Package 'SNPtools'

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Title S4 Tools for Reading and Organizing Genetic Data

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Description Provides S4-based structures to encapsulate the import, organization, and processing of genetic data from PLINK and FImpute files, with customizable arguments. Includes tools for combining SNP panels, summarizing genotype data, and facilitating downstream quality control and analysis workflows.

Depends R (>= 4.1.0),
snpStats,
tidyverse

Imports methods,
data.table,
fQC,
Rcpp

LinkingTo Rcpp

Suggests knitr,
rmarkdown

VignetteBuilder knitr

Encoding UTF-8

License GPL-3

RoxygenNote 7.3.2

Contents

`cbind_SnpMatrix` *Safe cbind for SnpMatrix preserving dimnames*

Description

This function performs a column-wise binding of multiple `SnpMatrix` objects, explicitly preserving row names and column names, avoiding unexpected "object has no names" warnings.

Usage

```
cbind_SnpMatrix(...)
```

Arguments

`...`	SnpMatrix objects to combine (must have identical row names).

Value

A single combined `SnpMatrix` with preserved row and column names.

Examples

```
## Not run:
cbind_SnpMatrix(matrix1, matrix2)

## End(Not run)
```

`check.sample.call.rate`

Check Sample Call Rate

Description

Identifies samples with call rate below a given threshold.

Usage

```
check.sample.call.rate(sample.summary, min.call.rate)
```

Arguments

`sample.summary`	A data frame with a "Call.rate" column for each sample.
`min.call.rate`	Minimum acceptable call rate (between 0 and 1).

Value

A character vector with the names of samples to remove.

`check.snp.same.position`

Check SNPs mapped to the same position

Description

Identifies groups of SNPs that are mapped to the exact same genomic position on each chromosome. Returns a list where each element corresponds to one group of overlapping SNPs.

Usage

```
check.snp.same.position(snpmap)
```

Arguments

`snpmap`	Data frame containing at least columns "Name", "Chromosome", and "Position".

Value

A list of character vectors, each with names of SNPs found at the same position.

combinarSNPData *Combine multiple SNPDataLong objects*

Description

This function merges a list of SNPDataLong objects, typically representing different SNP panels or datasets, into a single unified SNPDataLong object. It ensures that all genotype matrices have the same set of SNPs (filling missing SNPs with NA), and merges the marker map information while removing duplicate SNP entries.

Usage

```
combinarSNPData(lista)
```

Arguments

lista	A list of SNPDataLong objects to be combined.

Value

A single SNPDataLong object containing the combined genotype matrix, merged map, and a concatenated path string.

Examples

```
## Not run:
combined <- combinarSNPData(list(snp_obj1, snp_obj2, snp_obj3))

## End(Not run)
```

FImputeRunner *Build FImputeRunner object*

Description

A convenience function to construct a 'FImputeRunner' object from basic inputs.

Usage

```
FImputeRunner(object, path, exec_path = "FImpute3", name = "data")
```

Arguments

path	A character string indicating the directory to save FImpute files.
exec_path	Path to the FImpute executable (default = "FImpute3").
name	Name for the dataset (used internally, default = "gen_data").
geno	A SnpMatrix object.
map	A data.frame with SNP metadata (columns: Name, Chromosome, Position).

Value

An object of class 'FImputeRunner'.

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genoToDF *Convert geno slot from SNPDataLong to a data.frame*

Description

Converts the genotype matrix (geno slot) of a SNPDataLong object to a data.frame, with optional centering and scaling per SNP (column).

Usage

```
genoToDF(object, center = FALSE, scale = FALSE)
```

Arguments

object	An object of class SNPDataLong.
center	Logical or numeric. If TRUE (default FALSE), center columns to mean zero.
scale	Logical or numeric. If TRUE (default FALSE), scale columns to standard deviation one.

Value

A data.frame with individuals as rows and SNPs as columns (numeric 0/1/2, or centered/scaled values).

Examples

```
## Not run:
df <- genoToDF(nelore_imputed, center = TRUE, scale = TRUE)
head(df[, 1:5])

## End(Not run)
```

getGeno *Flexible and efficient genotype file reading with autodetection using fread*

Description

This generic and method allow flexible import of SNP genotype data from Illumina FinalReport files, supporting fast initial column detection using `data.table::fread`, followed by full genotype matrix construction via `snpStats::read.snps.long`.

Usage

```
getGeno(...)
```

Arguments

`path`	Path to the directory containing `FinalReport.txt`
`fields`	A list specifying column indices for sample, SNP, allele1, allele2, and confidence
`codes`	A character vector with allele codes (e.g., `c("A", "B")`)
`threshold`	Confidence threshold for genotype calling
`sep`	Field separator used in the files
`skip`	Number of lines to skip at the start of the file
`verbose`	Logical; if `TRUE`, displays progress messages
`every`	Frequency of progress update (number of SNPs)

Value

An `SNPDataLong` object containing the genotype matrix and map, or `NULL` if an error occurs

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importAllGenos *Import and combine multiple genotype configurations*

Description

This generic and method import genotype data from multiple configurations defined in an `SNPImportList` object, then combine them into a single unified `SNPDataLong` object.

Usage

```
importAllGenos(object)
```

Arguments

object	An object of class SNPImportList containing import configurations

Value

A single combined SNPDataLong object

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importFImputeResults *Import imputed FImpute results from disk*

Description

Reads existing imputed results from a given path and returns an object of class SNPDataLong.

Usage

```
importFImputeResults(path)
```

Arguments

path	Character. Path to the folder containing 'output_fimpute' (e.g., "fimpute_run_nelore").

Value

An object of class SNPDataLong containing the imputed genotypes and SNP map.

Examples

```
## Not run:
imputed_obj <- importFImputeResults("fimpute_run_nelore")
head(imputed_obj@map)

## End(Not run)
```

---

import_geno_list *Import multiple genotype datasets from a list of configurations*

Description

Reads and imports multiple genotype datasets specified in a list of configurations. Each configuration must include the path to the genotype data and information on field mapping. Optionally, you can also specify codes, quality threshold, separator, lines to skip, and a subset of IDs to retain. The function automatically fills the 'xref_path' slot per individual and combines maps into a single data.frame, adding a 'SourcePath' column indicating their origin and removing duplicated SNP rows (by Name). Prints progress messages indicating the current path being loaded (with counter).

Usage

```
import_geno_list(config_list)
```

Arguments

config_list	A list of configuration lists. Each element should contain: - ‘path‘ (character): Path to the genotype file or folder. - ‘fields‘ (list): Named list defining the columns (e.g., SNP ID, sample ID, alleles, confidence). - ‘codes‘ (character vector, optional): Allele codes (default is c("A", "B")). - ‘threshold‘ (numeric, optional): Maximum allowed missingness or confidence threshold (default 0.15). - ‘sep‘ (character, optional): Field separator in the input file (default tab "\t"). - ‘skip‘ (integer, optional): Number of lines to skip at the beginning of the file (default 0). - ‘verbose‘ (logical, optional): Whether to print detailed messages (default TRUE). - ‘subset‘ (character vector, optional): Vector of sample IDs to retain after import.

Value

An object of class ‘SNPDataLong‘ containing: - Combined genotype matrix (‘geno‘). - Combined map (‘map‘) as a single data.frame with ‘SourcePath‘ column and without duplicated rows. - Combined ‘xref_path‘ vector (one entry per individual). - ‘path‘ slot as a semicolon-separated string of all input dataset paths.

---

plotPCAgroups *Plot PCA groups from anticlustering result*

Description

Plot PCA groups from anticlustering result

Usage

```
plotPCAgroups(pca_res, groups, pcs = c(1, 2), filename = NULL)
```

Arguments

pca_res	A prcomp object.
groups	A factor or vector of group assignments.
pcs	Vector of length 2 indicating which PCs to plot (default: c(1, 2)).
filename	Optional. If provided, saves plot to this file (e.g., "antic.png").

Value

A ggplot object (also prints to screen).

Examples

```
## Not run:
res <- runAnticlusteringPCA(nelore_imputed, K = 2, n_pcs = 20)
plotPCAgroups(res$pca, res$groups)

## End(Not run)
```

`qcSamples` *Quality control on samples*

Description

Applies quality control (QC) procedures to samples in a ‘SNPDataLong‘ object, based on heterozygosity and call rate thresholds.

Usage

```
qcSamples(x, ...)

## S4 method for signature 'SNPDataLong'
qcSamples(
  x,
  heterozygosity = NULL,
  smp_cr = NULL,
  action = c("report", "filter", "both")
)
```

Arguments

`x`	An object of class ‘SNPDataLong‘.
`heterozygosity`	A numeric threshold or range for heterozygosity. Samples outside this threshold are removed.
`smp_cr`	Minimum acceptable sample call rate (between 0 and 1). Samples below this value are removed.
`action`	Character string indicating the action to perform. One of: - ‘"report"‘: only returns a list of samples to remove and those kept; - ‘"filter"‘: returns a filtered object without reporting; - ‘"both"‘: performs filtering and returns the filtered object.

Value

Depending on the ‘action‘ argument: - ‘"report"‘: returns a list with removed and kept samples; - ‘"filter"‘: returns a new ‘SNPDataLong‘ object with filtered genotypes; - ‘"both"‘: returns a list with: - ‘filtered‘: the filtered ‘SNPDataLong‘ object; - ‘report‘: a list of removed and kept samples.

qcSNPs *Quality Control for SNPDataLong with optional criteria*

Description

Applies flexible quality control filters on an object of class SNPDataLong. Supports call rate filtering, minor allele frequency (MAF), Hardy-Weinberg equilibrium (HWE), removal of monomorphic SNPs, exclusion of specific chromosomes, optionally removing SNPs without positions, and optionally removing SNPs at the same genomic position (keeping the one with highest MAF).

Usage

```
qcSNPs(x, ...)
```

Arguments

x	An object of class SNPDataLong.
missing_ind	Maximum allowed proportion of missing data per individual (currently not implemented).
missing_snp	Maximum allowed proportion of missing data per SNP (currently not implemented).
min_snp_cr	Minimum acceptable call rate for SNPs (e.g., 0.95). SNPs below this threshold are removed.
min_maf	Minimum minor allele frequency allowed for SNPs (e.g., 0.05). SNPs with lower MAF are removed.
hwe	p-value threshold for Hardy-Weinberg equilibrium test (e.g., 1e-6). SNPs violating this are removed.
snp_position	Logical. If TRUE, removes SNPs mapped to the same position, retaining only the one with highest MAF.
no_position	Logical. If TRUE, removes SNPs without defined genomic positions.
snp_mono	Logical. If TRUE, removes monomorphic SNPs (with no variation).
remove_chr	Character vector of chromosomes to exclude (e.g., c("X", "Y")).
action	One of "report" (returns a list of removed SNPs), "filter" (returns filtered SNPDataLong), or "both" (returns both).

Value

Depending on the action argument: - "report": list of SNPs removed by each filter and SNPs retained. - "filter": filtered SNPDataLong object. - "both": list containing the filtered object and detailed report.

Examples

```
## Not run:
set.seed(123)
mat <- matrix(sample(c(0, 1, 2, NA), 100, replace = TRUE, prob = c(0.4, 0.4, 0.15, 0.05)),
              nrow = 10, ncol = 10)
colnames(mat) <- paste0("snp", 1:10)
rownames(mat) <- paste0("ind", 1:10)
map <- data.frame(Name = colnames(mat), Chromosome = 1, Position = 1:10)
x <- new("SNPDataLong", geno = mat, map = map, path = "dummy_path", xref_path = rep("chip1", 10))

# Example using multiple filters
qcSNPs(x, min_snp_cr = 0.8, min_maf = 0.05, snp_mono = TRUE, no_position = TRUE, snp_position = TRUE, action = "filt

## End(Not run)
```

---

qc_header *Formatted header message*

Description

Prints a formatted message with a border for section titles in the console.

Usage

```
qc_header(title)
```

Arguments

title	Character string to be printed inside the header box.

Value

No return value. Used for side effects (message).

Examples

```
qc_header("Quality Control on Samples")
```

rbindSnpFlexible *Faster row-bind for SnpMatrix objects with differing columns*

Description

Combines multiple SnpMatrix objects by rows, automatically handling differing SNP columns, optimized for large matrices.

Usage

```
rbindSnpFlexible(...)
```

Arguments

...	One or more SnpMatrix objects.

Value

A single SnpMatrix object with all rows combined.

Examples

```
## Not run:
combined <- rbindSnpFlexible(brangus_geno, batch_BM@geno)

## End(Not run)
```

rbind_SnpMatrix *Safe rbind for SnpMatrix preserving dimnames*

Description

This function performs a row-wise binding of multiple `SnpMatrix` objects, explicitly preserving row names and column names, avoiding unexpected "object has no names" warnings.

Usage

```
rbind_SnpMatrix(...)
```

Arguments

...	SnpMatrix objects to combine (must have identical column names).

Value

A single combined `SnpMatrix` with preserved row and column names.

Examples

```
## Not run:
rbind_SnpMatrix(matrix1, matrix2)

## End(Not run)
```

`read.fimpute` *Read imputed genotypes from FImpute output and return SNPDataLong object*

Description

Reads imputed genotypes and SNP information from FImpute output, builds a SnpMatrix and a corresponding map, and returns an SNPDataLong object.

Usage

```
read.fimpute(file)
```

Arguments

`file`	Character. Path to the FImpute output directory (usually "output_fimpute").

Value

An object of class `SNPDataLong` containing the imputed genotypes and SNP map.

Examples

```
## Not run:
snp_long <- read.fimpute("output_fimpute")

## End(Not run)
```

`runAnticlusteringPCA` *Run PCA and Anticlustering on SNPDataLong*

Description

Converts a SNPDataLong object to a data.frame, runs PCA, and performs anticlustering grouping.

Usage

```
runAnticlusteringPCA(object, K = 2, n_pcs = 20, center = TRUE, scale = TRUE)
```

Arguments

object	An object of class SNPDataLong.
K	Number of groups for anticlustering.
n_pcs	Number of top principal components to use (default: 20).
center	Logical or numeric. Center columns before PCA (default: TRUE).
scale	Logical or numeric. Scale columns before PCA (default: TRUE).

Value

A list with: - groups: vector with group assignments. - pca: the PCA result object (prcomp). - pcs: matrix of top PCs used in anticlustering.

Examples

```
## Not run:
res <- runAnticlusteringPCA(nelore_imputed, K = 2, n_pcs = 20)
table(res$groups)

## End(Not run)
```

---

runFImpute *Run FImpute from a FImputeRunner object*

Description

This function runs the external FImpute software using a 'FImputeRunner' object, ensuring that all required input files are present and the results are imported.

Usage

```
runFImpute(object, verbose = TRUE)

## S4 method for signature 'FImputeRunner'
runFImpute(object, verbose = TRUE)
```

Arguments

object	An object of class 'FImputeRunner'.
verbose	Logical. If TRUE (default), FImpute output will be printed to the console.

Value

An updated 'FImputeRunner' object with the 'results' slot populated (SnpMatrix).

Examples

```
## Not run:
# Example: Running FImpute from a FImputeRunner object

path_fimpute <- "fimpute_run_example"
param_file <- file.path(path_fimpute, "fimpute.par")
fimpute_exec <- "FImpute3"  # assuming it is in PATH

export_obj <- new("FImputeExport",
                  geno = geno_obj@geno,
                  map = geno_obj@map,
                  path = path_fimpute)

runner <- new("FImputeRunner",
              export = export_obj,
              par_file = param_file,
              exec_path = fimpute_exec)

runner <- runFImpute(runner, verbose = TRUE)
head(runner@results)

## End(Not run)
```

`saveFImpute` *Save genotype and map files in FImpute format*

Description

S4 method to export genotype (.gen), map (.map), and parameter (fimpute.par) files compatible with [FImpute](https://www.aps.uoguelph.ca/~msargol/fimpute/).

Usage

```
saveFImpute(object, ...)

## S4 method for signature 'FImputeExport'
saveFImpute(object)

## S4 method for signature 'SNPDataLong'
saveFImpute(object, path = NULL)
```

Arguments

`object`	An object of class ‘FImputeExport‘ or ‘SNPDataLong‘.
`...`	Additional arguments passed to methods.
`path`	Output directory (default: "fimpute_run" for SNPDataLong).

Value

No return value. Files are saved to disk.

`saveFImputeRaw` *Export genotypes and map using basic arguments*

Description

Convenience function to export FImpute files directly from a ‘SnpMatrix‘ and map ‘data.frame‘.

Usage

```
saveFImputeRaw(geno, map, path, xref = NULL)
```

Arguments

`geno`	A ‘SnpMatrix‘ object.
`map`	A data.frame with columns ’Name’, ’Chromosome’, ’Position’, and ’SourcePath’.
`path`	Output directory.
`xref`	Optional vector of identifiers per individual (used to assign numeric chip IDs).

`savePlink` *Save SNPDataLong object to PLINK format*

Description

Saves genotype and map data from an SNPDataLong object in PLINK format (.ped/.map and optionally binary files).

Usage

```
savePlink(
  object,
  path = "plink_out",
  name = "plink_data",
  run_plink = TRUE,
  chunk_size = 1000
)
```

Arguments

object	An object of class SNPDataLong.
path	Character. Directory where files will be saved.
name	Character. Base name for PLINK output files.
run_plink	Logical. If TRUE (default), runs PLINK1 to convert to binary files. If FALSE, only .ped and .map files are saved.
chunk_size	Integer. Number of individuals per chunk for writing .ped file (default: 1000).

Value

No return value. Files are saved to disk.

Examples

```
## Not run:
savePlink(genotypes_qc, path = "plink_out", name = "nelore_qc", run_plink = TRUE, chunk_size = 2000)

## End(Not run)
```

Subset *Subset method for SNPDataLong*

Description

Subset method for SNPDataLong

Usage

```
Subset(object, index, margin = 1, keep = TRUE)
```

Arguments

object	A SNPDataLong object.
index	Character vector with row (individual) or column (SNP) names to filter.
margin	Integer: 1 = rows (individuals), 2 = columns (SNPs).
keep	Logical: TRUE to keep specified levels, FALSE to discard them.

Value

A new SNPDataLong object, subsetted accordingly.

summary,SNPDataLong-method
Summary for SNPDataLong objects

Description

Provides a detailed summary of an SNPDataLong object, including sample and SNP counts, proportion of missing data, and SNP distribution by chromosome if mapping information is available.

Usage

```
## S4 method for signature 'SNPDataLong'
summary(object, ...)
```

Arguments

object	An object of class SNPDataLong.

Value

Prints a summary to the console. Returns NULL (invisible).

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