement method for signature 'GbsrGenotypeData'
validMar(object) <- value
```

**Arguments**

|        |  |
|--------|--|
| object | A <a href="#">GbsrGenotypeData</a> object.   |
| chr    | A index to specify chromosome to get information.  |
| ...    | Unused.  |
| value  | A logical vector indicating valid markers with the length matching with the number of markers. |

**Value**

A logical vector of the same length with the number of total SNP markers

**Examples**

```
# Load data in the GDS file and instantiate a [GbsrGenotypeData] object.
gds_fn <- system.file("extdata", "sample.gds", package = "GBScleanR")
gds <- loadGDS(gds_fn)

validMar(gds)

# Close the connection to the GDS file.
closeGDS(gds)
```

---

|          |  |
|----------|--|
| validSam | <i>Return a logical vector indicating which are valid samples.</i> |
|----------|--|

---

### Description

Return a logical vector indicating which are valid samples.

### Usage

```
validSam(object, parents = FALSE, ...)  
  
validSam(object) <- value  
  
## S4 method for signature 'GbsrGenotypeData'  
validSam(object, parents)  
  
## S4 replacement method for signature 'GbsrGenotypeData'  
validSam(object) <- value
```

### Arguments

|         |  |
|---------|--|
| object  | A <a href="#">GbsrGenotypeData</a> object.   |
| parents | A logical value to indicate to set FALSE or TRUE to parental samples. If you specify parents = "only", this function returns a logical vector indicating TRUE for only parental samples. |
| ...     | Unused.  |
| value   | A logical vector indicating valid samples with the length matching with the number of samples  |

### Value

A logical vector of the same length with the number of total samples.

### Examples

```
# Load data in the GDS file and instantiate a [GbsrGenotypeData] object.  
gds_fn <- system.file("extdata", "sample.gds", package = "GBScleanR")  
gds <- loadGDS(gds_fn)  
  
validSam(gds)  
  
# Close the connection the GDS file.  
closeGDS(gds)
```

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