Package 'qtl2ggplot'

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Title Data Visualization for QTL Experiments

Description Functions to plot QTL (quantitative trait loci) analysis results and related diagnostics.
Part of 'qtl2', an upgrade of the 'qtl' package to better handle high-dimensional data and complex cross designs.

Depends R (>= 3.1.0)

Imports Rcpp (>= 0.12.7), assertthat, dplyr, ggplot2, purrr, stringr, tidyr, rlang, graphics, RColorBrewer, grid, qtl2, ggrepel

Suggests devtools, testthat, roxygen2, knitr, rmarkdown

VignetteBuilder knitr

License GPL-3

URL https://github.com/byandell/qtl2ggplot, https://kbroman.org/qtl2/

BugReports https://github.com/byandell/qtl2ggplot/issues

Encoding UTF-8

ByteCompile true

LinkingTo Rcpp

RoxygenNote 7.1.2

NeedsCompilation yes

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Repository CRAN

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R topics documented:

`color_patterns_get` *Set up col, pattern and group for plotting.*

Description

Set up col, pattern and group for plotting.

Usage

```
color_patterns_get(scan1ggdata, col, palette = NULL)
```

Arguments

`scan1ggdata`	data frame to be used for plotting
`col`	Color for `color` column in `scan1ggdata`
`palette`	for colors (default `NULL` uses `"Dark2"` from `RColorBrewer` package)

Value

list of `colors` and `shapes`.

color_patterns_pheno *Set up col, pattern, shape and group for plotting.*

Description

Set up col, pattern, shape and group for plotting.

Usage

```
color_patterns_pheno(
  scan1ggdata,
  lod,
  pattern,
  col,
  shape,
  patterns,
  facet = NULL
)
```

Arguments

scan1ggdata	data frame to be used for plotting
lod	matrix of LOD scores by position and pheno
pattern	allele pattern of form AB:CDEFGH
col	Color for color column in scan1ggdata
shape	Shape for shape column in scan1ggdata
patterns	Connect SDP patterns: one of c("none","all","hilit")
facet	use facet_wrap if not NULL

Value

data frame scan1ggdata with additional objects.

color_patterns_set *Set up colors for patterns or points*

Description

Set up colors for patterns or points

Usage

```
color_patterns_set(
  scan1output,
  snpinfo,
  patterns,
  col,
  pattern,
  show_all_snps,
  col_hilit,
  drop_hilit,
  maxlod
)
```

Arguments

scan1output	output of linear mixed model for phename (see scan1)
snpinfo	Data frame with snp information
patterns	Connect SDP patterns: one of c("none","all","hilit").
col	Color of other points, or colors for patterns
pattern	allele pattern as of form AB:CDEFGH
show_all_snps	show all SNPs if TRUE
col_hilit	Color of highlighted points
drop_hilit	SNPs with LOD score within this amount of the maximum SNP association will be highlighted.
maxlod	Maximum LOD for drop of drop_hilit

Value

list of col and pattern.

---

ggplot_coef *Plot QTL effects along chromosome*

Description

Plot estimated QTL effects along a chromosomes.

Usage

```
ggplot_coef(
  x,
  map,
  columns = NULL,
  col = NULL,
```

```
  scan1_output = NULL,
  gap = 25,
  ylim = NULL,
  bgcolor = "gray90",
  altbgcolor = "gray85",
  ylab = "QTL effects",
  xlim = NULL,
  ...
)

ggplot_coefCC(x, map, colors = qtl2::CCcolors, ...)

## S3 method for class 'scan1coef'
autoplot(x, ...)
```

Arguments

x	Estimated QTL effects ("coefficients") as obtained from scan1coef.
map	A list of vectors of marker positions, as produced by insert_pseudomarkers.
columns	Vector of columns to plot
col	Vector of colors, same length as columns. If NULL, some default choices are made.
scan1_output	If provided, we make a two-panel plot with coefficients on top and LOD scores below. Should have just one LOD score column; if multiple, only the first is used.
gap	Gap between chromosomes.
ylim	y-axis limits. If NULL, we use the range of the plotted coefficients.
bgcolor	Background color for the plot.
altbgcolor	Background color for alternate chromosomes.
ylab	y-axis label
xlim	x-axis limits. If NULL, we use the range of the plotted coefficients.
...	Additional graphics parameters.
colors	Colors to use for plotting.

Details

ggplot_coefCC() is the same as ggplot_coef(), but forcing columns=1:8 and using the Collaborative Cross colors, CCcolors.

Value

object of class ggplot.

See Also

ggplot_scan1, ggplot_snpasso

Examples

```
# read data
iron <- qtl2::read_cross2(system.file("extdata", "iron.zip", package="qtl2"))

# insert pseudomarkers into map
map <- qtl2::insert_pseudomarkers(iron$gmap, step=1)

# calculate genotype probabilities
probs <- qtl2::calc_genoprob(iron, map, error_prob=0.002)

# grab phenotypes and covariates; ensure that covariates have names attribute
pheno <- iron$pheno[,1]
covar <- match(iron$covar$sex, c("f", "m")) # make numeric
names(covar) <- rownames(iron$covar)

# calculate coefficients for chromosome 7
coef <- qtl2::scan1coef(probs[,7], pheno, addcovar=covar)

# plot QTL effects
ggplot2::autoplot(coef, map[7], columns=1:3)
```

---

ggplot_genes *Plot gene locations for a genomic interval*

Description

Plot gene locations for a genomic interval, as rectangles with gene symbol (and arrow indicating strand/direction) below.

Usage

```
ggplot_genes(
  genes,
  xlim = NULL,
  minrow = 4,
  padding = 0.2,
  colors = c("black", "red3", "green4", "blue3", "orange"),
  ...
)

## S3 method for class 'genes'
autoplot(x, ...)
```

Arguments

genes	Data frame containing `start` and `stop` in bp, `strand` (as `"-"`, `"+"`, or `NA`), and `Name`.

xlim	x-axis limits (in Mbp)
minrow	Minimum number of rows of genes
padding	Proportion to pad with white space around the genes
colors	Vectors of colors, used sequentially and then re-used.
...	Optional arguments passed to plot.
x	Object of class genes

Value

None.

Examples

```
filename <- file.path("https://raw.githubusercontent.com/rqtl",
                      "qtl2data/master/DOex",
                      "c2_genes.rds")
tmpfile <- tempfile()
download.file(filename, tmpfile, quiet=TRUE)
gene_tbl <- readRDS(tmpfile)
unlink(tmpfile)

ggplot_genes(gene_tbl)
```

---

ggplot_genes_internal *GGPlot internal routine for ggplot_genes*

Description

Plot genes at positions

Usage

```
ggplot_genes_internal(
  start,
  end,
  strand,
  rect_top,
  rect_bottom,
  colors,
  space,
  y,
  dir_symbol,
  name,
  xlim,
  xlab = "Position (Mbp)",
  ylab = "",
```

```
  bgcolor = "gray92",
  xat = NULL,
  legend.position = "none",
  vlines = NULL,
  ...
)
```

Arguments

`start`, `end`, `strand`, `rect_top`, `rect_bottom`, `colors`, `space`, `y`, `dir_symbol`, `name`, `xlim`	usual parameters
`legend.position`, `vlines`, `xlab`, `ylab`, `bgcolor`, `xat`	hidden parameters
`...`	Additional graphics parameters.

Value

object of class `ggplot`.

---

ggplot_listof_scan1coef

Plot of object of class listof_scan1coeff

Description

Plot object of class `listof_scan1coeff`, which is a list of objects of class `scan1coef`.

Usage

```
ggplot_listof_scan1coef(
  x,
  map,
  columns = NULL,
  col = NULL,
  scan1_output = NULL,
  facet = "pattern",
  ...
)

## S3 method for class 'listof_scan1coef'
autoplot(x, ...)
```

Arguments

x	object of class listof_scan1coeff
map	A list of vectors of marker positions, as produced by insert_pseudomarkers.
columns	Vector of columns to plot
col	Vector of colors, same length as columns. If NULL, some default choices are made.
scan1_output	If provided, we make a two-panel plot with coefficients on top and LOD scores below. Should have just one LOD score column; if multiple, only the first is used.
facet	Plot facets if multiple phenotypes and group provided (default = "pattern").
...	arguments for ggplot_coef
pattern	Use phenotype names as pattern.

Value

object of class ggplot

Author(s)

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---

ggplot_onegeno *Plot one individual's genome-wide genotypes*

Description

Plot one individual's genome-wide genotypes

Usage

```
ggplot_onegeno(
  geno,
  map,
  ind = 1,
  chr = NULL,
  col = NULL,
  shift = FALSE,
  chrwidth = 0.5,
  ...
)
```

Arguments

geno	Imputed phase-known genotypes, as a list of matrices (as produced by maxmarg) or a list of three-dimensional arrays (as produced by guess_phase).
map	Marker map (a list of vectors of marker positions).
ind	Individual to plot, either a numeric index or an ID (can be a vector).
chr	Selected chromosomes to plot; a vector of character strings.
col	Vector of colors for the different genotypes.
shift	If TRUE, shift the chromosomes so they all start at 0.
chrwidth	Total width of rectangles for each chromosome, as a fraction of the distance between them.
...	Additional graphics parameters

Value

object of class ggplot.

Examples

```
# load qtl2 package for data and genoprob calculation
library(qtl2)

# read data
iron <- read_cross2(system.file("extdata", "iron.zip", package="qtl2"))

# insert pseudomarkers into map
map <- insert_pseudomarkers(iron$gmap, step=1)

# calculate genotype probabilities
probs <- calc_genoprob(iron, map, error_prob=0.002)

# inferred genotypes
geno <- maxmarg(probs)

# plot the inferred genotypes for the first individual
ggplot_onegeno(geno, map, shift = TRUE)

# plot the inferred genotypes for the first four individuals
ggplot_onegeno(geno, map, ind=1:4)
```

---

ggplot_peaks *Plot QTL peak locations*

Description

Plot QTL peak locations (possibly with intervals) for multiple traits.

Usage

```
ggplot_peaks(
  peaks,
  map,
  chr = NULL,
  tick_height = 0.3,
  gap = 25,
  bgcolor = "gray90",
  altbgcolor = "gray85",
  ...
)
```

Arguments

peaks	Data frame such as that produced by find_peaks) containing columns chr, pos, lodindex, and lodcolumn. May also contain columns ci_lo and ci_hi, in which case intervals will be plotted.
map	Marker map, used to get chromosome lengths (and start and end positions).
chr	Selected chromosomes to plot; a vector of character strings.
tick_height	Height of tick marks at the peaks (a number between 0 and 1).
gap	Gap between chromosomes.
bgcolor	Background color for the plot.
altbgcolor	Background color for alternate chromosomes.
...	Additional graphics parameters

Value

None.

See Also

find_peaks

Examples

```
# load qtl2 package for data and genoprob calculation
library(qtl2)

# read data
iron <- read_cross2(system.file("extdata", "iron.zip", package="qtl2"))

# insert pseudomarkers into map
map <- insert_pseudomarkers(iron$gmap, step=1)

# calculate genotype probabilities
probs <- calc_genoprob(iron, map, error_prob=0.002)

# grab phenotypes and covariates; ensure that covariates have names attribute
```

```
pheno <- iron$pheno
covar <- match(iron$covar$sex, c("f", "m")) # make numeric
names(covar) <- rownames(iron$covar)
Xcovar <- get_x_covar(iron)

# perform genome scan
out <- scan1(probs, pheno, addcovar=covar, Xcovar=Xcovar)

# find peaks above lod=3.5 (and calculate 1.5-LOD support intervals)
peaks <- find_peaks(out, map, threshold=3.5, drop=1.5)

# color peaks above 6 red; only show chromosomes with peaks
plot_peaks(peaks, map)
peaks$col <- (peaks$lod > 6)

ggplot_peaks(peaks, map[names(map) %in% peaks$chr], col = c("blue","red"),
           legend.title = "LOD > 6")
```

---

ggplot_pxg *Plot phenotype vs genotype*

Description

Plot phenotype vs genotype for a single putative QTL and a single phenotype.

Usage

```
ggplot_pxg(
  geno,
  pheno,
  sort = TRUE,
  SEmult = NULL,
  pooledSD = TRUE,
  jitter = 0.2,
  bgcolor = "gray90",
  seg_width = 0.4,
  seg_lwd = 2,
  seg_col = "black",
  hlines = NULL,
  hlines_col = "white",
  hlines_lty = 1,
  hlines_lwd = 1,
  vlines_col = "gray80",
  vlines_lty = 1,
  vlines_lwd = 3,
  force_labels = TRUE,
  alternate_labels = FALSE,
  omit_points = FALSE,
```

```
  ...
)

mean_pxg(geno, pheno, dataframe = NULL)
```

Arguments

geno	Vector of genotypes, as produced by maxmarg with specific chr and pos.
pheno	Vector of phenotypes.
sort	If TRUE, sort genotypes from largest to smallest.
SEmult	If specified, interval estimates of the within-group averages will be displayed, as mean +/- SE * SEmult.
pooledSD	If TRUE and SEmult is specified, calculated a pooled within-group SD. Otherwise, get separate estimates of the within-group SD for each group.
jitter	Amount to jitter the points horizontally, if a vector of length > 0, it is taken to be the actual jitter amounts (with values between -0.5 and 0.5).
bgcolor	Background color for the plot.
seg_width	Width of segments at the estimated within-group averages
seg_lwd	Line width used to plot estimated within-group averages
seg_col	Line color used to plot estimated within-group averages
hlines	Locations of horizontal grid lines.
hlines_col	Color of horizontal grid lines
hlines_lty	Line type of horizontal grid lines
hlines_lwd	Line width of horizontal grid lines
vlines_col	Color of vertical grid lines
vlines_lty	Line type of vertical grid lines
vlines_lwd	Line width of vertical grid lines
force_labels	If TRUE, force all genotype labels to be shown.
alternate_labels	If TRUE, place genotype labels in two rows
omit_points	If TRUE, omit the points, just plotting the averages (and, potentially, the +/- SE intervals).
...	Additional graphics parameters, passed to plot.
dataframe	Supplied data frame, or constructed from geno and pheno if NULL.

Value

object of class ggplot.

See Also

plot_coef

Examples

```
# load qtl2 package for data and genoprob calculation
library(qtl2)

# read data
iron <- read_cross2(system.file("extdata", "iron.zip", package="qtl2"))

# insert pseudomarkers into map
map <- insert_pseudomarkers(iron$gmap, step=1)

# calculate genotype probabilities
probs <- calc_genoprob(iron, map, error_prob=0.002)

# inferred genotype at a 28.6 cM on chr 16
geno <- maxmarg(probs, map, chr=16, pos=28.6, return_char=TRUE)

# plot phenotype vs genotype
ggplot_pxg(geno, log10(iron$pheno[,1]), ylab=expression(log[10](Liver)))

# include +/- 2 SE intervals
ggplot_pxg(geno, log10(iron$pheno[,1]), ylab=expression(log[10](Liver)),
         SEmult=2)

# plot just the means
ggplot_pxg(geno, log10(iron$pheno[,1]), ylab=expression(log[10](Liver)),
         omit_points=TRUE)

# plot just the means +/- 2 SEs
ggplot_pxg(geno, log10(iron$pheno[,1]), ylab=expression(log[10](Liver)),
         omit_points=TRUE, SEmult=2)
```

`ggplot_scan1` *Plot a genome scan*

Description

Plot LOD curves for a genome scan

Plot LOD curves for a genome scan

Usage

```
ggplot_scan1(
  x,
  map,
  lodcolumn = 1,
  chr = NULL,
  gap = 25,
  bgcolor = "gray90",
  altbgcolor = "gray85",
```

```
  ...
)

## S3 method for class 'scan1'
autoplot(x, ...)

ggplot_scan1_internal(
  map,
  lod,
  gap = 25,
  col = NULL,
  shape = NULL,
  pattern = NULL,
  facet = NULL,
  patterns = c("none", "all", "hilit"),
  chrName = "Chr",
  ...
)
```

Arguments

x	Output of scan1.
map	Map of pseudomarker locations.
lodcolumn	LOD score column to plot (a numeric index, or a character string for a column name). One or more value(s) allowed.
chr	Selected chromosomes to plot; a vector of character strings.
gap	Gap between chromosomes.
bgcolor	Background color for the plot.
altbgcolor	Background color for alternate chromosomes.
...	Additional graphics parameters.
lod	Matrix of lod (or other) values.
col	Colors for points or lines, with labels.
shape	Shapes for points.
pattern	Use to group values for plotting (default = NULL); typically provided by plot_snpasso internal routine.
facet	Plot facets if multiple phenotypes and group provided (default = NULL).
patterns	Connect SDP patterns: one of c("none","all","hilit").
chrName	Add prefix chromosome name (default "Chr").

Value

None.

See Also

ggplot_coef, ggplot_snpasso

Examples

```
# load qtl2 package for data and genoprob calculation
library(qtl2)

# read data
iron <- read_cross2(system.file("extdata", "iron.zip", package="qtl2"))

# insert pseudomarkers into map
map <- insert_pseudomarkers(iron$gmap, step=1)

# calculate genotype probabilities
probs <- calc_genoprob(iron, map, error_prob=0.002)

# grab phenotypes and covariates; ensure that covariates have names attribute
pheno <- iron$pheno
covar <- match(iron$covar$sex, c("f", "m")) # make numeric
names(covar) <- rownames(iron$covar)
Xcovar <- get_x_covar(iron)

# perform genome scan
out <- scan1(probs, pheno, addcovar=covar, Xcovar=Xcovar)

# plot the results for selected chromosomes
chr <- c(2,7,8,9,15,16)
ggplot_scan1(out, map, lodcolumn=1:2, chr=chr, col=c("darkslateblue","violetred"),
     legend.position=c(0.1,0.9))

# plot just one chromosome
ggplot_scan1(out, map, chr=8, lodcolumn=1:2, col=c("darkblue","violetred"))

# can also use autoplot from ggplot2
# lodcolumn can also be a column name
library(ggplot2)
autoplot(out, map, chr=8, lodcolumn=c("liver","spleen"), col=c("darkblue","violetred"))
```

---

ggplot_snpasso *Plot SNP associations*

Description

Plot SNP associations, with possible expansion from distinct snps to all snps.

Usage

```
ggplot_snpasso(
  scan1output,
  snpinfo,
  genes = NULL,
  lodcolumn = 1,
```

```
  show_all_snps = TRUE,
  drop_hilit = NA,
  col_hilit = "violetred",
  col = "darkslateblue",
  ylim = NULL,
  gap = 25,
  minlod = 0,
  bgcolor = "gray90",
  altbgcolor = "gray85",
  ...
)
```

Arguments

scan1output	Output of scan1. Should contain an attribute, "snpinfo", as when scan1 are run with SNP probabilities produced by genoprob_to_snpprob.
snpinfo	Data frame with SNP information with the following columns (the last three are generally derived from with index_snps): • chr - Character string or factor with chromosome • pos - Position (in same units as in the "map" attribute in genoprobs. • sdp - Strain distribution pattern: an integer, between 1 and $2^n - 2$ where n is the number of strains, whose binary encoding indicates the founder genotypes • snp - Character string with SNP identifier (if missing, the rownames are used). • index - Indices that indicate equivalent groups of SNPs. • intervals - Indexes that indicate which marker intervals the SNPs reside. • on_map - Indicate whether SNP coincides with a marker in the genoprobs
genes	Optional data frame containing gene information for the region, with columns 'start' and 'stop' in Mbp, 'strand' (as '"-"', '"+"', or 'NA'), and 'Name'. If included, a two-panel plot is produced, with SNP associations above and gene locations below.
lodcolumn	LOD score column to plot (a numeric index, or a character string for a column name). One or more value(s) allowed.
show_all_snps	If TRUE, expand to show all SNPs.
drop_hilit	SNPs with LOD score within this amount of the maximum SNP association will be highlighted.
col_hilit	Color of highlighted points
col	Color of other points
ylim	y-axis limits
gap	Gap between chromosomes.
minlod	Minimum LOD to display. (Mostly for GWAS, in which case using 'minlod=1' will greatly increase the plotting speed, since the vast majority of points would be omittted.

bgcolor	Background color for the plot.
altbgcolor	Background color for alternate chromosomes.
...	Additional graphics parameters.

Value

object of class ggplot.

Hidden graphics parameters

A number of graphics parameters can be passed via '...'. For example, 'bgcolor' to control the background color and 'altbgcolor' to control the background color on alternate chromosomes. 'cex' for character expansion for the points (default 0.5), 'pch' for the plotting character for the points (default 16), and 'ylim' for y-axis limits.

See Also

ggplot_scan1, ggplot_coef

Examples

```
dirpath <- "https://raw.githubusercontent.com/rqtl/qtl2data/master/DOex"

# Read DOex example cross from 'qtl2data'
DOex <- subset(qtl2::read_cross2(file.path(dirpath, "DOex.zip")), chr = "2")

# Download genotype probabilities
tmpfile <- tempfile()
download.file(file.path(dirpath, "DOex_genoprobs_2.rds"), tmpfile, quiet=TRUE)
pr <- readRDS(tmpfile)
unlink(tmpfile)

# Download SNP info for DOex from web and read as RDS.
tmpfile <- tempfile()
download.file(file.path(dirpath, "c2_snpinfo.rds"), tmpfile, quiet=TRUE)
snpinfo <- readRDS(tmpfile)
unlink(tmpfile)
snpinfo <- dplyr::rename(snpinfo, pos = pos_Mbp)

# Convert to SNP probabilities
snpinfo <- qtl2::index_snps(DOex$pmap, snpinfo)
snppr <- qtl2::genoprob_to_snpprob(pr, snpinfo)

# Scan SNPs.
scan_snppr <- qtl2::scan1(snppr, DOex$pheno)

# plot results
ggplot_snpasso(scan_snppr, snpinfo, show_all_snps=FALSE, patterns="all", drop_hilit=1.5)


# can also just type autoplot() if ggplot2 attached
```

```
library(ggplot2)

# plot just subset of distinct SNPs
autoplot(scan_snppr, snpinfo, show_all_snps=FALSE, drop_hilit=1.5)

# highlight SDP patterns in SNPs; connect with lines.
autoplot(scan_snppr, snpinfo, patterns="all",drop_hilit=4)

# query function for finding genes in region
gene_dbfile <- system.file("extdata", "mouse_genes_small.sqlite", package="qtl2")
query_genes <- qtl2::create_gene_query_func(gene_dbfile)
genes <- query_genes(2, 97, 98)

# plot SNP association results with gene locations
autoplot(scan_snppr, snpinfo, patterns="hilit", drop_hilit=1.5, genes=genes)
)
```

`listof_scan1coef` *List of scan1coef objects*

Description

Create a list of scan1coef objects using `scan1coef`.

Summary of object of class `listof_scan1coef`, which is a list of objects of class `scan1coef`.

Summary of object of class `listof_scan1coef`, which is a list of objects of class `scan1coef`.

Subset of object of class `listof_scan1coef`, which is a list of objects of class `scan1coef`.

Usage

```
listof_scan1coef(
  probs,
  phe,
  K = NULL,
  covar = NULL,
  blups = FALSE,
  center = FALSE,
  ...
)

summary_listof_scan1coef(
  object,
  scan1_object,
  map,
  coef_names = dimnames(object[[1]])[[2]],
  center = TRUE,
  ...
```

```
)

## S3 method for class 'listof_scan1coef'
summary(object, ...)

summary_scan1coef(object, scan1_object, map, ...)

## S3 method for class 'scan1coef'
summary(object, ...)

subset_listof_scan1coef(x, elements, ...)

## S3 method for class 'listof_scan1coef'
subset(x, ...)

## S3 method for class 'listof_scan1coef'
x[...]
```

Arguments

probs	genotype probabilities object for one chromosome from calc_genoprob
phe	data frame of phenotypes
K	list of length 1 with kinship matrix
covar	matrix of covariates
blups	Create BLUPs if TRUE
center	center coefficients if TRUE
...	ignored
object	object of class listof_scan1coef
scan1_object	object from scan1
map	A list of vectors of marker positions, as produced by insert_pseudomarkers.
coef_names	names of effect coefficients (default is all coefficient names)
x	object of class listof_scan1coef
elements	indexes or names of list elements in x

Value

object of class listof_scan1coef

Author(s)

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Examples

```
# read data
iron <- qtl2::read_cross2(system.file("extdata", "iron.zip", package="qtl2"))

# insert pseudomarkers into map
map <- qtl2::insert_pseudomarkers(iron$gmap, step=1)

# calculate genotype probabilities
probs <- qtl2::calc_genoprob(iron, map, error_prob=0.002)

# Ensure that covariates have names attribute
covar <- match(iron$covar$sex, c("f", "m")) # make numeric
names(covar) <- rownames(iron$covar)

# Calculate scan1coef on all phenotypes,
# returning a list of \code{\link{scan1coef}} objects
out <- listof_scan1coef(probs[,7], iron$pheno, addcovar = covar, center = TRUE)

# Plot coefficients for all phenotypes
ggplot2::autoplot(out, map[7], columns = 1:3)

# Summary of coefficients at scan peak
scan_pr <- qtl2::scan1(probs[,7], iron$pheno)
summary(out, scan_pr, map[7])
```

`sdp_to_pattern` *Convert sdp to pattern*

Description

Convert strain distribution pattern (sdp) to letter pattern. Taken from package 'qtl2pattern' for internal use here.

Usage

```
sdp_to_pattern(sdp, haplos, symmetric = TRUE)
```

Arguments

`sdp`	vector of sdp values
`haplos`	letter codes for haplotypes (required)
`symmetric`	make patterns symmetric if `TRUE`

Value

vector of letter patterns

Author(s)

Brian S Yandell, <brian.yandell@wisc.edu>

---

summary_scan1 *Summary of scan1 object*

Description

Summary of scan1 object

Usage

```
summary_scan1(
  object,
  map,
  snpinfo = NULL,
  lodcolumn = seq_len(ncol(object)),
  chr = names(map),
  sum_type = c("common", "best"),
  drop = 1.5,
  show_all_snps = TRUE,
  ...
)

## S3 method for class 'scan1'
summary(object, ...)
```

Arguments

object	object from scan1
map	A list of vectors of marker positions, as produced by insert_pseudomarkers.
snpinfo	Data frame with SNP information with the following columns (the last three are generally derived from with index_snps):

- chr - Character string or factor with chromosome
- pos - Position (in same units as in the "map" attribute in genoprobs.
- sdp - Strain distribution pattern: an integer, between 1 and $2^n - 2$ where n is the number of strains, whose binary encoding indicates the founder genotypes
- snp - Character string with SNP identifier (if missing, the rownames are used).
- index - Indices that indicate equivalent groups of SNPs.
- intervals - Indexes that indicate which marker intervals the SNPs reside.
- on_map - Indicate whether SNP coincides with a marker in the genoprobs

lodcolumn	one or more lod columns

chr	one or more chromosome IDs
sum_type	type of summary
drop	LOD drop from maximum
show_all_snps	show all SNPs if TRUE
...	other arguments not used

Value

tbl summary

Author(s)

Brian S Yandell, <brian.yandell@wisc.edu>

Examples

```
# read data
iron <- qtl2::read_cross2(system.file("extdata", "iron.zip", package="qtl2"))
# insert pseudomarkers into map
map <- qtl2::insert_pseudomarkers(iron$gmap, step=1)

# calculate genotype probabilities
probs <- qtl2::calc_genoprob(iron, map, error_prob=0.002)

# grab phenotypes and covariates; ensure that covariates have names attribute
pheno <- iron$pheno
covar <- match(iron$covar$sex, c("f", "m")) # make numeric
names(covar) <- rownames(iron$covar)
Xcovar <- qtl2::get_x_covar(iron)

# perform genome scan
out <- qtl2::scan1(probs, pheno, addcovar=covar, Xcovar=Xcovar)

# summary
summary(out, map)
```

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