Package 'SNPtools'

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Title Ferramentas S4 para Leitura e Organização de Dados Genéticos

Version 0.1.0

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Description Estruturas baseadas em S4 para encapsular leitura de arquivos PLINK e FImpute com argumentos customizáveis.

Depends R (>= 4.1.0),
snpStats,
tidyverse

Imports methods,
data.table,
fQC

Suggests knitr,
rmarkdown

VignetteBuilder knitr

Encoding UTF-8

License GPL-3

RoxygenNote 7.3.2

Contents

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.

combinarSNPData   *Combina múltiplos objetos SNPDataLong (painéis diferentes)*

Description

Combina múltiplos objetos SNPDataLong (painéis diferentes)

Usage

```
combinarSNPData(lista)
```

Arguments

lista   Lista de objetos da classe SNPDataLong

Value

Objeto SNPDataLong unificado

getGeno	*Leitura flexível e eficiente de genótipos com autodetecção usando fread*

Description

Leitura flexível e eficiente de genótipos com autodetecção usando fread

Usage

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

Arguments

path	Caminho para o FinalReport.txt
fields	Lista com as colunas: sample, snp, allele1, allele2, confidence
codes	Vetor com os códigos de alelos (ex: c("A", "B"))
threshold	Corte para qualidade (confidence)
sep	Separador usado no arquivo
skip	Linhas a pular no topo
verbose	Exibir progresso?
every	Frequência de progresso

Value

Objeto da classe SNPDataLong ou NULL em caso de erro

importAllGenos	*Importa e combina múltiplas configurações de genótipos*

Description

Importa e combina múltiplas configurações de genótipos

Usage

```
importAllGenos(object)
```

Arguments

object	Objeto do tipo SNPImportList

Value

Objeto SNPDataLong combinado

import_geno_list	*Importa múltiplos conjuntos genotípicos a partir de uma lista de configurações*

Description

Importa múltiplos conjuntos genotípicos a partir de uma lista de configurações

Usage

```
import_geno_list(config_list)
```

Arguments

config_list   Lista com configurações (cada elemento é uma lista com path, fields, sep, etc.)

Value

Objeto SNPDataLong unificado

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.

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qcSNPs	*Controle de Qualidade para SNPDataLong com critérios opcionais*

Description

Permite análise de qualidade genotípica com critérios definidos pelo usuário.

Usage

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

Arguments

x	Objeto da classe SNPDataLong
missing_ind	Proporção máxima de dados faltantes permitida por indivíduo (opcional)
missing_snp	Proporção máxima de dados faltantes permitida por SNP (opcional)
min_snp_cr	Mínimo call rate aceitável para SNPs
min_maf	Frequência alélica mínima permitida para SNPs (opcional)
hwe	Identifica SNPs com desvio de HWE
snp_mono	Identifica SNPs monomórficos
remove_chr	Descarta SNPs localizados nos cromossomos listados
action	"report", "filter" ou "both"

Value

Dependendo do argumento action, retorna: - "report": lista com SNPs removidos por critério; - "filter": objeto SNPDataLong com SNPs filtrados; - "both": lista contendo o objeto filtrado e o relatório.

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), Chrom = 1, Position = 1:10)
x <- new("SNPDataLong", geno = mat, map = map)

qcSNPs(x, min_snp_cr = 0.8, min_maf = 0.05, snp_mono = TRUE, action = "report")
## End(Not run)
```

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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")
```

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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)

## S4 method for signature 'FImputeRunner'
runFImpute(object)
```

Arguments

object	An object of class 'FImputeRunner'

Value

An updated 'FImputeRunner' object with the 'results' slot populated.

---

saveFImpute	*Save genotype and map files in FImpute format*

Description

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

Usage

```
saveFImpute(object, ...)

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

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

Arguments

object	An object of class 'FImputeExport' or 'SNPDataLong'.
...	Further arguments passed to methods.
path	Character. Output directory where files will be written (only for 'SNPDataLong' method; default = '"fimpute_run"').

Value

No return value. Files are saved to disk.

Examples

```
## Not run:
if (requireNamespace("snpStats", quietly = TRUE)) {
  mat <- matrix(sample(c(0L, 1L, 2L), 50, replace = TRUE), nrow = 5)
  colnames(mat) <- paste0("snp", 1:10)
  rownames(mat) <- paste0("ind", 1:5)

  sm <- new("SnpMatrix", data = as.raw(mat))
  map <- data.frame(Name = colnames(mat), Chromosome = 1, Position = 1:10)
  x <- new("SNPDataLong", geno = sm, map = map)

  saveFImpute(x, path = tempdir())
}

## End(Not run)
```

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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)
```

Arguments

geno	A 'SnpMatrix' object (from the 'snpStats' package).
map	A 'data.frame' with columns 'Name', 'Chromosome', and 'Position'.
path	Path where the files will be saved.

Value

No return value. Files are saved to disk.

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summary,SNPDataLong-method
Summary para objetos da classe SNPDataLong

Description

Summary para objetos da classe SNPDataLong

Usage

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

Arguments

object   Objeto do tipo SNPDataLong

Value

Imprime resumo na tela

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