

# Package ‘qtl2’

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**Title** Quantitative Trait Locus Mapping in Experimental Crosses

**Description** Provides a set of tools to perform quantitative trait locus (QTL) analysis in experimental crosses. It is a reimplementaion of the 'R/qtl' package to better handle high-dimensional data and complex cross designs. Broman et al. (2019) <[doi:10.1534/genetics.118.301595](https://doi.org/10.1534/genetics.118.301595)>.

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**License** GPL-3

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---

add_threshold	<i>Add thresholds to genome scan plot</i>
---------------	---

---

## Description

Draw line segments at significance thresholds for a genome scan plot

## Usage

```
add_threshold(map, thresholdA, thresholdX = NULL, chr = NULL, gap = NULL, ...)
```

## Arguments

map	Marker map used in the genome scan plot
thresholdA	Autosomal threshold. Numeric or a list. (If a list, the "A" component is taken to be thresholdA and the "X" component is taken to be thresholdX.)
thresholdX	X chromosome threshold (if missing, assumed to be the same as thresholdA)
chr	Chromosomes that were included in the plot
gap	Gap between chromosomes in the plot. Default is 1% of the total genome length.
...	Additional arguments passed to <a href="#">graphics::segments()</a>

## Value

None.

## Examples

```
iron <- read_cross2(system.file("extdata", "iron.zip", package="qt12"))

map <- insert_pseudomarkers(iron$gmap, step=5)
probs <- calc_genoprob(iron, map, error_prob=0.002)
Xcovar <- get_x_covar(iron)
out <- scan1(probs, iron$pheno[,1], Xcovar=Xcovar)
# run just 3 permutations, as a fast illustration
operm <- scan1perm(probs, iron$pheno[,1], addcovar=Xcovar,
                  n_perm=3, perm_Xsp=TRUE, chr_lengths=chr_lengths(map))

plot(out, map)
add_threshold(map, summary(operm), col="violetred", lty=2)
```

---

`basic_summaries`*Basic summaries of a cross2 object*

---

**Description**

Basic summaries of a cross2 object.

**Usage**`n_ind(cross2)``n_ind_geno(cross2)``n_ind_pheno(cross2)``n_ind_covar(cross2)``n_ind_gnp(cross2)``ind_ids(cross2)``ind_ids_geno(cross2)``ind_ids_pheno(cross2)``ind_ids_covar(cross2)``ind_ids_gnp(cross2)``n_chr(cross2)``n_founders(cross2)``founders(cross2)``chr_names(cross2)``tot_mar(cross2)``n_mar(cross2)``marker_names(cross2)``n_pheno(cross2)``pheno_names(cross2)`

```
n_covar(cross2)
```

```
covar_names(cross2)
```

```
n_phenocovar(cross2)
```

```
phenocovar_names(cross2)
```

### Arguments

**cross2** An object of class "cross2", as output by [read\\_cross2\(\)](#). For details, see the [R/qtl2 developer guide](#).

### Value

Variously a number, vector of numbers, or vector of character strings.

### Functions

- `n_ind()`: Number of individuals (either genotyped or phenotyped)
- `n_ind_geno()`: Number of genotyped individuals
- `n_ind_pheno()`: Number of phenotyped individuals
- `n_ind_covar()`: Number of individuals with covariate data
- `n_ind_gnp()`: Number of individuals with both genotype and phenotype data
- `ind_ids()`: IDs of individuals (either genotyped or phenotyped)
- `ind_ids_geno()`: IDs of genotyped individuals
- `ind_ids_pheno()`: IDs of phenotyped individuals
- `ind_ids_covar()`: IDs of individuals with covariate data
- `ind_ids_gnp()`: IDs of individuals with both genotype and phenotype data
- `n_chr()`: Number of chromosomes
- `n_founders()`: Number of founder strains
- `founders()`: Names of founder strains
- `chr_names()`: Chromosome names
- `tot_mar()`: Total number of markers
- `n_mar()`: Number of markers on each chromosome
- `marker_names()`: Marker names
- `n_pheno()`: Number of phenotypes
- `pheno_names()`: Phenotype names
- `n_covar()`: Number of covariates
- `covar_names()`: Covariate names
- `n_phenocovar()`: Number of phenotype covariates
- `phenocovar_names()`: Phenotype covariate names

**See Also**[summary.cross2\(\)](#)

---

batch_cols	<i>Batch columns by pattern of missing values</i>
------------	---

---

**Description**

Identify batches of columns of a matrix that have the same pattern of missing values.

**Usage**

```
batch_cols(mat, max_batch = NULL)
```

**Arguments**

mat	A numeric matrix
max_batch	Maximum batch size

**Value**

A list containing the batches, each with two components: cols containing numeric indices of the columns in the corresponding batch, and omit containing a vector of row indices that have missing values in this batch.

**See Also**[batch\\_vec\(\)](#)**Examples**

```
x <- rbind(c( 1,  2,  3, 13, 16),
           c( 4,  5,  6, 14, 17),
           c( 7, NA,  8, NA, 18),
           c(NA, NA, NA, NA, 19),
           c(10, 11, 12, 15, 20))
batch_cols(x)
```



---

batch_vec	<i>Split vector into batches</i>
-----------	----------------------------------

---

**Description**

Split a vector into batches, each no longer than batch\_size and creating at least n\_cores batches, for use in parallel calculations.

**Usage**

```
batch_vec(vec, batch_size = NULL, n_cores = 1)
```

**Arguments**

- vec                   A vector to be split into batches
- batch\_size           Maximum size for each batch
- n\_cores              Number of compute cores, to be used as a minimum number of batches.

**Value**

A list of vectors, each no longer than batch\_size, and with at least n\_cores componenets.

**See Also**

```
batch\_cols\(\)
```

**Examples**

```
vec_split <- batch_vec(1:304, 50, 8)
vec_split2 <- batch_vec(1:304, 50)
```

---

bayes_int	<i>Calculate Bayes credible intervals</i>
-----------	---

---

**Description**

Calculate Bayes credible intervals for a single LOD curve on a single chromosome, with the ability to identify intervals for multiple LOD peaks.

**Usage**

```

bayes_int(
  scan1_output,
  map,
  chr = NULL,
  lodcolumn = 1,
  threshold = 0,
  peakdrop = Inf,
  prob = 0.95,
  expand2markers = TRUE
)

```

**Arguments**

scan1_output	An object of class "scan1" as returned by <code>scan1()</code> .
map	A list of vectors of marker positions, as produced by <code>insert_pseudomarkers()</code> .
chr	Chromosome ID to consider (must be a single value).
lodcolumn	LOD score column to consider (must be a single value).
threshold	Minimum LOD score for a peak.
peakdrop	Amount that the LOD score must drop between peaks, if multiple peaks are to be defined on a chromosome.
prob	Nominal coverage for the interval.
expand2markers	If TRUE, QTL intervals are expanded so that their endpoints are at genetic markers.

**Details**

We identify a set of peaks defined as local maxima that exceed the specified threshold, with the requirement that the LOD score must have dropped by at least peakdrop below the lowest of any two adjacent peaks.

At a given peak, if there are ties, with multiple positions jointly achieving the maximum LOD score, we take the average of these positions as the location of the peak.

The default is to use threshold=0, peakdrop=Inf, and prob=0.95. We then return results a single peak, no matter the maximum LOD score, and give a 95% Bayes credible interval.

**Value**

A matrix with three columns:

- ci\_lo - lower bound of interval
- pos - peak position
- ci\_hi - upper bound of interval

Each row corresponds to a different peak.

**See Also**

[lod\\_int\(\)](#), [find\\_peaks\(\)](#), [scan1\(\)](#)

**Examples**

```
# 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)

# 95% Bayes credible interval for QTL on chr 7, first phenotype
bayes_int(out, map, chr=7, lodcolumn=1)
```

---

calc\_entropy

---

*Calculate entropy of genotype probability distribution*


---

**Description**

For each individual at each genomic position, calculate the entropy of the genotype probability distribution, as a quantitative summary of the amount of missing information.

**Usage**

```
calc_entropy(probs, quiet = TRUE, cores = 1)
```

**Arguments**

probs	Genotype probabilities, as calculated from <a href="#">calc_genoprob()</a> .
quiet	IF FALSE, print progress messages.
cores	Number of CPU cores to use, for parallel calculations. (If 0, use <a href="#">parallel::detectCores()</a> . Alternatively, this can be links to a set of cluster sockets, as produced by <a href="#">parallel::makeCluster()</a> .

**Details**

We calculate  $-\sum(p \log_2 p)$ , where we take  $0 \log 0 = 0$ .

**Value**

A list of matrices (each matrix is a chromosome and is arranged as individuals x markers).

**Examples**

```
grav2 <- read_cross2(system.file("extdata", "grav2.zip", package="qt12"))

probs <- calc_genoprob(grav2, error_prob=0.002)
e <- calc_entropy(probs)
e <- do.call("cbind", e) # combine chromosomes into one big matrix

# summarize by individual
mean_ind <- rowMeans(e)

# summarize by marker
mean_marker <- colMeans(e)
```

---

calc_errorlod	<i>Calculate genotyping error LOD scores</i>
---------------	--

---

**Description**

Use the genotype probabilities calculated with [calc\\_genoprob\(\)](#) to calculate genotyping error LOD scores, to help identify potential genotyping errors (and problem markers and/or individuals).

**Usage**

```
calc_errorlod(cross, probs, quiet = TRUE, cores = 1)
```

**Arguments**

cross	Object of class "cross2". For details, see the <a href="#">R/qt12 developer guide</a> .
probs	Genotype probabilities as calculated from <a href="#">calc_genoprob()</a> .
quiet	If FALSE, print progress messages.
cores	Number of CPU cores to use, for parallel calculations. (If 0, use <a href="#">parallel::detectCores()</a> .) Alternatively, this can be links to a set of cluster sockets, as produced by <a href="#">parallel::makeCluster()</a> .

**Details**

Let  $O_k$  denote the observed marker genotype at position  $k$ , and  $g_k$  denote the corresponding true underlying genotype.

Following Lincoln and Lander (1992), we calculate  $\text{LOD} = \log_{10}[Pr(O_k|g_k = O_k)/Pr(O_k|g_k \neq O_k)]$

**Value**

A list of matrices of genotyping error LOD scores. Each matrix corresponds to a chromosome and is arranged as individuals x markers.

## References

Lincoln SE, Lander ES (1992) Systematic detection of errors in genetic linkage data. *Genomics* 14:604–610.

## See Also

[calc\\_genoprob\(\)](#)

## Examples

```
iron <- read_cross2(system.file("extdata", "iron.zip", package="qtl2"))
probs <- calc_genoprob(iron, error_prob=0.002, map_function="c-f")
errorlod <- calc_errorlod(iron, probs)

# combine into one matrix
errorlod <- do.call("cbind", errorlod)
```

---

calc_genoprob	<i>Calculate conditional genotype probabilities</i>
---------------	---

---

## Description

Uses a hidden Markov model to calculate the probabilities of the true underlying genotypes given the observed multipoint marker data, with possible allowance for genotyping errors.

## Usage

```
calc_genoprob(
  cross,
  map = NULL,
  error_prob = 0.0001,
  map_function = c("haldane", "kosambi", "c-f", "morgan"),
  lowmem = FALSE,
  quiet = TRUE,
  cores = 1
)
```

## Arguments

cross	Object of class "cross2". For details, see the <a href="#">R/qtl2 developer guide</a> .
map	Genetic map of markers. May include pseudomarker locations (that is, locations that are not within the marker genotype data). If NULL, the genetic map in cross is used.
error_prob	Assumed genotyping error probability
map_function	Character string indicating the map function to use to convert genetic distances to recombination fractions.

lowmem	If FALSE, split individuals into groups with common sex and crossinfo and then precalculate the transition matrices for a chromosome; potentially a lot faster but using more memory.
quiet	If FALSE, print progress messages.
cores	Number of CPU cores to use, for parallel calculations. (If 0, use <code>parallel::detectCores()</code> .) Alternatively, this can be links to a set of cluster sockets, as produced by <code>parallel::makeCluster()</code> .

## Details

Let  $O_k$  denote the observed marker genotype at position  $k$ , and  $g_k$  denote the corresponding true underlying genotype.

We use the forward-backward equations to calculate  $\alpha_{kv} = \log Pr(O_1, \dots, O_k, g_k = v)$  and  $\beta_{kv} = \log Pr(O_{k+1}, \dots, O_n | g_k = v)$

We then obtain  $Pr(g_k | O_1, \dots, O_n) = \exp(\alpha_{kv} + \beta_{kv}) / s$  where  $s = \sum_v \exp(\alpha_{kv} + \beta_{kv})$

## Value

An object of class "calc\_genoprob": a list of three-dimensional arrays of probabilities, individuals x genotypes x positions. (Note that the arrangement is different from R/qtl.) Also contains four attributes:

- crosstype - The cross type of the input cross.
- is\_x\_chr - Logical vector indicating whether chromosomes are to be treated as the X chromosome or not, from input cross.
- alleles - Vector of allele codes, from input cross.
- alleleprobs - Logical value (FALSE) that indicates whether the probabilities are compressed to allele probabilities, as from `genoprob_to_alleleprob()`.

## See Also

`insert_pseudomarkers()`

## Examples

```
grav2 <- read_cross2(system.file("extdata", "grav2.zip", package="qtl2"))
gmap_w_pmar <- insert_pseudomarkers(grav2$gmap, step=1)
probs <- calc_genoprob(grav2, gmap_w_pmar, error_prob=0.002)
```

---

calc_geno_freq	<i>Calculate genotype frequencies</i>
----------------	---------------------------------------

---

## Description

Calculate genotype frequencies, by individual or by marker

## Usage

```
calc_geno_freq(probs, by = c("individual", "marker"), omit_x = TRUE)
```

## Arguments

probs	List of arrays of genotype probabilities, as calculated by <a href="#">calc_genoprob()</a> .
by	Whether to summarize by individual or marker
omit_x	If TRUE, results are just for the autosomes. If FALSE, results are a list of length two, containing the results for the autosomes and those for the X chromosome.

## Value

If omit\_x=TRUE, the result is a matrix of genotype frequencies; columns are genotypes and rows are either individuals or markers.

If necessary (that is, if omit\_x=FALSE, the data include the X chromosome, and the set of genotypes on the X chromosome are different than on the autosomes), the result is a list with two components (for the autosomes and for the X chromosome), each being a matrix of genotype frequencies.

## See Also

[calc\\_raw\\_geno\\_freq\(\)](#), [calc\\_het\(\)](#)

## Examples

```
iron <- read_cross2(system.file("extdata", "iron.zip", package="qtl2"))
p <- calc_genoprob(iron, err=0.002)

# genotype frequencies by marker
tab_g <- calc_geno_freq(p, "marker")

# allele frequencies by marker
ap <- genoprob_to_alleleprob(p)
tab_a <- calc_geno_freq(ap, "marker")
```

---

calc_grid	<i>Calculate indicators of which marker/pseudomarker positions are along a fixed grid</i>
-----------	---

---

## Description

Construct vectors of logical indicators that indicate which positions correspond to locations along a grid

## Usage

```
calc_grid(map, step = 0, off_end = 0, tol = 0.01)
```

## Arguments

map	A list of numeric vectors; each vector gives marker positions for a single chromosome.
step	Distance between pseudomarkers and markers; if step=0 no pseudomarkers are inserted.
off_end	Distance beyond terminal markers in which to insert pseudomarkers.
tol	Tolerance for determining whether a pseudomarker would duplicate a marker position.

## Details

The function [insert\\_pseudomarkers\(\)](#), with stepwidth="fixed", will insert a grid of pseudomarkers, to a marker map. The present function gives a series of TRUE/FALSE vectors that indicate which positions fall on the grid. This is for use with [probs\\_to\\_grid\(\)](#), for reducing genotype probabilities, calculated with [calc\\_genoprob\(\)](#), to just the positions on the grid. The main value of this is to speed up genome scan computations in the case of very dense markers, by focusing on just a grid of positions rather than on all marker locations.

## Value

A list of logical (TRUE/FALSE) vectors that indicate, for a marker/pseudomarker map created by [insert\\_pseudomarkers\(\)](#) with step>0 and stepwidth="fixed", which positions correspond to the locations along the fixed grid.

## See Also

[insert\\_pseudomarkers\(\)](#), [probs\\_to\\_grid\(\)](#), [map\\_to\\_grid\(\)](#)

## Examples

```
iron <- read_cross2(system.file("extdata", "iron.zip", package="qtl2"))
gmap_w_pmar <- insert_pseudomarkers(iron$gmap, step=1)
grid <- calc_grid(iron$gmap, step=1)
```



---

calc_het	<i>Calculate heterozygosities</i>
----------	-----------------------------------

---

**Description**

Calculate heterozygosities, by individual or by marker

**Usage**

```
calc_het(probs, by = c("individual", "marker"), omit_x = TRUE, cores = 1)
```

**Arguments**

probs	List of arrays of genotype probabilities, as calculated by <a href="#">calc_genoprob()</a> .
by	Whether to summarize by individual or marker
omit_x	If TRUE, omit the X chromosome.
cores	Number of CPU cores to use, for parallel calculations. (If 0, use <a href="#">parallel::detectCores()</a> .) Alternatively, this can be links to a set of cluster sockets, as produced by <a href="#">parallel::makeCluster()</a> .

**Details**

calc\_het() looks at the genotype names (the 2nd dimension of the dimnames of the input probs), which must be two-letter names, and assumes that when the two letters are different it's a heterozygous genotype while if they're the same it's a homozygous genotype

**Value**

The result is a vector of estimated heterozygosities

**See Also**

[calc\\_raw\\_het\(\)](#), [calc\\_geno\\_freq\(\)](#)

**Examples**

```
iron <- read_cross2(system.file("extdata", "iron.zip", package="qtl2"))
p <- calc_genoprob(iron, err=0.002)

# heterozygosities by individual
het_ind <- calc_het(p)

# heterozygosities by marker
het_mar <- calc_het(p, "marker")
```

---

calc_kinship	<i>Calculate kinship matrix</i>
--------------	---------------------------------

---

## Description

Calculate genetic similarity among individuals (kinship matrix) from conditional genotype probabilities.

## Usage

```
calc_kinship(
  probs,
  type = c("overall", "loco", "chr"),
  omit_x = FALSE,
  use_allele_probs = TRUE,
  quiet = TRUE,
  cores = 1
)
```

## Arguments

probs	Genotype probabilities, as calculated from <a href="#">calc_genoprob()</a> .
type	Indicates whether to calculate the overall kinship ("overall", using all chromosomes), the kinship matrix leaving out one chromosome at a time ("loco"), or the kinship matrix for each chromosome ("chr").
omit_x	If TRUE, only use the autosomes; ignored when type="chr".
use_allele_probs	If TRUE, assess similarity with allele probabilities (that is, first run <a href="#">genoprob_to_alleleprob()</a> ); otherwise use the genotype probabilities.
quiet	IF FALSE, print progress messages.
cores	Number of CPU cores to use, for parallel calculations. (If 0, use <a href="#">parallel::detectCores()</a> .) Alternatively, this can be links to a set of cluster sockets, as produced by <a href="#">parallel::makeCluster()</a> .

## Details

If use\_allele\_probs=TRUE (the default), we first convert the genotype probabilities to allele probabilities (using [genoprob\\_to\\_alleleprob\(\)](#)).

We then calculate  $\sum_{kl} (p_{ikl} p_{jkl})$  where  $k$  = position,  $l$  = allele, and  $i, j$  are two individuals.

For crosses with just two possible genotypes (e.g., backcross), we don't convert to allele probabilities but just use the original genotype probabilities.

## Value

If type="overall" (the default), a matrix of proportion of matching alleles. Otherwise a list with one matrix per chromosome.

**Examples**

```
grav2 <- read_cross2(system.file("extdata", "grav2.zip", package="qtl2"))
map <- insert_pseudomarkers(grav2$gmap, step=1)
probs <- calc_genoprob(grav2, map, error_prob=0.002)
K <- calc_kinship(probs)

# using only markers/pseudomarkers on the grid
grid <- calc_grid(grav2$gmap, step=1)
probs_sub <- probs_to_grid(probs, grid)
K_grid <- calc_kinship(probs_sub)
```

---

calc\_raw\_founder\_maf    *Calculate founder minor allele frequencies from raw SNP genotypes*

---

**Description**

Calculate minor allele frequency from raw SNP genotypes in founders, by founder strain or by marker

**Usage**

```
calc_raw_founder_maf(cross, by = c("individual", "marker"))
```

**Arguments**

cross	Object of class "cross2". For details, see the <a href="#">R/qtl2 developer guide</a> .
by	Indicates whether to summarize by founder strain ("individual") or by marker.

**Value**

A vector of minor allele frequencies, one for each founder strain or marker.

**See Also**

[recode\\_snps\(\)](#), [calc\\_raw\\_maf\(\)](#)

**Examples**

```
## Not run:
# load example data and calculate genotype probabilities
file <- paste0("https://raw.githubusercontent.com/rqtl1/",
               "qtl2data/main/D0ex/D0ex.zip")
D0ex <- read_cross2(file)
D0ex_maf <- calc_raw_founder_maf(D0ex)

## End(Not run)
```

---

calc_raw_genotype_freq	<i>Calculate genotype frequencies from raw SNP genotypes</i>
------------------------	--

---

## Description

Calculate genotype frequencies from raw SNP genotypes, by individual or by marker

## Usage

```
calc_raw_genotype_freq(cross, by = c("individual", "marker"), cores = 1)
```

## Arguments

cross	Object of class "cross2". For details, see the <a href="#">R/ql2 developer guide</a> .
by	Indicates whether to summarize by individual or by marker.
cores	Number of CPU cores to use, for parallel calculations. (If 0, use <a href="#">parallel::detectCores()</a> .) Alternatively, this can be links to a set of cluster sockets, as produced by <a href="#">parallel::makeCluster()</a> .

## Value

A matrix of genotypes frequencies with 3 columns (AA, AB, and BB) and with rows being either individuals or markers.

## See Also

[calc\\_raw\\_maf\(\)](#), [calc\\_raw\\_het\(\)](#), [recode\\_snps\(\)](#), [calc\\_genotype\\_freq\(\)](#)

## Examples

```
## Not run:
# load example data and calculate genotype probabilities
file <- paste0("https://raw.githubusercontent.com/rqtl/",
               "ql2data/main/D0ex/D0ex.zip")
D0ex <- read_cross2(file)
gfreq <- calc_raw_genotype_freq(D0ex)

## End(Not run)
```

---

calc_raw_het	<i>Calculate estimated heterozygosity from raw SNP genotypes</i>
--------------	--

---

**Description**

Calculate estimated heterozygosity for each individual from raw SNP genotypes

**Usage**

```
calc_raw_het(cross, by = c("individual", "marker"))
```

**Arguments**

cross	Object of class "cross2". For details, see the <a href="#">R/qrtl2 developer guide</a> .
by	Indicates whether to summarize by founder strain ("individual") or by marker.

**Value**

A vector of heterozygosities, one for each individual or marker.

**See Also**

[recode\\_snps\(\)](#), [calc\\_raw\\_maf\(\)](#), [calc\\_raw\\_founder\\_maf\(\)](#), [calc\\_raw\\_geno\\_freq\(\)](#), [calc\\_het\(\)](#)

**Examples**

```
## Not run:
# load example data and calculate genotype probabilities
file <- paste0("https://raw.githubusercontent.com/rqtl/",
               "qrtl2data/main/D0ex/D0ex.zip")
D0ex <- read_cross2(file)
D0ex_het <- calc_raw_het(D0ex)

## End(Not run)
```

---

calc_raw_maf	<i>Calculate minor allele frequency from raw SNP genotypes</i>
--------------	--

---

**Description**

Calculate minor allele frequency from raw SNP genotypes, by individual or by marker

**Usage**

```
calc_raw_maf(cross, by = c("individual", "marker"))
```

**Arguments**

**cross**                      Object of class "cross2". For details, see the [R/ql2 developer guide](#).  
**by**                              Indicates whether to summarize by founder strain ("individual") or by marker.

**Value**

A vector of minor allele frequencies, one for each individual or marker.

**See Also**

[recode\\_snps\(\)](#), [calc\\_raw\\_founder\\_maf\(\)](#), [calc\\_raw\\_het\(\)](#), [calc\\_raw\\_geno\\_freq\(\)](#)

**Examples**

```
## Not run:
# load example data and calculate genotype probabilities
file <- paste0("https://raw.githubusercontent.com/rqtl/",
               "qt12data/main/D0ex/D0ex.zip")
D0ex <- read_cross2(file)
D0ex_maf <- calc_raw_maf(D0ex)

## End(Not run)
```

---

calc\_sdp

---

*Calculate strain distribution pattern from SNP genotypes*


---

**Description**

Calculate the strain distribution patterns (SDPs) from the strain genotypes at a set of SNPs.

**Usage**

```
calc_sdp(geno)
```

**Arguments**

**geno**                      Matrix of SNP genotypes, markers x strains, coded as 1 (AA) and 3 (BB). Markers with values other than 1 or 3 are omitted, and monomorphic markers, are omitted.

**Value**

A vector of strain distribution patterns: integers between 1 and  $2^n - 2$  where  $n$  is the number of strains, whose binary representation indicates the strain genotypes.

**See Also**

[invert\\_sdp\(\)](#), [sdp2char\(\)](#)

### Examples

```
x <- rbind(m1=c(3, 1, 1, 1, 1, 1, 1, 1),
           m2=c(1, 3, 3, 1, 1, 1, 1, 1),
           m3=c(1, 1, 1, 1, 3, 3, 3, 3))
calc_sdp(x)
```

---

cbind.calc_genoprob	<i>Join genotype probabilities for different chromosomes</i>
---------------------	--

---

### Description

Join multiple genotype probability objects, as produced by [calc\\_genoprob\(\)](#), for the same set of individuals but different chromosomes.

### Usage

```
## S3 method for class 'calc_genoprob'
cbind(...)
```

### Arguments

...                      Genotype probability objects as produced by [calc\\_genoprob\(\)](#). Must have the same set of individuals.

### Value

An object of class "calc\_genoprob", like the input; see [calc\\_genoprob\(\)](#).

### See Also

[rbind.calc\\_genoprob\(\)](#)

### Examples

```
grav2 <- read_cross2(system.file("extdata", "grav2.zip", package="qt12"))
map <- insert_pseudomarkers(grav2$gmap, step=1)
probsA <- calc_genoprob(grav2[1:5,1:2], map, error_prob=0.002)
probsB <- calc_genoprob(grav2[1:5,3:4], map, error_prob=0.002)
probs <- cbind(probsA, probsB)
```

---

cbind.scan1

*Join genome scan results for different phenotypes.*


---

## Description

Join multiple `scan1()` results for different phenotypes; must have the same map.

## Usage

```
## S3 method for class 'scan1'
cbind(...)
```

## Arguments

...                      Genome scan objects of class "scan1", as produced by `scan1()`. Must have the same map.

## Details

If components `addcovar()`, `Xcovar`, `intcovar`, `weights` do not match between objects, we omit this information.

If `hsq` present but has differing numbers of rows, we omit this information.

## Value

An object of class "scan1", like the inputs, but with the lod score columns from the inputs combined as multiple columns in a single object.

## See Also

`rbind.scan1()`, `scan1()`

## Examples

```
grav2 <- read_cross2(system.file("extdata", "grav2.zip", package="qt12"))
map <- insert_pseudomarkers(grav2$gmap, step=1)
probs <- calc_genoprob(grav2, map, error_prob=0.002)
phe1 <- grav2$pheno[,1,drop=FALSE]
phe2 <- grav2$pheno[,2,drop=FALSE]

out1 <- scan1(probs, phe1) # phenotype 1
out2 <- scan1(probs, phe2) # phenotype 2
out <- cbind(out1, out2)
```



---

cbind.scan1perm	<i>Combine columns from multiple scan1 permutation results</i>
-----------------	--

---

## Description

Column-bind multiple scan1perm objects with the same numbers of rows.

## Usage

```
## S3 method for class 'scan1perm'
cbind(...)
```

## Arguments

... A set of permutation results from [scan1perm\(\)](#) (objects of class "scan1perm". If different numbers of permutation replicates were used, those columns with fewer replicates are padded with missing values NA. However, if any include autosome/X chromosome-specific permutations, they must all be such.

## Details

The aim of this function is to concatenate the results from multiple runs of a permutation test with [scan1perm\(\)](#), generally with different phenotypes and/or methods, to be used in parallel with [rbind.scan1perm\(\)](#).

## Value

The combined column-binded input, as an object of class "scan1perm"; see [scan1perm\(\)](#).

## See Also

[rbind.scan1perm\(\)](#), [scan1perm\(\)](#), [scan1\(\)](#)

## Examples

```
# 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)

# permutations with genome scan (just 3 replicates, for illustration)
operm1 <- scan1perm(probs, pheno[,1,drop=FALSE], addcovar=covar, Xcovar=Xcovar, n_perm=3)
operm2 <- scan1perm(probs, pheno[,2,drop=FALSE], addcovar=covar, Xcovar=Xcovar, n_perm=3)

operm <- cbind(operm1, operm2)

```

---

cbind.sim\_geno

Join genotype imputations for different chromosomes

---

## Description

Join multiple genotype imputation objects, as produced by [sim\\_geno\(\)](#), for the same individuals but different chromosomes.

## Usage

```

## S3 method for class 'sim_geno'
cbind(...)

```

## Arguments

...                      Genotype imputation objects as produced by [sim\\_geno\(\)](#). Must have the same set of individuals.

## Value

An object of class "sim\_geno", like the input; see [sim\\_geno\(\)](#).

## See Also

[rbind.sim\\_geno\(\)](#), [sim\\_geno\(\)](#)

## Examples

```

grav2 <- read_cross2(system.file("extdata", "grav2.zip", package="qt12"))
map <- insert_pseudomarkers(grav2$gmap, step=1)
drawsA <- sim_geno(grav2[1:5,1:2], map, error_prob=0.002, n_draws=4)
drawsB <- sim_geno(grav2[1:5,3:4], map, error_prob=0.002, n_draws=4)
draws <- cbind(drawsA, drawsB)

```

---

cbind.viterbi	<i>Join viterbi results for different chromosomes</i>
---------------	---

---

**Description**

Join multiple viterbi objects, as produced by `viterbi()`, for the same set of individuals but different chromosomes.

**Usage**

```
## S3 method for class 'viterbi'
cbind(...)
```

**Arguments**

... Imputed genotype objects as produced by `viterbi()`. Must have the same set of individuals.

**Value**

An object of class "viterbi", like the input; see `viterbi()`.

**See Also**

`rbind.viterbi()`, `viterbi()`

**Examples**

```
grav2 <- read_cross2(system.file("extdata", "grav2.zip", package="qt12"))
map <- insert_pseudomarkers(grav2$gmap, step=1)
gA <- viterbi(grav2[1:5,1:2], map, error_prob=0.002)
gB <- viterbi(grav2[1:5,3:4], map, error_prob=0.002)
g <- cbind(gA, gB)
```

---

cbind_expand	<i>Combine matrices by columns, expanding and aligning rows</i>
--------------	---

---

**Description**

This is like `base::cbind()` but using row names to align the rows and expanding with missing values if there are rows in some matrices but not others.

**Usage**

```
cbind_expand(...)
```

**Arguments**

... A set of matrices or data frames

**Value**

The matrices combined by columns, using row names to align the rows, and expanding with missing values if there are rows in some matrices but not others.

**Examples**

```
df1 <- data.frame(x=c(1,2,3,NA,4), y=c(5,8,9,10,11), row.names=c("A", "B", "C", "D", "E"))
df2 <- data.frame(w=c(7,8,0,9,10), z=c(6,NA,NA,9,10), row.names=c("A", "B", "F", "C", "D"))
cbind_expand(df1, df2)
```

---

CCcolors

---

*Collaborative Cross colors*


---

**Description**

A vector of 8 colors for use with the mouse Collaborative Cross and Diversity Outbreds.

**Details**

CCorigcolors are the original eight colors for the Collaborative Cross founder strains. CCaltcolors are a slightly modified version, but still not color-blind friendly. CCcolors are derived from the the Okabe-Ito color blind friendly palette in Wong (2011) Nature Methods [doi:10.1038/nmeth.1618](https://doi.org/10.1038/nmeth.1618).

**Source**

<https://web.archive.org/web/20250215070655/https://csbio.unc.edu/CCstatus/index.py?run=AvailableLines.information>

**Examples**

```
data(CCcolors)
data(CCaltcolors)
data(CCorigcolors)
```

---

check_cross2	<i>Check a cross2 object</i>
--------------	------------------------------

---

**Description**

Check the integrity of the data within a cross2 object.

**Usage**

```
check_cross2(cross2)
```

**Arguments**

cross2	An object of class "cross2", as output by <a href="#">read_cross2()</a> . For details, see the <a href="#">R/qlt2 developer guide</a> .
--------	---

**Details**

Checks whether a cross2 object meets the specifications. Problems are issued as warnings.

**Value**

If everything is correct, returns TRUE; otherwise FALSE, with attributes that give the problems.

**Examples**

```
grav2 <- read_cross2(system.file("extdata", "grav2.zip", package="qlt2"))
check_cross2(grav2)
```

---

chisq_colpairs	<i>Chi-square test on all pairs of columns</i>
----------------	--

---

**Description**

Perform a chi-square test for independence for all pairs of columns of a matrix.

**Usage**

```
chisq_colpairs(x)
```

**Arguments**

x	A matrix of positive integers. NAs and values $\leq 0$ are treated as missing.
---	--

**Value**

A matrix of size  $p \times p$ , where  $p$  is the number of columns in the input matrix  $x$ , containing the chi-square test statistics for independence, applied to pairs of columns of  $x$ . The diagonal of the result will be all NAs.

**Examples**

```
z <- matrix(sample(1:2, 500, replace=TRUE), ncol=5)
chisq_colpairs(z)
```

---

chr_lengths	<i>Calculate chromosome lengths</i>
-------------	-------------------------------------

---

**Description**

Calculate chromosome lengths for a map object

**Usage**

```
chr_lengths(map, collapse_to_AX = FALSE)
```

**Arguments**

- map                   A list of vectors, each specifying locations of the markers.
- collapse\_to\_AX   If TRUE, collapse to the total lengths of the autosomes and X chromosome.

**Details**

We take `diff(range(v))` for each vector,  $v$ .

**Value**

A vector of chromosome lengths. If `collapse_to_AX=TRUE`, the result is a vector of length 2 (autosomal and X chromosome lengths).

**See Also**

```
scan1perm\(\)
```

---

clean	<i>Clean an object</i>
-------	------------------------

---

**Description**

Clean an object by removing messy values

**Usage**

```
clean(object, ...)
```

**Arguments**

object	Object to be cleaned
...	Other arguments

**Value**

Input object with messy values cleaned up

**See Also**

[clean.scan1\(\)](#), [clean.calc\\_genoprob\(\)](#)

---

clean_genoprob	<i>Clean genotype probabilities</i>
----------------	-------------------------------------

---

**Description**

Clean up genotype probabilities by setting small values to 0 and for a genotype column where the maximum value is rather small, set all values in that column to 0.

**Usage**

```
clean_genoprob(
  object,
  value_threshold = 0.000001,
  column_threshold = 0.01,
  ind = NULL,
  cores = 1,
  ...
)

## S3 method for class 'calc_genoprob'
clean(
```

```

    object,
    value_threshold = 0.000001,
    column_threshold = 0.01,
    ind = NULL,
    cores = 1,
    ...
)

```

## Arguments

<code>object</code>	Genotype probabilities as calculated by <code>calc_genoprob()</code> .
<code>value_threshold</code>	Probabilities below this value will be set to 0.
<code>column_threshold</code>	For genotype columns where the maximum value is below this threshold, all values will be set to 0. This must be less than $1/k$ where $k$ is the number of genotypes.
<code>ind</code>	Optional vector of individuals (logical, numeric, or character). If provided, only the genotype probabilities for these individuals will be cleaned, though the full set will be returned.
<code>cores</code>	Number of CPU cores to use, for parallel calculations. (If 0, use <code>parallel::detectCores()</code> .) Alternatively, this can be links to a set of cluster sockets, as produced by <code>parallel::makeCluster()</code> .
<code>...</code>	Ignored at this point.

## Details

In cases where a particular genotype is largely absent, `scan1coef()` and `fit1()` can give unstable estimates of the genotype effects. Cleaning up the genotype probabilities by setting small values to 0 helps to ensure that such effects get set to NA.

At each position and for each genotype column, we find the maximum probability across individuals. If that maximum is  $< \text{column\_threshold}$ , all values in that genotype column at that position are set to 0.

In addition, any genotype probabilities that are  $< \text{value\_threshold}$  (generally  $< \text{column\_threshold}$ ) are set to 0.

The probabilities are then re-scaled so that the probabilities for each individual at each position sum to 1.

If `ind` is provided, the function is applied only to the designated subset of individuals. This may be useful when only a subset of individuals have been phenotyped, as you may want to zero out genotype columns where that subset of individuals has only negligible probability values.

## Value

A cleaned version of the input genotype probabilities object, `object`.



**Examples**

```

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

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

# clean the genotype probabilities
# (doesn't really do anything in this case, because there are no small but non-zero values)
probs_clean <- clean(probs)

# clean only the females' genotype probabilities
probs_cleanf <- clean(probs, ind=names(iron$is_female)[iron$is_female])

```

clean\_scan1

*Clean scan1 output***Description**

Clean scan1 output by replacing negative values with NA and remove rows where all values are NA.

**Usage**

```

clean_scan1(object, ...)

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

```

**Arguments**

object	Output of <code>scan1()</code> .
...	Ignored at present

**Value**

The input object with negative values replaced with NAs and then rows with all NAs removed.

**Examples**

```

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

pr <- calc_genoprob(iron)
out <- scan1(pr, iron$pheno)

out <- clean(out)

```

---

compare_founder_geno	<i>Compare founders genotype data</i>
----------------------	---------------------------------------

---

## Description

Count the number of matching genotypes between all pairs of founder lines.

## Usage

```
compare_founder_geno(
  cross,
  omit_x = FALSE,
  proportion = TRUE,
  quiet = TRUE,
  cores = 1
)
```

## Arguments

cross	Object of class "cross2". For details, see the <a href="#">R/qt12 developer guide</a> .
omit_x	If TRUE, only use autosomal genotypes
proportion	If TRUE (the default), the upper triangle of the result contains the proportions of matching genotypes. If FALSE, the upper triangle contains counts of matching genotypes.
quiet	IF FALSE, print progress messages.
cores	Number of CPU cores to use, for parallel calculations. (If 0, use <a href="#">parallel::detectCores()</a> .) Alternatively, this can be links to a set of cluster sockets, as produced by <a href="#">parallel::makeCluster()</a> .

## Value

A square matrix; diagonal is number of observed genotypes for each founder line. The values in the lower triangle are the numbers of markers where both of a pair were genotyped. The values in the upper triangle are either proportions or counts of matching genotypes for each pair (depending on whether proportion=TRUE or =FALSE). The object is given class "compare\_geno".

## Examples

```
## Not run:
file <- paste0("https://raw.githubusercontent.com/rqt1/",
               "qt12data/main/D0ex/D0ex.zip")
D0ex <- read_cross2(file)
cg <- compare_founder_geno(D0ex)
summary(cg)

## End(Not run)
```

---

compare_geno	<i>Compare individuals' genotype data</i>
--------------	---

---

## Description

Count the number of matching genotypes between all pairs of individuals, to look for unusually closely related individuals.

## Usage

```
compare_geno(cross, omit_x = FALSE, proportion = TRUE, quiet = TRUE, cores = 1)
```

## Arguments

cross	Object of class "cross2". For details, see the <a href="#">R/qt12 developer guide</a> .
omit_x	If TRUE, only use autosomal genotypes
proportion	If TRUE (the default), the upper triangle of the result contains the proportions of matching genotypes. If FALSE, the upper triangle contains counts of matching genotypes.
quiet	If FALSE, print progress messages.
cores	Number of CPU cores to use, for parallel calculations. (If 0, use <a href="#">parallel::detectCores()</a> .) Alternatively, this can be links to a set of cluster sockets, as produced by <a href="#">parallel::makeCluster()</a> .

## Value

A square matrix; diagonal is number of observed genotypes for each individual. The values in the lower triangle are the numbers of markers where both of a pair were genotyped. The values in the upper triangle are either proportions or counts of matching genotypes for each pair (depending on whether proportion=TRUE or =FALSE). The object is given class "compare\_geno".

## Examples

```
grav2 <- read_cross2(system.file("extdata", "grav2.zip", package="qt12"))
cg <- compare_geno(grav2)
summary(cg)
```

---

compare_genoprob	<i>Compare two sets of genotype probabilities</i>
------------------	---

---

## Description

Compare two sets of genotype probabilities for one individual on a single chromosome.

## Usage

```
compare_genoprob(
  probs1,
  probs2,
  cross,
  ind = 1,
  chr = NULL,
  minprob = 0.95,
  minmarkers = 10,
  minwidth = 0,
  annotate = FALSE
)
```

## Arguments

probs1	Genotype probabilities (as produced by <a href="#">calc_genoprob()</a> ) or allele dosages (as produced by <a href="#">genoprob_to_alleleprob()</a> ).
probs2	A second set of genotype probabilities, just like probs1.
cross	Object of class "cross2". For details, see the <a href="#">R/qt12 developer guide</a> .
ind	Individual to plot, either a numeric index or an ID.
chr	Selected chromosome; a single character string.
minprob	Minimum probability for inferring genotypes (passed to <a href="#">maxmarg()</a> ).
minmarkers	Minimum number of markers in results.
minwidth	Minimum width in results.
annotate	If TRUE, add some annotations to the geno1 and geno2 columns to indicate, where they differ, which one matches what appears to be the best genotype. (* = matches the best genotype; - = lower match).

## Details

The function does the following:

- Reduce the probabilities to a set of common locations that also appear in cross.
- Use [maxmarg\(\)](#) to infer the genotype at every position using each set of probabilities.
- Identify intervals where the two inferred genotypes are constant.
- Within each segment, compare the observed SNP genotypes to the founders' genotypes.

**Value**

A data frame with each row corresponding to an interval over which probs1 and probs2 each have a fixed inferred genotype. Columns include the two inferred genotypes, the start and end points and width of the interval, and when founder genotypes are in cross, the proportions of SNPs where the individual matches each possible genotypes.

**See Also**

[plot\\_genoprobcomp\(\)](#)

**Examples**

```
iron <- read_cross2(system.file("extdata", "iron.zip", package="qtl2"))
iron <- iron[1,"2"] # subset to first individual on chr 2
map <- insert_pseudomarkers(iron$gmap, step=1)

# in presence of a genotyping error, how much does error_prob matter?
iron$geno[[1]][1,3] <- 3
pr_e <- calc_genoprob(iron, map, error_prob=0.002)
pr_ne <- calc_genoprob(iron, map, error_prob=1e-15)

compare_genoprob(pr_e, pr_ne, iron, minmarkers=1, minprob=0.5)
```

---

compare_maps	<i>Compare two marker maps</i>
--------------	--------------------------------

---

**Description**

Compare two marker maps, identifying markers that are only in one of the two maps, or that are in different orders on the two maps.

**Usage**

```
compare_maps(map1, map2)
```

**Arguments**

map1	A list of numeric vectors; each vector gives marker positions for a single chromosome.
map2	A second map, in the same format as map1.

**Value**

A data frame containing

- marker - marker name
- chr\_map1 - chromosome ID on map1
- pos\_map1 - position on map1
- chr\_map2 - chromosome ID on map2
- pos\_map2 - position on map2

**Examples**

```
# load some data
iron <- read_cross2( system.file("extdata", "iron.zip", package="qtl2") )
gmap <- iron$gmap
pmap <- iron$pmap

# omit a marker from each map
gmap[[7]] <- gmap[[7]][-3]
pmap[[8]] <- pmap[[8]][-7]
# swap order of a couple of markers on the physical map
names(pmap[[9]][3:4]) <- names(pmap[[9]][4:3])
# move a marker to a different chromosome
pmap[[10]] <- c(pmap[[10]], pmap[[1]][2])[c(1,3,2)]
pmap[[1]] <- pmap[[1]][-2]

# compare these messed-up maps
compare_maps(gmap, pmap)
```

---

convert2cross2

---

*Convert R/qtl cross object to new format*


---

**Description**

Convert a cross object from the R/qtl format to the R/qtl2 format

**Usage**

```
convert2cross2(cross)
```

**Arguments**

cross                    An object of class "cross"; see [qtl::read.cross\(\)](#) for details.

**Value**

Object of class "cross2". For details, see the [R/qtl2 developer guide](#).

**See Also**[read\\_cross2\(\)](#)**Examples**

```
library(qtl)
data(hyper)
hyper2 <- convert2cross2(hyper)
```

---

count_xo	<i>Count numbers of crossovers</i>
----------	------------------------------------

---

**Description**

Estimate the numbers of crossovers in each individual on each chromosome.

**Usage**

```
count_xo(geno, quiet = TRUE, cores = 1)
```

**Arguments**

geno	List of matrices of genotypes (output of <a href="#">maxmarg()</a> or <a href="#">viterbi()</a> ) or a list of 3d-arrays of genotypes (output of <a href="#">sim_geno()</a> ).
quiet	If FALSE, print progress messages.
cores	Number of CPU cores to use, for parallel calculations. (If 0, use <a href="#">parallel::detectCores()</a> .) Alternatively, this can be links to a set of cluster sockets, as produced by <a href="#">parallel::makeCluster()</a> .

**Value**

A matrix of crossover counts, individuals x chromosomes, or (if the input was the output of [sim\\_geno\(\)](#)) a 3d-array of crossover counts, individuals x chromosomes x imputations.

**See Also**[locate\\_xo\(\)](#)**Examples**

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

map <- insert_pseudomarkers(iron$gmap, step=1)
pr <- calc_genoprob(iron, map, error_prob=0.002, map_function="c-f")
g <- maxmarg(pr)
n_xo <- count_xo(g)

# imputations
imp <- sim_geno(iron, map, error_prob=0.002, map_function="c-f", n_draws=32)
```

```

n_xo_imp <- count_xo(imp)
# sums across chromosomes
tot_xo_imp <- apply(n_xo_imp, c(1,3), sum)
# mean and SD across imputations
summary_xo <- cbind(mean=rowMeans(tot_xo_imp),
                    sd=apply(tot_xo_imp, 1, sd))

```

---

```
create_gene_query_func
```

*Create a function to query genes*

---

## Description

Create a function that will connect to a SQLite database of gene information and return a data frame with gene information for a selected region.

## Usage

```

create_gene_query_func(
  dbfile = NULL,
  db = NULL,
  table_name = "genes",
  chr_field = "chr",
  start_field = "start",
  stop_field = "stop",
  name_field = "Name",
  strand_field = "strand",
  filter = NULL
)

```

## Arguments

dbfile	Name of database file
db	Optional database connection (provide one of file and db).
table_name	Name of table in the database
chr_field	Name of chromosome field
start_field	Name of field with start position (in basepairs)
stop_field	Name of field with stop position (in basepairs)
name_field	Name of field with gene name
strand_field	Name of field with strand (+/-)
filter	Additional SQL filter (as a character string).



## Details

Note that this function assumes that the database has `start` and `stop` fields that are in basepairs, but the selection uses positions in Mbp, and the output data frame should have `start` and `stop` columns in Mbp.

Also note that a SQLite database of MGI mouse genes is available at figshare: [doi:10.6084/m9.figshare.5286019.v7](https://doi.org/10.6084/m9.figshare.5286019.v7)

## Value

Function with three arguments, `chr`, `start`, and `end`, which returns a data frame with the genes overlapping that region, with `start` and `end` being in Mbp. The output should contain at least the columns `Name`, `chr`, `start`, and `stop`, the latter two being positions in Mbp.

## Examples

```
# create query function by connecting to file
dbfile <- system.file("extdata", "mouse_genes_small.sqlite", package="qt12")
query_genes <- create_gene_query_func(dbfile, filter="(source=='MGI')")
# query_genes will connect and disconnect each time
genes <- query_genes("2", 97.0, 98.0)

# connect and disconnect separately
library(RSQLite)
db <- dbConnect(SQLite(), dbfile)
query_genes <- create_gene_query_func(db=db, filter="(source=='MGI')")
genes <- query_genes("2", 97.0, 98.0)
dbDisconnect(db)
```

---

create_snpinfo	Create snp information table for a cross
----------------	--

---

## Description

Create a table of snp information from a cross, for use with `scan1snps()`.

## Usage

```
create_snpinfo(cross)
```

## Arguments

`cross` Object of class "cross2". For details, see the [R/qt12 developer guide](#).

**Value**

A data frame of SNP information with the following columns:

- chr - Character string or factor with chromosome
- pos - Position (in same units as in the "map" attribute in genoprobs).
- snp - Character string with SNP identifier (if missing, the rownames are used).
- 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 SNPs with missing founder genotypes are omitted.

**See Also**

[index\\_snps\(\)](#), [scan1snps\(\)](#), [genoprob\\_to\\_snpprob\(\)](#)

**Examples**

```
## Not run:
# load example data and calculate genotype probabilities
file <- paste0("https://raw.githubusercontent.com/rqtl/",
               "qt12data/main/DO_Recla/recla.zip")
recla <- read_cross2(file)
snpinfo <- create_snpinfo(recla)

# calculate genotype probabilities
pr <- calc_genoprob(recla, error_prob=0.002, map_function="c-f")

# index the snp information
snpinfo <- index_snps(recla$pmap, snpinfo)

# sex covariate
sex <- setNames((recla$covar$Sex=="female")*1, rownames(recla$covar))

# perform a SNP scan
out <- scan1snps(pr, recla$pmap, recla$pheno[, "bw"], addcovar=sex, snpinfo=snpinfo)

# plot the LOD scores
plot(out$lod, snpinfo, altcol="green3")

## End(Not run)
```

---

create\_variant\_query\_func

*Create a function to query variants*

---

**Description**

Create a function that will connect to a SQLite database of founder variant information and return a data frame with variants for a selected region.

**Usage**

```
create_variant_query_func(
  dbfile = NULL,
  db = NULL,
  table_name = "variants",
  chr_field = "chr",
  pos_field = "pos",
  id_field = "snp_id",
  sdp_field = "sdp",
  filter = NULL
)
```

**Arguments**

dbfile	Name of database file
db	Optional database connection (provide one of file and db).
table_name	Name of table in the database
chr_field	Name of chromosome field
pos_field	Name of position field
id_field	Name of SNP/variant ID field
sdp_field	Name of strain distribution pattern (SDP) field
filter	Additional SQL filter (as a character string)

**Details**

Note that this function assumes that the database has a pos field that is in basepairs, but the selection uses start and end positions in Mbp, and the output data frame should have pos in Mbp.

Also note that a SQLite database of variants in the founder strains of the mouse Collaborative Cross is available at figshare: [doi:10.6084/m9.figshare.5280229.v3](https://doi.org/10.6084/m9.figshare.5280229.v3)

**Value**

Function with three arguments, chr, start, and end, which returns a data frame with the variants in that region, with start and end being in Mbp. The output should contain at least the columns chr and pos, the latter being position in Mbp.

**Examples**

```
# create query function by connecting to file
dbfile <- system.file("extdata", "cc_variants_small.sqlite", package="qt12")
query_variants <- create_variant_query_func(dbfile)
# query_variants will connect and disconnect each time
variants <- query_variants("2", 97.0, 98.0)

# create query function to just grab SNPs
query_snps <- create_variant_query_func(dbfile, filter="type=='snp'")
# query_variants will connect and disconnect each time
```

```
snps <- query_snps("2", 97.0, 98.0)

# connect and disconnect separately
library(RSQLite)
db <- dbConnect(SQLite(), dbfile)
query_variants <- create_variant_query_func(db=db)
variants <- query_variants("2", 97.0, 98.0)
dbDisconnect(db)
```

---

decomp_kinship	<i>Calculate eigen decomposition of kinship matrix</i>
----------------	--

---

## Description

Calculate the eigen decomposition of a kinship matrix, or of a list of such matrices.

## Usage

```
decomp_kinship(kinship, cores = 1)
```

## Arguments

kinship	A square matrix, or a list of square matrices.
cores	Number of CPU cores to use, for parallel calculations. (If 0, use <a href="#">parallel::detectCores()</a> .) Alternatively, this can be links to a set of cluster sockets, as produced by <a href="#">parallel::makeCluster()</a> .

## Details

The result contains an attribute "eigen\_decomp".

## Value

The eigen values and the **transposed** eigen vectors, as a list containing a vector values and a matrix vectors.

## Examples

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

map <- insert_pseudomarkers(iron$gmap, step=1)
probs <- calc_genoprob(iron, map, error_prob=0.002)
K <- calc_kinship(probs)

Ke <- decomp_kinship(K)
```

---

drop_markers	<i>Drop markers from a cross2 object</i>
--------------	--

---

**Description**

Drop a vector of markers from a cross2 object.

**Usage**

```
drop_markers(cross, markers)
```

**Arguments**

cross	Object of class "cross2". For details, see the <a href="#">R/qlt2 developer guide</a> .
markers	A vector of marker names.

**Value**

The input cross with the specified markers removed.

**See Also**

[pull\\_markers\(\)](#), [drop\\_nullmarkers\(\)](#), [reduce\\_markers\(\)](#), [find\\_dup\\_markers\(\)](#)

**Examples**

```
grav2 <- read_cross2(system.file("extdata", "grav2.zip", package="qlt2"))
markers2drop <- c("BH.342C/347L-Col", "GH.94L", "EG.357C/359L-Col", "CD.245L", "ANL2")
grav2_rev <- drop_markers(grav2, markers2drop)
```

---

drop_nullmarkers	<i>Drop markers with no genotype data</i>
------------------	---

---

**Description**

Drop markers with no genotype data (or no informative genotypes)

**Usage**

```
drop_nullmarkers(cross, quiet = FALSE)
```

**Arguments**

cross	Object of class "cross2". For details, see the <a href="#">R/qlt2 developer guide</a> .
quiet	If FALSE, print information about how many markers were dropped.

**Details**

We omit any markers that have completely missing data, or if founder genotypes are present (e.g., for Diversity Outbreds), the founder genotypes are missing or are all the same.

**Value**

The input cross with the uninformative markers removed.

**See Also**

[drop\\_markers\(\)](#), [pull\\_markers\(\)](#)

**Examples**

```
grav2 <- read_cross2(system.file("extdata", "grav2.zip", package="qt12"))
# make a couple of markers missing
grav2$geno[[2]][,c(3,25)] <- 0
grav2_rev <- drop_nullmarkers(grav2)
```

---

est\_herit

*Estimate heritability with a linear mixed model*

---

**Description**

Estimate the heritability of a set of traits via a linear mixed model, with possible allowance for covariates.

**Usage**

```
est_herit(
  pheno,
  kinship,
  addcovar = NULL,
  weights = NULL,
  reml = TRUE,
  cores = 1,
  ...
)
```

**Arguments**

pheno	A numeric matrix of phenotypes, individuals x phenotypes.
kinship	A kinship matrix.
addcovar	An optional numeric matrix of additive covariates.
weights	An optional numeric vector of positive weights for the individuals. As with the other inputs, it must have names for individual identifiers.

reml	If true, use REML; otherwise, use maximum likelihood.
cores	Number of CPU cores to use, for parallel calculations. (If 0, use <code>parallel::detectCores()</code> .) Alternatively, this can be links to a set of cluster sockets, as produced by <code>parallel::makeCluster()</code> .
...	Additional control parameters (see details).

## Details

We fit the model  $y = X\beta + \epsilon$  where  $\epsilon$  is multivariate normal with mean 0 and covariance matrix  $\sigma^2[h^2(2K) + I]$  where  $K$  is the kinship matrix and  $I$  is the identity matrix.

If weights are provided, the covariance matrix becomes  $\sigma^2[h^2(2K) + D]$  where  $D$  is a diagonal matrix with the reciprocal of the weights.

For each of the inputs, the row names are used as individual identifiers, to align individuals.

If `reml=TRUE`, restricted maximum likelihood (reml) is used to estimate the heritability, separately for each phenotype.

Additional control parameters include `tol` for the tolerance for convergence, `quiet` for controlling whether messages will be display, `max_batch` for the maximum number of phenotypes in a batch, and `check_boundary` for whether the 0 and 1 boundary values for the estimated heritability will be checked explicitly.

## Value

A vector of estimated heritabilities, corresponding to the columns in `pheno`. The result has attributes `"sample_size"`, `"log10lik"` and `"resid_sd"`.

## Examples

```
# 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)

# kinship matrix
kinship <- calc_kinship(probs)

# 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)

# perform genome scan
hsq <- est_herit(pheno, kinship, covar)
```

---

est_map	<i>Estimate genetic maps</i>
---------	------------------------------

---

## Description

Uses a hidden Markov model to re-estimate the genetic map for an experimental cross, with possible allowance for genotyping errors.

## Usage

```
est_map(
  cross,
  error_prob = 0.0001,
  map_function = c("haldane", "kosambi", "c-f", "morgan"),
  lowmem = FALSE,
  maxit = 10000,
  tol = 0.000001,
  quiet = TRUE,
  save_rf = FALSE,
  cores = 1
)
```

## Arguments

cross	Object of class "cross2". For details, see the <a href="#">R/qt12 developer guide</a> .
error_prob	Assumed genotyping error probability
map_function	Character string indicating the map function to use to convert genetic distances to recombination fractions.
lowmem	If FALSE, precalculate initial and emission probabilities, and at each iteration calculate the transition matrices for a chromosome; potentially a lot faster but using more memory. Needs to be tailored somewhat to cross type. For example, multi-way RIL may need to reorder the transition matrix according to cross order, and AIL and DO need separate transition matrices for each generation.
maxit	Maximum number of iterations in EM algorithm.
tol	Tolerance for determining convergence
quiet	If FALSE, print progress messages.
save_rf	If TRUE, save the estimated recombination fractions as an attribute ("rf") of the result.
cores	Number of CPU cores to use, for parallel calculations. (If 0, use <a href="#">parallel::detectCores()</a> .) Alternatively, this can be links to a set of cluster sockets, as produced by <a href="#">parallel::makeCluster()</a> .

## Details

The map is estimated assuming no crossover interference, but a map function (by default, Haldane's) is used to derive the genetic distances.



**Value**

A list of numeric vectors, with the estimated marker locations (in cM). The location of the initial marker on each chromosome is kept the same as in the input cross.

**Examples**

```
grav2 <- read_cross2(system.file("extdata", "grav2.zip", package="qt12"))
gmap <- est_map(grav2, error_prob=0.002)
```

---

find_dup_markers	<i>Find markers with identical genotype data</i>
------------------	--

---

**Description**

Identify sets of markers with identical genotype data.

**Usage**

```
find_dup_markers(cross, chr, exact_only = TRUE, adjacent_only = FALSE)
```

**Arguments**

cross	Object of class "cross2". For details, see the <a href="#">R/qt12 developer guide</a> .
chr	Optional vector specifying which chromosomes to consider. This may be a logical, numeric, or character string vector.
exact_only	If TRUE, look only for markers that have matching genotypes and the same pattern of missing data; if FALSE, also look for cases where the observed genotypes at one marker match those at another, and where the first marker has missing genotype whenever the genotype for the second marker is missing.
adjacent_only	If TRUE, look only for sets of markers that are adjacent to each other.

**Details**

If `exact.only=TRUE`, we look only for groups of markers whose pattern of missing data and observed genotypes match exactly. One marker (chosen at random) is selected as the name of the group (in the output of the function).

If `exact.only=FALSE`, we look also for markers whose observed genotypes are contained in the observed genotypes of another marker. We use a pair of nested loops, working from the markers with the most observed genotypes to the markers with the fewest observed genotypes.

**Value**

A list of marker names; each component is a set of markers whose genotypes match one other marker, and the name of the component is the name of the marker that they match.

**See Also**

[drop\\_markers\(\)](#), [drop\\_nullmarkers\(\)](#), [reduce\\_markers\(\)](#)

**Examples**

```
grav2 <- read_cross2(system.file("extdata", "grav2.zip", package="qt12"))
dup <- find_dup_markers(grav2)
grav2_nodup <- drop_markers(grav2, unlist(dup))
```

---

find_ibd_segments	<i>Find IBD segments for a set of strains</i>
-------------------	---

---

**Description**

Find IBD segments (regions with a lot of shared SNP genotypes) for a set of strains

**Usage**

```
find_ibd_segments(geno, map, min_lod = 15, error_prob = 0.001, cores = 1)
```

**Arguments**

geno	List of matrices of founder genotypes. The matrices correspond to the genotypes on chromosomes and are arrayed as founders x markers.
map	List of vectors of marker positions
min_lod	Threshold for minimum LOD score for a segment
error_prob	Genotyping error/mutation probability
cores	Number of CPU cores to use, for parallel calculations. (If 0, use <a href="#">parallel::detectCores()</a> .) Alternatively, this can be links to a set of cluster sockets, as produced by <a href="#">parallel::makeCluster()</a> .

**Details**

For each strain pair on each chromosome, we consider all marker intervals and calculate a LOD score comparing the two hypotheses: that the strains are IBD in the interval, vs. that they are not. We assume that the two strains are homozygous at all markers, and use the model from Broman and Weber (1999), which assumes linkage equilibrium between markers and uses a simple model for genotype frequencies in the presence of genotyping errors or mutations.

Note that inference of IBD segments is heavily dependent on how SNPs were chosen to be genotyped. (For example, were the SNPs ascertained based on their polymorphism between a particular strain pair?)

**Value**

A data frame whose rows are IBD segments and whose columns are:

- Strain 1
- Strain 2
- Chromosome
- Left marker
- Right marker
- Left position
- Right position
- Left marker index
- Right marker index
- Interval length
- Number of markers
- Number of mismatches
- LOD score

**References**

Broman KW, Weber JL (1999) Long homozygous chromosomal segments in reference families from the Centre d'Étude du Polymorphisme Humain. *Am J Hum Genet* 65:1493–1500.

**Examples**

```
## Not run:  
# load DO data from Recla et al. (2014) Mamm Genome 25:211-222.  
recla <- read_cross2("https://raw.githubusercontent.com/rqtl/ql2data/main/DO_Recla/recla.zip")  
  
# grab founder genotypes and physical map  
fg <- recla$founder_genotype  
pmap <- recla$pmap  
  
# find shared segments  
(segs <- find_ibd_segments(fg, pmap, min_lod=10, error_prob=0.0001))  
  
## End(Not run)
```

---

find_index_snp	<i>Find name of indexed snp</i>
----------------	---------------------------------

---

## Description

For a particular SNP, find the name of the corresponding indexed SNP.

## Usage

```
find_index_snp(snpinfo, snp)
```

## Arguments

snpinfo	Data frame with SNP information with the following columns: <ul style="list-style-type: none"> <li>chr - Character string or factor with chromosome</li> <li>index - Numeric index of equivalent, indexed SNP, as produced by <a href="#">index_snps()</a>.</li> <li>snp - Character string with SNP identifier (if missing, the rownames are used).</li> </ul>
snp	Name of snp to look for (can be a vector).

## Value

A vector of SNP IDs (the corresponding indexed SNPs), with NA if a SNP is not found.

## See Also

[find\\_marker\(\)](#)

## Examples

```
## Not run:
# load example data and calculate genotype probabilities
file <- paste0("https://raw.githubusercontent.com/rqtl/",
               "qt12data/main/D0_Recla/recla.zip")
recla <- read_cross2(file)

# founder genotypes for a set of SNPs
snpgeno <- rbind(m1=c(3,1,1,3,1,1,1,1),
                 m2=c(3,1,1,3,1,1,1,1),
                 m3=c(1,1,1,1,3,3,3,3),
                 m4=c(1,3,1,3,1,3,1,3))
sdp <- calc_sdp(snpgeno)
snpinfo <- data.frame(chr=c("19", "19", "X", "X"),
                     pos=c(40.36, 40.53, 110.91, 111.21),
                     sdp=sdp,
                     snp=c("m1", "m2", "m3", "m4"), stringsAsFactors=FALSE)

# update snp info by adding the SNP index column
```

```
snpinfo <- index_snps(recla$pmap, snpinfo)

# find indexed snp for a particular snp
find_index_snp(snpinfo, "m3")

## End(Not run)
```

---

**find\_map\_gaps***Find gaps in a genetic map*

---

### Description

Find gaps between markers in a genetic map

### Usage

```
find_map_gaps(map, min_gap = 50)
```

### Arguments

map	Genetic map as a list of vectors (each vector is a chromosome and contains the marker positions).
min_gap	Minimum gap length to return.

### Value

Data frame with 6 columns: chromosome, marker to left of gap, numeric index of marker to left, marker to right of gap, numeric index of marker to right, and the length of the gap.

### See Also

[reduce\\_map\\_gaps\(\)](#)

### Examples

```
iron <- read_cross2(system.file("extdata", "iron.zip", package="qtl2"))
find_map_gaps(iron$gmap, 40)
```

---

find_marker	<i>Find markers by chromosome position</i>
-------------	--

---

## Description

Find markers closest to specified set of positions, or within a specified interval.

## Usage

```
find_marker(map, chr, pos = NULL, interval = NULL)
```

## Arguments

map	A map object: a list (corresponding to chromosomes) of vectors of marker positions. Can also be a snpinfo object (data frame with columns chr and pos; marker names taken from column snp or if that doesn't exist from the row names)
chr	A vector of chromosomes
pos	A vector of positions
interval	A pair of positions (provide either pos or interval but not both)

## Details

If pos is provided, interval should not be, and vice versa.

If pos is provided, then chr and pos should either be the same length, or one of them should have length 1 (to be expanded to the length of the other).

If interval is provided, then chr should have length 1.

## Value

A vector of marker names, either closest to the positions specified by pos, or within the interval defined by interval.

## See Also

[find\\_markerpos\(\)](#), [find\\_index\\_snp\(\)](#), [pull\\_genoprobp\(\)](#), [pull\\_genoprobint\(\)](#)

## Examples

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

# find markers by their genetic map positions
find_marker(iron$gmap, c(8, 11), c(37.7, 56.9))

# find markers by their physical map positions (two markers on chr 7)
find_marker(iron$pmap, 7, c(44.2, 108.9))
```

```
# find markers in an interval
find_marker(iron$pmap, 16, interval=c(35, 80))
```

---

find_markerpos	<i>Find positions of markers</i>
----------------	----------------------------------

---

## Description

Find positions of markers within a cross object

## Usage

```
find_markerpos(cross, markers, na.rm = TRUE)
```

## Arguments

cross	Object of class "cross2". For details, see the <a href="#">R/qt12 developer guide</a> . Can also be a map (as a list of vectors of marker positions).
markers	A vector of marker names.
na.rm	If TRUE, don't include not-found markers in the results (but issue a warning if some markers weren't found). If FALSE, include those markers with NA for chr and position.

## Value

A data frame with chromosome and genetic and physical positions (in columns "gmap" and "pmap"), with markers as row names. If the input cross is not a cross2 object but rather a map, the output contains chr and pos.

## See Also

[find\\_marker\(\)](#)

## Examples

```
iron <- read_cross2(system.file("extdata", "iron.zip", package="qt12"))

# find markers
find_markerpos(iron, c("D8Mit294", "D11Mit101"))
```

find\_peaks

*Find peaks in a set of LOD curves***Description**

Find peaks in a set of LOD curves (output from [scan1\(\)](#))

**Usage**

```
find_peaks(
  scan1_output,
  map,
  threshold = 3,
  peakdrop = Inf,
  drop = NULL,
  prob = NULL,
  thresholdX = NULL,
  peakdropX = NULL,
  dropX = NULL,
  probX = NULL,
  expand2markers = TRUE,
  sort_by = c("column", "pos", "lod"),
  cores = 1
)
```

**Arguments**

scan1_output	An object of class "scan1" as returned by <a href="#">scan1()</a> .
map	A list of vectors of marker positions, as produced by <a href="#">insert_pseudomarkers()</a> . Can also be an indexed SNP info table, as from <a href="#">index_snps()</a> or <a href="#">scan1snps()</a> .
threshold	Minimum LOD score for a peak (can be a vector with separate thresholds for each lod score column in scan1_output)
peakdrop	Amount that the LOD score must drop between peaks, if multiple peaks are to be defined on a chromosome. (Can be a vector with separate values for each lod score column in scan1_output.)
drop	If provided, LOD support intervals are included in the results, and this indicates the amount to drop in the support interval. (Can be a vector with separate values for each lod score column in scan1_output.) Must be $\leq$ peakdrop
prob	If provided, Bayes credible intervals are included in the results, and this indicates the nominal coverage. (Can be a vector with separate values for each lod score column in scan1_output.) Provide just one of drop and prob.
thresholdX	Separate threshold for the X chromosome; if unspecified, the same threshold is used for both autosomes and the X chromosome. (Like threshold, this can be a vector with separate thresholds for each lod score column.)



peakdropX	Like peakdrop, but for the X chromosome; if unspecified, the same value is used for both autosomes and the X chromosome. (Can be a vector with separate values for each lod score column in scan1_output.)
dropX	Amount to drop for LOD support intervals on the X chromosome. Ignored if drop is not provided. (Can be a vector with separate values for each lod score column in scan1_output.)
probX	Nominal coverage for Bayes intervals on the X chromosome. Ignored if prob is not provided. (Can be a vector with separate values for each lod score column in scan1_output.)
expand2markers	If TRUE (and if drop or prob is provided, so that QTL intervals are calculated), QTL intervals are expanded so that their endpoints are at genetic markers.
sort_by	Indicates whether to sort the rows by lod column, genomic position, or LOD score.
cores	Number of CPU cores to use, for parallel calculations. (If 0, use <code>parallel::detectCores()</code> .) Alternatively, this can be links to a set of cluster sockets, as produced by <code>parallel::makeCluster()</code> .

## Details

For each lod score column on each chromosome, we return a set of peaks defined as local maxima that exceed the specified threshold, with the requirement that the LOD score must have dropped by at least peakdrop below the lowest of any two adjacent peaks.

At a given peak, if there are ties, with multiple positions jointly achieving the maximum LOD score, we take the average of these positions as the location of the peak.

## Value

A data frame with each row being a single peak on a single chromosome for a single LOD score column, and with columns

- lodindex - lod column index
- lodcolumn - lod column name
- chr - chromosome ID
- pos - peak position
- lod - lod score at peak

If drop or prob is provided, the results will include two additional columns: ci\_lo and ci\_hi, with the endpoints of the LOD support intervals or Bayes credible wintervals.

## See Also

`scan1()`, `lod_int()`, `bayes_int()`

## Examples

```
# 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 just the highest peak on each chromosome
find_peaks(out, map, threshold=3)

# possibly multiple peaks per chromosome
find_peaks(out, map, threshold=3, peakdrop=1)

# possibly multiple peaks, also getting 1-LOD support intervals
find_peaks(out, map, threshold=3, peakdrop=1, drop=1)

# possibly multiple peaks, also getting 90% Bayes intervals
find_peaks(out, map, threshold=3, peakdrop=1, prob=0.9)
```

---

fit1

---

*Fit single-QTL model at a single position*


---

## Description

Fit a single-QTL model at a single putative QTL position and get detailed results about estimated coefficients and individuals contributions to the LOD score.

## Usage

```
fit1(
  genoprobs,
  pheno,
  kinship = NULL,
  addcovar = NULL,
  nullcovar = NULL,
  intcovar = NULL,
```

```

weights = NULL,
contrasts = NULL,
model = c("normal", "binary"),
zerosum = TRUE,
se = TRUE,
hsq = NULL,
reml = TRUE,
blup = FALSE,
...
)

```

## Arguments

genoprobs	A matrix of genotype probabilities, individuals x genotypes. If NULL, we create a single intercept column, matching the individual IDs in pheno.
pheno	A numeric vector of phenotype values (just one phenotype, not a matrix of them)
kinship	Optional kinship matrix.
addcovar	An optional numeric matrix of additive covariates.
nullcovar	An optional numeric matrix of additional additive covariates that are used under the null hypothesis (of no QTL) but not under the alternative (with a QTL). This is needed for the X chromosome, where we might need sex as a additive covariate under the null hypothesis, but we wouldn't want to include it under the alternative as it would be collinear with the QTL effects.
intcovar	An optional numeric matrix of interactive covariates.
weights	An optional numeric vector of positive weights for the individuals. As with the other inputs, it must have names for individual identifiers.
contrasts	An optional numeric matrix of genotype contrasts, size genotypes x genotypes. For an intercross, you might use <code>cbind(mu=c(1,1,1), a=c(-1, 0, 1), d=c(0, 1, 0))</code> to get mean, additive effect, and dominance effect. The default is the identity matrix.
model	Indicates whether to use a normal model (least squares) or binary model (logistic regression) for the phenotype. If <code>model="binary"</code> , the phenotypes must have values in $[0, 1]$ .
zerosum	If TRUE, force the genotype or allele coefficients sum to 0 by subtracting their mean and add another column with the mean. Ignored if contrasts is provided.
se	If TRUE, calculate the standard errors.
hsq	(Optional) residual heritability; used only if kinship provided.
reml	If kinship provided: if <code>reml=TRUE</code> , use REML; otherwise maximum likelihood.
blup	If TRUE, fit a model with QTL effects being random, as in <a href="#">scan1blup()</a> .
...	Additional control parameters; see Details;

## Details

For each of the inputs, the row names are used as individual identifiers, to align individuals.

If kinship is absent, Haley-Knott regression is performed. If kinship is provided, a linear mixed model is used, with a polygenic effect estimated under the null hypothesis of no (major) QTL, and then taken as fixed as known in the genome scan.

If contrasts is provided, the genotype probability matrix,  $P$ , is post-multiplied by the contrasts matrix,  $A$ , prior to fitting the model. So we use  $P \cdot A$  as the  $X$  matrix in the model. One might view the rows of  $A^{-1}$  as the set of contrasts, as the estimated effects are the estimated genotype effects pre-multiplied by  $A^{-1}$ .

The ... argument can contain several additional control parameters; suspended for simplicity (or confusion, depending on your point of view). `tol` is used as a tolerance value for linear regression by QR decomposition (in determining whether columns are linearly dependent on others and should be omitted); default  $1e-12$ . `maxit` is the maximum number of iterations for convergence of the iterative algorithm used when `model=binary`. `bintol` is used as a tolerance for convergence for the iterative algorithm used when `model=binary`. `eta_max` is the maximum value for the "linear predictor" in the case `model="binary"` (a bit of a technicality to avoid fitted values exactly at 0 or 1).

## Value

A list containing

- `coef` - Vector of estimated coefficients.
- `SE` - Vector of estimated standard errors (included if `se=TRUE`).
- `lod` - The overall lod score.
- `ind_lod` - Vector of individual contributions to the LOD score (not provided if kinship is used).
- `fitted` - Fitted values.
- `resid` - Residuals. If `blup==TRUE`, only `coef` and `SE` are included at present.

## References

Haley CS, Knott SA (1992) A simple regression method for mapping quantitative trait loci in line crosses using flanking markers. *Heredity* 69:315–324.

Kang HM, Zaitlen NA, Wade CM, Kirby A, Heckerman D, Daly MJ, Eskin E (2008) Efficient control of population structure in model organism association mapping. *Genetics* 178:1709–1723.

## See Also

[pull\\_genoprobpos\(\)](#), [find\\_marker\(\)](#)

## Examples

```
# read data
iron <- read_cross2(system.file("extdata", "iron.zip", package="qt12"))

# insert pseudomarkers into map
map <- insert_pseudomarkers(iron$gmap, step=5)
```

```

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

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

# scan chromosome 7 to find peak
out <- scan1(probs[, "7"], pheno, addcovar=covar)

# find peak position
max_pos <- max(out, map)

# genoprobs at max position
pr_max <- pull_genoprobpos(probs, map, max_pos$chr, max_pos$pos)

# fit QTL model just at that position
out_fit1 <- fit1(pr_max, pheno, addcovar=covar)

```

fread\_csv

*Read a csv file*

## Description

Read a csv file via `data.table::fread()` using a particular set of options, including the ability to transpose the result.

## Usage

```

fread_csv(
  filename,
  sep = ",",
  na.strings = c("NA", "-"),
  comment.char = "#",
  transpose = FALSE,
  rownames_included = TRUE
)

```

## Arguments

<code>filename</code>	Name of input file
<code>sep</code>	Field separator
<code>na.strings</code>	Missing value codes
<code>comment.char</code>	Comment character; rest of line after this character is ignored
<code>transpose</code>	If TRUE, transpose the result
<code>rownames_included</code>	If TRUE, the first column is taken to be row names.

Details

Initial two lines can contain comments with number of rows and columns. Number of columns includes an ID column; number of rows does not include the header row.  
The first column is taken to be a set of row names

Value

Data frame

See Also

[fread\\_csv\\_numer\(\)](#)

Examples

```
## Not run: mydata <- fread_csv("myfile.csv", transpose=TRUE)
```

---

fread_csv_numer	<i>Read a csv file that has numeric columns</i>
-----------------	---

---

Description

Read a csv file via [data.table::fread\(\)](#) using a particular set of options, including the ability to transpose the result. This version assumes that the contents other than the first column and the header row are strictly numeric.

Usage

```
fread_csv_numer(  
  filename,  
  sep = ",",  
  na.strings = c("NA", "-"),  
  comment.char = "#",  
  transpose = FALSE,  
  rownames_included = TRUE  
)
```

Arguments

- |                   |   |
|-------------------|---|
| filename          | Name of input file  |
| sep               | Field separator   |
| na.strings        | Missing value codes   |
| comment.char      | Comment character; rest of line after this character is ignored |
| transpose         | If TRUE, transpose the result                                   |
| rownames_included | If TRUE, the first column is taken to be row names.             |

**Details**

Initial two lines can contain comments with number of rows and columns. Number of columns includes an ID column; number of rows does not include the header row.

The first column is taken to be a set of row names

**Value**

Data frame

**See Also**

[fread\\_csv\(\)](#)

**Examples**

```
## Not run: mydata <- fread_csv_numer("myfile.csv", transpose=TRUE)
```

---

genoprob\_to\_alleleprob

*Convert genotype probabilities to allele probabilities*

---

**Description**

Reduce genotype probabilities (as calculated by [calc\\_genoprob\(\)](#)) to allele probabilities.

**Usage**

```
genoprob_to_alleleprob(probs, quiet = TRUE, cores = 1)
```

**Arguments**

probs	Genotype probabilities, as calculated from <a href="#">calc_genoprob()</a> .
quiet	IF FALSE, print progress messages.
cores	Number of CPU cores to use, for parallel calculations. (If 0, use <a href="#">parallel::detectCores()</a> .) Alternatively, this can be links to a set of cluster sockets, as produced by <a href="#">parallel::makeCluster()</a> .

**Value**

An object of class "calc\_genoprob", like the input probs, but with probabilities collapsed to alleles rather than genotypes. See [calc\\_genoprob\(\)](#).

**Examples**

```
iron <- read_cross2(system.file("extdata", "iron.zip", package="qtl2"))
gmap_w_pmar <- insert_pseudomarkers(iron, step=1)
probs <- calc_genoprob(iron, gmap_w_pmar, error_prob=0.002)
allele_probs <- genoprob_to_alleleprob(probs)
```

---

genoprob_to_snpprob	<i>Convert genotype probabilities to SNP probabilities</i>
---------------------	--

---

## Description

For multi-parent populations, convert use founder genotypes at a set of SNPs to convert founder-based genotype probabilities to SNP genotype probabilities.

## Usage

```
genoprob_to_snpprob(genoprobs, snpinfo)
```

## Arguments

- |           |   |
|-----------|---|
| genoprobs | Genotype probabilities as calculated by <a href="#">calc_genoprob()</a> .   |
| snpinfo   | Data frame with SNP information with the following columns (the last three are generally derived with <a href="#">index_snps()</a> ): <ul style="list-style-type: none"> <li>• chr - Character string or factor with chromosome</li> <li>• pos - Position (in same units as in the "map" attribute in genoprobs.</li> <li>• sdg - Strain distribution pattern: an integer, between 1 and <math>2^n - 2</math> where <math>n</math> is the number of strains, whose binary encoding indicates the founder genotypes</li> <li>• snp - Character string with SNP identifier (if missing, the rownames are used).</li> <li>• index - Indices that indicate equivalent groups of SNPs, calculated by <a href="#">index_snps()</a>.</li> <li>• intervals - Indexes that indicate which marker intervals the SNPs reside.</li> <li>• on_map - Indicate whether SNP coincides with a marker in the genoprobs</li> </ul> |

Alternatively, snpinfo can be a object of class "cross2", as output by [read\\_cross2\(\)](#), containing the data for a multi-parent population with founder genotypes, in which case the SNP information for all markers with complete founder genotype data is calculated and then used. But, in this case, the genotype probabilities must be at the markers in the cross.

## Details

We first split the SNPs by chromosome and use `snpinfo$index` to subset to non-equivalent SNPs. `snpinfo$interval` indicates the intervals in the genotype probabilities that contain each. For SNPs contained within an interval, we use the average of the probabilities for the two endpoints. We then collapse the probabilities according to the strain distribution pattern.



**Value**

An object of class "calc\_genoprob", like the input genoprobs, but with imputed genotype probabilities at the selected SNPs indicated in snpinfo\$index. See [calc\\_genoprob\(\)](#).

If the input genoprobs is for allele probabilities, the probs output has just two probability columns (for the two SNP alleles). If the input has a full set of  $n(n+1)/2$  probabilities for  $n$  strains, the probs output has 3 probabilities (for the three SNP genotypes). If the input has full genotype probabilities for the X chromosome ( $n(n+1)/2$  genotypes for the females followed by  $n$  hemizygous genotypes for the males), the output has 5 probabilities: the 3 female SNP genotypes followed by the two male hemizygous SNP genotypes.

**See Also**

[index\\_snps\(\)](#), [calc\\_genoprob\(\)](#), [scan1snps\(\)](#)

**Examples**

```
## Not run:
# load example data and calculate genotype probabilities
file <- paste0("https://raw.githubusercontent.com/rqtl/",
               "qtl2data/main/DO_Recla/recla.zip")
recla <- read_cross2(file)
recla <- recla[c(1:2,53:54), c("19", "X")] # subset to 4 mice and 2 chromosomes
probs <- calc_genoprob(recla, error_prob=0.002)

# founder genotypes for a set of SNPs
snpgeno <- rbind(m1=c(3,1,1,3,1,1,1,1),
                 m2=c(1,3,1,3,1,3,1,3),
                 m3=c(1,1,1,1,3,3,3,3),
                 m4=c(1,3,1,3,1,3,1,3))
sdp <- calc_sdp(snpgeno)
snpinfo <- data.frame(chr=c("19", "19", "X", "X"),
                     pos=c(40.36, 40.53, 110.91, 111.21),
                     sdp=sdp,
                     snp=c("m1", "m2", "m3", "m4"), stringsAsFactors=FALSE)

# identify groups of equivalent SNPs
snpinfo <- index_snps(recla$pmap, snpinfo)

# collapse to SNP genotype probabilities
snpprobs <- genoprob_to_snpprob(probs, snpinfo)

# could also first convert to allele probs
aprobs <- genoprob_to_alleleprob(probs)
snpprobs <- genoprob_to_snpprob(aprobs, snpinfo)

## End(Not run)
```

---

get_common_ids	<i>Get common set of IDs from objects</i>
----------------	---

---

## Description

For a set objects with IDs as row names (or, for a vector, just names), find the IDs that are present in all of the objects.

## Usage

```
get_common_ids(..., complete.cases = FALSE)
```

## Arguments

`...` A set of objects: vectors, lists, matrices, data frames, and/or arrays. If one is a character vector with no names attribute, it's taken to be a set of IDs, itself.

`complete.cases` If TRUE, look at matrices and non-character vectors and keep only individuals with no missing values.

## Details

This is used (mostly internally) to align phenotypes, genotype probabilities, and covariates in preparation for a genome scan. The `complete.cases` argument is used to omit individuals with any missing covariate values.

## Value

A vector of character strings for the individuals that are in common.

## Examples

```
x <- matrix(0, nrow=10, ncol=5); rownames(x) <- LETTERS[1:10]
y <- matrix(0, nrow=5, ncol=5); rownames(y) <- LETTERS[(1:5)+7]
z <- LETTERS[5:15]
get_common_ids(x, y, z)

x[8,1] <- NA
get_common_ids(x, y, z)
get_common_ids(x, y, z, complete.cases=TRUE)
```

---

get_x_covar	<i>Get X chromosome covariates</i>
-------------	------------------------------------

---

**Description**

Get the matrix of covariates to be used for the null hypothesis when performing QTL analysis with the X chromosome.

**Usage**

```
get_x_covar(cross)
```

**Arguments**

cross                      Object of class "cross2". For details, see the [R/qt12 developer guide](#).

**Details**

For most crosses, the result is either NULL (indicating no additional covariates are needed) or a matrix with a single column containing sex indicators (1 for males and 0 for females).

For an intercross, we also consider cross direction. There are four cases: (1) All male or all female but just one direction: no covariate; (2) All female but both directions: covariate indicating cross direction; (3) Both sexes, one direction: covariate indicating sex; (4) Both sexes, both directions: a covariate indicating sex and a covariate that is 1 for females from the reverse direction and 0 otherwise.

**Value**

A matrix of size individuals x no. covariates.

**Examples**

```
iron <- read_cross2(system.file("extdata", "iron.zip", package="qt12"))
xcovar <- get_x_covar(iron)
```

---

guess_phase	<i>Guess phase of imputed genotypes</i>
-------------	---

---

**Description**

Turn imputed genotypes into phased genotypes along chromosomes by attempting to pick the phase that leads to the fewest recombination events.

**Usage**

```
guess_phase(cross, geno, deterministic = FALSE, cores = 1)
```

Arguments

cross	Object of class "cross2". For details, see the <a href="#">R/qlt2 developer guide</a> .
geno	Imputed genotypes, as a list of matrices, as from <a href="#">maxmarg()</a> .
deterministic	If TRUE, preferentially put smaller allele first when there's uncertainty. If FALSE, the order of alleles is random in such cases.
cores	Number of CPU cores to use, for parallel calculations. (If 0, use <a href="#">parallel::detectCores()</a> .) Alternatively, this can be links to a set of cluster sockets, as produced by <a href="#">parallel::makeCluster()</a> .

Details

We randomly assign the pair of alleles at the first locus to two haplotypes, and then work left to right, assigning alleles to haplotypes one locus at a time seeking the fewest recombination events. The results are subject to arbitrary and random choices. For example, to the right of a homozygous region, either orientation is equally reasonable.

Value

If input cross is phase-known (e.g., recombinant inbred lines), the output will be the input geno. Otherwise, the output will be a list of three-dimensional arrays of imputed genotypes, individual x position x haplotype (1/2).

See Also

[maxmarg\(\)](#)

Examples

```
iron <- read_cross2(system.file("extdata", "iron.zip", package="qlt2"))
gmap <- insert_pseudomarkers(iron$gmap, step=1)
probs <- calc_genoprob(iron, gmap, error_prob=0.002)
imp_genotype <- maxmarg(probs)
ph_genotype <- guess_phase(iron, imp_genotype)
```

---

index_snps	<i>Create index of equivalent SNPs</i>
------------	--

---

Description

For a set of SNPs and a map of marker/pseudomarkers, partition the SNPs into groups that are contained within common intervals and have the same strain distribution pattern, and then create an index to a set of distinct SNPs, one per partition.

Usage

```
index_snps(map, snpinfo, tol = 0.00000001)
```

## Arguments

map	Physical map of markers and pseudomarkers; generally created from <code>insert_pseudomarkers()</code> and used for a set of genotype probabilities (calculated with <code>calc_genoprob()</code> ) that are to be used to interpolate SNP genotype probabilities (with <code>genoprob_to_snpprob()</code> ).
snpinfo	Data frame with SNP information with the following columns: <ul style="list-style-type: none"> <li>• chr - Character string or factor with chromosome</li> <li>• pos - Position (in same units as in the "map").</li> <li>• sdp - Strain distribution pattern: an integer, between 1 and <math>2^n - 2</math> where <math>n</math> is the number of strains, whose binary encoding indicates the founder genotypes</li> <li>• snp - Character string with SNP identifier (if missing, the rownames are used).</li> </ul>
tol	Tolerance for determining whether a SNP is exactly at a position at which genotype probabilities were already calculated.

## Details

We split the SNPs by chromosome and identify the intervals in the map that contain each. For SNPs within `tol` of a position at which the genotype probabilities were calculated, we take the SNP to be at that position. For each marker position or interval, we then partition the SNPs into groups that have distinct strain distribution patterns, and choose a single index SNP for each partition.

## Value

A data frame containing the input `snpinfo` with three added columns: "index" (which indicates the groups of equivalent SNPs), "interval" (which indicates the map interval containing the SNP, with values starting at 0), and `on_map` (which indicates that the SNP is within `tol` of a position on the map). The rows get reordered, so that they are ordered by chromosome and position, and the values in the "index" column are *by chromosome*.

## See Also

`genoprob_to_snpprob()`, `scan1snps()`, `find_index_snp()`

## Examples

```
## Not run:
# load example data and calculate genotype probabilities
file <- paste0("https://raw.githubusercontent.com/rqtl/",
               "qt12data/main/D0_Recla/recla.zip")
recla <- read_cross2(file)

# founder genotypes for a set of SNPs
snpgeno <- rbind(m1=c(3,1,1,3,1,1,1,1),
                 m2=c(1,3,1,3,1,3,1,3),
                 m3=c(1,1,1,1,3,3,3,3),
                 m4=c(1,3,1,3,1,3,1,3))
sdp <- calc_sdp(snpgeno)
snpinfo <- data.frame(chr=c("19", "19", "X", "X"),
```

```

pos=c(40.36, 40.53, 110.91, 111.21),
sdp=sdp,
snp=c("m1", "m2", "m3", "m4"), stringsAsFactors=FALSE)

# update snp info by adding the SNP index column
snpinfo <- index_snps(recla$pmap, snpinfo)

## End(Not run)

```

---

insert\_pseudomarkers    *Insert pseudomarkers into a marker map*

---

## Description

Insert pseudomarkers into a map of genetic markers

## Usage

```

insert_pseudomarkers(
  map,
  step = 0,
  off_end = 0,
  stepwidth = c("fixed", "max"),
  pseudomarker_map = NULL,
  tol = 0.01,
  cores = 1
)

```

## Arguments

map	A list of numeric vectors; each vector gives marker positions for a single chromosome.
step	Distance between pseudomarkers and markers; if step=0 no pseudomarkers are inserted.
off_end	Distance beyond terminal markers in which to insert pseudomarkers.
stepwidth	Indicates whether to use a fixed grid (stepwidth="fixed") or to use the maximal distance between pseudomarkers to ensure that no two adjacent markers/pseudomarkers are more than step apart.
pseudomarker_map	A map of pseudomarker locations; if provided the step, off_end, and stepwidth arguments are ignored.
tol	Tolerance for determining whether a pseudomarker would duplicate a marker position.
cores	Number of CPU cores to use, for parallel calculations. (If 0, use <a href="#">parallel::detectCores()</a> .) Alternatively, this can be links to a set of cluster sockets, as produced by <a href="#">parallel::makeCluster()</a> .

**Details**

If `stepwidth="fixed"`, a grid of pseudomarkers is added to the marker map.

If `stepwidth="max"`, a minimal set of pseudomarkers are added, so that the maximum distance between adjacent markers or pseudomarkers is at least `step`. If two adjacent markers are separated by less than `step`, no pseudomarkers will be added to the interval. If they are more than `step` apart, a set of equally-spaced pseudomarkers will be added.

If `pseudomarker_map` is provided, then the `step`, `off_end`, and `stepwidth` arguments are ignored, and the input `pseudomarker_map` is taken to be the set of pseudomarker positions.

**Value**

A list like the input map with pseudomarkers inserted. Will also have an attribute `"is_x_chr"`, taken from the input map.

**See Also**

[calc\\_genoprob\(\)](#), [calc\\_grid\(\)](#)

**Examples**

```
iron <- read_cross2(system.file("extdata", "iron.zip", package="qtl2"))
gmap_w_pmar <- insert_pseudomarkers(iron$gmap, step=1)
```

---

interp_genoprob	<i>Interpolate genotype probabilities</i>
-----------------	---

---

**Description**

Linear interpolation of genotype probabilities, mostly to get two sets onto the same map for comparison purposes.

**Usage**

```
interp_genoprob(probs, map, cores = 1)
```

**Arguments**

<code>probs</code>	Genotype probabilities, as calculated from <a href="#">calc_genoprob()</a> .
<code>map</code>	List of vectors of map positions.
<code>cores</code>	Number of CPU cores to use, for parallel calculations. (If 0, use <a href="#">parallel::detectCores()</a> .) Alternatively, this can be links to a set of cluster sockets, as produced by <a href="#">parallel::makeCluster()</a> .

### Details

We reduce probs to the positions present in map and then interpolate the genotype probabilities at additional positions in map by linear interpolation using the two adjacent positions. Off the ends, we just copy over the first or last value unchanged.

In general, it's better to use [insert\\_pseudomarkers\(\)](#) and [calc\\_genoprob\(\)](#) to get genotype probabilities at additional positions along a chromosome. This function is a **very** crude alternative that was implemented in order to compare genotype probabilities derived by different methods, where we first need to get them onto a common set of positions.

### Value

An object of class "calc\_genoprob", like the input, but with additional positions present in map. See [calc\\_genoprob\(\)](#).

### See Also

[calc\\_genoprob\(\)](#)

### Examples

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

probs <- calc_genoprob(iron, iron$gmap, error_prob=0.002)

# you generally wouldn't want to do this, but this is an illustration
map <- insert_pseudomarkers(iron$gmap, step=1)
probs_map <- interp_genoprob(probs, map)
```

---

interp\_map

*Interpolate between maps*

---

### Description

Use interpolate to convert from one map to another

### Usage

```
interp_map(map, oldmap, newmap)
```

### Arguments

map	The map to be interpolated; a list of vectors.
oldmap	Map with positions in the original scale, as in map.
newmap	Map with positions in the new scale.



**Value**

Object of same form as input map but in the units as in newmap.

**Examples**

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

# positions to interpolate from cM to Mbp
tointerp <- list("7" = c(pos7.1= 5, pos7.2=15, pos7.3=25),
                "9" = c(pos9.1=20, pos9.2=40))

interp_map(tointerp, iron$gmap, iron$pmap)
```

invert\_sdp

*Calculate SNP genotype matrix from strain distribution patterns***Description**

Calculate the matrix of SNP genotypes from a vector of strain distribution patterns (SDPs).

**Usage**

```
invert_sdp(sdp, n_strains)
```

**Arguments**

sdp	Vector of strain distribution patterns (integers between 1 and $2^n - 2$ where $n$ is the number of strains).
n_strains	Number of strains

**Value**

Matrix of SNP genotypes, markers x strains, coded as 1 (AA) and 3 (BB). Markers with values other than 1 or 3 are omitted, and monomorphic markers, are omitted.

**See Also**

[sdp2char\(\)](#), [calc\\_sdp\(\)](#)

**Examples**

```
sdp <- c(m1=1, m2=12, m3=240)
invert_sdp(sdp, 8)
```

---

locate_xo	<i>Locate crossovers</i>
-----------	--------------------------

---

**Description**

Estimate the locations of crossovers in each individual on each chromosome.

**Usage**

```
locate_xo(geno, map, quiet = TRUE, cores = 1)
```

**Arguments**

geno	List of matrices of genotypes (output of <a href="#">maxmarg()</a> or <a href="#">viterbi()</a> ).
map	List of vectors with the map positions of the markers.
quiet	If FALSE, print progress messages.
cores	Number of CPU cores to use, for parallel calculations. (If 0, use <a href="#">parallel::detectCores()</a> .) Alternatively, this can be links to a set of cluster sockets, as produced by <a href="#">parallel::makeCluster()</a> .

**Value**

A list of lists of estimated crossover locations, with crossovers placed at the midpoint of the intervals that contain them.

**See Also**

```
count\_xo\(\)
```

**Examples**

```
iron <- read_cross2(system.file("extdata", "iron.zip", package="qtl2"))
map <- insert_pseudomarkers(iron$gmap, step=1)
pr <- calc_genoprob(iron, map, error_prob=0.002, map_function="c-f")
g <- maxmarg(pr)
pos <- locate_xo(g, iron$gmap)
```

---

lod_int	<i>Calculate LOD support intervals</i>
---------	--

---

## Description

Calculate LOD support intervals for a single LOD curve on a single chromosome, with the ability to identify intervals for multiple LOD peaks.

## Usage

```
lod_int(
  scan1_output,
  map,
  chr = NULL,
  lodcolumn = 1,
  threshold = 0,
  peakdrop = Inf,
  drop = 1.5,
  expand2markers = TRUE
)
```

## Arguments

scan1_output	An object of class "scan1" as returned by <a href="#">scan1()</a> .
map	A list of vectors of marker positions, as produced by <a href="#">insert_pseudomarkers()</a> .
chr	Chromosome ID to consider (must be a single value).
lodcolumn	LOD score column to consider (must be a single value).
threshold	Minimum LOD score for a peak.
peakdrop	Amount that the LOD score must drop between peaks, if multiple peaks are to be defined on a chromosome.
drop	Amount to drop in the support interval. Must be $\leq$ peakdrop
expand2markers	If TRUE, QTL intervals are expanded so that their endpoints are at genetic markers.

## Details

We identify a set of peaks defined as local maxima that exceed the specified threshold, with the requirement that the LOD score must have dropped by at least peakdrop below the lowest of any two adjacent peaks.

At a given peak, if there are ties, with multiple positions jointly achieving the maximum LOD score, we take the average of these positions as the location of the peak.

The default is to use threshold=0, peakdrop=Inf, and drop=1.5. We then return results a single peak, no matter the maximum LOD score, and give a 1.5-LOD support interval.

**Value**

A matrix with three columns:

- ci\_lo - lower bound of interval
- pos - peak position
- ci\_hi - upper bound of interval

Each row corresponds to a different peak.

**See Also**

[bayes\\_int\(\)](#), [find\\_peaks\(\)](#), [scan1\(\)](#)

**Examples**

```
# 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)

# 1.5-LOD support interval for QTL on chr 7, first phenotype
lod_int(out, map, chr=7, lodcolum=1)
```

---

map\_to\_grid

---

*Subset a map to positions on a grid*


---

**Description**

Subset a map object to the locations on some grid.

**Usage**

```
map_to_grid(map, grid)
```

**Arguments**

map	A list of vectors of marker positions.
grid	A list of logical vectors (aligned with map), with TRUE indicating the position is on the grid.

**Details**

This is generally for the case of a map created with `insert_pseudomarkers()` with `step>0` and `stepwidth="fixed"`, so that the pseudomarkers form a grid along each chromosome.

**Value**

Same list as input, but subset to just include pseudomarkers along a grid.

**See Also**

`calc_grid()`, `probs_to_grid()`

**Examples**

```
grav2 <- read_cross2(system.file("extdata", "grav2.zip", package="qtl2"))
map_w_pmar <- insert_pseudomarkers(grav2$gmap, step=1)
sapply(map_w_pmar, length)
grid <- calc_grid(grav2$gmap, step=1)
map_sub <- map_to_grid(map_w_pmar, grid)
sapply(map_sub, length)
```

---

mat2strata	<i>Define strata based on rows of a matrix</i>
------------	--

---

**Description**

Use the rows of a matrix to define a set of strata for a stratified permutation test

**Usage**

```
mat2strata(mat)
```

**Arguments**

mat	A covariate matrix, as individuals x covariates
-----	---

**Value**

A vector of character strings: for each row of mat, we use `base::paste()` with `collapse="|"`.

**See Also**

`get_x_covar()`, `scan1perm()`

## Examples

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

Xcovar <- get_x_covar(iron)
perm_strata <- mat2strata(Xcovar)
```

---

maxlod	<i>Overall maximum LOD score</i>
--------	----------------------------------

---

## Description

Find overall maximum LOD score in genome scan results, across all positions and columns.

## Usage

```
maxlod(scan1_output, map = NULL, chr = NULL, lodcolumn = NULL)
```

## Arguments

scan1_output	An object of class "scan1" as returned by <a href="#">scan1()</a> .
map	A list of vectors of marker positions, as produced by <a href="#">insert_pseudomarkers()</a> .
chr	Optional vector of chromosomes to consider.
lodcolumn	An integer or character string indicating the LOD score column, either as a numeric index or column name. If NULL, return maximum for all columns.

## Value

A single number: the maximum LOD score across all columns and positions for the selected chromosomes.

## Examples

```
# 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)

# overall maximum
maxlod(out)

# maximum on chromosome 2
maxlod(out, map, "2")
```

---

maxmarg

*Find genotypes with maximum marginal probabilities*


---

## Description

For each individual at each position, find the genotype with the maximum marginal probability.

## Usage

```
maxmarg(
  probs,
  map = NULL,
  minprob = 0.95,
  chr = NULL,
  pos = NULL,
  return_char = FALSE,
  quiet = TRUE,
  cores = 1,
  tol = 0.0000000000001
)
```

## Arguments

probs	Genotype probabilities, as calculated from <a href="#">calc_genoprob()</a> .
map	Map of pseudomarkers in probs. Used only if chr and pos are provided.
minprob	Minimum probability for making a call. If maximum probability is less than this value, give NA.
chr	If provided (along with pos), consider only the single specified position.
pos	If provided (along with chr), consider only the single specified position.
return_char	If TRUE, return genotype names as character strings.
quiet	If FALSE, print progress messages.
cores	Number of CPU cores to use, for parallel calculations. (If 0, use <a href="#">parallel::detectCores()</a> .) Alternatively, this can be links to a set of cluster sockets, as produced by <a href="#">parallel::makeCluster()</a> .
tol	Tolerance value; genotypes with probability that are within tol of each other are treated as equivalent.

**Details**

If multiple genotypes share the maximum probability, one is chosen at random.

**Value**

If chr and pos are provided, a vector of genotypes is returned. In this case, map is needed.

Otherwise, the result is a object like that returned by `viterbi()`, A list of two-dimensional arrays of imputed genotypes, individuals x positions. Also includes these attributes:

- `crosstype` - The cross type of the input cross.
- `is_x_chr` - Logical vector indicating whether chromosomes are to be treated as the X chromosome or not, from input cross.
- `alleles` - Vector of allele codes, from input cross.

**See Also**

`sim_geno()`, `viterbi()`

**Examples**

```
# load data and calculate genotype probabilities
iron <- read_cross2(system.file("extdata", "iron.zip", package="qtl2"))
pr <- calc_genoprob(iron, error_prob=0.002)

# full set of imputed genotypes
ginf <- maxmarg(pr)

# imputed genotypes at a fixed position
g <- maxmarg(pr, iron$gmap, chr=8, pos=45.5)

# return genotype names rather than integers
g <- maxmarg(pr, iron$gmap, chr=8, pos=45.5, return_char=TRUE)
```

---

max\_compare\_geno

*Find pair with most similar genotypes*

---

**Description**

From results of `compare_geno()`, show the pair with most similar genotypes.

**Usage**

```
max_compare_geno(object, ...)

## S3 method for class 'compare_geno'
max(object, ...)
```



Arguments

object	A square matrix with genotype comparisons for pairs of individuals, as output by <a href="#">compare_geno()</a> .
...	Ignored

Value

Data frame with individual pair, proportion matches, number of mismatches, number of matches, and total markers genotyped.

Examples

```
grav2 <- read_cross2(system.file("extdata", "grav2.zip", package="qt12"))
cg <- compare_geno(grav2)
max(cg)
```

---

max_scan1	<i>Find position with maximum LOD score</i>
-----------	---

---

Description

Return data frame with the positions having maximum LOD score for a particular LOD score column

Usage

```
max_scan1(
  scan1_output,
  map = NULL,
  lodcolumn = 1,
  chr = NULL,
  na.rm = TRUE,
  ...
)

## S3 method for class 'scan1'
max(scan1_output, map = NULL, lodcolumn = 1, chr = NULL, na.rm = TRUE, ...)
```

Arguments

scan1_output	An object of class "scan1" as returned by <a href="#">scan1()</a> .
map	A list of vectors of marker positions, as produced by <a href="#">insert_pseudomarkers()</a> . Can also be an indexed SNP info table, as from <a href="#">index_snps()</a> or <a href="#">scan1snps()</a> .
lodcolumn	An integer or character string indicating the LOD score column, either as a numeric index or column name. If NULL, return maximum for all columns.
chr	Optional vector of chromosomes to consider.
na.rm	Ignored (take to be TRUE)
...	Ignored

**Value**

If map is NULL, the genome-wide maximum LOD score for the selected column is returned. If also lodcolumn is NULL, you get a vector with the maximum LOD for each column.

If map is provided, the return value is a data.frame with three columns: chr, pos, and lod score. But if lodcolumn is NULL, you get the maximum for each lod score column, in the format provided by [find\\_peaks\(\)](#), so a data.frame with five columns: lodindex, lodcolumn, chr, pos, and lod.

**Examples**

```
# 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)

# maximum of first column
max(out, map)

# maximum of spleen column
max(out, map, lodcolumn="spleen")

# maximum of first column on chr 2
max(out, map, chr="2")
```

---

n_missing	<i>Count missing genotypes</i>
-----------	--------------------------------

---

**Description**

Number (or proportion) of missing (or non-missing) genotypes by individual or marker

**Usage**

```
n_missing(
  cross,
  by = c("individual", "marker"),
```

```

    summary = c("count", "proportion")
  )

  n_typed(
    cross,
    by = c("individual", "marker"),
    summary = c("count", "proportion")
  )

```

### Arguments

cross	An object of class "cross2", as output by <code>read_cross2()</code> . For details, see the <a href="#">R/qrtl2 developer guide</a> .
by	Whether to summarize by individual or marker
summary	Whether to take count or proportion

### Value

Vector of counts (or proportions) of missing (or non-missing) genotypes.

### Functions

- `n_missing()`: Count missing genotypes
- `n_typed()`: Count genotypes

### Examples

```

iron <- read_cross2(system.file("extdata", "iron.zip", package="qrtl2"))
nmis_ind <- n_missing(iron)
pmis_mar <- n_typed(iron, "mar", "proportion")
plot(nmis_ind, xlab="Individual", ylab="No. missing genotypes")
plot(pmis_mar, xlab="Markers", ylab="Prop. genotyped")

```

---

plot\_coef

*Plot QTL effects along chromosome*

---

### Description

Plot estimated QTL effects along a chromosomes.

### Usage

```

plot_coef(
  x,
  map,
  columns = NULL,
  col = NULL,

```

```

    scan1_output = NULL,
    add = FALSE,
    gap = NULL,
    top_panel_prop = 0.65,
    legend = NULL,
    ...
)

plot_coefCC(
  x,
  map,
  columns = 1:8,
  col = qtl2::CCcolors,
  scan1_output = NULL,
  add = FALSE,
  gap = NULL,
  top_panel_prop = 0.65,
  legend = NULL,
  ...
)

## S3 method for class 'scan1coef'
plot(
  x,
  map,
  columns = 1,
  col = NULL,
  scan1_output = NULL,
  add = FALSE,
  gap = NULL,
  top_panel_prop = 0.65,
  legend = NULL,
  ...
)

```

### Arguments

x	Estimated QTL effects ("coefficients") as obtained from <a href="#">scan1coef()</a> .
map	A list of vectors of marker positions, as produced by <a href="#">insert_pseudomarkers()</a> .
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.
add	If TRUE, add to current plot (must have same map and chromosomes).
gap	Gap between chromosomes. The default is 1% of the total genome length.

top_panel_prop	If scan1_output provided, this gives the proportion of the plot that is devoted to the top panel.
legend	Location of legend, such as "bottomleft" or "topright" (NULL for no legend)
...	Additional graphics parameters.

### Details

plot\_coefCC() is the same as plot\_coef(), but forcing columns=1:8 and using the Collaborative Cross colors, [CCcolors](#).

### Value

None.

### Hidden graphics parameters

A number of graphics parameters can be passed via .... For example, bgcolor to control the background color, and things like ylab and ylim. These are not included as formal parameters in order to avoid cluttering the function definition.

In the case that scan1\_output is provided, col, ylab, and ylim all control the panel with estimated QTL effects, while col\_lod, ylab\_lod, and ylim\_lod control the LOD curve panel.

If legend is indicated so that a legend is shown, legend\_lab controls the labels in the legend, and legend\_ncol indicates the number of columns in the legend.

### See Also

[CCcolors](#), [plot\\_scan1\(\)](#), [plot\\_snpasso\(\)](#)

### Examples

```
# 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$pheno[,1]
covar <- match(iron$covar$sex, c("f", "m")) # make numeric
names(covar) <- rownames(iron$covar)

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

# plot QTL effects (note the need to subset the map object, for chromosome 7)
plot(coef, map[7], columns=1:3, col=c("slateblue", "violetred", "green3"))
```

---

plot_compare_geno	<i>Plot of compare_geno object.</i>
-------------------	-------------------------------------

---

### Description

From results of `compare_geno()`, plot histogram of

### Usage

```
plot_compare_geno(x, rug = TRUE, ...)

## S3 method for class 'compare_geno'
plot(x, rug = TRUE, ...)
```

### Arguments

x	A square matrix with genotype comparisons for pairs of individuals, as output by <code>compare_geno()</code> .
rug	If true, use <code>rug()</code> to plot tick marks at observed values below the histogram.
...	Additional graphics parameters passed to <code>hist()</code>

### Value

None.

### Examples

```
grav2 <- read_cross2(system.file("extdata", "grav2.zip", package="qt12"))
cg <- compare_geno(grav2)
plot(cg)
```

---

plot_genes	<i>Plot gene locations for a genomic interval</i>
------------	---

---

### Description

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

**Usage**

```
plot_genes(
  genes,
  minrow = 4,
  padding = 0.2,
  colors = c("black", "red3", "green4", "blue3", "orange"),
  scale_pos = 1,
  start_field = "start",
  stop_field = "stop",
  strand_field = "strand",
  name_field = "Name",
  ...
)
```

**Arguments**

genes	Data frame containing start and stop in Mbp, strand (as "-", "+", or NA), and Name.
minrow	Minimum number of rows of genes in the plot
padding	Proportion to pad with white space around the genes
colors	Vectors of colors, used sequentially and then re-used.
scale_pos	Factor by which to scale position (for example, to convert basepairs to Mbp)
start_field	Character string with name of column containing the genes' start positions.
stop_field	Character string with name of column containing the genes' stop positions.
strand_field	Character string with name of column containing the genes' strands. (The values of the corresponding field can be character strings "+" or "-", or numeric +1 or -1.)
name_field	Character string with name of column containing the genes' names.
...	Optional arguments passed to plot().

**Value**

None.

**Hidden graphics parameters**

Graphics parameters can be passed via ... For example, xlim to control the x-axis limits. These are not included as formal

**Examples**

```
genes <- data.frame(chr = c("6", "6", "6", "6", "6", "6", "6", "6"),
  start = c(139988753, 140680185, 141708118, 142234227, 142587862,
    143232344, 144398099, 144993835),
  stop = c(140041457, 140826797, 141773810, 142322981, 142702315,
    143260627, 144399821, 145076184),
```

```

strand = c("-", "+", "-", "-", "-", NA, "+", "-"),
Name = c("Plcz1", "Gm30215", "Gm5724", "Slco1a5", "Abcc9",
         "4930407I02Rik", "Gm31777", "Bcat1"),
stringsAsFactors=FALSE)

# use scale_pos=1e-6 because data in bp but we want the plot in Mbp
plot_genes(genes, xlim=c(140, 146), scale_pos=1e-6)

```

---

plot\_genoprob

---

*Plot genotype probabilities for one individual on one chromosome.*


---

## Description

Plot the genotype probabilities for one individual on one chromosome, as a heat map.

## Usage

```

plot_genoprob(
  probs,
  map,
  ind = 1,
  chr = NULL,
  geno = NULL,
  color_scheme = c("gray", "viridis"),
  col = NULL,
  threshold = 0,
  swap_axes = FALSE,
  ...
)

## S3 method for class 'calc_genoprob'
plot(x, ...)

```

## Arguments

probs	Genotype probabilities (as produced by <a href="#">calc_genoprob()</a> ) or allele dosages (as produced by <a href="#">genoprob_to_alleleprob()</a> ).
map	Marker map (a list of vectors of marker positions).
ind	Individual to plot, either a numeric index or an ID.
chr	Selected chromosome to plot; a single character string.
geno	Optional vector of genotypes or alleles to be shown (vector of integers or character strings)
color_scheme	Color scheme for the heatmap (ignored if col is provided).
col	Optional vector of colors for the heatmap.
threshold	Threshold for genotype probabilities; only genotypes that achieve this value somewhere on the chromosome will be shown.



swap_axes	If TRUE, swap the axes, so that the genotypes are on the x-axis and the chromosome position is on the y-axis.
...	Additional graphics parameters passed to <code>graphics::image()</code> .
x	Genotype probabilities (as produced by <code>calc_genoprob()</code> ) or allele dosages (as produced by <code>genoprob_to_alleleprob()</code> ). (For the S3 type plot function, this has to be called x.)

### Value

None.

### Hidden graphics parameters

A number of graphics parameters can be passed via .... For example, `hlines`, `hlines_col`, `hlines_lwd`, and `hlines_lty` to control the horizontal grid lines. (Use `hlines=NA` to avoid plotting horizontal grid lines.) Similarly `vlines`, `vlines_col`, `vlines_lwd`, and `vlines_lty` for vertical grid lines. You can also use many standard graphics parameters like `xlab` and `xlim`. These are not included as formal parameters in order to avoid cluttering the function definition.

### See Also

[plot\\_genoprobcomp\(\)](#)

### Examples

```
# load data and calculate genotype probabilities
iron <- read_cross2(system.file("extdata", "iron.zip", package="qtl2"))
iron <- iron[, "2"] # subset to chr 2
map <- insert_pseudomarkers(iron$gmap, step=1)
pr <- calc_genoprob(iron, map, error_prob=0.002)

# plot the probabilities for the individual labeled "262"
# (white = 0, black = 1)
plot_genoprob(pr, map, ind="262")

# change the x-axis label
plot_genoprob(pr, map, ind="262", xlab="Position (cM)")

# swap the axes so that the chromosome runs vertically
plot_genoprob(pr, map, ind="262", swap_axes=TRUE, ylab="Position (cM)")

# This is more interesting for a Diversity Outbred mouse example
## Not run:
file <- paste0("https://raw.githubusercontent.com/rqtl/",
               "qtl2data/main/D0ex/D0ex.zip")
D0ex <- read_cross2(file)
# subset to chr 2 and X and individuals labeled "232" and "256"
D0ex <- D0ex[c("232", "256"), c("2", "X")]
pr <- calc_genoprob(D0ex, error_prob=0.002)
# plot individual "256" on chr 2 (default is to pick first chr in the probs)
plot_genoprob(pr, D0ex$pmap, ind="256")
```

```

# omit states that never have probability >= 0.5
plot_genoprob(pr, DOex$pmap, ind="256", threshold=0.05)

# X chr male 232: just show the AY-HY genotype probabilities
plot_genoprob(pr, DOex$pmap, ind="232", chr="X", geno=paste0(LETTERS[1:8], "Y"))
# could also indicate genotypes by number
plot_genoprob(pr, DOex$pmap, ind="232", chr="X", geno=37:44)
# and can use negative indexes
plot_genoprob(pr, DOex$pmap, ind="232", chr="X", geno=-(1:36))

# X chr female 256: just show the first 36 genotype probabilities
plot_genoprob(pr, DOex$pmap, ind="256", chr="X", geno=1:36)

# again, can give threshold to omit genotypes whose probabilities never reach that threshold
plot_genoprob(pr, DOex$pmap, ind="256", chr="X", geno=1:36, threshold=0.5)

# can also look at the allele dosages
apr <- genoprob_to_alleleprob(pr)
plot_genoprob(apr, DOex$pmap, ind="232")

## End(Not run)

```

---

plot\_genoprobcomp

*Plot comparison of two sets of genotype probabilities*


---

## Description

Plot a comparison of two sets of genotype probabilities for one individual on one chromosome, as a heat map.

## Usage

```

plot_genoprobcomp(
  probs1,
  probs2,
  map,
  ind = 1,
  chr = NULL,
  geno = NULL,
  threshold = 0,
  n_colors = 256,
  swap_axes = FALSE,
  ...
)

```

**Arguments**

probs1	Genotype probabilities (as produced by <a href="#">calc_genoprob()</a> ) or allele dosages (as produced by <a href="#">genoprob_to_alleleprob()</a> ).
probs2	A second set of genotype probabilities, just like probs1.
map	Marker map (a list of vectors of marker positions).
ind	Individual to plot, either a numeric index or an ID.
chr	Selected chromosome to plot; a single character string.
geno	Optional vector of genotypes or alleles to be shown (vector of integers or character strings)
threshold	Threshold for genotype probabilities; only genotypes that achieve this value somewhere on the chromosome (in one or the other set of probabilities) will be shown.
n_colors	Number of colors in each color scale.
swap_axes	If TRUE, swap the axes, so that the genotypes are on the x-axis and the chromosome position is on the y-axis.
...	Additional graphics parameters passed to <a href="#">graphics::image()</a> .

**Details**

We plot the first set of probabilities in the range white to blue and the second set in the range white to red and attempt to combine them, for colors that are white, some amount of blue or red, or where both are large something like blackish purple.

**Value**

None.

**See Also**

[plot\\_genoprob\(\)](#)

**Examples**

```
iron <- read_cross2(system.file("extdata", "iron.zip", package="qtl2"))
iron <- iron[228,"1"] # subset to one individual on chr 1
map <- insert_pseudomarkers(iron$gmap, step=5)

# introduce genotype error and look at difference in genotype probabilities
pr_ne <- calc_genoprob(iron, map, error_prob=0.002)
iron$geno[[1]][1,2] <- 3
pr_e <- calc_genoprob(iron, map, error_prob=0.002)

# image of probabilities + comparison

par(mfrow=c(3,1))
plot_genoprob(pr_ne, map, main="No error")
plot_genoprob(pr_e, map, main="With an error")
```

```
plot_genoprobcomp(pr_ne, pr_e, map, main="Comparison")
```

---

plot\_lodpeaks

*Plot LOD scores vs QTL peak locations*


---

### Description

Create a scatterplot of LOD scores vs QTL peak locations (possibly with intervals) for multiple traits.

### Usage

```
plot_lodpeaks(peaks, map, chr = NULL, gap = NULL, intervals = FALSE, ...)
```

### Arguments

peaks	Data frame such as that produced by <a href="#">find_peaks()</a> 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.
gap	Gap between chromosomes. The default is 1% of the total genome length.
intervals	If TRUE and peaks contains QTL intervals, plot the intervals.
...	Additional graphics parameters

### Value

None.

### 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. These are not included as formal parameters in order to avoid cluttering the function definition.

### See Also

[find\\_peaks\(\)](#), [plot\\_peaks\(\)](#)

**Examples**

```
# 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)

plot_lodpeaks(peaks, map)
```

plot\_onegeno

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

Plot one individual's genome-wide genotypes

**Usage**

```
plot_onegeno(
  geno,
  map,
  ind = 1,
  chr = NULL,
  col = NULL,
  na_col = "white",
  swap_axes = FALSE,
  border = "black",
  shift = FALSE,
  chrwidth = 0.5,
  ...
)
```

**Arguments**

geno	Imputed phase-known genotypes, as a list of matrices (as produced by <code>maxmarg()</code> ) or a list of three-dimensional arrays (as produced by <code>guess_phase()</code> ).
map	Marker map (a list of vectors of marker positions).
ind	Individual to plot, either a numeric index or an ID.
chr	Selected chromosomes to plot; a vector of character strings.
col	Vector of colors for the different genotypes.
na_col	Color for missing segments.
swap_axes	If TRUE, swap the axes, so that the chromosomes run horizontally.
border	Color of outer border around chromosome rectangles.
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**

None.

**Hidden graphics parameters**

A number of graphics parameters can be passed via .... For example, `bgcolor` to control the background color. These are not included as formal parameters in order to avoid cluttering the function definition.

**Examples**

```
# load data and calculate genotype probabilities
iron <- read_cross2(system.file("extdata", "iron.zip", package="qtl2"))
iron <- iron["146", ] # subset to individual 146
map <- insert_pseudomarkers(iron$gmap, step=1)
pr <- calc_genoprob(iron, map, error_prob=0.002)

# infer genotypes, as those with maximal marginal probability
m <- maxmarg(pr)

# guess phase
ph <- guess_phase(iron, m)

# plot phased genotypes
plot_onegeno(ph, map, shift=TRUE, col=c("slateblue", "Orchid"))

# this is more interesting for Diversity Outbred mouse data
## Not run:
file <- paste0("https://raw.githubusercontent.com/rqtl/",
               "qtl2data/main/D0ex/D0ex.zip")
D0ex <- read_cross2(file)
```

```

# subset to individuals labeled "232" and "256"
D0ex <- D0ex[c("232", "256"), ]
pr <- calc_genoprob(D0ex, error_prob=0.002)

# infer genotypes, as those with maximal marginal probability
m <- maxmarg(pr, minprob=0.5)
# guess phase
ph <- guess_phase(D0ex, m)

# plot phased genotypes
plot_onegeno(ph, D0ex$gmap, shift=TRUE)
plot_onegeno(ph, D0ex$gmap, ind="256", shift=TRUE)

## End(Not run)

```

---

plot_peaks	<i>Plot QTL peak locations</i>
------------	--------------------------------

---

## Description

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

## Usage

```

plot_peaks(
  peaks,
  map,
  chr = NULL,
  tick_height = 0.3,
  gap = NULL,
  lod_labels = FALSE,
  ...
)

```

## Arguments

peaks	Data frame such as that produced by <a href="#">find_peaks()</a> 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. The default is 1% of the total genome length.

lod_labels	If TRUE, plot LOD scores near the intervals. Uses three hidden graphics parameters, label_gap (distance between CI and LOD text label), label_left (vector that indicates whether the labels should go on the left side; TRUE=on left, FALSE=on right, NA=put into larger gap on that chromosome), and label_cex that controls the size of these labels
...	Additional graphics parameters

**Value**

None.

**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. These are not included as formal parameters in order to avoid cluttering the function definition.

**See Also**

[find\\_peaks\(\)](#), [plot\\_lodpeaks\(\)](#)

**Examples**

```
# 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)

plot_peaks(peaks, map)

# show LOD scores
plot_peaks(peaks, map, lod_labels=TRUE)

# show LOD scores, controlling whether they go on the left or right
```



```
plot_peaks(peaks, map, lod_labels=TRUE,
           label_left=c(TRUE, TRUE, TRUE, FALSE, TRUE, FALSE))
```

plot\_pvg

*Plot phenotype vs genotype*

## Description

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

## Usage

```
plot_pvg(
  geno,
  pheno,
  sort = TRUE,
  SEMult = NULL,
  pooledSD = TRUE,
  swap_axes = FALSE,
  jitter = 0.2,
  force_labels = TRUE,
  alternate_labels = FALSE,
  omit_points = FALSE,
  ...
)
```

## Arguments

geno	Vector of genotypes, for example as produced by <code>maxmarg()</code> 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.
swap_axes	If TRUE, swap the axes, so that the genotypes are on the y-axis and the phenotype is on the x-axis.
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).
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 <code>plot()</code> .

**Value**

(Invisibly) A matrix with rows being the genotype groups and columns for the means and (if `SEmult` is specified) the SEs.

**Hidden graphics parameters**

A number of graphics parameters can be passed via `....`. For example, `bgcolor` to control the background color, and `seg_width`, `seg_lwd`, and `seg_col` to control the lines at the confidence intervals. Further, `hlines`, `hlines_col`, `hlines_lwd`, and `hlines_lty` to control the horizontal grid lines. (Use `hlines=NA` to avoid plotting horizontal grid lines.) Similarly `vlines`, `vlines_col`, `vlines_lwd`, and `vlines_lty` for vertical grid lines. These are not included as formal parameters in order to avoid cluttering the function definition.

**See Also**

[plot\\_coef\(\)](#)

**Examples**

```
# 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
plot_pxxg(geno, log10(iron$pheno[,1]), ylab=expression(log[10](Liver)))

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

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

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

---

plot_scan1	<i>Plot a genome scan</i>
------------	---------------------------

---

## Description

Plot LOD curves for a genome scan

## Usage

```
plot_scan1(x, map, lodcolumn = 1, chr = NULL, add = FALSE, gap = NULL, ...)
```

```
## S3 method for class 'scan1'
```

```
plot(x, map, lodcolumn = 1, chr = NULL, add = FALSE, gap = NULL, ...)
```

## Arguments

x	An object of class "scan1", as output by <a href="#">scan1()</a> .
map	A list of vectors of marker positions, as produced by <a href="#">insert_pseudomarkers()</a> .
lodcolumn	LOD score column to plot (a numeric index, or a character string for a column name). Only one value allowed.
chr	Selected chromosomes to plot; a vector of character strings.
add	If TRUE, add to current plot (must have same map and chromosomes).
gap	Gap between chromosomes. The default is 1% of the total genome length.
...	Additional graphics parameters.

## Value

None.

## 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. col controls the color of lines/curves; altcol can be used if you want alternative chromosomes in different colors. These are not included as formal parameters in order to avoid cluttering the function definition.

## See Also

[plot\\_coef\(\)](#), [plot\\_coefCC\(\)](#), [plot\\_snpasso\(\)](#)

**Examples**

```

# 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
ylim <- c(0, maxlod(out)*1.02) # need to strip class to get overall max LOD
chr <- c(2,7,8,9,15,16)
plot(out, map, chr=chr, ylim=ylim)
plot(out, map, lodcolumn=2, chr=chr, col="violetred", add=TRUE)
legend("topleft", lwd=2, col=c("darkslateblue", "violetred"), colnames(out),
      bg="gray90")

# plot just one chromosome
plot(out, map, chr=8, ylim=ylim)
plot(out, map, chr=8, lodcolumn=2, col="violetred", add=TRUE)

# lodcolumn can also be a column name
plot(out, map, lodcolumn="liver", ylim=ylim)
plot(out, map, lodcolumn="spleen", col="violetred", add=TRUE)

```

---

plot\_sdp

*plot strain distribution patterns for SNPs*


---

**Description**

plot the strain distribution patterns of SNPs using tracks of tick-marks for each founder strain

**Usage**

```
plot_sdp(pos, sdp, strain_labels = names(qtl2::CCcolors), ...)
```

**Arguments**

pos                      vector of SNP positions

sdp	vector of strain distribution patterns (as integers)
strain_labels	names of the strains
...	additional graphic arguments

### Details

Additional arguments, such as xlab, ylab, xlim, and main, are passed via ...; also bgcolor to control the color of the background, and col and lwd to control the color and thickness of the tick marks.

### Value

None.

### See Also

[calc\\_sdp\(\)](#), [invert\\_sdp\(\)](#)

### Examples

```
n_tick <- 50
plot_sdp(runif(n_tick, 0, 100), sample(0:255, n_tick, replace=TRUE))
```

---

plot_snpasso	<i>Plot SNP associations</i>
--------------	------------------------------

---

### Description

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

### Usage

```
plot_snpasso(
  scan1output,
  snpinfo,
  genes = NULL,
  lodcolumn = 1,
  show_all_snps = TRUE,
  chr = NULL,
  add = FALSE,
  drop_hilit = NA,
  col_hilit = "violetred",
  col = "darkslateblue",
  gap = NULL,
  minlod = 0,
  sdp_panel = FALSE,
  strain_labels = names(qtl2::CCcolors),
  ...
)
```

**Arguments**

scan1output	Output of <code>scan1()</code> using SNP probabilities derived by <code>genoprob_to_snpprob()</code> .
snpinfo	Data frame with SNP information with the following columns (the last three are generally derived from with <code>index_snps()</code> ): <ul style="list-style-type: none"> <li>• chr - Character string or factor with chromosome</li> <li>• pos - Position (in same units as in the "map" attribute in genoprobs.</li> <li>• sdp - Strain distribution pattern: an integer, between 1 and <math>2^n - 2</math> where <math>n</math> is the number of strains, whose binary encoding indicates the founder genotypes</li> <li>• snp - Character string with SNP identifier (if missing, the rownames are used).</li> <li>• index - Indices that indicate equivalent groups of SNPs.</li> <li>• intervals - Indexes that indicate which marker intervals the SNPs reside.</li> <li>• on_map - Indicate whether SNP coincides with a marker in the genoprobs</li> </ul>
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). Only one value allowed.
show_all_snps	If TRUE, expand to show all SNPs.
chr	Vector of character strings with chromosome IDs to plot.
add	If TRUE, add to current plot (must have same map and chromosomes).
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
gap	Gap between chromosomes. The default is 1% of the total genome length.
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 omitted.
sdp_panel	Include a panel with the strain distribution patterns for the highlighted SNPs
strain_labels	Labels for the strains, if sdp_panel=TRUE.
...	Additional graphics parameters.

**Value**

None.

### Hidden graphics parameters

A number of graphics parameters can be passed via .... For example, `bgcolor` to control the background color, `altbgcolor` to control the background color on alternate chromosomes, `altcol` to control the point 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. If you are including genes and/or SDP panels, you can use `panel_prop` to control the relative heights of the panels, from top to bottom.

### See Also

[plot\\_scan1\(\)](#), [plot\\_coef\(\)](#), [plot\\_coefCC\(\)](#)

### Examples

```
## Not run:
# load example D0 data from web
file <- paste0("https://raw.githubusercontent.com/rqt1/",
               "qt12data/main/D0ex/D0ex.zip")
D0ex <- read_cross2(file)

# subset to chr 2
D0ex <- D0ex[, "2"]

# calculate genotype probabilities and convert to allele probabilities
pr <- calc_genoprob(D0ex, error_prob=0.002)
apr <- genoprob_to_alleleprob(pr)

# query function for grabbing info about variants in region
snp_dbfile <- system.file("extdata", "cc_variants_small.sqlite", package="qt12")
query_variants <- create_variant_query_func(snp_dbfile)

# SNP association scan
out_snps <- scan1snps(apr, D0ex$pmap, D0ex$pheno, query_func=query_variants,
                     chr=2, start=97, end=98, keep_all_snps=TRUE)

# plot results
plot_snpasso(out_snps$lod, out_snps$snpinfo)

# can also just type plot()
plot(out_snps$lod, out_snps$snpinfo)

# plot just subset of distinct SNPs
plot(out_snps$lod, out_snps$snpinfo, show_all_snps=FALSE)

# highlight the top snps (with LOD within 1.5 of max)
plot(out_snps$lod, out_snps$snpinfo, drop_hilit=1.5)

# query function for finding genes in region
gene_dbfile <- system.file("extdata", "mouse_genes_small.sqlite", package="qt12")
query_genes <- create_gene_query_func(gene_dbfile)
genes <- query_genes(2, 97, 98)
```

```
# plot SNP association results with gene locations
plot(out_snps$lod, out_snps$snpinfo, drop_hilit=1.5, genes=genes)

# plot SNP asso results with genes plus SDPs of highlighted SNPs
plot(out_snps$lod, out_snps$snpinfo, drop_hilit=2, genes=genes, sdp_panel=TRUE)

## End(Not run)
```

---

predict_snpgeno	<i>Predict SNP genotypes</i>
-----------------	------------------------------

---

## Description

Predict SNP genotypes in a multiparent population from inferred genotypes plus founder strains' SNP alleles.

## Usage

```
predict_snpgeno(cross, geno, cores = 1)
```

## Arguments

cross	Object of class "cross2". For details, see the <a href="#">R/qt12 developer guide</a> .
geno	Imputed genotypes, as a list of matrices, as from <a href="#">maxmarg()</a> .
cores	Number of CPU cores to use, for parallel calculations. (If 0, use <a href="#">parallel::detectCores()</a> .) Alternatively, this can be links to a set of cluster sockets, as produced by <a href="#">parallel::makeCluster()</a> .

## Value

A list of matrices with inferred SNP genotypes, coded 1/2/3.

## See Also

[maxmarg\(\)](#), [viterbi\(\)](#), [calc\\_errorlod\(\)](#)

## Examples

```
## Not run:
# load example data and calculate genotype probabilities
file <- paste0("https://raw.githubusercontent.com/rqt1/",
               "qt12data/main/D0ex/D0ex.zip")
D0ex <- read_cross2(file)
probs <- calc_genoprob(D0ex, error_prob=0.002)

# inferred genotypes
m <- maxmarg(probs, minprob=0.5)
```



```
# inferred SNP genotypes
inferg <- predict_snpgeno(D0ex, m)

## End(Not run)
```

---

print.cross2	<i>Print a cross2 object</i>
--------------	------------------------------

---

### Description

Print a summary of a cross2 object

### Usage

```
## S3 method for class 'cross2'
print(x, ...)
```

### Arguments

x	An object of class "cross2", as output by <a href="#">read_cross2()</a> . For details, see the <a href="#">R/qlt2 developer guide</a> .
...	Ignored.

### Value

None.

---

print.summary.scan1perm	<i>Print summary of scan1perm permutations</i>
-------------------------	--

---

### Description

Print summary of scan1perm permutations

### Usage

```
## S3 method for class 'summary.scan1perm'
print(x, digits = 3, ...)
```

### Arguments

x	Object of class "summary.scan1perm", as produced by <a href="#">summary_scan1perm()</a> .
digits	Number of digits in printing significance thresholds; passed to <a href="#">base::print()</a> .
...	Ignored.

**Details**

This is to go with `summary_scan1perm()`, so that the summary output is printed in a nice format. Generally not called directly, but it can be in order to control the number of digits that appear.

**Value**

Invisibly returns the input, x.

**Examples**

```
# 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)

# permutations with genome scan (just 3 replicates, for illustration)
operm <- scan1perm(probs, pheno, addcovar=covar, Xcovar=Xcovar,
                  n_perm=3)

print( summary(operm, alpha=c(0.20, 0.05)), digits=8 )
```

---

probs\_to\_grid

---

*Subset genotype probability array to pseudomarkers on a grid*


---

**Description**

Subset genotype probability array (from `calc_genoprob()`) to a grid of pseudomarkers along each chromosome.

**Usage**

```
probs_to_grid(probs, grid)
```

**Arguments**

probs	Genotype probabilities as output from <code>calc_genoprob()</code> with <code>stepwidth="fixed"</code> .
grid	List of logical vectors that indicate which positions are on the grid and should be retained.

**Details**

This only works if `calc_genoprob()` was run with `stepwidth="fixed"`, so that the genotype probabilities were calculated at a grid of markers/pseudomarkers. When this is the case, we omit all but the probabilities on this grid. Use `calc_grid()` to find the grid positions.

**Value**

An object of class "calc\_genoprob", like the input, subset to just include pseudomarkers along a grid. See `calc_genoprob()`.

**See Also**

`calc_grid()`, `map_to_grid()`

**Examples**

```
grav2 <- read_cross2(system.file("extdata", "grav2.zip", package="qt12"))
map_w_pmar <- insert_pseudomarkers(grav2$gmap, step=1)
probs <- calc_genoprob(grav2, map_w_pmar, error_prob=0.002)
sapply(probs, dim)
grid <- calc_grid(grav2$gmap, step=1)
probs_sub <- probs_to_grid(probs, grid)
sapply(probs_sub, dim)
```

---

<code>pull_genoprobint</code>	<i>Pull genotype probabilities for an interval</i>
-------------------------------	--

---

**Description**

Pull out the genotype probabilities for a given genomic interval

**Usage**

```
pull_genoprobint(genoprobs, map, chr, interval)
```

**Arguments**

<code>genoprobs</code>	Genotype probabilities as calculated by <code>calc_genoprob()</code> .
<code>map</code>	The marker map for the genotype probabilities
<code>chr</code>	Chromosome ID (single character sting)
<code>interval</code>	Interval (pair of numbers)

**Value**

A list containing a single 3d array of genotype probabilities, like the input `genoprobs` but for the designated interval.

**See Also**

[find\\_marker\(\)](#), [pull\\_genoprobpos\(\)](#)

**Examples**

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

gmap <- insert_pseudomarkers(iron$gmap, step=1)
pr <- calc_genoprob(iron, gmap, error_prob=0.002)

pr_sub <- pull_genoprobint(pr, gmap, "8", c(25, 35))
```

---

<code>pull_genoprobpos</code>	<i>Pull genotype probabilities for a particular position</i>
-------------------------------	--

---

**Description**

Pull out the genotype probabilities for a particular position (by name)

**Usage**

```
pull_genoprobpos(genoprobs, map = NULL, chr = NULL, pos = NULL, marker = NULL)
```

**Arguments**

<code>genoprobs</code>	Genotype probabilities as calculated by <a href="#">calc_genoprob()</a> .
<code>map</code>	A map object: a list (corresponding to chromosomes) of vectors of marker positions. Can also be a <code>snpinfo</code> object (data frame with columns <code>chr</code> and <code>pos</code> ; marker names taken from column <code>snp</code> or if that doesn't exist from the row names)
<code>chr</code>	A chromosome ID
<code>pos</code>	A numeric position
<code>marker</code>	A single character string with the name of the position to pull out.

**Details**

Provide either a marker/pseudomarker name (with the argument `marker`) or all of `map`, `chr`, and `pos`.

**Value**

A matrix of genotype probabilities for the specified position.

**See Also**

[find\\_marker\(\)](#), [fit1\(\)](#), [pull\\_genoprobint\(\)](#)

**Examples**

```

iron <- read_cross2(system.file("extdata", "iron.zip", package="qt12"))

gmap <- insert_pseudomarkers(iron$gmap, step=1)
pr <- calc_genoprob(iron, gmap, error_prob=0.002)

pmar <- find_marker(gmap, 8, 40)
pr_8_40 <- pull_genoprobpos(pr, pmar)

pr_8_40_alt <- pull_genoprobpos(pr, gmap, 8, 40)

```

---

pull_markers	<i>Drop all but a specified set of markers</i>
--------------	--

---

**Description**

Drop all markers from a cross2 object except those in a specified vector.

**Usage**

```
pull_markers(cross, markers)
```

**Arguments**

cross	Object of class "cross2". For details, see the <a href="#">R/qt12 developer guide</a> .
markers	A vector of marker names.

**Value**

The input cross with only the specified markers.

**See Also**

[drop\\_markers\(\)](#), [drop\\_nullmarkers\(\)](#)

**Examples**

```

grav2 <- read_cross2(system.file("extdata", "grav2.zip", package="qt12"))
markers2drop <- c("BH.342C/347L-Co1", "GH.94L", "EG.357C/359L-Co1", "CD.245L", "ANL2")
grav2_rev <- pull_markers(grav2, markers2drop)

```

---

qt12version	<i>Installed version of R/qt12</i>
-------------	------------------------------------

---

**Description**

Get installed version of R/qt12

**Usage**

```
qt12version()
```

**Value**

A character string with the installed version of the R/qt12 package.

**Examples**

```
qt12version()
```

---

rbind.calc_genoprob	<i>Join genotype probabilities for different individuals</i>
---------------------	--

---

**Description**

Join multiple genotype probability objects, as produced by [calc\\_genoprob\(\)](#), for the same set of markers and genotypes but for different individuals.

**Usage**

```
## S3 method for class 'calc_genoprob'
rbind(...)
```

**Arguments**

...                      Genotype probability objects as produced by [calc\\_genoprob\(\)](#). Must have the same set of markers and genotypes.

**Value**

An object of class "calc\_genoprob", like the input; see [calc\\_genoprob\(\)](#).

**See Also**

[cbind.calc\\_genoprob\(\)](#)

**Examples**

```
grav2 <- read_cross2(system.file("extdata", "grav2.zip", package="qt12"))
map <- insert_pseudomarkers(grav2$gmap, step=1)
probsA <- calc_genoprob(grav2[1:5,], map, error_prob=0.002)
probsB <- calc_genoprob(grav2[6:12,], map, error_prob=0.002)
probs <- rbind(probsA, probsB)
```

---

rbind.scan1	<i>Join genome scan results for different chromosomes.</i>
-------------	--

---

**Description**

Join multiple [scan1\(\)](#) results for different chromosomes; must have the same set of lod score column.

**Usage**

```
## S3 method for class 'scan1'
rbind(...)
```

**Arguments**

... Genome scan objects of class "scan1", as produced by [scan1\(\)](#). Must have the same lod score columns.

**Details**

If components addcovar, Xcovar, intcovar, weights, sample\_size do not match between objects, we omit this information.

If hsq present, we simply rbind() the contents.

**Value**

An object of class "scan1", like the inputs, but with the results for different sets of chromosomes combined.

**See Also**

[cbind.scan1\(\)](#), [scan1\(\)](#)

**Examples**

```

grav2 <- read_cross2(system.file("extdata", "grav2.zip", package="qt12"))
map <- insert_pseudomarkers(grav2$gmap, step=1)
probs <- calc_genoprob(grav2, map, error_prob=0.002)
phe <- grav2$pheno[,1,drop=FALSE]

out1 <- scan1(probs[,1], phe) # chr 1
out2 <- scan1(probs[,5], phe) # chr 5
out <- rbind(out1, out2)

```

rbind.scan1perm

*Combine data from scan1perm objects***Description**

Row-bind multiple scan1perm objects with the same set of columns

**Usage**

```

## S3 method for class 'scan1perm'
rbind(...)

## S3 method for class 'scan1perm'
c(...)

```

**Arguments**

... A set of permutation results from [scan1perm\(\)](#) (objects of class "scan1perm"). They must have the same set of columns. If any include autosome/X chromosome-specific permutations, they must all be such.

**Details**

The aim of this function is to concatenate the results from multiple runs of a permutation test with [scan1perm\(\)](#), to assist in the case that such permutations are done on multiple processors in parallel.

**Value**

The combined row-binded input, as an object of class "scan1perm"; see [scan1perm\(\)](#).

**See Also**

[cbind.scan1perm\(\)](#), [scan1perm\(\)](#), [scan1\(\)](#)



**Examples**

```
# 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)

# permutations with genome scan (just 3 replicates, for illustration)
operm1 <- scan1perm(probs, pheno, addcovar=covar, Xcovar=Xcovar, n_perm=3)
operm2 <- scan1perm(probs, pheno, addcovar=covar, Xcovar=Xcovar, n_perm=3)

operm <- rbind(operm1, operm2)
```

rbind.sim\_geno

*Join genotype imputations for different individuals***Description**

Join multiple genotype imputation objects, as produced by [sim\\_geno\(\)](#), for the same set of markers but for different individuals.

**Usage**

```
## S3 method for class 'sim_geno'
rbind(...)
```

**Arguments**

... Genotype imputation objects as produced by [sim\\_geno\(\)](#). Must have the same set of markers and genotypes.

**Value**

An object of class "sim\_geno", like the input; see [sim\\_geno\(\)](#).

**See Also**

[cbind.sim\\_geno\(\)](#), [sim\\_geno\(\)](#)

## Examples

```
grav2 <- read_cross2(system.file("extdata", "grav2.zip", package="qtl2"))
map <- insert_pseudomarkers(grav2$gmap, step=1)
drawsA <- sim_geno(grav2[1:5,], map, error_prob=0.002, n_draws=4)
drawsB <- sim_geno(grav2[6:12,], map, error_prob=0.002, n_draws=4)
draws <- rbind(drawsA, drawsB)
```

---

rbind.viterbi

Join Viterbi results for different individuals

---

## Description

Join multiple imputed genotype objects, as produced by `viterbi()`, for the same set of markers but for different individuals.

## Usage

```
## S3 method for class 'viterbi'
rbind(...)
```

## Arguments

... Imputed genotype objects as produced by `viterbi()`. Must have the same set of markers.

## Value

An object of class "viterbi", like the input; see `viterbi()`.

## See Also

`cbind.viterbi()`, `viterbi()`

## Examples

```
grav2 <- read_cross2(system.file("extdata", "grav2.zip", package="qtl2"))
map <- insert_pseudomarkers(grav2$gmap, step=1)
gA <- viterbi(grav2[1:5,], map, error_prob=0.002)
gB <- viterbi(grav2[6:12,], map, error_prob=0.002)
g <- rbind(gA, gB)
```

---

read_cross2	<i>Read QTL data from files</i>
-------------	---------------------------------

---

## Description

Read QTL data from a set of files

## Usage

```
read_cross2(file, quiet = TRUE)
```

## Arguments

file	Character string with path to the <b>YAML</b> or <b>JSON</b> file containing all of the control information. This could instead be a zip file containing all of the data files, in which case the contents are unzipped to a temporary directory and then read.
quiet	If FALSE, print progress messages.

## Details

A control file in **YAML** or **JSON** format contains information about basic parameters as well as the names of the series of data files to be read. See the [sample data files](#) and the [vignette describing the input file format](#).

## Value

Object of class "cross2". For details, see the [R/ql2 developer guide](#).

## See Also

[read\\_pheno\(\)](#), [write\\_control\\_file\(\)](#), sample data files at <https://kbroman.org/ql2/pages/sampled.html> and <https://github.com/rql/ql2data>

## Examples

```
## Not run:
yaml_file <- "https://kbroman.org/ql2/assets/sampled/grav2/grav2.yaml"
grav2 <- read_cross2(yaml_file)

## End(Not run)
zip_file <- system.file("extdata", "grav2.zip", package="ql2")
grav2 <- read_cross2(zip_file)
```

---

read_pheno	<i>Read phenotype data</i>
------------	----------------------------

---

### Description

Read phenotype data from a CSV file (and, optionally, phenotype covariate data from a separate CSV file). The CSV files may be contained in zip files, separately or together.

### Usage

```
read_pheno(
  file,
  phenocovarfile = NULL,
  sep = ",",
  na.strings = c("-", "NA"),
  comment.char = "#",
  transpose = FALSE,
  quiet = TRUE
)
```

### Arguments

file	Character string with path to the phenotype data file (or a zip file containing both the phenotype and phenotype covariate files).
phenocovarfile	Character string with path to the phenotype covariate file. This can be a separate CSV or zip file; if a zip file, it must contain exactly one CSV file. Alternatively, if the file argument indicates a zip file that contains two files (phenotypes and phenotype covariates), then this phenocovarfile argument must indicate the base name for the phenotype covariate file.
sep	the field separator character
na.strings	a character vector of strings which are to be interpreted as NA values.
comment.char	A character vector of length one containing a single character to denote comments within the CSV files.
transpose	If TRUE, the phenotype data will be transposed. The phenotype covariate information is <b>never</b> transposed.
quiet	If FALSE, print progress messages.

### Value

Either a matrix of phenotype data, or a list containing pheno (phenotype matrix) and phenocovar (phenotype covariate matrix).

### See Also

`read_cross2()`, sample data files at <https://kbroman.org/ql2/pages/sampleddata.html> and <https://github.com/rqtl/ql2data>

**Examples**

```
## Not run:
file <- paste0("https://raw.githubusercontent.com/rqtl/",
               "qt12data/main/Gough/gough_pheno.csv")
phe <- read_pheno(file)

phecovfile <- paste0("https://raw.githubusercontent.com/rqtl/",
                    "qt12data/main/Gough/gough_phenocovar.csv")
phe_list <- read_pheno(file, phecovfile)

## End(Not run)
```

recode\_snps

*Recode SNPs by major allele***Description**

For multi-parent populations with founder genotypes, recode the raw SNP genotypes so that 1 means homozygous for the major allele in the founders.

**Usage**

```
recode_snps(cross)
```

**Arguments**

cross                      Object of class "cross2". For details, see the [R/qt12 developer guide](#).

**Value**

The input cross object with the raw SNP genotypes recoded so that 1 is homozygous for the major alleles in the founders.

**See Also**

[calc\\_raw\\_founder\\_maf\(\)](#), [calc\\_raw\\_maf\(\)](#)

**Examples**

```
## Not run:
# load example data and calculate genotype probabilities
file <- paste0("https://raw.githubusercontent.com/rqtl/",
               "qt12data/main/D0ex/D0ex.zip")
D0ex <- read_cross2(file)
D0ex <- recode_snps(D0ex)

## End(Not run)
```

---

reduce_map_gaps	<i>Reduce the lengths of gaps in a map</i>
-----------------	--

---

**Description**

Reduce the lengths of gaps in a map

**Usage**

```
reduce_map_gaps(map, min_gap = 50)
```

**Arguments**

map	Genetic map as a list of vectors (each vector is a chromosome and contains the marker positions).
min_gap	Minimum gap length to return.

**Value**

Input map with any gaps greater than min\_gap reduced to min\_gap.

**See Also**

[find\\_map\\_gaps\(\)](#)

**Examples**

```
iron <- read_cross2(system.file("extdata", "iron.zip", package="qt12"))
rev_map <- reduce_map_gaps(iron$gmap, 30)
```

---

reduce_markers	<i>Reduce markers to a subset of more-evenly-spaced ones</i>
----------------	--

---

**Description**

Find the largest subset of markers such that no two adjacent markers are separated by less than some distance.

**Usage**

```
reduce_markers(
  map,
  min_distance = 1,
  weights = NULL,
  max_batch = 10000,
  batch_distance_mult = 1,
  cores = 1
)
```

**Arguments**

map	A list with each component being a vector with the marker positions for a chromosome.
min_distance	Minimum distance between markers.
weights	A (optional) list of weights on the markers; same size as map.
max_batch	Maximum number of markers to consider in a batch
batch_distance_mult	If working with batches of markers, reduce min_distance by this multiple.
cores	Number of CPU cores to use, for parallel calculations. (If 0, use <a href="#">parallel::detectCores()</a> .) Alternatively, this can be links to a set of cluster sockets, as produced by <a href="#">parallel::makeCluster()</a> .

**Details**

Uses a dynamic programming algorithm to find, for each chromosome, the subset of markers for which  $\max(\text{weights})$  is maximal, subject to the constraint that no two adjacent markers may be separated by more than min\_distance.

The computation time for the algorithm grows with like the square of the number of markers, like 1 sec for 10k markers but 30 sec for 50k markers. If the number of markers on a chromosome is greater than max\_batch, the markers are split into batches and the algorithm applied to each batch with min\_distance smaller by a factor min\_distance\_mult, and then merged together for one last pass.

**Value**

A list like the input map, but with the selected subset of markers.

**References**

Broman KW, Weber JL (1999) Method for constructing confidently ordered linkage maps. *Genet Epidemiol* 16:337–343

**See Also**

[find\\_dup\\_markers\(\)](#), [drop\\_markers\(\)](#)

**Examples**

```
# read data
grav2 <- read_cross2(system.file("extdata", "grav2.zip", package="qt12"))

# grab genetic map
gmap <- grav2$gmap

# subset to markers that are >= 1 cM apart
gmap_sub <- reduce_markers(gmap, 1)

# drop all of the other markers from the cross
markers2keep <- unlist(lapply(gmap_sub, names))
grav2_sub <- pull_markers(grav2, markers2keep)
```

---

replace_ids	<i>Replace individual IDs</i>
-------------	-------------------------------

---

**Description**

Replace the individual IDs in an object with new ones

**Usage**

```
replace_ids(x, ids)

## S3 method for class 'cross2'
replace_ids(x, ids)

## S3 method for class 'calc_genoprob'
replace_ids(x, ids)

## S3 method for class 'viterbi'
replace_ids(x, ids)

## S3 method for class 'sim_geno'
replace_ids(x, ids)

## S3 method for class 'matrix'
replace_ids(x, ids)

## S3 method for class 'data.frame'
replace_ids(x, ids)
```

**Arguments**

x	Object whose IDs will be replaced
ids	Vector of character strings with the new individual IDs, with the names being the original IDs.



**Value**

The input `x` object, but with individual IDs replaced.

**Methods (by class)**

- `replace_ids(cross2)`: Replace IDs in a "cross2" object
- `replace_ids(calc_genoprob)`: Replace IDs in output from `calc_genoprob()`
- `replace_ids(viterbi)`: Replace IDs in output from `viterbi()`
- `replace_ids(sim_geno)`: Replace IDs in output from `sim_geno()`
- `replace_ids(matrix)`: Replace IDs in a matrix
- `replace_ids(data.frame)`: Replace IDs in a data frame

**Examples**

```
iron <- read_cross2(system.file("extdata", "iron.zip", package="qtl2"))
ids <- as.numeric(ind_ids(iron))

# replace the numeric IDs with IDs like "mouse003"
new_ids <- setNames( sprintf("mouse%03d", as.numeric(ids)), ids)

iron <- replace_ids(iron, new_ids)
```

---

scale\_kinship

*Scale kinship matrix*


---

**Description**

Scale kinship matrix to be like a correlation matrix.

**Usage**

```
scale_kinship(kinship)
```

**Arguments**

`kinship` A kinship matrix, or a list of such in the case of the "leave one chromosome out" method, as calculated by `calc_kinship()`.

**Details**

We take  $c_{ij} = k_{ij} / \sqrt{k_{ii}k_{jj}}$

**Value**

A matrix or list of matrices, as with the input, but with the matrices scaled to be like correlation matrices.

**Examples**

```
grav2 <- read_cross2(system.file("extdata", "grav2.zip", package="qt12"))
map <- insert_pseudomarkers(grav2$gmap, step=1)
probs <- calc_genoprob(grav2, map, error_prob=0.002)
K <- calc_kinship(probs)
Ka <- scale_kinship(K)
```

scan1

*Genome scan with a single-QTL model***Description**

Genome scan with a single-QTL model by Haley-Knott regression or a linear mixed model, with possible allowance for covariates.

**Usage**

```
scan1(
  genoprobs,
  pheno,
  kinship = NULL,
  addcovar = NULL,
  Xcovar = NULL,
  intcovar = NULL,
  weights = NULL,
  reml = TRUE,
  model = c("normal", "binary"),
  hsq = NULL,
  cores = 1,
  ...
)
```

**Arguments**

genoprobs	Genotype probabilities as calculated by <code>calc_genoprob()</code> .
pheno	A numeric matrix of phenotypes, individuals x phenotypes.
kinship	Optional kinship matrix, or a list of kinship matrices (one per chromosome), in order to use the LOCO (leave one chromosome out) method.
addcovar	An optional numeric matrix of additive covariates.
Xcovar	An optional numeric matrix with additional additive covariates used for null hypothesis when scanning the X chromosome.
intcovar	An numeric optional matrix of interactive covariates.
weights	An optional numeric vector of positive weights for the individuals. As with the other inputs, it must have names for individual identifiers.
reml	If kinship provided: if reml=TRUE, use REML; otherwise maximum likelihood.

model	Indicates whether to use a normal model (least squares) or binary model (logistic regression) for the phenotype. If model="binary", the phenotypes must have values in $[0, 1]$ .
hsq	Considered only if kinship is provided, in which case this is taken as the assumed value for the residual heritability. It should be a vector with length corresponding to the number of columns in pheno, or (if kinship corresponds to a list of LOCO kinship matrices) a matrix with dimension $\text{length}(\text{kinship}) \times \text{ncol}(\text{pheno})$ .
cores	Number of CPU cores to use, for parallel calculations. (If 0, use <code>parallel::detectCores()</code> .) Alternatively, this can be links to a set of cluster sockets, as produced by <code>parallel::makeCluster()</code> .
...	Additional control parameters; see Details.

### Details

We first fit the model  $y = X\beta + \epsilon$  where  $X$  is a matrix of covariates (or just an intercept) and  $\epsilon$  is multivariate normal with mean 0 and covariance matrix  $\sigma^2[h^2(2K) + I]$  where  $K$  is the kinship matrix and  $I$  is the identity matrix.

We then take  $h^2$  as fixed and then scan the genome, at each genomic position fitting the model  $y = P\alpha + X\beta + \epsilon$  where  $P$  is a matrix of genotype probabilities for the current position and again  $X$  is a matrix of covariates  $\epsilon$  is multivariate normal with mean 0 and covariance matrix  $\sigma^2[h^2(2K) + I]$ , taking  $h^2$  to be known.

Note that if weights are provided, the covariance matrix becomes  $\sigma^2[h^2(2K) + D]$  where  $D$  is a diagonal matrix with the reciprocal of the weights.

For each of the inputs, the row names are used as individual identifiers, to align individuals. The `genoprobs` object should have a component "is\_x\_chr" that indicates which of the chromosomes is the X chromosome, if any.

The ... argument can contain several additional control parameters; suspended for simplicity (or confusion, depending on your point of view). `tol` is used as a tolerance value for linear regression by QR decomposition (in determining whether columns are linearly dependent on others and should be omitted); default  $1e-12$ . `intcovar_method` indicates whether to use a high-memory (but potentially faster) method or a low-memory (and possibly slower) method, with values "highmem" or "lowmem"; default "lowmem". `max_batch` indicates the maximum number of phenotypes to run together; default is unlimited. `maxit` is the maximum number of iterations for convergence of the iterative algorithm used when model=binary. `bintol` is used as a tolerance for convergence for the iterative algorithm used when model=binary. `eta_max` is the maximum value for the "linear predictor" in the case model="binary" (a bit of a technicality to avoid fitted values exactly at 0 or 1).

If kinship is absent, Haley-Knott regression is performed. If kinship is provided, a linear mixed model is used, with a polygenic effect estimated under the null hypothesis of no (major) QTL, and then taken as fixed as known in the genome scan.

If kinship is a single matrix, then the `hsq` in the results is a vector of heritabilities (one value for each phenotype). If kinship is a list (one matrix per chromosome), then `hsq` is a matrix, chromosomes x phenotypes.

### Value

An object of class "scan1": a matrix of LOD scores, positions x phenotypes. Also contains one or more of the following attributes:

- `sample_size` - Vector of sample sizes used for each phenotype
- `hsq` - Included if kinship provided: A matrix of estimated heritabilities under the null hypothesis of no QTL. Columns are the phenotypes. If the "loco" method was used with `calc_kinship()` to calculate a list of kinship matrices, one per chromosome, the rows of `hsq` will be the heritabilities for the different chromosomes (well, leaving out each one). If `Xcovar` was not NULL, there will at least be an autosome and X chromosome row.

## References

Haley CS, Knott SA (1992) A simple regression method for mapping quantitative trait loci in line crosses using flanking markers. *Heredity* 69:315–324.

Kang HM, Zaitlen NA, Wade CM, Kirby A, Heckerman D, Daly MJ, Eskin E (2008) Efficient control of population structure in model organism association mapping. *Genetics* 178:1709–1723.

## See Also

`scan1perm()`, `scan1coef()`, `cbind.scan1()`, `rbind.scan1()`, `scan1max()`

## Examples

```
# 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)

# leave-one-chromosome-out kinship matrices
kinship <- calc_kinship(probs, "loco")

# genome scan with a linear mixed model
out_lmm <- scan1(probs, pheno, kinship, covar, Xcovar)
```

scan1blup

*Calculate BLUPs of QTL effects in scan along one chromosome***Description**

Calculate BLUPs of QTL effects in scan along one chromosome, with a single-QTL model treating the QTL effects as random, with possible allowance for covariates and for a residual polygenic effect.

**Usage**

```
scan1blup(
  genoprobs,
  pheno,
  kinship = NULL,
  addcovar = NULL,
  nullcovar = NULL,
  contrasts = NULL,
  se = FALSE,
  reml = TRUE,
  tol = 0.000000000001,
  cores = 1,
  quiet = TRUE
)
```

**Arguments**

genoprobs	Genotype probabilities as calculated by <a href="#">calc_genoprob()</a> .
pheno	A numeric vector of phenotype values (just one phenotype, not a matrix of them)
kinship	Optional kinship matrix, or a list of kinship matrices (one per chromosome), in order to use the LOCO (leave one chromosome out) method.
addcovar	An optional numeric matrix of additive covariates.
nullcovar	An optional numeric matrix of additional additive covariates that are used under the null hypothesis (of no QTL) but not under the alternative (with a QTL). This is needed for the X chromosome, where we might need sex as a additive covariate under the null hypothesis, but we wouldn't want to include it under the alternative as it would be collinear with the QTL effects. Only used if kinship is provided but <code>hsq</code> is not, to get estimate of residual heritability.
contrasts	An optional numeric matrix of genotype contrasts, size genotypes x genotypes. For an intercross, you might use <code>cbind(mu=c(1,0,0), a=c(-1, 0, 1), d=c(0, 1, 0))</code> to get mean, additive effect, and dominance effect. The default is the identity matrix.
se	If TRUE, also calculate the standard errors.
reml	If <code>reml=TRUE</code> , use REML to estimate variance components; otherwise maximum likelihood.

tol	Tolerance value for convergence of linear mixed model fit.
cores	Number of CPU cores to use, for parallel calculations. (If 0, use <code>parallel::detectCores()</code> .) Alternatively, this can be links to a set of cluster sockets, as produced by <code>parallel::makeCluster()</code> .
quiet	If FALSE, print message about number of cores used when multi-core.

## Details

For each of the inputs, the row names are used as individual identifiers, to align individuals.

If kinship is provided, the linear mixed model accounts for a residual polygenic effect, with a the polygenic variance estimated under the null hypothesis of no (major) QTL, and then taken as fixed as known in the scan to estimate QTL effects.

If contrasts is provided, the genotype probability matrix,  $P$ , is post-multiplied by the contrasts matrix,  $A$ , prior to fitting the model. So we use  $P \cdot A$  as the  $X$  matrix in the model. One might view the rows of  $A^{-1}$  as the set of contrasts, as the estimated effects are the estimated genotype effects pre-multiplied by  $A^{-1}$ .

## Value

An object of class "scan1coef": a matrix of estimated regression coefficients, of dimension positions x number of effects. The number of effects is `n_genotypes + n_addcovar`. May also contain the following attributes:

- SE - Present if `se=TRUE`: a matrix of estimated standard errors, of same dimension as `coef`.
- `sample_size` - Vector of sample sizes used for each phenotype

## References

Haley CS, Knott SA (1992) A simple regression method for mapping quantitative trait loci in line crosses using flanking markers. *Heredity* 69:315–324.

Kang HM, Zaitlen NA, Wade CM, Kirby A, Heckerman D, Daly MJ, Eskin E (2008) Efficient control of population structure in model organism association mapping. *Genetics* 178:1709–1723.

Robinson GK (1991) That BLUP is a good thing: The estimation of random effects. *Statist Sci* 6:15–32.

## Examples

```
# 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)

# convert to allele probabilities
aprobs <- genoprob_to_alleleprob(probs)
```

```

# 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 BLUPs of coefficients for chromosome 7
blup <- scan1blup(aprobs[, "7"], pheno, addcovar=covar)

# leave-one-chromosome-out kinship matrix for chr 7
kinship7 <- calc_kinship(probs, "loco")[[ "7" ]]

# calculate BLUPs of coefficients for chromosome 7, adjusting for residual polygenic effect
blup_pg <- scan1blup(aprobs[, "7"], pheno, kinship7, addcovar=covar)

```

scan1coef

*Calculate QTL effects in scan along one chromosome*

## Description

Calculate QTL effects in scan along one chromosome with a single-QTL model using Haley-Knott regression or a linear mixed model (the latter to account for a residual polygenic effect), with possible allowance for covariates.

## Usage

```

scan1coef(
  genoprobs,
  pheno,
  kinship = NULL,
  addcovar = NULL,
  nullcovar = NULL,
  intcovar = NULL,
  weights = NULL,
  contrasts = NULL,
  model = c("normal", "binary"),
  zerosum = TRUE,
  se = FALSE,
  hsq = NULL,
  reml = TRUE,
  ...
)

```

## Arguments

genoprobs	Genotype probabilities as calculated by <a href="#">calc_genoprob()</a> .
pheno	A numeric vector of phenotype values (just one phenotype, not a matrix of them)

kinship	Optional kinship matrix, or a list of kinship matrices (one per chromosome), in order to use the LOCO (leave one chromosome out) method.
addcovar	An optional numeric matrix of additive covariates.
nullcovar	An optional numeric matrix of additional additive covariates that are used under the null hypothesis (of no QTL) but not under the alternative (with a QTL). This is needed for the X chromosome, where we might need sex as a additive covariate under the null hypothesis, but we wouldn't want to include it under the alternative as it would be collinear with the QTL effects. Only used if kinship is provided but <code>hsq</code> is not, to get estimate of residual heritability.
intcovar	An optional numeric matrix of interactive covariates.
weights	An optional numeric vector of positive weights for the individuals. As with the other inputs, it must have names for individual identifiers.
contrasts	An optional numeric matrix of genotype contrasts, size genotypes x genotypes. For an intercross, you might use <code>cbind(mu=c(1,1,1), a=c(-1, 0, 1), d=c(0, 1, 0))</code> to get mean, additive effect, and dominance effect. The default is the identity matrix.
model	Indicates whether to use a normal model (least squares) or binary model (logistic regression) for the phenotype. If <code>model="binary"</code> , the phenotypes must have values in $[0, 1]$ .
zerosum	If TRUE, force the genotype or allele coefficients sum to 0 by subtracting their mean and add another column with the mean. Ignored if <code>contrasts</code> is provided.
se	If TRUE, also calculate the standard errors.
hsq	(Optional) residual heritability; used only if kinship provided.
reml	If kinship provided: if <code>reml=TRUE</code> , use REML; otherwise maximum likelihood.
...	Additional control parameters; see Details;

## Details

For each of the inputs, the row names are used as individual identifiers, to align individuals.

If kinship is absent, Haley-Knott regression is performed. If kinship is provided, a linear mixed model is used, with a polygenic effect estimated under the null hypothesis of no (major) QTL, and then taken as fixed as known in the genome scan.

If `contrasts` is provided, the genotype probability matrix,  $P$ , is post-multiplied by the contrasts matrix,  $A$ , prior to fitting the model. So we use  $P \cdot A$  as the  $X$  matrix in the model. One might view the rows of  $A^{-1}$  as the set of contrasts, as the estimated effects are the estimated genotype effects pre-multiplied by  $A^{-1}$ .

The ... argument can contain several additional control parameters; suspended for simplicity (or confusion, depending on your point of view). `tol` is used as a tolerance value for linear regression by QR decomposition (in determining whether columns are linearly dependent on others and should be omitted); default  $1e-12$ . `maxit` is the maximum number of iterations for convergence of the iterative algorithm used when `model=binary`. `bintol` is used as a tolerance for convergence for the iterative algorithm used when `model=binary`. `eta_max` is the maximum value for the "linear predictor" in the case `model="binary"` (a bit of a technicality to avoid fitted values exactly at 0 or 1).



**Value**

An object of class "scan1coef": a matrix of estimated regression coefficients, of dimension positions x number of effects. The number of effects is `n_genotypes + n_addcovar + (n_genotypes-1)*n_intcovar`. May also contain the following attributes:

- SE - Present if `se=TRUE`: a matrix of estimated standard errors, of same dimension as `coef`.
- `sample_size` - Vector of sample sizes used for each phenotype

**References**

Haley CS, Knott SA (1992) A simple regression method for mapping quantitative trait loci in line crosses using flanking markers. *Heredity* 69:315–324.

Kang HM, Zaitlen NA, Wade CM, Kirby A, Heckerman D, Daly MJ, Eskin E (2008) Efficient control of population structure in model organism association mapping. *Genetics* 178:1709–1723.

**Examples**

```
# 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$pheno[,1]
covar <- match(iron$covar$sex, c("f", "m")) # make numeric
names(covar) <- rownames(iron$covar)

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

# leave-one-chromosome-out kinship matrix for chr 7
kinship7 <- calc_kinship(probs, "loco")[[ "7" ]]

# calculate coefficients for chromosome 7, adjusting for residual polygenic effect
coef_pg <- scan1coef(probs[, "7"], pheno, kinship7, addcovar=covar)
```

---

scan1max

---

*Maximum LOD score from genome scan with a single-QTL model*


---

**Description**

Maximum LOD score from genome scan with a single-QTL model by Haley-Knott regression or a linear mixed model, with possible allowance for covariates.

**Usage**

```
scan1max(
  genoprobs,
  pheno,
  kinship = NULL,
  addcovar = NULL,
  Xcovar = NULL,
  intcovar = NULL,
  weights = NULL,
  reml = TRUE,
  model = c("normal", "binary"),
  hsq = NULL,
  by_chr = FALSE,
  cores = 1,
  ...
)
```

**Arguments**

genoprobs	Genotype probabilities as calculated by <a href="#">calc_genoprob()</a> .
pheno	A numeric matrix of phenotypes, individuals x phenotypes.
kinship	Optional kinship matrix, or a list of kinship matrices (one per chromosome), in order to use the LOCO (leave one chromosome out) method.
addcovar	An optional numeric matrix of additive covariates.
Xcovar	An optional numeric matrix with additional additive covariates used for null hypothesis when scanning the X chromosome.
intcovar	An numeric optional matrix of interactive covariates.
weights	An optional numeric vector of positive weights for the individuals. As with the other inputs, it must have names for individual identifiers.
reml	If kinship provided: if reml=TRUE, use REML; otherwise maximum likelihood.
model	Indicates whether to use a normal model (least squares) or binary model (logistic regression) for the phenotype. If model="binary", the phenotypes must have values in [0, 1].
hsq	Considered only if kinship is provided, in which case this is taken as the assumed value for the residual heritability. It should be a vector with length corresponding to the number of columns in pheno, or (if kinship corresponds to a list of LOCO kinship matrices) a matrix with dimension length(kinship) x ncol(pheno).
by_chr	If TRUE, save the individual chromosome maxima.
cores	Number of CPU cores to use, for parallel calculations. (If 0, use <a href="#">parallel::detectCores()</a> .) Alternatively, this can be links to a set of cluster sockets, as produced by <a href="#">parallel::makeCluster()</a> .
...	Additional control parameters; see Details.

**Details**

Equivalent to running `scan1()` and then saving the column maxima, with some savings in memory usage.

**Value**

Either a vector of genome-wide maximum LOD scores, or if `by_chr` is `TRUE`, a matrix with the chromosome-specific maxima, with the rows being the chromosomes and the columns being the phenotypes.

**See Also**

[scan1\(\)](#), [scan1perm\(\)](#)

**Examples**

```
# 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 <- scan1max(probs, pheno, addcovar=covar, Xcovar=Xcovar)
```

---

scan1perm

---

*Permutation test for genome scan with a single-QTL model*


---

**Description**

Permutation test for a genome scan with a single-QTL model by Haley-Knott regression or a linear mixed model, with possible allowance for covariates.

**Usage**

```
scan1perm(
  genoprobs,
  pheno,
  kinship = NULL,
  addcovar = NULL,
  Xcovar = NULL,
  intcovar = NULL,
```

```

weights = NULL,
reml = TRUE,
model = c("normal", "binary"),
n_perm = 1,
perm_Xsp = FALSE,
perm_strata = NULL,
chr_lengths = NULL,
cores = 1,
...
)

```

## Arguments

genoprobs	Genotype probabilities as calculated by <a href="#">calc_genoprob()</a> .
pheno	A numeric matrix of phenotypes, individuals x phenotypes.
kinship	Optional kinship matrix, or a list of kinship matrices (one per chromosome), in order to use the LOCO (leave one chromosome out) method.
addcovar	An optional numeric matrix of additive covariates.
Xcovar	An optional numeric matrix with additional additive covariates used for null hypothesis when scanning the X chromosome.
intcovar	An optional numeric matrix of interactive covariates.
weights	An optional numeric vector of positive weights for the individuals. As with the other inputs, it must have names for individual identifiers.
reml	If kinship provided: if reml=TRUE, use REML; otherwise maximum likelihood.
model	Indicates whether to use a normal model (least squares) or binary model (logistic regression) for the phenotype. If model="binary", the phenotypes must have values in [0, 1].
n_perm	Number of permutation replicates.
perm_Xsp	If TRUE, do separate permutations for the autosomes and the X chromosome.
perm_strata	Vector of strata, for a stratified permutation test. Should be named in the same way as the rows of pheno. The unique values define the strata.
chr_lengths	Lengths of the chromosomes; needed only if perm_Xsp=TRUE. See <a href="#">chr_lengths()</a> .
cores	Number of CPU cores to use, for parallel calculations. (If 0, use <a href="#">parallel::detectCores()</a> .) Alternatively, this can be links to a set of cluster sockets, as produced by <a href="#">parallel::makeCluster()</a> .
...	Additional control parameters; see Details.

## Details

If kinship is not provided, so that analysis proceeds by Haley-Knott regression, we permute the rows of the phenotype data; the same permutations are also applied to the rows of the covariates (addcovar, Xcovar, and intcovar) are permuted.

If kinship is provided, we instead permute the rows of the genotype data and fit an LMM with the same residual heritability (estimated under the null hypothesis of no QTL).

If Xcovar is provided and perm\_strata=NULL, we do a stratified permutation test with the strata defined by the rows of Xcovar. If a simple permutation test is desired, provide perm\_strata that is a vector containing a single repeated value.

The ... argument can contain several additional control parameters; suspended for simplicity (or confusion, depending on your point of view). tol is used as a tolerance value for linear regression by QR decomposition (in determining whether columns are linearly dependent on others and should be omitted); default 1e-12. maxit is the maximum number of iterations for convergence of the iterative algorithm used when model=binary. bintol is used as a tolerance for convergence for the iterative algorithm used when model=binary. eta\_max is the maximum value for the "linear predictor" in the case model="binary" (a bit of a technicality to avoid fitted values exactly at 0 or 1).

### Value

If perm\_Xsp=FALSE, the result is matrix of genome-wide maximum LOD scores, permutation replicates x phenotypes. If perm\_Xsp=TRUE, the result is a list of two matrices, one for the autosomes and one for the X chromosome. The object is given class "scan1perm".

### References

- Churchill GA, Doerge RW (1994) Empirical threshold values for quantitative trait mapping. *Genetics* 138:963–971.
- Manichaikul A, Palmer AA, Sen S, Broman KW (2007) Significance thresholds for quantitative trait locus mapping under selective genotyping. *Genetics* 177:1963–1966.
- Haley CS, Knott SA (1992) A simple regression method for mapping quantitative trait loci in line crosses using flanking markers. *Heredity* 69:315–324.
- Kang HM, Zaitlen NA, Wade CM, Kirby A, Heckerman D, Daly MJ, Eskin E (2008) Efficient control of population structure in model organism association mapping. *Genetics* 178:1709–1723.

### See Also

[scan1\(\)](#), [chr\\_lengths\(\)](#), [mat2strata\(\)](#)

### Examples

```
# 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)

# strata for permutations
perm_strata <- mat2strata(Xcovar)

# permutations with genome scan (just 3 replicates, for illustration)
operm <- scan1perm(probs, pheno, addcovar=covar, Xcovar=Xcovar,
                  n_perm=3, perm_strata=perm_strata)
summary(operm)

# leave-one-chromosome-out kinship matrices
kinship <- calc_kinship(probs, "loco")

# permutations of genome scan with a linear mixed model
operm_lmm <- scan1perm(probs, pheno, kinship, covar, Xcovar, n_perm=3,
                      perm_Xsp=TRUE, perm_strata=perm_strata,
                      chr_lengths=chr_lengths(map))
summary(operm_lmm)

```

---

scan1snps

---

*Single-QTL genome scan at imputed SNPs*


---

## Description

Perform a single-QTL scan across the genome or a defined region at SNPs genotyped in the founders, by Haley-Knott regression or a linear mixed model, with possible allowance for covariates.

## Usage

```

scan1snps(
  genoprobs,
  map,
  pheno,
  kinship = NULL,
  addcovar = NULL,
  Xcovar = NULL,
  intcovar = NULL,
  weights = NULL,
  reml = TRUE,
  model = c("normal", "binary"),
  query_func = NULL,
  chr = NULL,
  start = NULL,
  end = NULL,
  snpinfo = NULL,
  batch_length = 20,

```

```

    keep_all_snps = FALSE,
    cores = 1,
    ...
)

```

## Arguments

genoprobs	Genotype probabilities as calculated by <a href="#">calc_genoprob()</a> .
map	Physical map for the positions in the genoprobs object: A list of numeric vectors; each vector gives marker positions for a single chromosome.
pheno	A numeric matrix of phenotypes, individuals x phenotypes.
kinship	Optional kinship matrix, or a list of kinship matrices (one per chromosome), in order to use the LOCO (leave one chromosome out) method.
addcovar	An optional numeric matrix of additive covariates.
Xcovar	An optional numeric matrix with additional additive covariates used for null hypothesis when scanning the X chromosome.
intcovar	An optional numeric matrix of interactive covariates.
weights	An optional numeric vector of positive weights for the individuals. As with the other inputs, it must have names for individual identifiers.
reml	If kinship provided: if reml=TRUE, use REML; otherwise maximum likelihood.
model	Indicates whether to use a normal model (least squares) or binary model (logistic regression) for the phenotype. If model="binary", the phenotypes must have values in $[0, 1]$ .
query_func	Function for querying SNP information; see <a href="#">create_variant_query_func()</a> . Takes arguments chr, start, end, (with start and end in the units in map, generally Mbp), and returns a data frame containing the columns snp, chr, pos, and sdp. (See snpinfo below.)
chr	Chromosome or chromosomes to scan
start	Position defining the start of an interval to scan. Should be a single number, and if provided, chr should also have length 1.
end	Position defining the end of an interval to scan. Should be a single number, and if provided, chr should also have length 1.
snpinfo	Optional data frame of SNPs to scan; if provided, query_func, chr, start, and end are ignored. Should contain the following columns: <ul style="list-style-type: none"> <li>• chr - Character string or factor with chromosome</li> <li>• pos - Position (in same units as in the "map").</li> <li>• sdp - Strain distribution pattern: an integer, between 1 and <math>2^n - 2</math> where <math>n</math> is the number of strains, whose binary encoding indicates the founder genotypes</li> <li>• snp - Character string with SNP identifier (if missing, the rownames are used).</li> </ul>
batch_length	Interval length (in units of map, generally Mbp) to scan at one time.

keep_all_snps	SNPs are grouped into equivalence classes based on position and founder genotypes; if keep_all_snps=FALSE, the return value will contain information only on the indexed SNPs (one per equivalence class).
cores	Number of CPU cores to use, for parallel calculations. (If 0, use <code>parallel::detectCores()</code> .) Alternatively, this can be links to a set of cluster sockets, as produced by <code>parallel::makeCluster()</code> .
...	Additional control parameters passed to <code>scan1()</code>

## Details

The analysis proceeds as follows:

- Call `query_func()` to grab all SNPs over a region.
- Use `index_snps()` to group SNPs into equivalence classes.
- Use `genoprob_to_snpprob()` to convert genoprobs to SNP probabilities.
- Use `scan1()` to do a single-QTL scan at the SNPs.

## Value

A list with two components: `lod` (matrix of LOD scores) and `snpinfo` (a data frame of SNPs that were scanned, including columns `index` which indicates groups of equivalent SNPs)

## See Also

`scan1()`, `genoprob_to_snpprob()`, `index_snps()`, `create_variant_query_func()`, `plot_snpasso()`

## Examples

```
## Not run:
# load example data and calculate genotype probabilities
file <- paste0("https://raw.githubusercontent.com/rqtl/",
               "qt12data/main/D0ex/D0ex.zip")
D0ex <- read_cross2(file)
probs <- calc_genoprob(D0ex, error_prob=0.002)

snpdb_file <- system.file("extdata", "cc_variants_small.sqlite", package="qt12")
queryf <- create_variant_query_func(snpdb_file)

out <- scan1snps(probs, D0ex$pmap, D0ex$pheno, query_func=queryf, chr=2, start=97, end=98)

## End(Not run)
```



---

sdp2char	<i>Convert strain distribution patterns to character strings</i>
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---

### Description

Convert a vector of numeric codes for strain distribution patterns to character strings.

### Usage

```
sdp2char(sdp, n_strains = NULL, strains = NULL)
```

### Arguments

sdp	Vector of strain distribution patterns (integers between 1 and $2^n - 2$ where $n$ is the number of strains).
n_strains	Number of founder strains (if missing but strains is provided, we use the length of strains)
strains	Vector of single-letter codes for the strains

### Value

Vector of character strings with the two groups of alleles separated by a vertical bar (|).

### See Also

[invert\\_sdp\(\)](#), [calc\\_sdp\(\)](#)

### Examples

```
sdp <- c(m1=1, m2=12, m3=240)
sdp2char(sdp, 8)
sdp2char(sdp, strains=c("A", "B", "I", "D", "Z", "C", "P", "W"))
```

---

sim_geno	<i>Simulate genotypes given observed marker data</i>
----------	--

---

### Description

Uses a hidden Markov model to simulate from the joint distribution  $\Pr(g | O)$  where  $g$  is the underlying sequence of true genotypes and  $O$  is the observed multipoint marker data, with possible allowance for genotyping errors.

**Usage**

```
sim_geno(
  cross,
  map = NULL,
  n_draws = 1,
  error_prob = 0.0001,
  map_function = c("haldane", "kosambi", "c-f", "morgan"),
  lowmem = FALSE,
  quiet = TRUE,
  cores = 1
)
```

**Arguments**

cross	Object of class "cross2". For details, see the <a href="#">R/qt12 developer guide</a> .
map	Genetic map of markers. May include pseudomarker locations (that is, locations that are not within the marker genotype data). If NULL, the genetic map in cross is used.
n_draws	Number of simulations to perform.
error_prob	Assumed genotyping error probability
map_function	Character string indicating the map function to use to convert genetic distances to recombination fractions.
lowmem	If FALSE, split individuals into groups with common sex and crossinfo and then precalculate the transition matrices for a chromosome; potentially a lot faster but using more memory.
quiet	If FALSE, print progress messages.
cores	Number of CPU cores to use, for parallel calculations. (If 0, use <a href="#">parallel::detectCores()</a> .) Alternatively, this can be links to a set of cluster sockets, as produced by <a href="#">parallel::makeCluster()</a> .

**Details**

After performing the backward equations, we draw from  $Pr(g_1 = v|O)$  and then  $Pr(g_{k+1} = v|O, g_k = u)$ .

**Value**

An object of class "sim\_geno": a list of three-dimensional arrays of imputed genotypes, individuals x positions x draws. Also contains three attributes:

- crosstype - The cross type of the input cross.
- is\_x\_chr - Logical vector indicating whether chromosomes are to be treated as the X chromosome or not, from input cross.
- alleles - Vector of allele codes, from input cross.

**See Also**

[cbind.sim\\_geno\(\)](#), [rbind.sim\\_geno\(\)](#)

Examples

```
grav2 <- read_cross2(system.file("extdata", "grav2.zip", package="qt12"))
map_w_pmar <- insert_pseudomarkers(grav2$gmap, step=1)
draws <- sim_geno(grav2, map_w_pmar, n_draws=4, error_prob=0.002)
```

---

smooth_gmap	<i>Smooth genetic map</i>
-------------	---------------------------

---

Description

Smooth a genetic map by mixing it with a bit of constant recombination (using a separate recombination rate for each chromosome), to eliminate intervals that have exactly 0 recombination.

Usage

```
smooth_gmap(gmap, pmap, alpha = 0.02)
```

Arguments

gmap	Genetic map, as a list of numeric vectors; each vector gives marker positions for a single chromosome.
pmap	Physical map, as a list of numeric vectors; each vector gives marker positions for a single chromosome, with the same chromosomes and markers as gmap.
alpha	Proportion of mixture to take from constant recombination.

Details

An interval of genetic length  $d_g$  and physical length  $d_p$  is changed to have length  $(1 - \alpha)d_g + \alpha d_p r$  where  $r = L_g/L_p$  is the chromosome-specific recombination rate.

Value

A genetic map like the input gmap, but smoothed by mixing it with a proportion alpha of constant recombination on each chromosome.

See Also

```
unsmooth\_gmap\(\)
```

Examples

```
iron <- read_cross2(system.file("extdata", "iron.zip", package="qt12"))
gmap_adj <- smooth_gmap(iron$gmap, iron$pmap)
```

---

subset.calc\_genoprob    *Subsetting genotype probabilities*


---

## Description

Pull out a specified set of individuals and/or chromosomes from the results of `calc_genoprob()`.

## Usage

```
## S3 method for class 'calc_genoprob'
subset(x, ind = NULL, chr = NULL, ...)

## S3 method for class 'calc_genoprob'
x[ind = NULL, chr = NULL]
```

## Arguments

<code>x</code>	Genotype probabilities as output from <code>calc_genoprob()</code> .
<code>ind</code>	A vector of individuals: numeric indices, logical values, or character string IDs
<code>chr</code>	A vector of chromosomes: logical values, or character string IDs. Numbers are interpreted as character string IDs.
<code>...</code>	Ignored.

## Value

An object of class "calc\_genoprob", like the input, with the selected individuals and/or chromosomes; see `calc_genoprob()`.

## Examples

```
grav2 <- read_cross2(system.file("extdata", "grav2.zip", package="qt12"))

pr <- calc_genoprob(grav2)
# keep just individuals 1:5, chromosome 2
prsub <- pr[1:5,2]
# keep just chromosome 2
prsub2 <- pr[,2]
```

---

subset.cross2*Subsetting data for a QTL experiment*

---

### Description

Pull out a specified set of individuals and/or chromosomes from a `cross2` object.

### Usage

```
## S3 method for class 'cross2'
subset(x, ind = NULL, chr = NULL, ...)

## S3 method for class 'cross2'
x[ind = NULL, chr = NULL]
```

### Arguments

<code>x</code>	An object of class "cross2", as output by <code>read_cross2()</code> . For details, see the <a href="#">R/qtl2 developer guide</a> .
<code>ind</code>	A vector of individuals: numeric indices, logical values, or character string IDs.
<code>chr</code>	A vector of chromosomes: numeric indices, logical values, or character string IDs
<code>...</code>	Ignored.

### Details

When subsetting by individual, if `ind` is numeric, they're assumed to be numeric indices; if character strings, they're assumed to be individual IDs. `ind` can be numeric or logical only if the genotype, phenotype, and covariate data all have the same individuals in the same order.

When subsetting by chromosome, `chr` is *always* converted to character strings and treated as chromosome IDs. So if there are three chromosomes with IDs "18", "19", and "X", `mycross[, 18]` will give the first of the chromosomes (labeled "18") and `mycross[, 3]` will give an error.

When using character string IDs for `ind` or `chr`, you can use "negative" subscripts to indicate exclusions, for example `mycross[, c("-18", "-X")]` or `mycross["-Mouse2501", ]`. But you can't mix "positive" and "negative" subscripts, and if any of the individuals has an ID that begins with "-", you can't use negative subscripts like this.

### Value

The input `cross2` object, with the selected individuals and/or chromosomes.

### Warning

The order of the two arguments is reversed relative to the related function in [R/qtl](#).

**Examples**

```
grav2 <- read_cross2(system.file("extdata", "grav2.zip", package="qt12"))
# keep individuals 1-20 and chromosomes 3 and 4
grav2sub <- grav2[1:20, c(3,4)]
# keep just chromosome 1
grav2_c1 <- grav2[,1]
```

subset.sim\_geno

*Subsetting imputed genotypes***Description**

Pull out a specified set of individuals and/or chromosomes from the results of [sim\\_geno\(\)](#).

**Usage**

```
## S3 method for class 'sim_geno'
subset(x, ind = NULL, chr = NULL, ...)

## S3 method for class 'sim_geno'
x[ind = NULL, chr = NULL]
```

**Arguments**

x	Imputed genotypes as output from <a href="#">sim_geno()</a> .
ind	A vector of individuals: numeric indices, logical values, or character string IDs
chr	A vector of chromosomes: logical values, or character string IDs. Numbers are interpreted as character string IDs.
...	Ignored.

**Value**

An object of class "sim\_geno", like the input with the selected individuals and/or chromosomes; see [sim\\_geno\(\)](#).

**Examples**

```
grav2 <- read_cross2(system.file("extdata", "grav2.zip", package="qt12"))

dr <- sim_geno(grav2, n_draws=4)
# keep just individuals 1:5, chromosome 2
drsub <- dr[1:5,2]
# keep just chromosome 2
drsub2 <- dr[,2]
```

---

subset.viterbi	<i>Subsetting Viterbi results</i>
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## Description

Pull out a specified set of individuals and/or chromosomes from the results of `viterbi()`

## Usage

```
## S3 method for class 'viterbi'
subset(x, ind = NULL, chr = NULL, ...)

## S3 method for class 'viterbi'
x[ind = NULL, chr = NULL]
```

## Arguments

<code>x</code>	Imputed genotypes as output from <code>viterbi()</code> .
<code>ind</code>	A vector of individuals: numeric indices, logical values, or character string IDs
<code>chr</code>	A vector of chromosomes: logical values, or character string IDs. Numbers are interpreted as character string IDs.
<code>...</code>	Ignored.

## Value

An object of class "viterbi", like the input, with the selected individuals and/or chromosomes; see `viterbi()`.

## Examples

```
grav2 <- read_cross2(system.file("extdata", "grav2.zip", package="qt12"))

g <- viterbi(grav2)
# keep just individuals 1:5, chromosome 2
gsub <- g[1:5,2]
# keep just chromosome 2
gsub2 <- g[,2]
```

---

subset_scan1	<i>Subset scan1 output</i>
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## Description

Subset the output of [scan1\(\)](#) by chromosome or column

## Usage

```
subset_scan1(x, map = NULL, chr = NULL, lodcolumn = NULL, ...)
```

```
## S3 method for class 'scan1'
```

```
subset(x, map = NULL, chr = NULL, lodcolumn = NULL, ...)
```

## Arguments

x	An object of class "scan1" as returned by <a href="#">scan1()</a> .
map	A list of vectors of marker positions, as produced by <a href="#">insert_pseudomarkers()</a> .
chr	Vector of chromosomes.
lodcolumn	Vector of integers or character strings indicating the LOD score columns, either as a numeric indexes or column names.
...	Ignored

## Value

Object of class "scan1", like the input, but subset by chromosome and/or column. See [scan1\(\)](#).

## Examples

```
# 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)

# pull out chromosome 8
```



```
out_c8 <- subset(out, map, chr="8")

# just the second column on chromosome 2
out_c2_spleen <- subset(out, map, "2", "spleen")

# all positions, but just the "liver" column
out_spleen <- subset(out, map, lodcolumn="spleen")
```

---

summary.cross2	<i>Summary of cross2 object</i>
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---

**Description**

Summarize a cross2 object

**Usage**

```
## S3 method for class 'cross2'
summary(object, ...)
```

**Arguments**

- object      An object of class "cross2", as output by [read\\_cross2\(\)](#). For details, see the [R/qt12 developer guide](#).
- ...      Ignored.

**Value**

None.

**See Also**

[basic\\_summaries](#)

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summary_compare_genotype	<i>Basic summary of compare_genotype object</i>
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**Description**

From results of [compare\\_genotype\(\)](#), show pairs of individuals with similar genotypes.

Usage

```
summary_compare_geno(object, threshold = 0.9, ...)

## S3 method for class 'compare_geno'
summary(object, threshold = 0.9, ...)

## S3 method for class 'summary.compare_geno'
print(x, digits = 2, ...)
```

Arguments

object	A square matrix with genotype comparisons for pairs of individuals, as output by <code>compare_geno()</code> .
threshold	Minimum proportion matches for a pair of individuals to be shown.
...	Ignored
x	Results of <code>summary.compare_geno()</code>
digits	Number of digits to print

Value

Data frame with names of individuals in pair, proportion matches, number of mismatches, number of matches, and total markers genotyped. Last two columns are the numeric indexes of the individuals in the pair.

Examples

```
grav2 <- read_cross2(system.file("extdata", "grav2.zip", package="qt12"))
cg <- compare_geno(grav2)
summary(cg)
```

---

summary_scan1perm	<i>Summarize scan1perm results</i>
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---

Description

Summarize permutation test results from `scan1perm()`, as significance thresholds.

Usage

```
summary_scan1perm(object, alpha = 0.05)

## S3 method for class 'scan1perm'
summary(object, alpha = 0.05, ...)
```

**Arguments**

object	An object of class "scanoneperm", as output by <code>scan1perm()</code>
alpha	Vector of significance levels
...	Ignored

**Details**

In the case of X-chromosome-specific permutations (when `scan1perm()` was run with `perm_Xsp=TRUE`, we follow the approach of Broman et al. (2006) to get separate thresholds for the autosomes and X chromosome, using

Let  $L_A$  and  $L_X$  be total the genetic lengths of the autosomes and X chromosome, respectively, and let  $L_T = L_A + L_X$ . Then in place of  $\alpha$ , we use

$$\alpha_A = 1 - (1 - \alpha)^{L_A/L_T}$$

as the significance level for the autosomes and

$$\alpha_X = 1 - (1 - \alpha)^{L_X/L_T}$$

as the significance level for the X chromosome.

**Value**

An object of class `summary.scan1perm`. If `scan1perm()` was run with `perm_Xsp=FALSE`, this is a single matrix of significance thresholds, with rows being significance levels and columns being the columns in the input. If `scan1perm()` was run with `perm_Xsp=TRUE`, this is a list of two matrices, with the significance thresholds for the autosomes and X chromosome, respectively.

The result has an attribute "n\_perm" that has the numbers of permutation replicates (either a matrix or a list of two matrices).

**References**

Broman KW, Sen Ś, Owens SE, Manichaikul A, Southard-Smith EM, Churchill GA (2006) The X chromosome in quantitative trait locus mapping. *Genetics* 174:2151-2158

**Examples**

```
# 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)

# permutations with genome scan (just 3 replicates, for illustration)
operm <- scan1perm(probs, pheno, addcovar=covar, Xcovar=Xcovar,
                  n_perm=3)

summary(operm, alpha=c(0.20, 0.05))

```

---

top\_snps

---

*Create table of top snp associations*


---

## Description

Create a table of the top snp associations

## Usage

```

top_snps(
  scan1_output,
  snpinfo,
  lodcolumn = 1,
  chr = NULL,
  drop = 1.5,
  show_all_snps = TRUE
)

```

## Arguments

- |              |   |
|--------------|---|
| scan1_output | Output of <a href="#">scan1()</a> . Should contain a component "snpinfo", as when <a href="#">scan1()</a> is run with SNP probabilities produced by <a href="#">genoprob_to_snpprob()</a> .   |
| snpinfo      | <p>Data frame with SNP information with the following columns (the last three are generally derived with <a href="#">index_snps()</a>):</p> <ul style="list-style-type: none"> <li>• chr - Character string or factor with chromosome</li> <li>• pos - Position (in same units as in the "map" attribute in genoprobs.</li> <li>• sdp - Strain distribution pattern: an integer, between 1 and <math>2^n - 2</math> where <math>n</math> is the number of strains, whose binary encoding indicates the founder genotypes</li> <li>• snp - Character string with SNP identifier (if missing, the rownames are used).</li> <li>• index - Indices that indicate equivalent groups of SNPs, calculated by <a href="#">index_snps()</a>.</li> <li>• intervals - Indexes that indicate which marker intervals the SNPs reside.</li> <li>• on_map - Indicate whether SNP coincides with a marker in the genoprobs</li> </ul> |

lodcolumn	Selected LOD score column to (a numeric index, or a character string for a column name). Only one value allowed.
chr	Selected chromosome; only one value allowed.
drop	Show all SNPs with LOD score within this amount of the maximum SNP association.
show_all_snps	If TRUE, expand to show all SNPs.

### Value

Data frame like the input `snpinfo` with just the selected subset of rows, and with an added column with the LOD score.

### See Also

[index\\_snps\(\)](#), [genoprob\\_to\\_snpprob\(\)](#), [scan1snps\(\)](#), [plot\\_snpasso\(\)](#)

### Examples

```
## Not run:
# load example D0 data from web
file <- paste0("https://raw.githubusercontent.com/rqt1/",
               "qt12data/main/D0ex/D0ex.zip")
D0ex <- read_cross2(file)

# subset to chr 2
D0ex <- D0ex[, "2"]

# calculate genotype probabilities and convert to allele probabilities
pr <- calc_genoprob(D0ex, error_prob=0.002)
apr <- genoprob_to_alleleprob(pr)

# query function for grabbing info about variants in region
dbfile <- system.file("extdata", "cc_variants_small.sqlite", package="qt12")
query_variants <- create_variant_query_func(dbfile)

# SNP association scan, keep information on all SNPs
out_snps <- scan1snps(apr, D0ex$pmap, D0ex$pheno, query_func=query_variants,
                     chr=2, start=97, end=98, keep_all_snps=TRUE)

# table with top SNPs
top_snps(out_snps$lod, out_snps$snpinfo)

# top SNPs among the distinct subset at which calculations were performed
top_snps(out_snps$lod, out_snps$snpinfo, show_all_snps=FALSE)

# top SNPs within 0.5 LOD of max
top_snps(out_snps$lod, out_snps$snpinfo, drop=0.5)

## End(Not run)
```

---

unsmooth_gmap	<i>Unsmooth genetic map</i>
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---

### Description

Performs the reverse operation of `smooth_gmap()`, in case one wants to go back to the original genetic map.

### Usage

```
unsmooth_gmap(gmap, pmap, alpha = 0.02)
```

### Arguments

<code>gmap</code>	Genetic map, as a list of numeric vectors; each vector gives marker positions for a single chromosome.
<code>pmap</code>	Physical map, as a list of numeric vectors; each vector gives marker positions for a single chromosome, with the same chromosomes and markers as <code>gmap</code> .
<code>alpha</code>	Proportion of mixture to take from constant recombination.

### Details

An interval of genetic length  $d_g$  and physical length  $d_p$  is changed to have length  $(d_g - \alpha d_p r)/(1 - \alpha)$  where  $r = L_g/L_p$  is the chromosome-specific recombination rate.

### Value

A genetic map like the input `gmap`, but with the reverse operation of `smooth_gmap()` applied, provided that exactly the same physical map and `alpha` are used.

### See Also

[smooth\\_gmap\(\)](#)

### Examples

```
iron <- read_cross2(system.file("extdata", "iron.zip", package="qtl2"))
gmap_adj <- smooth_gmap(iron$gmap, iron$pmap)
gmap_back <- unsmooth_gmap(gmap_adj, iron$pmap)
```

---

viterbi	<i>Calculate most probable sequence of genotypes</i>
---------	--

---

## Description

Uses a hidden Markov model to calculate  $\arg \max \Pr(g \mid O)$  where  $g$  is the underlying sequence of true genotypes and  $O$  is the observed multipoint marker data, with possible allowance for genotyping errors.

## Usage

```
viterbi(
  cross,
  map = NULL,
  error_prob = 0.0001,
  map_function = c("haldane", "kosambi", "c-f", "morgan"),
  lowmem = FALSE,
  quiet = TRUE,
  cores = 1
)
```

## Arguments

cross	Object of class "cross2". For details, see the <a href="#">R/qt12 developer guide</a> .
map	Genetic map of markers. May include pseudomarker locations (that is, locations that are not within the marker genotype data). If NULL, the genetic map in cross is used.
error_prob	Assumed genotyping error probability
map_function	Character string indicating the map function to use to convert genetic distances to recombination fractions.
lowmem	If FALSE, split individuals into groups with common sex and crossinfo and then precalculate the transition matrices for a chromosome; potentially a lot faster but using more memory.
quiet	If FALSE, print progress messages.
cores	Number of CPU cores to use, for parallel calculations. (If 0, use <a href="#">parallel::detectCores()</a> .) Alternatively, this can be links to a set of cluster sockets, as produced by <a href="#">parallel::makeCluster()</a> .

## Details

We use a hidden Markov model to find, for each individual on each chromosome, the most probable sequence of underlying genotypes given the observed marker data.

Note that we break ties at random, and our method for doing this may introduce some bias.

Consider the results with caution; the most probable sequence can have very low probability, and can have features that are quite unusual (for example, the number of recombination events can be too small). In most cases, the results of a single imputation with [sim\\_geno\(\)](#) will be more realistic.

**Value**

An object of class "viterbi": a list of two-dimensional arrays of imputed genotypes, individuals x positions. Also contains three attributes:

- crosstype - The cross type of the input cross.
- is\_x\_chr - Logical vector indicating whether chromosomes are to be treated as the X chromosome or not, from input cross.
- alleles - Vector of allele codes, from input cross.

**See Also**

`sim_geno()`, `maxmarg()`, `cbind.viterbi()`, `rbind.viterbi()`

**Examples**

```
grav2 <- read_cross2(system.file("extdata", "grav2.zip", package="qtl2"))
map_w_pmar <- insert_pseudomarkers(grav2$gmap, step=1)
g <- viterbi(grav2, map_w_pmar, error_prob=0.002)
```

---

write_control_file	<i>Write a control file for QTL data</i>
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---

**Description**

Write the control file (in **YAML** or **JSON**) needed by `read_cross2()` for a set of QTL data.

**Usage**

```
write_control_file(
  output_file,
  crosstype = NULL,
  geno_file = NULL,
  founder_geno_file = NULL,
  gmap_file = NULL,
  pmap_file = NULL,
  pheno_file = NULL,
  covar_file = NULL,
  phenocovar_file = NULL,
  sex_file = NULL,
  sex_covar = NULL,
  sex_codes = NULL,
  crossinfo_file = NULL,
  crossinfo_covar = NULL,
  crossinfo_codes = NULL,
  geno_codes = NULL,
  alleles = NULL,
  xchr = NULL,
```



```

sep = ",",
na.strings = c("-", "NA"),
comment.char = "#",
geno_transposed = FALSE,
founder_geno_transposed = FALSE,
pheno_transposed = FALSE,
covar_transposed = FALSE,
phenocovar_transposed = FALSE,
description = NULL,
comments = NULL,
overwrite = FALSE
)

```

### Arguments

output_file	File name (with path) of the <b>YAML</b> or <b>JSON</b> file to be created, as a character string. If extension is .json, JSON format is used; otherwise, YAML is used.
crosstype	Character string with the cross type.
geno_file	File name for genotype data.
founder_geno_file	File name for the founder genotype data.
gmap_file	File name for genetic map.
pmap_file	File name for the physical map.
pheno_file	File name for the phenotype data.
covar_file	File name for the covariate data.
phenocovar_file	File name for the phenotype covariate data (i.e., metadata about the phenotypes).
sex_file	File name for the individuals' sex. (Specify just one of sex_file or sex_covar.)
sex_covar	Column name in the covariate data that corresponds to sex. (Specify just one of sex_file or sex_covar.)
sex_codes	Named vector of character strings specifying the encoding of sex. The names attribute should be the codes used in the data files; the values within the vector should be "female" and "male".
crossinfo_file	File name for the cross_info data. (Specify just one of crossinfo_file or crossinfo_covar.)
crossinfo_covar	Column name in the covariate data that corresponds to the cross_info data. (Specify just one of crossinfo_file or crossinfo_covar.)
crossinfo_codes	In the case that there is a single cross info column (whether in a file or as a covariate), you can provide a named vector of character strings specifying the encoding of cross_info. The names attribute should be the codes used; the values within the vector should be the codes to which they will be converted (for example, 0 and 1 for an intercross).

geno_codes	Named vector specifying the encoding of genotypes. The names attribute has the codes used within the genotype and founder genotype data files; the values within the vector should be the integers to which the genotypes will be converted.
alleles	Vector of single-character codes for the founder alleles.
xchr	Character string with the ID for the X chromosome.
sep	Character string that separates columns in the data files.
na.strings	Vector of character strings with codes to be treated as missing values.
comment.char	Character string that is used as initial character in a set of leading comment lines in the data files.
geno_transposed	If TRUE, genotype file is transposed (with markers as rows).
founder_geno_transposed	If TRUE, founder genotype file is transposed (with markers as rows).
pheno_transposed	If TRUE, phenotype file is transposed (with phenotypes as rows).
covar_transposed	If TRUE, covariate file is transposed (with covariates as rows).
phenocovar_transposed	If TRUE, phenotype covariate file is transposed (with phenotype covariates as rows).
description	Optional character string describing the data.
comments	Vector of character strings to be inserted as comments at the top of the file (in the case of YAML), with each string as a line. For JSON, the comments are instead included within the control object.
overwrite	If TRUE, overwrite file if it exists. If FALSE (the default) and the file exists, stop with an error.

## Details

This function takes a set of parameters and creates the control file (in **YAML** or **JSON** format) needed for the new input data file format for **R/qt12**. See the [sample data files](#) and the [vignette describing the input file format](#).

## Value

(Invisibly) The data structure that was written.

## See Also

[read\\_cross2\(\)](#), sample data files at [https://kbroman.org/qt12/pages/sampledata.html](https://kbroman.org/qt12/pages/sampleddata.html)

## Examples

```
# Control file for the sample dataset, grav2
grav2_control_file <- file.path(tempdir(), "grav2.yaml")
write_control_file(grav2_control_file,
  crosstype="riself",
  geno_file="grav2_geno.csv",
  gmap_file="grav2_gmap.csv",
  pheno_file="grav2_pheno.csv",
  phenocovar_file="grav2_phenocovar.csv",
  geno_codes=c(L=1L, C=2L),
  alleles=c("L", "C"),
  na.strings=c("-", "NA"))

# Control file for the sample dataset, iron
iron_control_file <- file.path(tempdir(), "iron.yaml")
write_control_file(iron_control_file,
  crosstype="f2",
  geno_file="iron_geno.csv",
  gmap_file="iron_gmap.csv",
  pheno_file="iron_pheno.csv",
  covar_file="iron_covar.csv",
  phenocovar_file="iron_phenocovar.csv",
  geno_codes=c(SS=1L, SB=2L, BB=3L),
  sex_covar="sex",
  sex_codes=c(f="female", m="male"),
  crossinfo_covar="cross_direction",
  crossinfo_codes=c("(SxB)x(SxB)"=0L, "(BxS)x(BxS)"=1L),
  xchr="X",
  alleles=c("S", "B"),
  na.strings=c("-", "NA"))

# Remove these files, to clean up temporary directory
unlink(c(grav2_control_file, iron_control_file))
```

---

xpos\_scan1

*Get x-axis position for genomic location*


---

## Description

For a plot of `scan1()` results, get the x-axis location that corresponds to a particular genomic location (chromosome ID and position).

## Usage

```
xpos_scan1(map, chr = NULL, gap = NULL, thechr, thepos)
```

## Arguments

`map` A list of vectors of marker positions, as produced by `insert_pseudomarkers()`.

chr	Selected chromosomes that were plotted (if used in the call to <code>plot_scan1()</code> ).
gap	The gap between chromosomes used in the call to <code>plot_scan1()</code> .
thechr	Vector of chromosome IDs
thepos	Vector of chromosomal positions

### Details

thechr and thepos should be the same length, or should have length 1 (in which case they are expanded to the length of the other vector).

### Value

A vector of x-axis locations.

### Examples

```
# 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
ylim <- c(0, maxlod(out)*1.02) # need to strip class to get overall max LOD
chr <- c(2,7,8,9,15,16)
plot(out, map, chr=chr, ylim=ylim)
plot(out, map, lodcolumn=2, chr=chr, col="violetred", add=TRUE)
legend("topleft", lwd=2, col=c("darkslateblue", "violetred"), colnames(out),
      bg="gray90")

# Use xpos_scan1 to add points at the peaks
# first find the peaks with LOD > 3
peaks <- find_peaks(out, map)

# keep just the peaks for chromosomes that were plotted
peaks <- peaks[peaks$chr %in% chr,]

# find x-axis positions
xpos <- xpos_scan1(map, chr=chr, thechr=peaks$chr, thepos=peaks$pos)
```

```
# point colors
ptcolor <- c("darkslateblue", "violetred")[match(peaks$lodcolumn, c("liver", "spleen"))]

# plot points
points(xpos, peaks$lod, pch=21, bg=ptcolor)
```

---

zip_datafiles	<i>Zip a set of data files</i>
---------------	--------------------------------

---

## Description

Zip a set of data files (in format read by [read\\_cross2\(\)](#)).

## Usage

```
zip_datafiles(control_file, zip_file = NULL, overwrite = FALSE, quiet = TRUE)
```

## Arguments

control_file	Character string with path to the control file ( <b>YAML</b> or <b>JSON</b> ) containing all of the control information.
zip_file	Name of zip file to use. If NULL, we use the stem of control_file but with a .zip extension.
overwrite	If TRUE, overwrite file if it exists. If FALSE (the default) and the file exists, stop with an error.
quiet	If FALSE, print progress messages.

## Details

The input control\_file is the control file (in **YAML** or **JSON** format) to be read by [read\\_cross2\(\)](#). (See the [sample data files](#) and the [vignette describing the input file format](#).)

The `utils::zip()` function is used to do the zipping.

The files should all be contained within the directory where the control\_file sits, or in a subdirectory of that directory. If file paths use `..`, these get stripped by zip, and so the resulting zip file may not work with [read\\_cross2\(\)](#).

## Value

Character string with the file name of the zip file that was created.

## See Also

[read\\_cross2\(\)](#), sample data files at [https://kbroman.org/ql2/pages/sampledata.html](https://kbroman.org/ql2/pages/sampleddata.html)

**Examples**

```
## Not run:  
zipfile <- file.path(tempdir(), "grav2.zip")  
zip_datafiles("grav2.yaml", zipfile)  
  
## End(Not run)
```

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