Package 'BGData'

October 5, 2021

Version 2.3.0

License MIT + file LICENSE

Title A Suite of Packages for Analysis of Big Genomic Data

Description An umbrella package providing a phenotype/genotype data structure and scalable and efficient computational methods for large genomic datasets in combination with several other packages: 'BEDMatrix', 'LinkedMatrix', and 'symDMatrix'.

URL https://github.com/QuantGen/BGData

BugReports https://github.com/QuantGen/BGData/issues

Depends R (>= 3.0.2), BEDMatrix (>= 1.4.0), LinkedMatrix (>= 1.3.0), symDMatrix (>= 2.0.0)

Imports methods, parallel, crochet (>= 2.1.0), bigmemory, synchronicity, ff, bit

Suggests data.table (>= 1.9.6), lme4, SKAT, testthat

NeedsCompilation yes

Author Gustavo de los Campos [aut], Alexander Grueneberg [aut, cre], Paulino Perez [ctb], Ana Vazquez [ctb]

Maintainer Alexander Grueneberg <cran@agrueneberg.info>

Repository CRAN

Date/Publication 2021-10-05 10:00:05 UTC

R topics documented:

`BGData-package` *A Suite of Packages for Analysis of Big Genomic Data*

Description

Modern genomic datasets are big (large n), high-dimensional (large p), and multi-layered. The challenges that need to be addressed are memory requirements and computational demands. Our goal is to develop software that will enable researchers to carry out analyses with big genomic data within the R environment.

Details

We have identified several approaches to tackle those challenges within R:

- File-backed matrices: The data is stored in on the hard drive and users can read in smaller chunks when they are needed.
- Linked arrays: For very large datasets a single file-backed array may not be enough or convenient. A linked array is an array whose content is distributed over multiple file-backed nodes.
- Multiple dispatch: Methods are presented to users so that they can treat these arrays pretty much as if they were RAM arrays.
- Multi-level parallelism: Exploit multi-core and multi-node computing.
- Inputs: Users can create these arrays from standard formats (e.g., PLINK .bed).

The `BGData` package is an umbrella package that comprises several packages: `BEDMatrix`, `LinkedMatrix`, and `symDMatrix`. It features scalable and efficient computational methods for large genomic datasets such as genome-wide association studies (GWAS) or genomic relationship matrices (G matrix). It also contains a container class called `BGData` that holds genotypes, sample information, and variant information.

Example dataset

The `extdata` folder contains example files that were generated from the 250k SNP and phenotype data in Atwell et al. (2010). Only the first 300 SNPs of chromosome 1, 2, and 3 were included to keep the size of the example dataset small. PLINK was used to convert the data to .bed and .raw files. `FT10` has been chosen as a phenotype and is provided as an alternate phenotype file. The file is intentionally shuffled to demonstrate that the additional phenotypes are put in the same order as the rest of the phenotypes.

See Also

`BEDMatrix-package`, `LinkedMatrix-package`, and `symDMatrix-package` for an introduction to the respective packages.

`file-backed-matrices` for more information on file-backed matrices. `multi-level-parallelism` for more information on multi-level parallelism.

`as.BGData` *Convert Other Objects to BGData Objects*

Description

Converts other objects to `BGData` objects by loading supplementary phenotypes and map files referenced by the object to be used for the sample information and variant information, respectively.

Currently supported are `BEDMatrix` objects, plain or nested in `ColumnLinkedMatrix` objects.

Usage

```
as.BGData(x, alternatePhenotypeFile = NULL, ...)

## S3 method for class 'BEDMatrix'
as.BGData(x, alternatePhenotypeFile = NULL, ...)

## S3 method for class 'ColumnLinkedMatrix'
as.BGData(x, alternatePhenotypeFile = NULL,
  ...)

## S3 method for class 'RowLinkedMatrix'
as.BGData(x, alternatePhenotypeFile = NULL,
  ...)
```

Arguments

`x`	An object. Currently supported are `BEDMatrix` objects, plain or nested in `ColumnLinkedMatrix` objects.
`alternatePhenotypeFile`	Path to an alternate phenotype file.
`...`	Additional arguments to the `read.table` or `fread` call (if data.table package is installed) call to parse the alternate pheno file.

Details

The .ped and .raw formats only allows for a single phenotype. If more phenotypes are required it is possible to store them in an alternate phenotype file. The path to such a file can be provided with `alternatePhenotypeFile` and will be merged with the existing sample information. The first and second columns of that file must contain family and within-family IDs, respectively.

For `BEDMatrix` objects: If a .fam file (which corresponds to the first six columns of a .ped or .raw file) of the same name and in the same directory as the .bed file exists, the sample information will be populated with the data stored in that file. Otherwise a stub that only contains an `IID` column populated with the rownames of `geno(x)` will be generated. The same will happen for a .bim file for the variant information.

For `ColumnLinkedMatrix` objects: See the case for `BEDMatrix` objects, but only the .fam file of the first node of the `LinkedMatrix` will be read and used for the sample information, and the .bim files of all nodes will be combined and used for the variant information.

Value

A `BGData` object.

See Also

`readRAW()` to convert text files to `BGData` objects. `BGData-class`, `BEDMatrix-class`, `ColumnLinkedMatrix-class` for more information on the above mentioned classes. `read.table` and `fread` to learn more about extra arguments that can be passed via `...`.

Examples

```
# Path to example data
path <- system.file("extdata", package = "BGData")

# Convert a single BEDMatrix object to a BGData object
chr1 <- BEDMatrix::BEDMatrix(paste0(path, "/chr1.bed"))
bg1 <- as.BGData(chr1)

# Convert multiple BEDMatrix objects in a ColumnLinkedMatrix to a BGData object
chr2 <- BEDMatrix::BEDMatrix(paste0(path, "/chr2.bed"))
chr3 <- BEDMatrix::BEDMatrix(paste0(path, "/chr3.bed"))
clm <- ColumnLinkedMatrix(chr1, chr2, chr3)
bg2 <- as.BGData(clm)

# Load additional (alternate) phenotypes
bg3 <- as.BGData(clm, alternatePhenotypeFile = paste0(path, "/pheno.txt"))
```

BGData *Creates a New BGData Instance*

Description

This function constructs a new `BGData` object.

Usage

```
BGData(geno, pheno = NULL, map = NULL)
```

Arguments

geno	A geno object that contains genotypes.
pheno	A data.frame that contains sample information (including phenotypes). A stub that only contains a sample_id column populated with either the rownames of geno or a sequence starting with sample_ will be generated if NULL
map	A data.frame that contains variant information. A stub that only contains a variant_id column populated with either the colnames of geno or a sequence starting with variant_ will be generated if NULL

See Also

BGData-class and geno-class for more information on the above mentioned classes.

BGData-class *Container for Phenotype and Genotype Data*

Description

The BGData class is a container for genotypes, sample information, and variant information. The class is inspired by the .bed/.fam/.bim (binary) and .ped/.fam/.map (text) phenotype/genotype file formats of PLINK. It is used by several functions of this package such as GWAS for performing a Genome Wide Association Study or getG for calculating a genomic relationship matrix.

Details

There are several ways to create an instance of this class:

- from arbitrary phenotype/genotype data using the BGData constructor function.
- from a .bed file using as.BGData and BEDMatrix.
- from a previously saved BGData object using load.BGData.
- from multiple files (even a mixture of different file types) using LinkedMatrix.
- from a .raw file (or a .ped-like file) using readRAW, readRAW_matrix, or readRAW_big.matrix.

A .ped file can be recoded to a .raw file in PLINK using plink --file myfile --recodeA, or converted to a .bed file using plink --file myfile --make-bed. Conversely, a .bed file can be transformed back to a .ped file using plink --bfile myfile --recode or to a .raw file using plink --bfile myfile --recodeA without losing information.

Accessors

In the following code snippets, x is a BGData object.

`geno(x)`, `geno(x) <- value`: Get or set genotypes.

`pheno(x)`, `pheno(x) <- value`: Get or set sample information.

`map(x)`, `map(x) <- value`: Get or set variant information.

See Also

`BGData`, `as.BGData`, `load.BGData`, `readRAW` to create BGData objects.

`LinkedMatrix-class` and `BEDMatrix-class` for more information on the above mentioned classes.

Examples

```
X <- matrix(data = rnorm(100), nrow = 10, ncol = 10)
Y <- data.frame(y = runif(10))
MAP <- data.frame(means = colMeans(X), freqNA = colMeans(is.na(X)))
DATA <- BGData(geno = X, pheno = Y, map = MAP)

dim(geno(DATA))
head(pheno(DATA))
head(map(DATA))
```

---

chunkedApply *Applies a Function on Each Row or Column of a File-Backed Matrix*

Description

Similar to `apply`, but designed for file-backed matrices. The function brings chunks of an object into physical memory by taking subsets, and applies a function on either the rows or the columns of the chunks using an optimized version of `apply`. If `nCores` is greater than 1, the function will be applied in parallel using `mclapply`. In that case the subsets of the object are taken on the slaves.

Usage

```
chunkedApply(X, MARGIN, FUN, i = seq_len(nrow(X)),
  j = seq_len(ncol(X)), chunkSize = 5000L,
  nCores = getOption("mc.cores", 2L), verbose = FALSE, ...)
```

Arguments

X	A file-backed matrix, typically the genotypes of a BGData object.
MARGIN	The subscripts which the function will be applied over. 1 indicates rows, 2 indicates columns.
FUN	The function to be applied.

i	Indicates which rows of X should be used. Can be integer, boolean, or character. By default, all rows are used.
j	Indicates which columns of X should be used. Can be integer, boolean, or character. By default, all columns are used.
chunkSize	The number of rows or columns of X that are brought into physical memory for processing per core. If NULL, all elements in i or j are used. Defaults to 5000.
nCores	The number of cores (passed to mclapply). Defaults to the number of cores as detected by detectCores.
verbose	Whether progress updates will be posted. Defaults to FALSE.
...	Additional arguments to be passed to the apply like function.

See Also

file-backed-matrices for more information on file-backed matrices. multi-level-parallelism for more information on multi-level parallelism. BGData-class for more information on the BGData class.

Examples

```
# Restrict number of cores to 1 on Windows
if (.Platform$OS.type == "windows") {
    options(mc.cores = 1)
}

# Load example data
bg <- BGData:::loadExample()

# Compute standard deviation of columns
chunkedApply(X = geno(bg), MARGIN = 2, FUN = sd)
```

---

chunkedMap *Applies a Function on Each Chunk of a File-Backed Matrix*

Description

Similar to lapply, but designed for file-backed matrices. The function brings chunks of an object into physical memory by taking subsets, and applies a function on them. If nCores is greater than 1, the function will be applied in parallel using mclapply. In that case the subsets of the object are taken on the slaves.

Usage

```
chunkedMap(X, FUN, i = seq_len(nrow(X)), j = seq_len(ncol(X)),
  chunkBy = 2L, chunkSize = 5000L, nCores = getOption("mc.cores",
  2L), verbose = FALSE, ...)
```

Arguments

X	A file-backed matrix, typically the genotypes of a BGData object.
FUN	The function to be applied on each chunk.
i	Indicates which rows of X should be used. Can be integer, boolean, or character. By default, all rows are used.
j	Indicates which columns of X should be used. Can be integer, boolean, or character. By default, all columns are used.
chunkBy	Whether to extract chunks by rows (1) or by columns (2). Defaults to columns (2).
chunkSize	The number of rows or columns of X that are brought into physical memory for processing per core. If NULL, all elements in i or j are used. Defaults to 5000.
nCores	The number of cores (passed to mclapply). Defaults to the number of cores as detected by detectCores.
verbose	Whether progress updates will be posted. Defaults to FALSE.
...	Additional arguments to be passed to the apply like function.

See Also

file-backed-matrices for more information on file-backed matrices. multi-level-parallelism for more information on multi-level parallelism. BGData-class for more information on the BGData class.

Examples

```
# Restrict number of cores to 1 on Windows
if (.Platform$OS.type == "windows") {
    options(mc.cores = 1)
}

# Load example data
bg <- BGData:::loadExample()

# Compute column sums of each chunk
chunkedMap(X = geno(bg), FUN = colSums)
```

---

file-backed-matrices *File-Backed Matrices*

Description

Functions with the chunkSize parameter work best with file-backed matrices such as BEDMatrix objects. To avoid loading the whole, potentially very large matrix into memory, these functions will load chunks of the file-backed matrix into memory and perform the operations on one chunk at a time. The size of the chunks is determined by the chunkSize parameter. Care must be taken to not set chunkSize too high to avoid memory shortage, particularly when combined with parallel computing.

See Also

BEDMatrix-class as an example of a file-backed matrix.

`findRelated` *Find related individuals in a relationship matrix*

Description

Find related individuals in a relationship matrix.

Usage

```
findRelated(x, ...)

## S3 method for class 'matrix'
findRelated(x, cutoff = 0.03, ...)

## S3 method for class 'symDMatrix'
findRelated(x, cutoff = 0.03, verbose = FALSE,
  ...)
```

Arguments

`x`	A matrix-like object with dimnames.
`...`	Additional arguments for methods.
`cutoff`	The cutoff between 0 and 1 for related individuals to be included in the output. Defaults to 0.03.
`verbose`	Whether progress updates will be posted. Defaults to `FALSE`.

Value

A vector of names or indices of related individuals.

Methods (by class)

- `matrix`: Find related individuals in matrices
- `symDMatrix`: Find related individuals in symDMatrix objects

Examples

```
# Load example data
bg <- BGData:::loadExample()

G <- getG(geno(bg))
findRelated(G)
```

geno *Getting/Setting Genotypes, Sample Information, and Variant Information*

Description

A set of generic functions for getting/setting the genotypes, sample information, and variant information.

Usage

```
geno(x)
geno(x) <- value

pheno(x)
pheno(x) <- value

map(x)
map(x) <- value
```

Arguments

x	The object from/on which to get/set genotypes, sample information, and variant information. Typically a BGData object.
value	Typically a geno object for the geno setter. Typically a data.frame object for the pheno setter. Typically a data.frame object for the map setter.

See Also

- BGData-class
- geno-class

Examples

```
# Load example data
bg <- BGData:::loadExample()

# Access genotypes
geno(bg)

# Access sample information
pheno(bg)

# Access variant information
map(bg)
```

geno-class *An Abstract S4 Class Union of Matrix-Like Types*

Description

geno is a class union of several matrix-like types, many of them suitable for very large datasets.

Currently supported are LinkedMatrix, BEDMatrix, big.matrix,ff_matrix, and matrix.

See Also

LinkedMatrix-class, BEDMatrix-class, big.matrix-class, ff, and matrix for more information on each matrix-like type.

BGData-class for more information on the BGData class, in particular its geno accessor that accepts geno objects.

getG *Computes a Genomic Relationship Matrix*

Description

Computes a positive semi-definite symmetric genomic relation matrix G=XX' offering options for centering and scaling the columns of X beforehand.

Usage

```
getG(X, center = TRUE, scale = TRUE, impute = TRUE, scaleG = TRUE,
  minVar = 1e-05, i = seq_len(nrow(X)), j = seq_len(ncol(X)), i2 = NULL,
  chunkSize = 5000L, nCores = getOption("mc.cores", 2L), verbose = FALSE)
```

Arguments

X	A matrix-like object, typically the genotypes of a BGData object.
center	Either a logical value or a numeric vector of length equal to the number of columns of X. Numeric vector required if i2 is used. If FALSE, no centering is done. Defaults to TRUE.
scale	Either a logical value or a numeric vector of length equal to the number of columns of X. Numeric vector required if i2 is used. If FALSE, no scaling is done. Defaults to TRUE.
impute	Indicates whether missing values should be imputed. Defaults to TRUE.
scaleG	Whether XX' should be scaled. Defaults to TRUE.
minVar	Columns with variance lower than this value will not be used in the computation (only if scale is not FALSE).

i	Indicates which rows of X should be used. Can be integer, boolean, or character. By default, all rows are used.
j	Indicates which columns of X should be used. Can be integer, boolean, or character. By default, all columns are used.
i2	Indicates which rows should be used to compute a block of the genomic relationship matrix. Will compute XY' where X is determined by i and j and Y by i2 and j. Can be integer, boolean, or character. If NULL, the whole genomic relationship matrix XX' is computed. Defaults to NULL.
chunkSize	The number of columns of X that are brought into physical memory for processing per core. If NULL, all columns of X are used. Defaults to 5000.
nCores	The number of cores (passed to mclapply). Defaults to the number of cores as detected by detectCores.
verbose	Whether progress updates will be posted. Defaults to FALSE.

Details

If center = FALSE, scale = FALSE and scaleG = FALSE, getG produces the same outcome than tcrossprod.

Value

A positive semi-definite symmetric numeric matrix.

See Also

file-backed-matrices for more information on file-backed matrices. multi-level-parallelism for more information on multi-level parallelism. BGData-class for more information on the BGData class.

Examples

```
# Restrict number of cores to 1 on Windows
if (.Platform$OS.type == "windows") {
    options(mc.cores = 1)
}

# Load example data
bg <- BGData:::loadExample()

# Compute a scaled genomic relationship matrix from centered and scaled
# genotypes
g1 <- getG(X = geno(bg))

# Disable scaling of G
g2 <- getG(X = geno(bg), scaleG = FALSE)

# Disable centering of genotypes
g3 <- getG(X = geno(bg), center = FALSE)
```

```
# Disable scaling of genotypes
g4 <- getG(X = geno(bg), scale = FALSE)

# Provide own scales
scales <- chunkedApply(X = geno(bg), MARGIN = 2, FUN = sd)
g4 <- getG(X = geno(bg), scale = scales)

# Provide own centers
centers <- chunkedApply(X = geno(bg), MARGIN = 2, FUN = mean)
g5 <- getG(X = geno(bg), center = centers)

# Only use the first 50 individuals (useful to account for population structure)
g6 <- getG(X = geno(bg), i = 1:50)

# Only use the first 100 markers (useful to ignore some markers)
g7 <- getG(X = geno(bg), j = 1:100)

# Compute unscaled G matrix by combining blocks of $XX_{i2}'$ where $X_{i2}$ is
# a horizontal partition of X. This is useful for distributed computing as each
# block can be computed in parallel. Centers and scales need to be precomputed.
block1 <- getG(X = geno(bg), i2 = 1:100, center = centers, scale = scales)
block2 <- getG(X = geno(bg), i2 = 101:199, center = centers, scale = scales)
g8 <- cbind(block1, block2)

# Compute unscaled G matrix by combining blocks of $X_{i}X_{i2}'$ where both
# $X_{i}$ and $X_{i2}$ are horizontal partitions of X. Similarly to the example
# above, this is useful for distributed computing, in particular to compute
# very large G matrices. Centers and scales need to be precomputed. This
# approach is similar to the one taken by the symDMatrix package, but the
# symDMatrix package adds memory-mapped blocks, only stores the upper side of
# the triangular matrix, and provides a type that allows for indexing as if the
# full G matrix is in memory.
block11 <- getG(X = geno(bg), i = 1:100, i2 = 1:100, center = centers, scale = scales)
block12 <- getG(X = geno(bg), i = 1:100, i2 = 101:199, center = centers, scale = scales)
block21 <- getG(X = geno(bg), i = 101:199, i2 = 1:100, center = centers, scale = scales)
block22 <- getG(X = geno(bg), i = 101:199, i2 = 101:199, center = centers, scale = scales)
g9 <- rbind(
    cbind(block11, block12),
    cbind(block21, block22)
)
```

`getG_symDMatrix` *Computes a Very Large Genomic Relationship Matrix*

Description

Computes a positive semi-definite symmetric genomic relation matrix G=XX' offering options for centering and scaling the columns of `X` beforehand.

Usage

```
getG_symDMatrix(X, center = TRUE, scale = TRUE, impute = TRUE, scaleG = TRUE,
  minVar = 1e-05, blockSize = 5000L,
  folderOut = paste0("symDMatrix_", randomString()), vmode = "double",
  i = seq_len(nrow(X)), j = seq_len(ncol(X)), chunkSize = 5000L,
  nCores = getOption("mc.cores", 2L), verbose = FALSE)
```

Arguments

X	A matrix-like object, typically the genotypes of a BGData object.
center	Either a logical value or a numeric vector of length equal to the number of columns of X. If FALSE, no centering is done. Defaults to TRUE.
scale	Either a logical value or a numeric vector of length equal to the number of columns of X. If FALSE, no scaling is done. Defaults to TRUE.
impute	Indicates whether missing values should be imputed. Defaults to TRUE.
scaleG	TRUE/FALSE whether xx' must be scaled.
minVar	Columns with variance lower than this value will not be used in the computation (only if scale is not FALSE).
blockSize	The number of rows and columns of each block. If NULL, a single block of the same length as i will be created. Defaults to 5000.
folderOut	The path to the folder where to save the symDMatrix object. Defaults to a random string prefixed with "symDMatrix_".
vmode	vmode of ff objects.
i	Indicates which rows of X should be used. Can be integer, boolean, or character. By default, all rows are used.
j	Indicates which columns of X should be used. Can be integer, boolean, or character. By default, all columns are used.
chunkSize	The number of columns of X that are brought into physical memory for processing per core. If NULL, all columns of X are used. Defaults to 5000.
nCores	The number of cores (passed to mclapply). Defaults to the number of cores as detected by detectCores.
verbose	Whether progress updates will be posted. Defaults to FALSE.

Details

Even very large genomic relationship matrices are supported by partitioning X into blocks and calling getG on these blocks. This function performs the block computations sequentially, which may be slow. In an HPC environment, performance can be improved by manually distributing these operations to different nodes.

Value

A symDMatrix object.

See Also

multi-level-parallelism for more information on multi-level parallelism. symDMatrix-class and BGData-class for more information on the BGData class. getG to learn more about the underlying method.

GWAS *Performs Single Marker Regressions Using BGData Objects*

Description

Implements single marker regressions. The regression model includes all the covariates specified in the right-hand-side of the formula plus one column of the genotypes at a time. The data from the association tests is obtained from a BGData object.

Usage

```
GWAS(formula, data, method = "lsfit", i = seq_len(nrow(geno(data))),
  j = seq_len(ncol(geno(data))), chunkSize = 5000L,
  nCores = getOption("mc.cores", 2L), verbose = FALSE, ...)
```

Arguments

formula	The formula for the GWAS model without the variant, e.g. y ~ 1 or y ~ factor(sex) + age. The variables included in the formula must be column names in the sample information of the BGData object.
data	A BGData object.
method	The regression method to be used. Currently, the following methods are implemented: rayOLS (see below), lsfit, lm, lm.fit, glm, lmer, and SKAT. Defaults to lsfit.
i	Indicates which rows of the genotypes should be used. Can be integer, boolean, or character. By default, all rows are used.
j	Indicates which columns of the genotypes should be used. Can be integer, boolean, or character. By default, all columns are used.
chunkSize	The number of columns of the genotypes that are brought into physical memory for processing per core. If NULL, all elements in j are used. Defaults to 5000.
nCores	The number of cores (passed to mclapply). Defaults to the number of cores as detected by detectCores.
verbose	Whether progress updates will be posted. Defaults to FALSE.
...	Additional arguments for chunkedApply and regression method.

Details

The rayOLS method is a regression through the origin that can only be used with a y ~ 1 formula, i.e. it only allows for one quantitative response variable y and one variant at a time as an explanatory variable (the variant is not included in the formula, hence 1 is used as a dummy). If covariates are needed, consider preadjustment of y. Among the provided methods, it is by far the fastest.

Some regression methods may require the data to not contain columns with variance 0 or too many missing values. We suggest running summarize to detect variants that do not clear the desired minor-allele frequency and rate of missing genotype calls, and filtering these variants out using the j parameter of the GWAS function (see example below).

Value

The same matrix that would be returned by coef(summary(model)).

See Also

file-backed-matrices for more information on file-backed matrices. multi-level-parallelism for more information on multi-level parallelism. BGData-class for more information on the BGData class. lsfit, lm, lm.fit, glm, lmer, and SKAT for more information on regression methods.

Examples

```
# Restrict number of cores to 1 on Windows
if (.Platform$OS.type == "windows") {
    options(mc.cores = 1)
}

# Load example data
bg <- BGData:::loadExample()

# Detect variants that do not pass MAF and missingness thresholds
summaries <- summarize(geno(bg))
maf <- ifelse(summaries$allele_freq > 0.5, 1 - summaries$allele_freq,
    summaries$allele_freq)
exclusions <- maf < 0.01 | summaries$freq_na > 0.05

# Perform a single marker regression
res1 <- GWAS(formula = FT10 ~ 1, data = bg, j = !exclusions)

# Draw a Manhattan plot
plot(-log10(res1[, 4]))

# Use lm instead of lsfit (the default)
res2 <- GWAS(formula = FT10 ~ 1, data = bg, method = "lm", j = !exclusions)

# Use glm instead of lsfit (the default)
y <- pheno(bg)$FT10
pheno(bg)$FT10.01 <- y > quantile(y, 0.8, na.rm = TRUE)
res3 <- GWAS(formula = FT10.01 ~ 1, data = bg, method = "glm", j = !exclusions)

# Perform a single marker regression on the first 50 markers (useful for
```

```
# distributed computing)
res4 <- GWAS(formula = FT10 ~ 1, data = bg, j = 1:50)
```

---

load.BGData *Loads BGData (and Other) Objects from .RData Files*

Description

This function is similar to load, but also initializes the different types of objects that can be used as genotypes in a BGData object.

Currently supported are ff_matrix, big.matrix, and BEDMatrix objects. If the object is of type LinkedMatrix, all nodes will be initialized with their appropriate method.

Usage

```
load.BGData(file, envir = parent.frame())
```

Arguments

file	The name of the .RData file to be loaded.
envir	The environment where to load the data.

See Also

BGData-class, ff, big.matrix-class, BEDMatrix-class, and LinkedMatrix-class for more information on the above mentioned classes.

---

multi-level-parallelism

Multi-Level Parallelism

Description

Functions with the nCores, i, and j parameters provide capabilities for both parallel and distributed computing.

For parallel computing, nCores determines the number of cores the code is run on. Memory usage can be an issue for higher values of nCores as R is not particularly memory-efficient. As a rule of thumb, at least around (nCores * object_size(chunk)) + object_size(result) MB of total memory will be needed for operations on file-backed matrices, not including potential copies of your data that might be created (for example lsfit runs cbind(1,X)). i and j can be used to include or exclude certain rows or columns. Internally, the mclapply function is used and therefore parallel computing will not work on Windows machines.

For distributed computing, i and j determine the subset of the input matrix that the code runs on. In an HPC environment, this can be used not just to include or exclude certain rows or columns, but also to partition the task among many nodes rather than cores. Scheduler-specific code and code to aggregate the results need to be written by the user. It is recommended to set nCores to 1 as nodes are often cheaper than cores.

See Also

mclapply to learn more about the function used to implement parallel computing. detectCores to detect the number of available cores.

---

orderedMerge *Merge Two Data Frames Keeping the Order of the First*

Description

This is a simplified version of merge useful for merging additional data into a BGData object while keeping the order of the data in the BGData object.

Usage

```
orderedMerge(x, y, by = c(1L, 2L))
```

Arguments

x	Data frame
y	Data frame
by	Specifications of the columns used for merging. Defaults to the first two columns of the data frame, which traditionally has the family ID and the individual ID.

Value

Merged data frame

See Also

BGData-class for more information on the BGData class.

---

preprocess *Center, scale, and impute data*

Description

A faster version of scale with a similar interface that also allows for imputation. The main difference is that this version scales by the standard deviation regardless of whether centering is enabled or not. If centering is enabled, missing values are imputed by 0, otherwise by the mean of the column that contains the value.

Usage

```
preprocess(X, center = FALSE, scale = FALSE, impute = FALSE,
  nCores = getOption("mc.cores", 2L))
```

Arguments

X	A numeric matrix.
center	Either a logical value or numeric vector of length equal to the number of columns of X.
scale	Either a logical value or numeric vector of length equal to the number of columns of X.
impute	Indicates whether missing values should be imputed.
nCores	The number of cores (passed to mclapply). Defaults to the number of cores as detected by detectCores.

Value

The centered, scaled, and imputed matrix.

See Also

scale, which this function tries to improve upon.

Examples

```
# Load example data
bg <- BGData:::loadExample()

# Center and scale genotypes
W <- preprocess(as.matrix(geno(bg)), center = TRUE, scale = TRUE)
```

---

readRAW *Creates a BGData Object From a .raw File or a .ped-Like File*

Description

Creates a BGData object from a .raw file (generated with --recodeA in PLINK). Other text-based file formats are supported as well by tweaking some of the parameters as long as the records of individuals are in rows, and phenotypes, covariates and markers are in columns.

Usage

```
readRAW(fileIn, header = TRUE, dataType = integer(), n = NULL,
  p = NULL, sep = "", na.strings = "NA", nColSkip = 6L,
  idCol = c(1L, 2L), nNodes = NULL, linked.by = "rows",
  folderOut = paste0("BGData_", sub("\\.[[:alnum:]]+$", "",
  basename(fileIn))), outputType = "byte", dimorder = if (linked.by ==
  "rows") 2L:1L else 1L:2L, verbose = FALSE)

readRAW_matrix(fileIn, header = TRUE, dataType = integer(), n = NULL,
  p = NULL, sep = "", na.strings = "NA", nColSkip = 6L,
```

```
  idCol = c(1L, 2L), verbose = FALSE)

readRAW_big.matrix(fileIn, header = TRUE, dataType = integer(),
  n = NULL, p = NULL, sep = "", na.strings = "NA", nColSkip = 6L,
  idCol = c(1L, 2L), folderOut = paste0("BGData_",
  sub("\\.[[:alnum:]]+$", "", basename(fileIn))), outputType = "char",
  verbose = FALSE)
```

Arguments

fileIn	The path to the plaintext file.
header	Whether fileIn contains a header. Defaults to TRUE.
dataType	The coding type of genotypes in fileIn. Use integer() or double() for numeric coding. Alpha-numeric coding is currently not supported for readRAW and readRAW_big.matrix: use the --recodeA option of PLINK to convert the .ped file into a .raw file. Defaults to integer().
n	The number of individuals. Auto-detect if NULL. Defaults to NULL.
p	The number of markers. Auto-detect if NULL. Defaults to NULL.
sep	The field separator character. Values on each line of the file are separated by this character. If sep = "" (the default for readRAW the separator is "white space", that is one or more spaces, tabs, newlines or carriage returns.
na.strings	The character string used in the plaintext file to denote missing value. Defaults to NA.
nColSkip	The number of columns to be skipped to reach the genotype information in the file. Defaults to 6.
idCol	The index of the ID column. If more than one index is given, both columns will be concatenated with "_". Defaults to c(1,2), i.e. a concatenation of the first two columns.
nNodes	The number of nodes to create. Auto-detect if NULL. Defaults to NULL.
linked.by	If columns a column-linked matrix (ColumnLinkedMatrix) is created, if rows a row-linked matrix (RowLinkedMatrix). Defaults to rows.
folderOut	The path to the folder where to save the binary files. Defaults to the name of the input file (fileIn) without extension prefixed with "BGData_".
outputType	The vmode for ff and type for big.matrix objects. Default to byte for ff and char for big.matrix objects.
dimorder	The physical layout of the underlying ff object of each node.
verbose	Whether progress updates will be posted. Defaults to FALSE.

Details

The data included in the first couple of columns (up to nColSkip) is used to populate the sample information of a BGData object, and the remaining columns are used to fill the genotypes. If the first row contains a header (header = TRUE), data in this row is used to determine the column names for sample information and genotypes.

The genotypes can take several forms, depending on the function that is called (readRAW, readRAW_matrix, or readRAW_big.matrix). The following sections illustrate each function in detail.

readRAW

Genotypes are stored in a LinkedMatrix object where each node is an ff instance. Multiple ff files are used because the array size in ff is limited to the largest integer which can be represented on the system (.Machine$integer.max) and for genetic data this limitation is often exceeded. The LinkedMatrix package makes it possible to link several ff files together by columns or by rows and treat them similarly to a single matrix. By default a ColumnLinkedMatrix is used for the genotypes, but the user can modify this using the linked.by argument. The number of nodes to generate is either specified by the user using the nNodes argument or determined internally so that each ff object has a number of cells that is smaller than .Machine$integer.max / 1.2. A folder (see folderOut) that contains the binary flat files (named geno_*.bin) and an external representation of the BGData object in BGData.RData is created.

readRAW_matrix

Genotypes are stored in a regular matrix object. Therefore, this function will only work if the .raw file is small enough to fit into memory.

readRAW_big.matrix

Genotypes are stored in a filebacked big.matrix object. A folder (see folderOut) that contains the binary flat file (named BGData.bin), a descriptor file (named BGData.desc), and an external representation of the BGData object in BGData.RData are created.

Reloading a BGData object

To reload a BGData object, it is recommended to use the load.BGData function instead of the load function as load does not initialize ff objects or attach big.matrix objects.

See Also

load.BGData() to load a previously saved BGData object, as.BGData() to create BGData objects from non-text files (e.g. .bed files). BGData-class, ColumnLinkedMatrix-class, RowLinkedMatrix-class, big.matrix-class, and ff for more information on the above mentioned classes.

Examples

```
# Path to example data
path <- system.file("extdata", package = "BGData")

# Convert RAW files of chromosome 1 to a BGData object
bg <- readRAW(fileIn = paste0(path, "/chr1.raw"))

unlink("BGData_chr1", recursive = TRUE)
```

segments *Find non-overlapping segments based on a summary statistic*

Description

Given a summary statistic and a threshold, this function computes the number of non-overlapping segments, each defined as a discovery (i.e., `statistic[i] <= threshold`) +/- a gap, in the same units as `bp` (often base-pair position).

Usage

```
segments(statistic, chr, bp, threshold, gap, trim = FALSE, verbose = FALSE)
```

Arguments

`statistic`	A statistic (e.g., BFDR or p-values).
`chr`	A vector containing the chromosome for each value of `statistic`.
`bp`	A vector containing the base-pair positions for each value of `statistic`.
`threshold`	The threshold to determine 'significance' (e.g., `1e-5` for p-values).
`gap`	1/2 of the length of the desired segments.
`trim`	Whether to collapse segments that were artifically inflated by `gap`. Defaults to `FALSE`.
`verbose`	Whether progress updates will be posted. Defaults to `FALSE`.

Value

A data frame containing the following information:

`chr`	Chromosome
`start`	Index where segment starts within `statistic`.
`end`	Index where segment ends within `statistic`.
`length`	Length of segment.
`bpStart`	Base-pair position where segment starts.
`bpEnd`	Base-pair position where segment ends.
`bpLength`	Length of segment in base-pair positions.
`minValue`	Smallest value of `statistic` within segment.
`minValuePos`	Position of variant with the smallest value of `statistic` within segment.

Examples

```
library(BGData)

# Load example data
bg <- BGData:::loadExample()

# Perform GWAS
pValues <- GWAS(
    formula = FT10 ~ 1,
    data = bg,
    method = "rayOLS"
)

# Determine segments within +/- 1MB from a significant variant
segments <- segments(
    statistic = pValues[, 4],
    chr = map(bg)$chromosome,
    bp = map(bg)$base_pair_position,
    threshold = 1e-5,
    gap = 1e6,
    trim = FALSE,
    verbose = FALSE
)
```

---

summarize *Generates Various Summary Statistics*

Description

Computes the frequency of missing values, the (minor) allele frequency, and standard deviation of each column of X.

Usage

```
summarize(X, i = seq_len(nrow(X)), j = seq_len(ncol(X)),
  chunkSize = 5000L, nCores = getOption("mc.cores", 2L),
  verbose = FALSE)
```

Arguments

X	A matrix-like object, typically the genotypes of a BGData object.
i	Indicates which rows of X should be used. Can be integer, boolean, or character. By default, all rows are used.
j	Indicates which columns of X should be used. Can be integer, boolean, or character. By default, all columns are used.
chunkSize	The number of columns of X that are brought into physical memory for processing per core. If NULL, all elements in j are used. Defaults to 5000.

nCores	The number of cores (passed to mclapply). Defaults to the number of cores as detected by detectCores.
verbose	Whether progress updates will be posted. Defaults to FALSE.

Value

A data.frame with three columns: freq_na for frequencies of missing values, allele_freq for allele frequencies of the counted allele, and sd for standard deviations.

See Also

file-backed-matrices for more information on file-backed matrices. multi-level-parallelism for more information on multi-level parallelism. BGData-class for more information on the BGData class.

Examples

```
# Restrict number of cores to 1 on Windows
if (.Platform$OS.type == "windows") {
    options(mc.cores = 1)
}

# Load example data
bg <- BGData:::loadExample()

# Summarize the whole dataset
sum1 <- summarize(X = geno(bg))

# Summarize the first 50 individuals
sum2 <- summarize(X = geno(bg), i = 1:50)

# Summarize the first 1000 markers (useful for distributed computing)
sum3 <- summarize(X = geno(bg), j = 1:100)

# Summarize the first 50 individuals on the first 1000 markers
sum4 <- summarize(X = geno(bg), i = 1:50, j = 1:100)

# Summarize by names
sum5 <- summarize(X = geno(bg), j = c("snp81233_C", "snp81234_C", "snp81235_T"))

# Convert to minor allele frequencies (useful if the counted alleles are not
# the minor alleles)
maf <- ifelse(sum1$allele_freq > 0.5, 1 - sum1$allele_freq, sum1$allele_freq)
```

Index