Package 'snplinkage'

May 9, 2026

Title Single Nucleotide Polymorphisms Linkage Disequilibrium Visualizations

Version 1.2.0

Description Linkage disequilibrium visualizations of up to several hundreds of single nucleotide polymorphisms (SNPs), annotated with chromosomic positions and gene names. Two types of plots are available for small numbers of SNPs (<40) and for large numbers (tested up to 500). Both can be extended by combining other ggplots, e.g. association studies results, and functions enable to directly visualize the effect of SNP selection methods, as minor allele frequency filtering and TagSNP selection, with a second correlation heatmap. The SNPs correlations are computed on Genotype Data objects from the 'GWASTools' package using the 'SNPRelate' package, and the plots are customizable 'ggplot2' and 'gtable' objects and are annotated using the 'biomaRt' package. Usage is detailed in the vignette with example data and results from up to 500 SNPs of 1,200 scans are in Charlon T. (2019) <doi:10.13097/archive-ouverte/unige:161795>.

Imports biomaRt, cowplot, data.table, gdsfmt, ggplot2, ggrepel, grid, grDevices, gtable, knitr, magrittr, methods, parallel, reshape2, SNPRelate, stats, utils

Depends R (>= 2.15), GWASTools (>= 1.10.1)

Suggests rmarkdown, testthat

biocViews GeneticVariability, MicroArray, SNP

URL https://gitlab.com/thomaschln/snplinkage

BugReports https://gitlab.com/thomaschln/snplinkage/-/issues

VignetteBuilder knitr

License GPL-3

Encoding UTF-8

RoxygenNote 7.3.2

NeedsCompilation no

Author Thomas Charlon [aut, cre] (ORCID: <https://orcid.org/0000-0001-7497-0470>), Karl Forner [aut],

Alessandro Di Cara [aut],
Jérôme Wojcik [aut]

Maintainer Thomas Charlon <charlon@protonmail.com>

Repository CRAN

Date/Publication 2024-09-09 19:10:02 UTC

Contents

`chisq_pvalues` *Compute Chi-squared p-values*

Description

Compute Chi-squared p-values

Usage

```
chisq_pvalues(
  m_data,
  response,
  adjust_method = "fdr",
  mlog10_transform = TRUE,
  n_cores = 1,
  ...
)
```

Arguments

`m_data`	Data matrix of observations by variables
`response`	Response vector of length the number of observations
`adjust_method`	Multiple testing p-value adjustment method. Passed to stats::p.adjust. 'fdr' by default.
`mlog10_transform`	Logical, transform p-values by minus log10. True by default.
`n_cores`	Number of cores
`...`	Passed to stats::chisq.test

Value

Chi-squared p-values

`chisq_pvalues_gdata` *Compute Chi-squared p-values on a Genotype data object*

Description

Compute Chi-squared p-values on a Genotype data object

Usage

```
chisq_pvalues_gdata(
  gdata,
  snp_idxs,
  response_column = "region",
  response_value = "Europe",
  threshold = 2,
  ...
)
```

Arguments

`gdata`	Genotype data object
`snp_idxs`	SNPs indexes
`response_column`	Response column in gdata scans annotations data frame
`response_value`	Response value. The response vector will be a logical, true if equal to the value, false otherwise.
`threshold`	Keep only associations greater than the threshold
`...`	Passed to chisq_pvalues

Value

SNPs annotation data frame, chi-squared p-values in column pvalues

crohn *Crohn's disease data*

Description

The data set consist of 103 common (>5% minor allele frequency) SNPs genotyped in 129 trios from an European-derived population. These SNPs are in a 500-kb region on human chromosome 5q31 implicated as containing a genetic risk factor for Crohn disease.

Imported from the gap R package.

An example use of the data is with the following paper, Kelly M. Burkett, Celia M. T. Greenwood, BradMcNeney, Jinko Graham. Gene genealogies for genetic association mapping, with application to Crohn's disease. Fron Genet 2013, 4(260) doi: 10.3389/fgene.2013.00260

Usage

```
data(crohn)
```

Format

A data frame containing 387 rows and 212 columns

Source

MJ Daly, JD Rioux, SF Schaffner, TJ Hudson, ES Lander (2001) High-resolution haplotype structure in the human genome Nature Genetics 29:229-232

diamond_annots *Get diamond ggplot layer.*

Description

Diamond ggplot layer for ggplot_ld

Usage

```
diamond_annots(data, x = "x", y = "y", color = "color", size = 0.5)
```

Arguments

data	Data frame of 3 columns defining the diamonds
x	Name of the column for horizontal positions
y	Name of the column for vertical positions
color	Name of the column for color values
size	Radius of the diamonds

Value

gglayers

`fetch_allele1.default` *Fetch allele 1 (default object)*

Description

Fetch allele 1 (default object)

Usage

```
## Default S3 method:
fetch_allele1(obj, snps_idx)
```

Arguments

`obj`	Default object
`snps_idx`	SNPs indexes

`fetch_allele1.GdsGenotypeReader`
Fetch allele 1 (GdsGenotypeReader object)

Description

Fetch allele 1 (GdsGenotypeReader object)

Usage

```
## S3 method for class 'GdsGenotypeReader'
fetch_allele1(obj, snps_idx)
```

Arguments

`obj`	GenotypeData object
`snps_idx`	SNPs indexes

Value

Allele 1

`fetch_allele1.GenotypeData`
Fetch allele 1 (GenotypeData object)

Description

Fetch allele 1 (GenotypeData object)

Usage

```
## S3 method for class 'GenotypeData'
fetch_allele1(obj, ...)
```

Arguments

`obj`	GenotypeData object
`...`	Passed to getAlleleA

Value

Allele 1

`fetch_allele1.GenotypeDataSubset`
Fetch allele 1 (GenotypeDataSubset object)

Description

Fetch allele 1 (GenotypeDataSubset object)

Usage

```
## S3 method for class 'GenotypeDataSubset'
fetch_allele1(obj, snps_idx)
```

Arguments

`obj`	GenotypeDataSubset object
`snps_idx`	SNPs indexes

Value

Allele 1

fetch_allele2.default *Fetch allele 2 (default object)*

Description

Fetch allele 2 (default object)

Usage

```
## Default S3 method:
fetch_allele2(obj, snps_idx)
```

Arguments

obj	Default object
snps_idx	SNPs indexes

fetch_allele2.GdsGenotypeReader *Fetch allele 2 (GdsGenotypeReader object)*

Description

Fetch allele 2 (GdsGenotypeReader object)

Usage

```
## S3 method for class 'GdsGenotypeReader'
fetch_allele2(obj, snps_idx)
```

Arguments

obj	GenotypeData object
snps_idx	SNPs indexes

Value

Allele 2

`fetch_allele2.GenotypeData` *Fetch allele 2 (GenotypeData object)*

Description

Fetch allele 2 (GenotypeData object)

Usage

```
## S3 method for class 'GenotypeData'
fetch_allele2(obj, ...)
```

Arguments

`obj`	GenotypeData object
`...`	Passed to getAlleleB

Value

Allele 2

`fetch_allele2.GenotypeDataSubset` *Fetch allele 1 (GenotypeDataSubset object)*

Description

Fetch allele 1 (GenotypeDataSubset object)

Usage

```
## S3 method for class 'GenotypeDataSubset'
fetch_allele2(obj, snps_idx)
```

Arguments

`obj`	GenotypeDataSubset object
`snps_idx`	SNPs indexes

Value

Allele 2

fetch_gds.default *Fetch GDS (default)*

Description

Fetch GDS (default)

Usage

```
## Default S3 method:
fetch_gds(obj, ...)
```

Arguments

obj	Default object
...	Not passed

fetch_gds.GdsGenotypeReader *Fetch GDS (GdsGenotypeReader)*

Description

Fetch GDS (GdsGenotypeReader)

Usage

```
## S3 method for class 'GdsGenotypeReader'
fetch_gds(obj, ...)
```

Arguments

obj	GdsGenotypeReader object
...	Not passed

Value

S4 slot 'handler' of obj

`fetch_gds.GenotypeData` *Fetch GDS (GenotypeData)*

Description

Fetch GDS (GenotypeData)

Usage

```
## S3 method for class 'GenotypeData'
fetch_gds(obj, ...)
```

Arguments

`obj`	GenotypeData object
`...`	Not passed

Value

fetch_gds output on S4 slot 'data' of obj

`fetch_gds.GenotypeDataSubset` *Fetch GDS (GenotypeDataSubset)*

Description

Fetch GDS (GenotypeDataSubset)

Usage

```
## S3 method for class 'GenotypeDataSubset'
fetch_gds(obj, ...)
```

Arguments

`obj`	GenotypeDataSubset object
`...`	Not passed

gdata_add_gene_annots *gdata_add_gene_annots*

Description

Add biomaRt gene annotations to Genotype Data object.

Usage

```
gdata_add_gene_annots(
  gdata,
  snp_idxs,
  rsids_colname = "probe_id",
  biomart_metadb = get_biomart_metadb()
)
```

Arguments

gdata	Genotype Data object
snp_idxs	SNP indexes
rsids_colname	Column of SNP annotation data frame with rs identifiers
biomart_metadb	List with slots snpmart and ensembl, corresponding to the biomart databases to query for SNP identifiers and gene names, respectively. See get_biomart_metadb function.

Value

Genotype Data object

gdata_add_gene_annots_aim_example *gdata_add_gene_annots_aim_example*

Description

Add ancestry informative markers gene annotations to Genotype Data object. Convenience function for the vignette to avoid querying biomaRt on build.

Usage

```
gdata_add_gene_annots_aim_example(gdata, aim_idxs)
```

Arguments

gdata	Genotype Data object
aim_idxs	AIM indexes in the example Genotype data object

Value

Genotype Data object

`gdata_add_gene_annots_hladr_example` *gdata_add_gene_annots_hladr_example*

Description

Add HLA-DR gene annotations to Genotype Data object. Convenience function for the vignette to avoid querying biomaRt on build.

Usage

```
gdata_add_gene_annots_hladr_example(gdata, hla_dr_idxs)
```

Arguments

`gdata`	Genotype Data object
`hla_dr_idxs`	HLA-DR indexes in the example Genotype data object

Value

Genotype Data object

`gdata_scans_annots` *gdata_scan_annots*

Description

Get scans annotations from a Genotype Data object or a subset.

Usage

```
gdata_scans_annots(gdata, scan_ids)
```

Arguments

`gdata`	Genotype Data object
`scan_ids`	Scan identifiers to subset

Value

Scans annotations data frame

gdata_snps_annots *gdata_snp_annots*

Description

Get SNPs annotations from a Genotype Data object or a subset.

Usage

```
gdata_snps_annots(gdata, snp_ids = NULL)
```

Arguments

gdata	Genotype Data object
snp_ids	SNP identifiers to subset

Value

SNP annotation data frame

get_biomart_metadb *get_biomart_metadb*

Description

To query gene names of SNPs, it is necessary to retrieve two objects using biomaRt::useMart. First, the object required to map SNP rs identifiers to ENSEMBL identifiers. Second, the object required to map ENSEMBL identifiers to common gene names. The function returns a list of two slots named snpmart and ensembl corresponding to each one, respectively. Once obtained it is saved to a local file.

Usage

```
get_biomart_metadb(
  filepath = extdata_filepath("bmart_meta.rds"),
  host = "https://grch37.ensembl.org"
)
```

Arguments

filepath	Path to save the biomaRt objects
host	BiomaRt Ensembl host, by default https://grch37.ensembl.org

Value

List of slots snpmart and ensembl as detailed above

get_scan_annot.GenotypeData *Get scans annotations (GenotypeData object)*

Description

Get scans annotations (GenotypeData object)

Usage

```
## S3 method for class 'GenotypeData'
get_scan_annot(obj, ...)
```

Arguments

obj	GenotypeData object
...	Not passed

Value

Data frame

get_scan_annot.GenotypeDataSubset *Get scans annotations (GenotypeDataSubset object)*

Description

Get scans annotations (GenotypeDataSubset object)

Usage

```
## S3 method for class 'GenotypeDataSubset'
get_scan_annot(obj, ...)
```

Arguments

obj	GenotypeDataSubset object
...	Not passed

Value

Data frame

`get_snp_annot.GenotypeData` *Get SNPs annotations (GenotypeData object)*

Description

Get SNPs annotations (GenotypeData object)

Usage

```
## S3 method for class 'GenotypeData'
get_snp_annot(obj, ...)
```

Arguments

`obj`	GenotypeData object
`...`	Not passed

Value

Data frame

`get_snp_annot.GenotypeDataSubset` *Get SNPs annotations (GenotypeDataSubset object)*

Description

Get SNPs annotations (GenotypeDataSubset object)

Usage

```
## S3 method for class 'GenotypeDataSubset'
get_snp_annot(obj, ...)
```

Arguments

`obj`	GenotypeDataSubset object
`...`	Not passed

Value

Data frame

`ggplot_associations` *Ggplot associations*

Description

Get SNPs associations ggplot, either as points or as a linked area. Optionally add labels to most associated points using ggrepel.

Usage

```
ggplot_associations(
  df_snp,
  pvalue_colname = "pvalues",
  labels_colname = "probe_id",
  n_labels = 10,
  nudge = c(0, 1),
  linked_area = FALSE,
  byindex = linked_area,
  colors = if (linked_area) snp_position_colors(nrow(df_snp)) else "black"
)
```

Arguments

`df_snp`	SNP annotation data frame with columns chromosome, position, and as specified by parameters pvalue_colname and optionally labels_colname.
`pvalue_colname`	Column name of df_snp with association values
`labels_colname`	Optional column name of df_snp with labels. Set to NULL to remove.
`n_labels`	Number of labels of most associated points to display.
`nudge`	Nudge parameter passed to ggrepel::geom_label_repel.
`linked_area`	Add a linked area to associations points, default FALSE
`byindex`	Display by SNP index or chromosomic position (default)
`colors`	Colors of SNPs

Value

ggplot

ggplot_ld *Ggplot linkage disequilibrium*

Description

Display SNP r2 correlations using points or diamonds with text.

Usage

```
ggplot_ld(
  df_ld,
  diamonds = length(unique(df_ld$SNP_A)) < 40,
  point_size = 120/sqrt(nrow(df_ld)),
  reverse = FALSE,
  reindex = TRUE
)
```

Arguments

df_ld	Data frame with columns SNP_A, SNP_B, and R2. As returned by the snprelate_ld function.
diamonds	Should the values be displayed as diamonds or points ? Default is TRUE for less than 40 SNPs.
point_size	Size for geom_point. Ignored if diamonds is TRUE.
reverse	Reverse the display (horizontal symmetry)
reindex	If FALSE, SNPs are positionned following their IDs

Value

ggplot

ggplot_snp_pos *Ggplot SNPs position*

Description

Get SNPs position ggplot with mappings to combine with other ggplots. Optionally add labels and an upper subset.

Usage

```
ggplot_snp_pos(
  df_snp,
  upper_subset = NULL,
  labels_colname = NULL,
  colors = snp_position_colors(nrow(df_snp))
)
```

Arguments

df_snp	SNP annotation data frame with a column named position and, if specified, one named as the labels_colname parameter.
upper_subset	Subset of df_snp for the positions on the upper side
labels_colname	Optional column name of df_snp to use as SNP labels.
colors	Colors for each SNP

Value

ggplot

---

gtable_ld *Gtable of linkage disequilibrium and chromosomic positions*

Description

Creates a gtable of linkage disequilibrium and chromosomic positions ggplots. A biplot_subset parameter is available to add a second linkage disequibrium ggplot to visualize the effect of a SNP selection.

Usage

```
gtable_ld(
  df_ld,
  df_snp,
  biplot_subset = NULL,
  labels_colname = NULL,
  diamonds = length(unique(df_ld$SNP_A)) < 40,
  point_size = ifelse(is.null(biplot_subset), 120, 80)/sqrt(nrow(df_ld)),
  title = "",
  title_biplot = "",
  ...
)
```

Arguments

df_ld	Data frame returned by snprelate_ld
df_snp	SNP annotations with columns snpID and position
biplot_subset	SNP indexes of the subset for the second ld plot
labels_colname	Column name of df_snp to use as SNP labels
diamonds	Display the values as diamonds or as points Default is TRUE for less than 40 SNPs.
point_size	Size for geom_point. Ignored if diamonds is TRUE.
title	Plot title
title_biplot	Optional biplot title
...	Passed to ggplot_ld

Value

gtable of ggplots

Examples

```
library(snplinkage)
gds_path <- save_hgdp_as_gds()
gdata <- load_gds_as_genotype_data(gds_path)
qc <- snprelate_qc(gdata, tagsnp = .99)
snp_idxs_8p23 <- select_region_idxs(qc$gdata, chromosome = 8,
  position_min = 11e6, position_max = 12e6)

df_ld <- snprelate_ld(qc$gdata, snps_idx = snp_idxs_8p23, quiet = TRUE)
plt <- gtable_ld(df_ld, df_snp = gdata_snps_annots(qc$gdata))
```

---

gtable_ld_associations

Gtable of linkage disequilibrium and associations

Description

Creates a gtable of a linkage disequilibrium, chromosomic positions, and association scores ggplots.

Usage

```
gtable_ld_associations(
  df_assocs,
  df_ld,
  pvalue_colname = "pvalues",
  labels_colname = "probe_id",
  n_labels = 5,
  diamonds = nrow(df_assocs) <= 40,
  linked_area = diamonds,
  point_size = 150/nrow(df_assocs),
  colors = snp_position_colors(nrow(df_assocs)),
  ...
)
```

Arguments

df_assocs	SNP annotation data frame with columns chromosome, position, and as specified by parameters pvalue_colname and optionally labels_colname.
df_ld	Data frame with columns SNP_A, SNP_B, and R2, as returned by the snprelate_ld function.
pvalue_colname	Column name of df_snp with association values
labels_colname	Optional column name of df_snp with labels. Set NULL to remove labels.

n_labels	Number of labels of most associated SNPs to display.
diamonds	Should the values be displayed as diamonds or points ? Default is TRUE for up to 40 SNPs.
linked_area	Add a linked area to associations points. Default same as diamonds.
point_size	Point size for ggplot_ld, ignored if diamonds is TRUE.
colors	Colors of SNPs
...	Passed to ggplot_associations

Value

gtable

`gtable_ld_associations_combine`

Build gtable by combining ggplots

Description

Build gtable by combining ggplots

Usage

```
gtable_ld_associations_combine(ggplots, diamonds)
```

Arguments

ggplots	List of ggplots
diamonds	Does the LD visualization use diamond-type layout

Value

gtable of ggplots

Examples

```
library(snplinkage)

# example rnaseq data frame, 20 variables of 20 patients
m_rna = matrix(runif(20 ^ 2), nrow = 20)

# pair-wise correlation matrix
m_ld = cor(m_rna) ^ 2

# keep only upper triangle and reshape to data frame
m_ld[lower.tri(m_ld, diag = TRUE)] = NA
df_ld = reshape2::melt(m_ld) |> na.omit()
```

```
# rename for SNPLinkage
names(df_ld) = c('SNP_A', 'SNP_B', 'R2')

# visualize with ggplot_ld
gg_ld = ggplot_ld(df_ld)

# let's imagine the 20 variables came from 3 physically close regions
positions = c(runif(7, 10e5, 15e5), runif(6, 25e5, 30e5),
              runif(7, 45e5, 50e5)) |> sort()

# build the dataframe
df_snp_pos = data.frame(position = positions)
df_snp_pos$label = c(rep('HLA-A', 7), rep('HLA-B', 6), rep('HLA-C', 7))

gg_pos_biplot = ggplot_snp_pos(df_snp_pos, labels_colname = 'label',
                               upper_subset = TRUE)

# let's assume HLA-B is more associated with the outcome than the other genes
pvalues = c(runif(7, 1e-3, 1e-2), runif(6, 1e-8, 1e-6), runif(7, 1e-3, 1e-2))
log10_pvals = -log10(pvalues)

# we can reuse the df_snp_pos object
df_snp_pos$pvalues = log10_pvals

# add the chromosome column
df_snp_pos$chromosome = 6

gg_assocs = ggplot_associations(df_snp_pos, labels_colname = 'label',
                                linked_area = TRUE, nudge = c(0, 0.5),
                                n_labels = 12)

l_ggs = list(pos = gg_pos_biplot, ld = gg_ld, pval = gg_assocs)
gt_ld = gtable_ld_associations_combine(l_ggs, diamonds = TRUE)
grid::grid.draw(gt_ld)
```

`gtable_ld_associations_gdata` *Gtable of linkage disequilibrium and associations using a GenotypeData object*

Description

Compute linkage disequilibrium using snprelate_ld on the set of SNPs in the associations data frame and call gtable_ld_associations. Creates a gtable of a linkage disequilibrium, chromosomic positions, and association scores ggplots.

Usage

```
gtable_ld_associations_gdata(
```

```
  df_assocs,
  gdata,
  pvalue_colname = "pvalues",
  labels_colname = "probe_id",
  diamonds = nrow(df_assocs) <= 40,
  window = 15,
  ...
)
```

Arguments

df_assocs	SNP annotation data frame with columns chromosome, position, and as specified by parameters pvalue_colname and optionally labels_colname.
gdata	GenotypeData object, as returned by load_gds_as_genotype_data
pvalue_colname	Column name of df_snp with association values
labels_colname	Optional column name of df_snp with labels. Set NULL to remove labels.
diamonds	Should the values be displayed as diamonds or points ? Default is TRUE for up to 40 SNPs.
window	Window size for snprelate_ld. Forced to the total number of SNPs if diamonds is FALSE
...	Passed to gtable_ld_associations

Value

gtable

Examples

```
library(snplinkage)
gds_path <- save_hgdp_as_gds()
gdata <- load_gds_as_genotype_data(gds_path)
qc <- snprelate_qc(gdata, tagsnp = .99)

snp_idxs_mhc <- select_region_idxs(qc$gdata,
  chromosome = 6, position_min = 29e6, position_max = 33e6)
df_assocs <- chisq_pvalues_gdata(qc$gdata, snp_idxs_mhc)

df_top_aim <- subset(df_assocs, rank(-pvalues, ties.method = 'first') <= 20)

#qc$gdata <- gdata_add_gene_annots(qc$gdata, rownames(df_top_aim))
qc$gdata <- gdata_add_gene_annots_aim_example(qc$gdata, rownames(df_top_aim))

plt <- gtable_ld_associations_gdata(df_top_aim, qc$gdata,
  labels_colname = 'gene')
```

gtable_ld_gdata *Gtable of linkage disequilibrium and positions using a GenotypeData object*

Description

Compute linkage disequilibrium using snprelate_ld on a set of SNP indexes and call gtable_ld. Two parameters are available to compute and compare minor allele frequency filtering and TagSNP selection by displaying two LD plots with their positions in the center. The maf and r2 parameters are used similarly and as follows: - compare baseline with MAF 5 gtable_ld(gdata, snps_idx, maf = 0.05) - compare baseline with TagSNP r2 = 0.8 gtable_ld(gdata, snps_idx, r2 = 0.8) - compare 5 gtable_ld(gdata, snps_idx, maf = c(0.05, 0.05), r2 = 0.8) - compare MAF 5 gtable_ld(gdata, snps_idx, maf = c(0.05, 0.1), r2 = c(0.8, 0.6))

Usage

```
gtable_ld_gdata(
  gdata,
  snps_idx,
  maf = NULL,
  r2 = NULL,
  diamonds = length(snps_idx) < 40,
  window = 15,
  autotitle = TRUE,
  autotitle_bp = TRUE,
  double_title = FALSE,
  ...
)
```

Arguments

gdata	GenotypeData object returned by load_gds_as_genotype_data
snps_idx	SNPs indexes to select
maf	Minor allele frequency threshold(s), see description
r2	TagSNP r2 threshold(s), see description
diamonds	Display the values as diamonds or as points Default is TRUE for less than 40 SNPs.
window	Window size for snprelate_ld. Forced to the total number of SNPs if diamonds is FALSE
autotitle	Set title to feature selection method(s), number of SNPs and chromosome
autotitle_bp	Set biplot title to feature selection method(s), number of SNPs and chromosome
double_title	Logical, if false (default) keep only biplot title
...	Passed to gtable_ld

Value

gtable of ggplots

Examples

```
library(snplinkage)
gds_path <- save_hgdp_as_gds()
gdata <- load_gds_as_genotype_data(gds_path)
qc <- snprelate_qc(gdata, tagsnp = .99)

snp_idxs_1p13_large <- select_region_idxs(qc$gdata, chromosome = 1,
  position_min = 114e6, n_snps = 100)
plt <- gtable_ld_gdata(qc$gdata, snp_idxs_1p13_large)
```

---

gtable_ld_grobs *Build gtable by combining ggplots*

Description

Build gtable by combining ggplots

Usage

```
gtable_ld_grobs(plots, labels_colname, title)
```

Arguments

plots	List of ggplots
labels_colname	Does the SNP position plot contain labels
title	Title text string

Value

gtable of ggplots

Examples

```
library(snplinkage)

# example rnaseq data frame, 20 variables of 20 patients
m_rna = matrix(runif(20 ^ 2), nrow = 20)

# pair-wise correlation matrix
m_ld = cor(m_rna) ^ 2

# keep only upper triangle and reshape to data frame
m_ld[lower.tri(m_ld, diag = TRUE)] = NA
```

```
df_ld = reshape2::melt(m_ld) |> na.omit()

# rename for SNPLinkage
names(df_ld) = c('SNP_A', 'SNP_B', 'R2')

# visualize with ggplot_ld
gg_ld = ggplot_ld(df_ld)
# let's imagine the 20 variables came from 3 physically close regions
positions = c(runif(7, 10e5, 15e5), runif(6, 25e5, 30e5),
              runif(7, 45e5, 50e5)) |> sort()

# build the dataframe
df_snp_pos = data.frame(position = positions)
df_snp_pos$label = c(rep('HLA-A', 7), rep('HLA-B', 6), rep('HLA-C', 7))
gg_snp_pos = ggplot_snp_pos(df_snp_pos, labels_colname = 'label')

l_ggs = list(snp_pos = gg_snp_pos, ld = gg_ld)
gt_ld = gtable_ld_grobs(l_ggs, labels_colname = TRUE,
                        title = 'RNASeq correlations')
grid::grid.draw(gt_ld)
```

`is_snp_first_dim.default` *Is SNP first dimension (default)*

Description

Is SNP first dimension (default)

Usage

```
## Default S3 method:
is_snp_first_dim(obj, ...)
```

Arguments

`obj`	Default object
`...`	Not passed

Value

NA

is_snp_first_dim.gds.class *Is SNP first dimension (GDS object)*

Description

Is SNP first dimension (GDS object)

Usage

```
## S3 method for class 'gds.class'
is_snp_first_dim(obj, ...)
```

Arguments

obj	GDS object
...	Not passed

Value

Logical, TRUE if SNP is first dimension

is_snp_first_dim.GdsGenotypeReader *Is SNP first dimension (GdsGenotypeReader object)*

Description

Is SNP first dimension (GdsGenotypeReader object)

Usage

```
## S3 method for class 'GdsGenotypeReader'
is_snp_first_dim(obj, ...)
```

Arguments

obj	GdsGenotypeReader object
...	Not passed

Value

is_snp_first_dim output on S4 slot 'handler'

`is_snp_first_dim.GenotypeData`
Is SNP first dimension (GenotypeData object)

Description

Is SNP first dimension (GenotypeData object)

Usage

```
## S3 method for class 'GenotypeData'
is_snp_first_dim(obj, ...)
```

Arguments

`obj`	Genotype data object
`...`	Not passed

Value

is_snp_first_dim output on S4 slot 'data'

`is_snp_first_dim.MatrixGenotypeReader`
Is SNP first dimension (MatrixGenotypeReader object)

Description

Is SNP first dimension (MatrixGenotypeReader object)

Usage

```
## S3 method for class 'MatrixGenotypeReader'
is_snp_first_dim(obj, ...)
```

Arguments

`obj`	MatrixGenotypeReader object
`...`	Not passed

Value

TRUE

is_snp_first_dim.NcdfGenotypeReader

Is SNP first dimension (NcdfGenotypeReader object)

Description

Is SNP first dimension (NcdfGenotypeReader object)

Usage

```
## S3 method for class 'NcdfGenotypeReader'
is_snp_first_dim(obj, ...)
```

Arguments

obj	NcdfGenotypeReader object
...	Not passed

Value

TRUE

load_gds_as_genotype_data

Load GDS as Genotype Data

Description

Open a connection to a snpgds file (cf. SNPRelate package) as a Genotype Data object.

Usage

```
load_gds_as_genotype_data(
  gds_file,
  read_snp_annot = TRUE,
  read_scan_annot = TRUE
)
```

Arguments

gds_file	Path of snpgds file
read_snp_annot	Read the SNPs' annotations
read_scan_annot	Read the scans' annotations

Value

Genotype Data object

Examples

```
library(snplinkage)
gds_path <- save_hgdp_as_gds()
gdata <- load_gds_as_genotype_data(gds_path)
```

`parallel_apply` *Separate a matrix in a list of matrices of length the number of cores and apply a function on the columns in parallel*

Description

Separate a matrix in a list of matrices of length the number of cores and apply a function on the columns in parallel

Usage

```
parallel_apply(m_data, apply_fun, n_cores = 1, ...)
```

Arguments

`m_data`	Data matrix
`apply_fun`	Function to apply
`n_cores`	Number of cores
`...`	Passed to apply_fun

Value

apply_fun return

print_qc_as_tex_table *print_qc_as_tex_table*

Description

Print information about quality control performed by the snprelate_qc function.

Usage

```
print_qc_as_tex_table(
  gdata_qc,
  label = "qc",
  caption = paste("Quality control and feature selection of the subset of the",
    "human genome diversity project dataset.")
)
```

Arguments

gdata_qc	Genotype Data object object returned by snprelate_qc
label	Label of the Tex table
caption	Caption of the Tex table

Value

Prints knitr::kable object using cat

save_hgdp_as_gds *save_hgdp_as_gds*

Description

Save the HGDP SNP data text file as a Genomic Data Structure file

Usage

```
save_hgdp_as_gds(paths = hgdp_filepaths(), outpath = tempfile(), ...)
```

Arguments

paths	Paths of the zip, txt, and gds files
outpath	Output GDS file path
...	Passed to save_genotype_data_as_gds

Value

Path of the saved gds file

`select_region_idxs` *select_region_idxs*

Description

Select SNP indexes corresponding to a specific genomic region.

Usage

```
select_region_idxs(
  gdata,
  chromosome,
  position_min = -Inf,
  position_max = Inf,
  n_snps = 0,
  offset = 0
)
```

Arguments

`gdata`	Genotype Data object
`chromosome`	Chromosome to select
`position_min`	Minimum base pair position to select
`position_max`	Maximum base pair position to select
`n_snps`	Maximum number of SNPs to return
`offset`	Number of SNPs to offset

Value

SNP indexes of Genotype Data object

`snprelate_allele_frequencies`
Compute allele frequencie and snp missing rate

Description

Wrapper over SNPRelate::snpgdsSNPRateFreq

Usage

```
snprelate_allele_frequencies(
  gdata,
  snps_idx = NULL,
  scans_idx = NULL,
  quiet = FALSE
)
```

Arguments

gdata	A GenotypeData object
snps_idx	Vector of snps indices
scans_idx	Vector of scans indices
quiet	Whether to be quiet

Value

A data frame of snps_idx, snps_ids, allele1, allele2, maf, missing where allele1 and allele2 are the rates of the alleles, and maf the minimum of the 2. Missing is the missing rate. N.B: the allele rates are computed on the non missing genotypes, i.e. their sum equals 1.

---

snprelate_ld *Wrapper for snpgdsLDMat to compute r2*

Description

Wrapper for snpgdsLDMat to compute r2

Usage

```
snprelate_ld(
  gdata,
  window_size = 0,
  min_r2 = 0,
  snps_idx = NULL,
  scans_idx = NULL,
  threads = 1,
  quiet = FALSE
)
```

Arguments

gdata	A GenotypeData object
window_size	Max number of SNPs in LD window, 0 for no window
min_r2	Minimum r2 value to report

snps_idx	Indices of snps to use
scans_idx	Indices of scans to use
threads	The number of threads to use
quiet	Whether to be quiet

Value

A data frame with columns SNP_A, SNP_B, R2 for r2 >= min_r2

`snprelate_ld_select` *Wrapper for snpgdsLDpruning to select Tag SNPs*

Description

The tagged snp set is (by sliding window) representative and strongly not redundant.

Usage

```
snprelate_ld_select(
  gdata,
  window_length = 500L,
  min_r2,
  window_size = NA,
  snps_idx = NULL,
  scans_idx = NULL,
  remove.monosnp = FALSE,
  autosome.only = FALSE,
  method = "r",
  threads = 1,
  quiet = FALSE,
  ...
)
```

Arguments

gdata	A GenotypeData object
window_length	Max length in kb of the window
min_r2	Minimum r2 value to report
window_size	Max number of SNPs in LD window
snps_idx	Indices of snps to use
scans_idx	Indices of scans to use
remove.monosnp	if TRUE, remove monomorphic SNPs
autosome.only	if TRUE, use autosomal SNPs only; if it is a numeric or character value, keep SNPs according to the specified chromosome

method	"composite", "r", "dprime", "corr", see details
threads	The number of threads to use, currently ignored
quiet	Whether to be quiet
...	Forwarded to SNPRelate::snpgdsLDpruning

Value

A list of SNP IDs stratified by chromosomes.

---

snprelate_qc *snprelate_qc*

Description

Quality control using SNPRelate functions.

Usage

```
snprelate_qc(
  gdata,
  samples_nas = 0.03,
  ibs = 0.99,
  keep_ids = NULL,
  snps_nas = 0.01,
  maf = 0.05,
  tagsnp = 0.8,
  n_cores = 1
)
```

Arguments

gdata	Genotype data object
samples_nas	NA threshold for samples, default 3 pct
ibs	Samples identity by state threshold, default 99 pct
keep_ids	Samples ids to keep even if IBS is higher than threshold. Used for monozygotic twins.
snps_nas	NA threshold for SNPs, default 1 pct
maf	Minor allele frequency threshold, default 5 pct
tagsnp	TagSNP r2 correlation threshold, default 0.8
n_cores	Number of cores

Value

List of gdata, Genotype data object, and df_qc, QC info data frame

Examples

```
library(snplinkage)
gds_path <- save_hgdp_as_gds()
gdata <- load_gds_as_genotype_data(gds_path)
qc <- snprelate_qc(gdata, tagsnp = .99)
```

`%<>%` *Assignment pipe*

Description

Pipe an object forward into a function or call expression and update the ‘lhs‘ object with the resulting value. Magrittr imported function, see details and examples in the magrittr package.

Arguments

`lhs`	An object which serves both as the initial value and as target.
`rhs`	a function call using the magrittr semantics.

Value

None, used to update the value of lhs.

`%$%` *Exposition pipe*

Description

Expose the names in ‘lhs‘ to the ‘rhs‘ expression. Magrittr imported function, see details and examples in the magrittr package.

Arguments

`lhs`	A list, environment, or a data.frame.
`rhs`	An expression where the names in lhs is available.

Value

Result of rhs applied to one or several names of lhs.

`%>%` *Pipe*

Description

Pipe an object forward into a function or call expression. Magrittr imported function, see details and examples in the magrittr package.

Arguments

`lhs`	A value or the magrittr placeholder.
`rhs`	A function call using the magrittr semantics.

Value

Result of rhs applied to lhs, see details in magrittr package.

Index