

# Package ‘bigsnpr’

November 7, 2022

**Encoding** UTF-8

**Type** Package

**Title** Analysis of Massive SNP Arrays

**Version** 1.11.6

**Date** 2022-11-07

**Description** Easy-to-use, efficient, flexible and scalable tools for analyzing massive SNP arrays. Privé et al. (2018) <[doi:10.1093/bioinformatics/bty185](https://doi.org/10.1093/bioinformatics/bty185)>.

**License** GPL-3

**LazyData** TRUE

**Language** en-US

**ByteCompile** TRUE

**SystemRequirements** A few functions from package 'bigsnpr' wrap existing software such as 'PLINK' <[www.cog-genomics.org/plink2](http://www.cog-genomics.org/plink2)>. Functions are provided to download these software. Note that these external software might not work for some operating systems (e.g. 'PLINK' might not work on Solaris).

**Depends** R (>= 3.4), bigstatsr (>= 1.5.11)

**Imports** bigassertr (>= 0.1.3), bigparallelr, bigsparser (>= 0.6), bigreadr, bigutilsr (>= 0.3.3), data.table (>= 1.12.4), doRNG, foreach, ggplot2, magrittr, Matrix, methods, Rcpp, runonce (>= 0.2.3), stats, vctrs

**LinkingTo** bigsparser, bigstatsr, Rcpp, RcppArmadillo (>= 0.9.600), rmio, roptim (>= 0.1.6)

**Suggests** bindata, covr, dbplyr (>= 1.4), dplyr, gaston, glue, Hmisc, microbenchmark, pcadapt (>= 4.1), quadprog, RhpcBLASctl, rmutl, RSpectra, RSQLite, R.utils, spelling, testthat, tibble, xgboost

**RoxygenNote** 7.1.1

**URL** <https://privefl.github.io/bigsnpr/>

**BugReports** <https://github.com/privefl/bigsnpr/issues>

**NeedsCompilation** yes

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**Repository** CRAN

**Date/Publication** 2022-11-07 11:40:11 UTC

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---

bed-class	<i>Class bed</i>
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## Description

A reference class for storing a pointer to a mapped version of a bed file.

## Usage

```
bed(bedfile)
```

## Arguments

bedfile	Path to file with extension ".bed" to read. You need the corresponding ".bim" and ".fam" in the same directory.
---------	---

## Details

A bed object has many field:

- `$address`: address of the external pointer containing the underlying C++ object, to be used internally as a `XPtr<bed>` in C++ code
- `$extptr`: use `$address` instead
- `$bedfile`: path to the bed file
- `$bimfile`: path to the corresponding bim file
- `$famfile`: path to the corresponding fam file
- `$prefix`: path without extension
- `$nrow`: number of samples in the bed file
- `$ncol`: number of variants in the bed file
- `$map`: data frame read from `$bimfile`
- `$fam`: data frame read from `$famfile`
- `$.map`: use `$map` instead
- `$.fam`: use `$fam` instead
- `$light`: get a lighter version of this object for parallel algorithms to not have to transfer e.g. `$.map`.

## Examples

```
bedfile <- system.file("extdata", "example-missing.bed", package = "bigsnpr")
(obj.bed <- bed(bedfile))
```

---

bed\_clumping

*LD clumping*

---

## Description

For a bigSNP:

- `snp_pruning()`: LD pruning. Similar to "`--indep-pairwise (size+1) 1 thr.r2`" in **PLINK**. **This function is deprecated (see [this article](#))**.
- `snp_clumping()` (and `bed_clumping()`): LD clumping. If you do not provide any statistic to rank SNPs, it would use minor allele frequencies (MAFs), making clumping similar to pruning.
- `snp_indLRLDR()`: Get SNP indices of long-range LD regions for the human genome.

**Usage**

```

bed_clumping(
  obj.bed,
  ind.row = rows_along(obj.bed),
  S = NULL,
  thr.r2 = 0.2,
  size = 100/thr.r2,
  exclude = NULL,
  ncores = 1
)

snp_clumping(
  G,
  infos.chr,
  ind.row = rows_along(G),
  S = NULL,
  thr.r2 = 0.2,
  size = 100/thr.r2,
  infos.pos = NULL,
  is.size.in.bp = NULL,
  exclude = NULL,
  ncores = 1
)

snp_pruning(
  G,
  infos.chr,
  ind.row = rows_along(G),
  size = 49,
  is.size.in.bp = FALSE,
  infos.pos = NULL,
  thr.r2 = 0.2,
  exclude = NULL,
  nploidy = 2,
  ncores = 1
)

snp_indLRDR(infos.chr, infos.pos, LD.regions = LD.wiki34)

```

**Arguments**

obj.bed	Object of type <code>bed</code> , which is the mapping of some bed file. Use <code>obj.bed &lt;- bed(bedfile)</code> to get this object.
ind.row	An optional vector of the row indices (individuals) that are used. If not specified, all rows are used. <b>Don't use negative indices.</b>
S	A vector of column statistics which express the importance of each SNP (the more important is the SNP, the greater should be the corresponding statistic).

For example, if  $S$  follows the standard normal distribution, and "important" means significantly different from 0, you must use  $\text{abs}(S)$  instead.

**If not specified, MAFs are computed and used.**

thr.r2	Threshold over the squared correlation between two SNPs. Default is 0.2.
size	For one SNP, window size around this SNP to compute correlations. Default is $100 / \text{thr.r2}$ for clumping (0.2 -> 500; 0.1 -> 1000; 0.5 -> 200). If not providing <code>infos.pos</code> (NULL, the default), this is a window in number of SNPs, otherwise it is a window in kb (genetic distance). I recommend that you provide the positions if available.
exclude	Vector of SNP indices to exclude anyway. For example, can be used to exclude long-range LD regions (see Price2008). Another use can be for thresholding with respect to p-values associated with $S$ .
ncores	Number of cores used. Default doesn't use parallelism. You may use <code>nb_cores</code> .
G	A <code>FBM.code256</code> (typically <code>&lt;bigSNP&gt;\$genotypes</code> ). <b>You shouldn't have missing values.</b> Also, remember to do quality control, e.g. some algorithms in this package won't work if you use SNPs with 0 MAF.
infos.chr	Vector of integers specifying each SNP's chromosome. Typically <code>&lt;bigSNP&gt;\$map\$chromosome</code> .
infos.pos	Vector of integers specifying the physical position on a chromosome (in base pairs) of each SNP. Typically <code>&lt;bigSNP&gt;\$map\$physical.pos</code> .
is.size.in.bp	Deprecated.
nploidy	Number of trials, parameter of the binomial distribution. Default is 2, which corresponds to diploidy, such as for the human genome.
LD.regions	A data.frame with columns "Chr", "Start" and "Stop". Default use the table of 34 long-range LD regions that you can find <a href="#">there</a> .

## Value

- `snp_clumping()` (and `bed_clumping()`): SNP indices that are **kept**.
- `snp_indLRLDR()`: SNP indices to be used as (part of) the 'exclude' parameter of `snp_clumping()`.

## References

Price AL, Weale ME, Patterson N, et al. Long-Range LD Can Confound Genome Scans in Admixed Populations. *Am J Hum Genet.* 2008;83(1):132-135. doi:10.1016/j.ajhg.2008.06.005

## Examples

```
test <- snp_attachExtdata()
G <- test$genotypes

# clumping (prioritizing higher MAF)
ind.keep <- snp_clumping(G, infos.chr = test$map$chromosome,
                        infos.pos = test$map$physical.pos,
                        thr.r2 = 0.1)
```

```
# keep most of them -> not much LD in this simulated dataset
length(ind.keep) / ncol(G)
```

---

bed_counts	<i>Counts</i>
------------	---------------

---

## Description

Counts the number of 0s, 1s, 2s and NAs by variants in the bed file.

## Usage

```
bed_counts(
  obj.bed,
  ind.row = rows_along(obj.bed),
  ind.col = cols_along(obj.bed),
  byrow = FALSE,
  ncores = 1
)
```

## Arguments

obj.bed	Object of type <a href="#">bed</a> , which is the mapping of some bed file. Use <code>obj.bed &lt;- bed.bedfile)</code> to get this object.
ind.row	An optional vector of the row indices (individuals) that are used. If not specified, all rows are used. <b>Don't use negative indices.</b>
ind.col	An optional vector of the column indices (SNPs) that are used. If not specified, all columns are used. <b>Don't use negative indices.</b>
byrow	Whether to count by individual rather than by variant? Default is FALSE (count by variant).
ncores	Number of cores used. Default doesn't use parallelism. You may use <a href="#">nb_cores</a> .

## Value

A matrix of with 4 rows and `length(ind.col)` columns.

## Examples

```
bedfile <- system.file("extdata", "example-missing.bed", package = "bigsnpr")
obj.bed <- bed.bedfile)

bed_counts(obj.bed, ind.col = 1:5)

bed_counts(obj.bed, ind.row = 1:5, byrow = TRUE)
```

---

bed_cprodVec	<i>Cross-product with a vector</i>
--------------	------------------------------------

---

### Description

Cross-product between a "bed" object and a vector.

Missing values are replaced by 0 (after centering), as if they had been imputed using parameter center.

### Usage

```
bed_cprodVec(
  obj.bed,
  y.row,
  ind.row = rows_along(obj.bed),
  ind.col = cols_along(obj.bed),
  center = rep(0, length(ind.col)),
  scale = rep(1, length(ind.col)),
  ncores = 1
)
```

### Arguments

obj.bed	Object of type <a href="#">bed</a> , which is the mapping of some bed file. Use <code>obj.bed &lt;- bed.bedfile</code> to get this object.
y.row	A vector of same size as <code>ind.row</code> .
ind.row	An optional vector of the row indices (individuals) that are used. If not specified, all rows are used. <b>Don't use negative indices.</b>
ind.col	An optional vector of the column indices (SNPs) that are used. If not specified, all columns are used. <b>Don't use negative indices.</b>
center	Vector of same length of <code>ind.col</code> to subtract from columns of $X$ .
scale	Vector of same length of <code>ind.col</code> to divide from columns of $X$ .
ncores	Number of cores used. Default doesn't use parallelism. You may use <a href="#">nb_cores</a> .

### Value

$X^T \cdot y$ .

### Examples

```
bedfile <- system.file("extdata", "example.bed", package = "bigsnpr")
obj.bed <- bed.bedfile)
```



```
y.row <- rep(1, nrow(obj.bed))
str.bed_cprodVec(obj.bed, y.row)
```

---

bed_MAF	<i>Allele frequencies</i>
---------	---------------------------

---

### Description

Allele frequencies of a `bed` object.

### Usage

```
bed_MAF(
  obj.bed,
  ind.row = rows_along(obj.bed),
  ind.col = cols_along(obj.bed),
  ncores = 1
)
```

### Arguments

<code>obj.bed</code>	Object of type <code>bed</code> , which is the mapping of some bed file. Use <code>obj.bed &lt;- bed.bedfile</code> to get this object.
<code>ind.row</code>	An optional vector of the row indices (individuals) that are used. If not specified, all rows are used. <b>Don't use negative indices.</b>
<code>ind.col</code>	An optional vector of the column indices (SNPs) that are used. If not specified, all columns are used. <b>Don't use negative indices.</b>
<code>ncores</code>	Number of cores used. Default doesn't use parallelism. You may use <code>nb_cores</code> .

### Value

A `data.frame` with

- `$ac`: allele counts,
- `$mac`: minor allele counts,
- `$af`: allele frequencies,
- `$maf`: minor allele frequencies,
- `$N`: numbers of non-missing values.

### Examples

```
bedfile <- system.file("extdata", "example-missing.bed", package = "bigsnpr")
obj.bed <- bed.bedfile)
```

```
bed_MAF(obj.bed, ind.col = 1:5)
```

---

bed_prodVec	<i>Product with a vector</i>
-------------	------------------------------

---

### Description

Product between a "bed" object and a vector.

Missing values are replaced by 0 (after centering), as if they had been imputed using parameter center.

### Usage

```
bed_prodVec(
  obj.bed,
  y.col,
  ind.row = rows_along(obj.bed),
  ind.col = cols_along(obj.bed),
  center = rep(0, length(ind.col)),
  scale = rep(1, length(ind.col)),
  ncores = 1
)
```

### Arguments

obj.bed	Object of type <code>bed</code> , which is the mapping of some bed file. Use <code>obj.bed &lt;- bed.bedfile</code> to get this object.
y.col	A vector of same size as <code>ind.col</code> .
ind.row	An optional vector of the row indices (individuals) that are used. If not specified, all rows are used. <b>Don't use negative indices.</b>
ind.col	An optional vector of the column indices (SNPs) that are used. If not specified, all columns are used. <b>Don't use negative indices.</b>
center	Vector of same length of <code>ind.col</code> to subtract from columns of <code>X</code> .
scale	Vector of same length of <code>ind.col</code> to divide from columns of <code>X</code> .
ncores	Number of cores used. Default doesn't use parallelism. You may use <code>nb_cores</code> .

### Value

$X \cdot y$ .

### Examples

```
bedfile <- system.file("extdata", "example.bed", package = "bigsnpr")
obj.bed <- bed.bedfile)
```

```
y.col <- rep(1, ncol(obj.bed))
str(bed_prodVec(obj.bed, y.col))
```

---

bed_projectPCA	<i>Projecting PCA</i>
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---

## Description

Computing and projecting PCA of reference dataset to a target dataset.

## Usage

```
bed_projectPCA(
  obj.bed.ref,
  obj.bed.new,
  k = 10,
  ind.row.new = rows_along(obj.bed.new),
  ind.row.ref = rows_along(obj.bed.ref),
  ind.col.ref = cols_along(obj.bed.ref),
  strand_flip = TRUE,
  join_by_pos = TRUE,
  match.min.prop = 0.5,
  build.new = "hg19",
  build.ref = "hg19",
  liftOver = NULL,
  ...,
  verbose = TRUE,
  ncores = 1
)
```

## Arguments

obj.bed.ref	Object of type bed, which is the mapping of the bed file of the reference data. Use <code>obj.bed &lt;- bed(bedfile)</code> to get this object.
obj.bed.new	Object of type bed, which is the mapping of the bed file of the target data. Use <code>obj.bed &lt;- bed(bedfile)</code> to get this object.
k	Number of principal components to compute and project.
ind.row.new	Rows to be used in the target data. Default uses them all.
ind.row.ref	Rows to be used in the reference data. Default uses them all.
ind.col.ref	Columns to be potentially used in the reference data. Default uses all the ones in common with target data.
strand_flip	Whether to try to flip strand? (default is TRUE) If so, ambiguous alleles A/T and C/G are removed.
join_by_pos	Whether to join by chromosome and position (default), or instead by rsid.

match.min.prop	Minimum proportion of variants in the smallest data to be matched, otherwise stops with an error. Default is 20%.
build.new	Genome build of the target data. Default is hg19.
build.ref	Genome build of the reference data. Default is hg19.
liftOver	Path to liftOver executable. Binaries can be downloaded at <a href="https://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/liftOver">https://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/liftOver</a> for Mac and at <a href="https://hgdownload.cse.ucsc.edu/admin/exe/linux.x86_64/liftOver">https://hgdownload.cse.ucsc.edu/admin/exe/linux.x86_64/liftOver</a> for Linux.
...	Arguments passed on to <code>bed_autoSVD</code>
fun.scaling	A function with parameters <code>X</code> (or <code>obj.bed</code> ), <code>ind.row</code> and <code>ind.col</code> , and that returns a data.frame with <code>\$center</code> and <code>\$scale</code> for the columns corresponding to <code>ind.col</code> , to scale each of their elements such as followed: $\frac{X_{i,j} - center_j}{scale_j}$ <p>Default uses binomial scaling. You can also provide your own center and scale by using <code>as_scaling_fun()</code>.</p>
roll.size	Radius of rolling windows to smooth log-p-values. Default is 50.
int.min.size	Minimum number of consecutive outlier SNPs in order to be reported as long-range LD region. Default is 20.
thr.r2	Threshold over the squared correlation between two SNPs. Default is 0.2. Use NA if you want to skip the clumping step.
alpha.tukey	Default is 0.1. The type-I error rate in outlier detection (that is further corrected for multiple testing).
min.mac	Minimum minor allele count (MAC) for variants to be included. Default is 10.
max.iter	Maximum number of iterations of outlier detection. Default is 5.
size	For one SNP, window size around this SNP to compute correlations. Default is $100 / thr.r2$ for clumping (0.2 -> 500; 0.1 -> 1000; 0.5 -> 200). If not providing <code>infos.pos</code> (NULL, the default), this is a window in number of SNPs, otherwise it is a window in kb (genetic distance). I recommend that you provide the positions if available.
verbose	Output some information on the iterations? Default is TRUE.
ncores	Number of cores used. Default doesn't use parallelism. You may use <code>nb_cores</code> .

## Value

A list of 3 elements:

- `$obj.svd.ref`: `big_SVD` object computed from reference data.
- `$simple_proj`: simple projection of new data into space of reference PCA.
- `$OADP_proj`: Online Augmentation, Decomposition, and Procrustes (OADP) projection of new data into space of reference PCA.

---

bed\_projectSelfPCA      *Projecting PCA*

---

### Description

Projecting PCA using individuals from one dataset to other individuals from the same dataset.

### Usage

```
bed_projectSelfPCA(
  obj.svd,
  obj.bed,
  ind.row,
  ind.col = attr(obj.svd, "subset"),
  ncores = 1
)
```

### Arguments

obj.svd	List with v, d, center and scale. Typically the an object of type "big_SVD".
obj.bed	Object of type bed, which is the mapping of the bed file of the data containing both the individuals that were used to compute the PCA and the other individuals to be projected.
ind.row	Rows (individuals) to be projected.
ind.col	Columns that were used for computing PCA. If <a href="#">bed_autoSVD</a> was used, then <code>attr(obj.svd, "subset")</code> is automatically used by default. Otherwise (e.g. if <a href="#">bed_randomSVD</a> was used), you have to pass <code>ind.col</code> .
ncores	Number of cores used. Default doesn't use parallelism. You may use <a href="#">nb_cores</a> .

### Value

A list of 3 elements:

- `$obj.svd.ref`: big\_SVD object computed from reference data.
- `$simple_proj`: simple projection of new data into space of reference PCA.
- `$OADP_proj`: Online Augmentation, Decomposition, and Procrustes (OADP) projection of new data into space of reference PCA.

---

bed_randomSVD	<i>Randomized partial SVD</i>
---------------	-------------------------------

---

### Description

Partial SVD (or PCA) of a genotype matrix stored as a PLINK (.bed) file.#'

### Usage

```
bed_randomSVD(
  obj.bed,
  fun.scaling = bed_scaleBinom,
  ind.row = rows_along(obj.bed),
  ind.col = cols_along(obj.bed),
  k = 10,
  tol = 1e-04,
  verbose = FALSE,
  ncores = 1
)
```

### Arguments

`obj.bed` Object of type `bed`, which is the mapping of some bed file. Use `obj.bed <- bed(bedfile)` to get this object.

`fun.scaling` A function with parameters `X`, `ind.row` and `ind.col`, and that returns a data.frame with `$center` and `$scale` for the columns corresponding to `ind.col`, to scale each of their elements such as followed:

$$\frac{X_{i,j} - center_j}{scale_j}.$$

Default doesn't use any scaling. You can also provide your own center and scale by using `as_scaling_fun()`.

`ind.row` An optional vector of the row indices (individuals) that are used. If not specified, all rows are used.  
**Don't use negative indices.**

`ind.col` An optional vector of the column indices (SNPs) that are used. If not specified, all columns are used.  
**Don't use negative indices.**

`k` Number of singular vectors/values to compute. Default is 10. **This algorithm should be used to compute only a few singular vectors/values.**

`tol` Precision parameter of `svds`. Default is 1e-4.

`verbose` Should some progress be printed? Default is FALSE.

`ncores` Number of cores used. Default doesn't use parallelism. You may use `nb_cores`.

**Value**

A named list (an S3 class "big\_SVD") of

- d, the singular values,
- u, the left singular vectors,
- v, the right singular vectors,
- niter, the number of the iteration of the algorithm,
- nops, number of Matrix-Vector multiplications used,
- center, the centering vector,
- scale, the scaling vector.

Note that to obtain the Principal Components, you must use [predict](#) on the result. See examples.

**Examples**

```
bedfile <- system.file("extdata", "example.bed", package = "bigsnpr")
obj.bed <- bed(bedfile)

str(bed_randomSVD(obj.bed))
```

---

bed\_scaleBinom                      *Binomial(2, p) scaling*

---

**Description**

Binomial(2, p) scaling where p is estimated.

**Usage**

```
bed_scaleBinom(
  obj.bed,
  ind.row = rows_along(obj.bed),
  ind.col = cols_along(obj.bed),
  ncores = 1
)
```

**Arguments**

obj.bed	Object of type <a href="#">bed</a> , which is the mapping of some bed file. Use <code>obj.bed &lt;- bed(bedfile)</code> to get this object.
ind.row	An optional vector of the row indices (individuals) that are used. If not specified, all rows are used. <b>Don't use negative indices.</b>
ind.col	An optional vector of the column indices (SNPs) that are used. If not specified, all columns are used. <b>Don't use negative indices.</b>
ncores	Number of cores used. Default doesn't use parallelism. You may use <a href="#">nb_cores</a> .

**Details**

You will probably not use this function as is but as parameter `fun.scaling` of other functions (e.g. `bed_autoSVD` and `bed_randomSVD`).

**Value**

A data frame with `$center` and `$scale`.

**References**

This scaling is widely used for SNP arrays. Patterson N, Price AL, Reich D (2006). Population Structure and Eigenanalysis. PLoS Genet 2(12): e190. doi:10.1371/journal.pgen.0020190.

**Examples**

```
bedfile <- system.file("extdata", "example-missing.bed", package = "bigsnpr")
obj.bed <- bed(bedfile)

str(bed_scaleBinom(obj.bed))

str(bed_randomSVD(obj.bed, bed_scaleBinom))
```

---

bed\_tcrossprodSelf      *tcrossprod / GRM*

---

**Description**

Compute  $GG^T$  from a bed object, with possible filtering and scaling of G. For example, this can be used to compute GRMs.

**Usage**

```
bed_tcrossprodSelf(
  obj.bed,
  fun.scaling = bed_scaleBinom,
  ind.row = rows_along(obj.bed),
  ind.col = cols_along(obj.bed),
  block.size = block_size(length(ind.row))
)
```

**Arguments**

`obj.bed`      Object of type `bed`, which is the mapping of some bed file. Use `obj.bed <- bed(bedfile)` to get this object.



fun.scaling A function with parameters X (or obj.bed), ind.row and ind.col, and that returns a data.frame with \$center and \$scale for the columns corresponding to ind.col, to scale each of their elements such as followed:

$$\frac{X_{i,j} - center_j}{scale_j}.$$

Default uses binomial scaling. You can also provide your own center and scale by using `as_scaling_fun()`.

ind.row An optional vector of the row indices (individuals) that are used. If not specified, all rows are used.

**Don't use negative indices.**

ind.col An optional vector of the column indices (SNPs) that are used. If not specified, all columns are used.

**Don't use negative indices.**

block.size Maximum number of columns read at once. Default uses `block_size`.

### Value

A temporary `FBM`, with the following two attributes:

- a numeric vector center of column scaling,
- a numeric vector scale of column scaling.

### Matrix parallelization

Large matrix computations are made block-wise and won't be parallelized in order to not have to reduce the size of these blocks. Instead, you may use `Microsoft R Open` or `OpenBLAS` in order to accelerate these block matrix computations. You can also control the number of cores used with `bigparallelr::set_blas_ncores()`.

### Examples

```
bedfile <- system.file("extdata", "example.bed", package = "bigsnpr")
obj.bed <- bed(bedfile)
```

```
K <- bed_tcrossprodSelf(obj.bed)
K[1:4, 1:6] / ncol(obj.bed)
```

---

bigSNP-class

*Class bigSNP*

---

### Description

An S3 class for representing information on massive SNP arrays.

**Value**

A named list with at least 3 slots:

**genotypes** A [FBM.code256](#) which is a special Filebacked Big Matrix encoded with type raw (one byte unsigned integer), representing genotype calls and possibly imputed allele dosages. Rows are individuals and columns are SNPs.

**fam** A `data.frame` containing some information on the individuals (read from a ".fam" file).

**map** A `data.frame` giving some information on the variants (read from a ".bim" file).

**See Also**

[snp\\_readBed](#)

---

coef\_to\_liab

*Liability scale*

---

**Description**

Coefficient to convert to the liability scale. E.g.  $h2\_liab = coef * h2\_obs$ .

**Usage**

```
coef_to_liab(K_pop, K_gwas = 0.5)
```

**Arguments**

`K_pop` Prevalence in the population.

`K_gwas` Prevalence in the GWAS. You should provide this if you used  $(n\_case + n\_control)$  as sample size. If using the effective sample size  $4 / (1 / n\_case + 1 / n\_control)$  instead, you should keep the default value of `K_gwas = 0.5` as the GWAS case-control ascertainment is already accounted for in the effective sample size.

**Value**

Scaling coefficient to convert e.g. heritability to the liability scale.

**Examples**

```
h2 <- 0.2
h2 * coef_to_liab(0.02)
```

---

download_1000G	<i>Download 1000G</i>
----------------	-----------------------

---

**Description**

Download 1000 genomes project (phase 3) data in PLINK bed/bim/fam format, including 2490 (mostly unrelated) individuals and ~1.7M SNPs in common with either HapMap3 or the UK Biobank.

**Usage**

```
download_1000G(dir, overwrite = FALSE, delete_zip = TRUE)
```

**Arguments**

dir	The directory where to put the downloaded files.
overwrite	Whether to overwrite files when downloading and unzipping? Default is FALSE.
delete_zip	Whether to delete zip after decompressing the file in it? Default is TRUE.

**Value**

The path of the downloaded bed file.

---

download_beagle	<i>Download Beagle 4.1</i>
-----------------	----------------------------

---

**Description**

Download Beagle 4.1 from <https://faculty.washington.edu/browning/beagle/beagle.html>

**Usage**

```
download_beagle(dir = tempdir())
```

**Arguments**

dir	The directory where to put the Beagle Java Archive. Default is a temporary directory.
-----	---

**Value**

The path of the downloaded Beagle Java Archive.

---

download\_plink            *Download PLINK*

---

### Description

Download PLINK 1.9 from <https://www.cog-genomics.org/plink2>.

Download PLINK 2.0 from <https://www.cog-genomics.org/plink/2.0/>.

### Usage

```
download_plink(dir = tempdir(), overwrite = FALSE, verbose = TRUE)
```

```
download_plink2(
  dir = tempdir(),
  AVX2 = TRUE,
  overwrite = FALSE,
  verbose = TRUE
)
```

### Arguments

dir	The directory where to put the PLINK executable. Default is a temporary directory.
overwrite	Whether to overwrite file? Default is FALSE.
verbose	Whether to output details of downloading. Default is TRUE.
AVX2	Whether to download the AVX2 version? This is only available for 64 bits architectures. Default is TRUE.

### Value

The path of the downloaded PLINK executable.

---

LD.wiki34            *Long-range LD regions*

---

### Description

34 long-range Linkage Disequilibrium (LD) regions for the human genome based on some [wiki table](#).

### Usage

```
LD.wiki34
```

**Format**

A data frame with 34 rows (regions) and 4 variables:

- Chr: region's chromosome
- Start: starting position of the region (in bp)
- Stop: stopping position of the region (in bp)
- ID: some ID of the region.

---

same_ref	<i>Determine reference divergence</i>
----------	---------------------------------------

---

**Description**

Determine reference divergence while accounting for strand flips. **This does not remove ambiguous alleles.**

**Usage**

```
same_ref(ref1, alt1, ref2, alt2)
```

**Arguments**

ref1	The reference alleles of the first dataset.
alt1	The alternative alleles of the first dataset.
ref2	The reference alleles of the second dataset.
alt2	The alternative alleles of the second dataset.

**Value**

A logical vector whether the references alleles are the same. Missing values can result from missing values in the inputs or from ambiguous matching (e.g. matching A/C and A/G).

**See Also**

[snp\\_match\(\)](#)

**Examples**

```
same_ref(ref1 = c("A", "C", "T", "G", NA),
         alt1 = c("C", "T", "C", "A", "A"),
         ref2 = c("A", "C", "A", "A", "C"),
         alt2 = c("C", "G", "G", "G", "A"))
```

SCT

*Stacked C+T (SCT)***Description**

Polygenic Risk Scores for a grid of clumping and thresholding parameters.

Stacking over many Polygenic Risk Scores, corresponding to a grid of many different parameters for clumping and thresholding.

**Usage**

```
snp_grid_clumping(
  G,
  infos.chr,
  infos.pos,
  lpS,
  ind.row = rows_along(G),
  grid.thr.r2 = c(0.01, 0.05, 0.1, 0.2, 0.5, 0.8, 0.95),
  grid.base.size = c(50, 100, 200, 500),
  infos.imp = rep(1, ncol(G)),
  grid.thr.imp = 1,
  groups = list(cols_along(G)),
  exclude = NULL,
  ncores = 1
)

snp_grid_PRS(
  G,
  all_keep,
  betas,
  lpS,
  n_thr_lpS = 50,
  grid.lpS.thr = 0.9999 * seq_log(max(0.1, min(lpS, na.rm = TRUE)), max(lpS, na.rm =
    TRUE), n_thr_lpS),
  ind.row = rows_along(G),
  backingfile = tempfile(),
  type = c("float", "double"),
  ncores = 1
)

snp_grid_stacking(
  multi_PRS,
  y.train,
  alphas = c(1, 0.01, 1e-04),
  ncores = 1,
  ...
)
```

**Arguments**

G	A <a href="#">FBM.code256</a> (typically <code>&lt;bigSNP&gt;\$genotypes</code> ). <b>You shouldn't have missing values.</b> Also, remember to do quality control, e.g. some algorithms in this package won't work if you use SNPs with 0 MAF.
infos.chr	Vector of integers specifying each SNP's chromosome. Typically <code>&lt;bigSNP&gt;\$map\$chromosome</code> .
infos.pos	Vector of integers specifying the physical position on a chromosome (in base pairs) of each SNP. Typically <code>&lt;bigSNP&gt;\$map\$physical.pos</code> .
lpS	Numeric vector of $-\log_{10}(\text{p-value})$ associated with betas.
ind.row	An optional vector of the row indices (individuals) that are used. If not specified, all rows are used. <b>Don't use negative indices.</b>
grid.thr.r2	Grid of thresholds over the squared correlation between two SNPs for clumping. Default is <code>c(0.01, 0.05, 0.1, 0.2, 0.5, 0.8, 0.95)</code> .
grid.base.size	Grid for base window sizes. Sizes are then computed as <code>base.size / thr.r2</code> (in kb). Default is <code>c(50, 100, 200, 500)</code> .
infos.imp	Vector of imputation scores. Default is all 1 if you do not provide it.
grid.thr.imp	Grid of thresholds over <code>infos.imp</code> (default is 1), but you should change it (e.g. <code>c(0.3, 0.6, 0.9, 0.95)</code> ) if providing <code>infos.imp</code> .
groups	List of vectors of indices to define your own categories. This could be used e.g. to derive C+T scores using two different GWAS summary statistics, or to include other information such as functional annotations. Default just makes one group with all variants.
exclude	Vector of SNP indices to exclude anyway.
ncores	Number of cores used. Default doesn't use parallelism. You may use <a href="#">nb_cores</a> .
all_keep	Output of <code>snp_grid_clumping()</code> (indices passing clumping).
betas	Numeric vector of weights (effect sizes from GWAS) associated with each variant (column of G). If alleles are reversed, make sure to multiply corresponding effects by -1.
n_thr_lpS	Length for default <code>grid.lpS.thr</code> . Default is 50.
grid.lpS.thr	Sequence of thresholds to apply on <code>lpS</code> . Default is a grid (of length <code>n_thr_lpS</code> ) evenly spaced on a logarithmic scale, i.e. on a log-log scale for p-values.
backingfile	Prefix for backingfiles where to store scores of C+T. As we typically use a large grid, this can result in a large matrix so that we store it on disk. Default uses a temporary file.
type	Type of <code>backingfile</code> values. Either "float" (the default) or "double". Using "float" requires half disk space.
multi_PRS	Output of <code>snp_grid_PRS()</code> .
y.train	Vector of phenotypes. If there are two levels (binary 0/1), it uses <a href="#">big_splLogReg()</a> for stacking, otherwise <a href="#">big_splLinReg()</a> .

alphas            Vector of values for grid-search. See `big_spLogReg()`. Default for this function is `c(1, 0.01, 0.0001)`.

...                Other parameters to be passed to `big_spLogReg()`. For example, using `covar.train`, you can add covariates in the model with all C+T scores. You can also use `pf.covar` if you do not want to penalize these covariates.

### Value

`snp_grid_PRS()`: An FBM (matrix on disk) that stores the C+T scores for all parameters of the grid (and for each chromosome separately). It also stores as attributes the input parameters `all_keep`, `betas`, `lpS` and `grid.lpS.thr` that are also needed in `snp_grid_stacking()`.

---

<code>seq_log</code>	<i>Sequence, evenly spaced on a logarithmic scale</i>
----------------------	---

---

### Description

Sequence, evenly spaced on a logarithmic scale

### Usage

```
seq_log(from, to, length.out)
```

### Arguments

`from`            the starting and (maximal) end values of the sequence. Of length 1 unless just `from` is supplied as an unnamed argument.

`to`                the starting and (maximal) end values of the sequence. Of length 1 unless just `from` is supplied as an unnamed argument.

`length.out`      desired length of the sequence. A non-negative number, which for `seq` and `seq.int` will be rounded up if fractional.

### Value

A sequence of length `length.out`, evenly spaced on a logarithmic scale between `from` and `to`.

### Examples

```
seq_log(1, 1000, 4)
seq_log(1, 100, 5)
```



---

snp\_ancestry\_summary *Estimation of ancestry proportions*

---

## Description

Estimation of ancestry proportions. Make sure to match summary statistics using `snp_match()` (and to reverse frequencies correspondingly).

## Usage

```
snp_ancestry_summary(freq, info_freq_ref, projection, correction)
```

## Arguments

freq	Vector of frequencies from which to estimate ancestry proportions.
info_freq_ref	A data frame (or matrix) with the set of frequencies to be used as reference (one population per column).
projection	Matrix of "loadings" for each variant/PC to be used to project allele frequencies.
correction	Coefficients to correct for shrinkage when projecting.

## Value

vector of coefficients representing the ancestry proportions.

## Examples

```
## Not run:

# GWAS summary statistics for Epilepsy (supposedly in EUR+EAS+AFR)
gz <- runonce::download_file(
  "http://www.epigad.org/gwas_ilae2018_16loci/all_epilepsy_METAL.gz",
  dir = "tmp-data")
readLines(gz, n = 3)

library(dplyr)
sumstats <- bigreadr::fread2(
  gz, select = c("CHR", "BP", "Allele2", "Allele1", "Freq1"),
  col.names = c("chr", "pos", "a0", "a1", "freq")
) %>%
  mutate_at(3:4, toupper)
# It is a good idea to filter for similar per-variant N (when available..)

all_freq <- bigreadr::fread2(
  runonce::download_file("https://figshare.com/ndownloader/files/31620968",
    dir = "tmp-data", fname = "ref_freqs.csv.gz"))
projection <- bigreadr::fread2(
  runonce::download_file("https://figshare.com/ndownloader/files/31620953",
    dir = "tmp-data", fname = "projection.csv.gz"))
```

```

matched <- snp_match(
  mutate(sumstats, chr = as.integer(chr), beta = 1),
  all_freq[1:5],
  return_flip_and_rev = TRUE
) %>%
  mutate(freq = ifelse(`_REV_`, 1 - freq, freq))

res <- snp_ancestry_summary(
  freq = matched$freq,
  info_freq_ref = all_freq[matched$`_NUM_ID_`, -(1:5)],
  projection = projection[matched$`_NUM_ID_`, -(1:5)],
  correction = c(1, 1, 1, 1.008, 1.021, 1.034, 1.052, 1.074, 1.099,
                 1.123, 1.15, 1.195, 1.256, 1.321, 1.382, 1.443)
)

# Some ancestry groups are very close to each other, and should be merged
group <- colnames(all_freq)[-(1:5)]
group[group %in% c("Scandinavia", "United Kingdom", "Ireland")] <- "Europe (North West)"
group[group %in% c("Europe (South East)", "Europe (North East)")] <- "Europe (East)"

tapply(res, factor(group, unique(group)), sum)

## End(Not run)

```

---

snp\_asGeneticPos      *Interpolate to genetic positions*

---

## Description

Use genetic maps available at <https://github.com/joepickrell/1000-genomes-genetic-maps/> to interpolate physical positions (in bp) to genetic positions (in cM).

## Usage

```

snp_asGeneticPos(
  infos.chr,
  infos.pos,
  dir = tempdir(),
  ncores = 1,
  rsid = NULL,
  type = c("OMNI", "hapmap")
)

```

## Arguments

`infos.chr`      Vector of integers specifying each SNP's chromosome.  
Typically `<bigSNP>$map$chromosome`.

infos.pos	Vector of integers specifying the physical position on a chromosome (in base pairs) of each SNP. Typically <code>&lt;bigSNP&gt;\$map\$physical.pos</code> .
dir	Directory where to download and decompress files. Default is <code>tempdir()</code> . Directly use <i>uncompressed</i> files there if already present. You can use <code>R.utils::gunzip()</code> to uncompress local files.
ncores	Number of cores used. Default doesn't use parallelism. You may use <code>nb_cores</code> .
rsid	If providing rsIDs, the matching is performed using those (instead of positions) and variants not matched are interpolated using spline interpolation of variants that have been matched.
type	Whether to use the genetic maps interpolated from "OMNI" (the default), or from "hapmap".

**Value**

The new vector of genetic positions.

---

snp_attach	<i>Attach a "bigSNP" from backing files</i>
------------	---

---

**Description**

Load a [bigSNP](#) from backing files into R.

**Usage**

```
snp_attach(rdsfile)
```

**Arguments**

rdsfile      The path of the ".rds" which stores the bigSNP object.

**Details**

This is often just a call to [readRDS](#). But it also checks if you have moved the two (".bk" and ".rds") backing files to another directory.

**Value**

The bigSNP object.

**Examples**

```
(bedfile <- system.file("extdata", "example.bed", package = "bigsnpr"))

# Reading the bedfile and storing the data in temporary directory
rds <- snp_readBed(bedfile, backingfile = tempfile())

# Loading the data from backing files
test <- snp_attach(rds)

str(test)
dim(G <- test$genotypes)
G[1:8, 1:8]
```

---

snp\_attachExtdata      *Attach a "bigSNP" for examples and tests*

---

**Description**

Attach a "bigSNP" for examples and tests

**Usage**

```
snp_attachExtdata(bedfile = c("example.bed", "example-missing.bed"))
```

**Arguments**

bedfile              Name of one example bed file. Either

- "example.bed" (the default),
- "example-missing.bed".

**Value**

The example "bigSNP", filebacked in the "/tmp/" directory.

---

snp\_autoSVD              *Truncated SVD while limiting LD*

---

**Description**

Fast truncated SVD with initial pruning and that iteratively removes long-range LD regions. Some variants are removing due to the initial clumping, then more and more variants are removed at each iteration. You can access the indices of the remaining variants with `attr(*, "subset")`. If some of the variants removed are contiguous, the regions are reported in `attr(*, "lrldr")`.

**Usage**

```
snp_autoSVD(
  G,
  infos.chr,
  infos.pos = NULL,
  ind.row = rows_along(G),
  ind.col = cols_along(G),
  fun.scaling = snp_scaleBinom(),
  thr.r2 = 0.2,
  size = 100/thr.r2,
  k = 10,
  roll.size = 50,
  int.min.size = 20,
  alpha.tukey = 0.05,
  min.mac = 10,
  max.iter = 5,
  is.size.in.bp = NULL,
  ncores = 1,
  verbose = TRUE
)
```

```
bed_autoSVD(
  obj.bed,
  ind.row = rows_along(obj.bed),
  ind.col = cols_along(obj.bed),
  fun.scaling = bed_scaleBinom,
  thr.r2 = 0.2,
  size = 100/thr.r2,
  k = 10,
  roll.size = 50,
  int.min.size = 20,
  alpha.tukey = 0.05,
  min.mac = 10,
  max.iter = 5,
  ncores = 1,
  verbose = TRUE
)
```

**Arguments**

G	A <a href="#">FBM.code256</a> (typically <bigSNP>\$genotypes). <b>You shouldn't have missing values.</b> Also, remember to do quality control, e.g. some algorithms in this package won't work if you use SNPs with 0 MAF.
infos.chr	Vector of integers specifying each SNP's chromosome. Typically <bigSNP>\$map\$chromosome.
infos.pos	Vector of integers specifying the physical position on a chromosome (in base pairs) of each SNP. Typically <bigSNP>\$map\$physical.pos.

ind.row	An optional vector of the row indices (individuals) that are used. If not specified, all rows are used. <b>Don't use negative indices.</b>
ind.col	An optional vector of the column indices (SNPs) that are used. If not specified, all columns are used. <b>Don't use negative indices.</b>
fun.scaling	A function with parameters $X$ (or obj.bed), ind.row and ind.col, and that returns a data.frame with \$center and \$scale for the columns corresponding to ind.col, to scale each of their elements such as followed: $\frac{X_{i,j} - center_j}{scale_j}$ Default uses binomial scaling. You can also provide your own center and scale by using <code>as_scaling_fun()</code> .
thr.r2	Threshold over the squared correlation between two SNPs. Default is 0.2. Use NA if you want to skip the clumping step.
size	For one SNP, window size around this SNP to compute correlations. Default is $100 / thr.r2$ for clumping (0.2 -> 500; 0.1 -> 1000; 0.5 -> 200). If not providing infos.pos (NULL, the default), this is a window in number of SNPs, otherwise it is a window in kb (genetic distance). I recommend that you provide the positions if available.
k	Number of singular vectors/values to compute. Default is 10. <b>This algorithm should be used to compute a few singular vectors/values.</b>
roll.size	Radius of rolling windows to smooth log-p-values. Default is 50.
int.min.size	Minimum number of consecutive outlier SNPs in order to be reported as long-range LD region. Default is 20.
alpha.tukey	Default is 0.1. The type-I error rate in outlier detection (that is further corrected for multiple testing).
min.mac	Minimum minor allele count (MAC) for variants to be included. Default is 10.
max.iter	Maximum number of iterations of outlier detection. Default is 5.
is.size.in.bp	Deprecated.
ncores	Number of cores used. Default doesn't use parallelism. You may use <code>nb_cores</code> .
verbose	Output some information on the iterations? Default is TRUE.
obj.bed	Object of type <code>bed</code> , which is the mapping of some bed file. Use <code>obj.bed &lt;- bed.bedfile)</code> to get this object.

## Details

If you don't have any information about SNPs, you can try using

- `infos.chr = rep(1, ncol(G))`,
- `size = ncol(G)` (if SNPs are not sorted),
- `roll.size = 0` (if SNPs are not sorted).

**Value**

A named list (an S3 class "big\_SVD") of

- d, the singular values,
- u, the left singular vectors,
- v, the right singular vectors,
- niter, the number of the iteration of the algorithm,
- nops, number of Matrix-Vector multiplications used,
- center, the centering vector,
- scale, the scaling vector.

Note that to obtain the Principal Components, you must use [predict](#) on the result. See examples.

**Examples**

```
ex <- snp_attachExtdata()
G <- ex$genotypes

obj.svd <- snp_autoSVD(G,
                      infos.chr = ex$map$chromosome,
                      infos.pos = ex$map$physical.position)

str(obj.svd)
```

---

snp\_beagleImpute

*Imputation*

---

**Description**

Imputation using **Beagle** version 4.

**Usage**

```
snp_beagleImpute(
  beagle.path,
  plink.path,
  bedfile.in,
  bedfile.out = NULL,
  memory.max = 3,
  ncores = 1,
  extra.options = "",
  plink.options = "",
  verbose = TRUE
)
```

### Arguments

beagle.path	Path to the executable of Beagle v4+.
plink.path	Path to the executable of PLINK 1.9.
bedfile.in	Path to the input bedfile.
bedfile.out	Path to the output bedfile. Default is created by appending "_impute" to prefix.in (bedfile.in without extension).
memory.max	Max memory (in GB) to be used. It is internally rounded to be an integer. Default is 3.
ncores	Number of cores used. Default doesn't use parallelism. You may use <a href="#">nb_cores</a> .
extra.options	Other options to be passed to Beagle as a string. More options can be found at Beagle's website.
plink.options	Other options to be passed to PLINK as a string. More options can be found at <a href="https://www.cog-genomics.org/plink2/filter">https://www.cog-genomics.org/plink2/filter</a> .
verbose	Whether to show PLINK log? Default is TRUE.

### Details

Downloads and more information can be found at the following websites

- [PLINK](#),
- [Beagle](#).

### Value

The path of the new bedfile.

### References

Browning, Brian L., and Sharon R. Browning. "Genotype imputation with millions of reference samples." *The American Journal of Human Genetics* 98.1 (2016): 116-126.

### See Also

[download\\_plink](#) [download\\_beagle](#)

---

snp\_cor

*Correlation matrix*

---

### Description

Get significant (Pearson) correlations between nearby SNPs of the same chromosome (p-values are computed using a two-sided t-test).



**Usage**

```
snp_cor(
  Gna,
  ind.row = rows_along(Gna),
  ind.col = cols_along(Gna),
  size = 500,
  alpha = 1,
  thr_r2 = 0,
  fill.diag = TRUE,
  infos.pos = NULL,
  ncores = 1
)

bed_cor(
  obj.bed,
  ind.row = rows_along(obj.bed),
  ind.col = cols_along(obj.bed),
  size = 500,
  alpha = 1,
  thr_r2 = 0,
  fill.diag = TRUE,
  infos.pos = NULL,
  ncores = 1
)
```

**Arguments**

Gna	A <a href="#">FBM.code256</a> (typically <code>&lt;bigSNP&gt;\$genotypes</code> ). You can have missing values in these data.
ind.row	An optional vector of the row indices (individuals) that are used. If not specified, all rows are used. <b>Don't use negative indices.</b>
ind.col	An optional vector of the column indices (SNPs) that are used. If not specified, all columns are used. <b>Don't use negative indices.</b>
size	For one SNP, window size around this SNP to compute correlations. Default is 500. If not providing <code>infos.pos</code> (NULL, the default), this is a window in number of SNPs, otherwise it is a window in kb (genetic distance).
alpha	Type-I error for testing correlations. Default is 1 (no threshold is applied).
thr_r2	Threshold to apply on squared correlations. Default is 0.
fill.diag	Whether to fill the diagonal with 1s (the default) or to keep it as 0s.
infos.pos	Vector of integers specifying the physical position on a chromosome (in base pairs) of each SNP. Typically <code>&lt;bigSNP&gt;\$map\$physical.pos</code> .
ncores	Number of cores used. Default doesn't use parallelism. You may use <a href="#">nb_cores</a> .
obj.bed	Object of type <a href="#">bed</a> , which is the mapping of some bed file. Use <code>obj.bed &lt;- bed.bedfile)</code> to get this object.

**Value**

The (Pearson) correlation matrix. This is a sparse symmetric matrix.

**Examples**

```
test <- snp_attachExtdata()
G <- test$genotypes

corr <- snp_cor(G, ind.col = 1:1000)
corr[1:10, 1:10]

# Sparsity
length(corr@x) / length(corr)
```

---

snp\_fastImpute

*Fast imputation*


---

**Description**

Fast imputation algorithm based on local XGBoost models.

**Usage**

```
snp_fastImpute(
  Gna,
  infos.chr,
  alpha = 1e-04,
  size = 200,
  p.train = 0.8,
  n.cor = nrow(Gna),
  seed = NA,
  ncores = 1
)
```

**Arguments**

Gna	A <a href="#">FBM.code256</a> (typically <bigSNP>\$genotypes). You can have missing values in these data.
infos.chr	Vector of integers specifying each SNP's chromosome. Typically <bigSNP>\$map\$chromosome.
alpha	Type-I error for testing correlations. Default is 1e-4.
size	Number of neighbor SNPs to be possibly included in the model imputing this particular SNP. Default is 200.
p.train	Proportion of non missing genotypes that are used for training the imputation model while the rest is used to assess the accuracy of this imputation model. Default is 0.8.

n.cor	Number of rows that are used to estimate correlations. Default uses them all.
seed	An integer, for reproducibility. Default doesn't use seeds.
ncores	Number of cores used. Default doesn't use parallelism. You may use <a href="#">nb_cores</a> .

**Value**

An [FBM](#) with

- the proportion of missing values by SNP (first row),
- the estimated proportion of imputation errors by SNP (second row).

**See Also**

[snp\\_fastImputeSimple\(\)](#)

**Examples**

```
## Not run:

fake <- snp_attachExtdata("example-missing.bed")
G <- fake$genotypes
CHR <- fake$map$chromosome
infos <- snp_fastImpute(G, CHR)
infos[, 1:5]

# Still missing values
big_counts(G, ind.col = 1:10)
# You need to change the code of G
# To make this permanent, you need to save (modify) the file on disk
fake$genotypes$code256 <- CODE_IMPUTE_PRED
fake <- snp_save(fake)
big_counts(fake$genotypes, ind.col = 1:10)

# Plot for post-checking
## Here there is no SNP with more than 1% error (estimated)
pvals <- c(0.01, 0.005, 0.002, 0.001); colvals <- 2:5
df <- data.frame(pNA = infos[1, ], pError = infos[2, ])

# base R
plot(subset(df, pNA > 0.001), pch = 20)
idc <- lapply(seq_along(pvals), function(i) {
  curve(pvals[i] / x, from = 0, lwd = 2,
        col = colvals[i], add = TRUE)
})
legend("topright", legend = pvals, title = "p(NA & Error)",
      col = colvals, lty = 1, lwd = 2)

# ggplot2
library(ggplot2)
Reduce(function(p, i) {
  p + stat_function(fun = function(x) pvals[i] / x, color = colvals[i])
})
```

```

}, x = seq_along(pvals), init = ggplot(df, aes(pNA, pError))) +
  geom_point() +
  coord_cartesian(ylim = range(df$pError, na.rm = TRUE)) +
  theme_bigstatsr()

## End(Not run)

```

---

snp\_fastImputeSimple *Fast imputation*

---

### Description

Fast imputation via mode, mean, sampling according to allele frequencies, or 0.

### Usage

```

snp_fastImputeSimple(
  Gna,
  method = c("mode", "mean0", "mean2", "random"),
  ncores = 1
)

```

### Arguments

Gna	A <a href="#">FBM.code256</a> (typically <bigSNP>\$genotypes). You can have missing values in these data.
method	Either "random" (sampling according to allele frequencies), "mean0" (rounded mean), "mean2" (rounded mean to 2 decimal places), "mode" (most frequent call).
ncores	Number of cores used. Default doesn't use parallelism. You may use <a href="#">nb_cores</a> .

### Value

A new [FBM.code256](#) object (same file, but different code).

### See Also

[snp\\_fastImpute\(\)](#)

### Examples

```

big SNP <- snp_attachExtdata("example-missing.bed")
G <- big SNP$genotypes
G[, 2] # some missing values
G2 <- snp_fastImputeSimple(G)
G2[, 2] # no missing values anymore
G[, 2] # imputed, but still returning missing values
G$copy(code = CODE_IMPUTE_PRED)[, 2] # need to decode imputed values

```

```
G$copy(code = c(0, 1, 2, rep(0, 253)))[, 2] # "imputation" by 0
```

---

snp_fst	<i>Fixation index (Fst)</i>
---------	-----------------------------

---

### Description

Fixation index (Fst), either per variant, or genome-wide

### Usage

```
snp_fst(list_df_af, min_maf = 0, overall = FALSE)
```

### Arguments

list_df_af	List of data frames with \$af (allele frequency per variant) and \$N (sample size per variant). Typically, the outputs of <code>bed_MAF()</code> . Each new data frame of the list should correspond to a different population.
min_maf	Minimum MAF threshold (for the average of populations) to be included in the final results. Default is 0 (remove monomorphic variants).
overall	Whether to compute Fst genome-wide (TRUE) or per variant (FALSE, the default).

### Value

If overall, then one value, otherwise a value for each variant with missing values for the variants not passing min\_maf. This should be equivalent to using `'--fst --within'` in PLINK.

### References

Weir, B. S., & Cockerham, C. C. (1984). Estimating F-statistics for the analysis of population structure. *Evolution*, 1358-1370.

### Examples

```
bedfile <- system.file("extdata", "example.bed", package = "bigsnpr")
obj.bed <- bed(bedfile)

pop <- rep(1:3, c(143, 167, 207))
ind_pop <- split(seq_along(pop), pop)
list_df_af <- lapply(ind_pop, function(ind) bed_MAF(obj.bed, ind.row = ind))

snp_fst(list_df_af)
snp_fst(list_df_af[c(1, 2)], overall = TRUE)
snp_fst(list_df_af[c(1, 3)], overall = TRUE)
snp_fst(list_df_af[c(3, 2)], overall = TRUE)
```

---

`snp_gc`*Genomic Control*

---

**Description**

Genomic Control

**Usage**`snp_gc(gwas)`**Arguments**

`gwas` A `mhtest` object with the p-values associated with each SNP. Typically, the output of `big_univLinReg`, `big_univLogReg` or `snp_pcadapt`.

**Value**

A `ggplot2` object. You can plot it using the `print` method. You can modify it as you wish by adding layers. You might want to read [this chapter](#) to get more familiar with the package **ggplot2**.

**References**

Devlin, B., & Roeder, K. (1999). Genomic control for association studies. *Biometrics*, 55(4), 997-1004.

**Examples**

```
set.seed(9)

test <- snp_attachExtdata()
G <- test$genotypes
y <- rnorm(nrow(G))

gwas <- big_univLinReg(G, y)
snp_qq(gwas)
gwas_gc <- snp_gc(gwas) # change attr(gwas_gc, "transfo")

snp_qq(gwas_gc)
# The next plot should be prettier with a real dataset
snp_manhattan(gwas_gc,
              infos.chr = test$map$chromosome,
              infos.pos = test$map$physical.pos)

p <- snp_qq(gwas_gc) + ggplot2::aes(text = asPlotlyText(test$map))
## Not run: plotly::ggplotly(p, tooltip = "text")
```

---

snp\_getSampleInfos      *Get sample information*

---

## Description

Get information of individuals by matching from an external file.

## Usage

```
snp_getSampleInfos(  
  x,  
  df.or.files,  
  col.family.ID = 1,  
  col.sample.ID = 2,  
  col.infos = -c(1, 2),  
  pair.sep = "-_",  
  ...  
)
```

## Arguments

x	A <a href="#">bigSNP</a> .
df.or.files	Either <ul style="list-style-type: none"><li>• A <code>data.frame</code>,</li><li>• A character vector of file names where to find at the information you want. You should have one column for family IDs and one for sample IDs.</li></ul>
col.family.ID	Index of the column containing the family IDs to match with those of the study. Default is the second one.
col.sample.ID	Index of the column containing the sample IDs to match with those of the study. Default is the first one.
col.infos	Indices of the column containing the information you want. Default is all but the first and the second columns.
pair.sep	Separator used for concatenation family and sample IDs in order to match easier. Default is "-_".
...	Any additional parameter to pass to <code>bigreadr::fread2()</code> . Particularly, option <code>header = FALSE</code> is sometimes needed.

## Value

The requested information as a `data.frame`.

## See Also

[list.files](#)

**Examples**

```

test <- snp_attachExtdata()
# Just after reading
rle(test$fam$family.ID)
# Get populations clusters from external files
files <- system.file("extdata", paste0("cluster", 1:3), package = "bigsnp")
bigreadr::fread2(files[1])
# need header option
bigreadr::fread2(files[1], header = FALSE)
infos <- snp_getSampleInfos(test, files, header = FALSE)
rle(infos[[1]])

```

---

snp\_lassosum2

*lassosum2*


---

**Description**

lassosum2

**Usage**

```

snp_lassosum2(
  corr,
  df_beta,
  delta = c(0.001, 0.01, 0.1, 1),
  nlambda = 30,
  lambda.min.ratio = 0.01,
  dfmax = 2e+05,
  maxiter = 1000,
  tol = 1e-05,
  ncores = 1
)

```

**Arguments**

corr	Sparse correlation matrix as an <a href="#">SFBM</a> . If corr is a dsCMatrix or a dgCMatrix, you can use as_SFBM(corr).
df_beta	A data frame with 3 columns: <ul style="list-style-type: none"> <li>• \$beta: effect size estimates</li> <li>• \$beta_se: standard errors of effect size estimates</li> <li>• \$n_eff: sample size when estimating beta (in the case of binary traits, this is <math>4 / (1 / n_{\text{control}} + 1 / n_{\text{case}})</math>)</li> </ul>
delta	Vector of shrinkage parameters to try (L2-regularization). Default is $c(0.001, 0.01, 0.1, 1)$ .
nlambda	Number of different lambdas to try (L1-regularization). Default is 30.



lambda.min.ratio	Ratio between last and first lambdas to try. Default is 0.01.
dfmax	Maximum number of non-zero effects in the model. Default is 200e3.
maxiter	Maximum number of iterations before convergence. Default is 1000.
tol	Tolerance parameter for assessing convergence. Default is 1e-5.
ncores	Number of cores used. Default doesn't use parallelism. You may use <a href="#">nb_cores</a> .

**Value**

A matrix of effect sizes, one vector (column) for each row in `attr(<res>, "grid_param")`. Missing values are returned when strong divergence is detected.

---

snp_ldpred2_inf	<i>LDpred2</i>
-----------------	----------------

---

**Description**

LDpred2. Tutorial at <https://privefl.github.io/bigsnpr/articles/LDpred2.html>.

**Usage**

```
snp_ldpred2_inf(corr, df_beta, h2)
```

```
snp_ldpred2_grid(
  corr,
  df_beta,
  grid_param,
  burn_in = 50,
  num_iter = 100,
  ncores = 1,
  return_sampling_betas = FALSE
)
```

```
snp_ldpred2_auto(
  corr,
  df_beta,
  h2_init,
  vec_p_init = 0.1,
  burn_in = 500,
  num_iter = 200,
  sparse = FALSE,
  verbose = FALSE,
  report_step = num_iter + 1L,
  allow_jump_sign = TRUE,
  shrink_corr = 1,
  alpha_bounds = c(-1.5, 0.5),
  ncores = 1
)
```

**Arguments**

corr	Sparse correlation matrix as an <a href="#">SFBM</a> . If corr is a dsCMatrix or a dgCMatrix, you can use <code>as_SFBM(corr)</code> .
df_beta	A data frame with 3 columns: <ul style="list-style-type: none"> <li>• <code>\$beta</code>: effect size estimates</li> <li>• <code>\$beta_se</code>: standard errors of effect size estimates</li> <li>• <code>\$n_eff</code>: sample size when estimating beta (in the case of binary traits, this is <math>4 / (1 / n_{\text{control}} + 1 / n_{\text{case}})</math>)</li> </ul>
h2	Heritability estimate.
grid_param	A data frame with 3 columns as a grid of hyper-parameters: <ul style="list-style-type: none"> <li>• <code>\$p</code>: proportion of causal variants</li> <li>• <code>\$h2</code>: heritability (captured by the variants used)</li> <li>• <code>\$sparse</code>: boolean, whether a sparse model is sought They can be run in parallel by changing <code>ncores</code>.</li> </ul>
burn_in	Number of burn-in iterations.
num_iter	Number of iterations after burn-in.
ncores	Number of cores used. Default doesn't use parallelism. You may use <a href="#">nb_cores</a> .
return_sampling_betas	Whether to return all sampling betas (after burn-in)? This is useful for assessing the uncertainty of the PRS at the individual level (see <a href="#">doi:10.1101/2020.11.30.403188</a> ). Default is FALSE (only returns the averaged final vectors of betas). If TRUE, only one set of parameters is allowed.
h2_init	Heritability estimate for initialization.
vec_p_init	Vector of initial values for p. Default is 0.1.
sparse	In LDpred2-auto, whether to also report a sparse solution by running LDpred2-grid with the estimates of p and h2 from LDpred2-auto, and sparsity enabled. Default is FALSE.
verbose	Whether to print "p // h2" estimates at each iteration. Disabled when parallelism is used.
report_step	Step to report sampling betas (after burn-in and before unscaling). Nothing is reported by default. If using <code>num_iter = 200</code> and <code>report_step = 20</code> , then 10 vectors of sampling betas are reported (as a sparse matrix with 10 columns).
allow_jump_sign	Whether to allow for effects sizes to change sign in consecutive iterations? Default is TRUE (normal sampling). You can use FALSE to force effects to go through 0 first before changing sign. Setting this parameter to FALSE could be useful to prevent instability (oscillation and ultimately divergence) of the Gibbs sampler. This would also be useful for accelerating convergence of chains with a large initial value for p.
shrink_corr	Shrinkage multiplicative coefficient to apply to off-diagonal elements of the correlation matrix. Default is 1 (unchanged). You can use e.g. 0.95 to add a bit of regularization.
alpha_bounds	Boundaries for the estimates of $\alpha$ . Default is <code>c(-1.5, 0.5)</code> . You can use the same value twice to fix $\alpha$ .

**Details**

For reproducibility, `set.seed()` can be used to ensure that two runs of LDpred2 give the exact same results (since v1.10).

**Value**

`snp_ldpred2_inf`: A vector of effects, assuming an infinitesimal model.

`snp_ldpred2_grid`: A matrix of effect sizes, one vector (column) for each row of `grid_param`. Missing values are returned when strong divergence is detected. If using `return_sampling_betas`, each column corresponds to one iteration instead (after burn-in).

`snp_ldpred2_auto`: A list (over `vec_p_init`) of lists with

- `$beta_est`: vector of effect sizes (on the allele scale)
- `$beta_est_sparse` (only when `sparse = TRUE`): sparse vector of effect sizes
- `$postp_est`: vector of posterior probabilities of being causal
- `$corr_est`, the "imputed" correlations between variants and phenotypes, which can be used for post-QCing variants by comparing those to `with(df_beta, beta / sqrt(n_eff * beta_se^2 + beta^2))`
- `$sample_beta`: sparse matrix of sampling betas (see parameter `report_step`), *not* on the allele scale, for which you need to multiply by `with(df_beta, sqrt(n_eff * beta_se^2 + beta^2))`
- `$path_p_est`: full path of p estimates (including burn-in); useful to check convergence of the iterative algorithm
- `$path_h2_est`: full path of h2 estimates (including burn-in); useful to check convergence of the iterative algorithm
- `$path_alpha_est`: full path of alpha estimates (including burn-in); useful to check convergence of the iterative algorithm
- `$h2_est`: estimate of the (SNP) heritability (also see [coef\\_to\\_liab](#))
- `$p_est`: estimate of p, the proportion of causal variants
- `$alpha_est`: estimate of alpha, the parameter controlling the relationship between allele frequencies and expected effect sizes
- `$h2_init` and `$p_init`: input parameters, for convenience

---

snp\_ldsc

*LD score regression*


---

**Description**

LD score regression

**Usage**

```
snp_ldsc(
  ld_score,
  ld_size,
  chi2,
  sample_size,
  blocks = 200,
  intercept = NULL,
  chi2_thr1 = 30,
  chi2_thr2 = Inf,
  ncores = 1
)
```

```
snp_ldsc2(corr, df_beta, blocks = NULL, intercept = 1, ncores = 1, ...)
```

**Arguments**

ld_score	Vector of LD scores.
ld_size	Number of variants used to compute ld_score.
chi2	Vector of chi-squared statistics.
sample_size	Sample size of GWAS corresponding to chi-squared statistics. Possibly a vector, or just a single value.
blocks	Either a single number specifying the number of blocks, or a vector of integers specifying the block number of each chi2 value. Default is 200 for snp_ldsc(), dividing into 200 blocks of approximately equal size. NULL can also be used to skip estimating standard errors, which is the default for snp_ldsc2().
intercept	You can constrain the intercept to some value (e.g. 1). Default is NULL in snp_ldsc() (the intercept is estimated) and is 1 in snp_ldsc2() (the intercept is fixed to 1). This is equivalent to parameter --intercept-h2.
chi2_thr1	Threshold on chi2 in step 1. Default is 30. This is equivalent to parameter --two-step.
chi2_thr2	Threshold on chi2 in step 2. Default is Inf (none).
ncores	Number of cores used. Default doesn't use parallelism. You may use <a href="#">nb_cores</a> .
corr	Sparse correlation matrix. Can also be an <a href="#">SFBM</a> .
df_beta	A data frame with 3 columns: <ul style="list-style-type: none"> <li>• \$beta: effect size estimates</li> <li>• \$beta_se: standard errors of effect size estimates</li> <li>• \$n_eff: sample size when estimating beta (in the case of binary traits, this is <math>4 / (1 / n_{\text{control}} + 1 / n_{\text{case}})</math>)</li> </ul>
...	Arguments passed on to <a href="#">snp_ldsc</a>

**Value**

Vector of 4 values (or only the first 2 if blocks = NULL):

- [["int"]]: LDSC regression intercept,
- [["int\_se"]]: SE of this intercept,
- [["h2"]]: LDSC regression estimate of (SNP) heritability (also see [coef\\_to\\_liab](#)),
- [["h2\_se"]]: SE of this heritability estimate.

**Examples**

```
big SNP <- snp_attachExtdata()
G <- big SNP$genotypes
y <- big SNP$fam$affection - 1
corr <- snp_cor(G, ind.col = 1:1000)

gwas <- big_univLogReg(G, y, ind.col = 1:1000)
df_beta <- data.frame(beta = gwas$estim, beta_se = gwas$std.err,
                     n_eff = 4 / (1 / sum(y == 0) + 1 / sum(y == 1)))

snp_ldsc2(corr, df_beta)
snp_ldsc2(corr, df_beta, blocks = 20, intercept = NULL)
```

---

snp\_ldsplit

*Independent LD blocks*


---

**Description**

Split a correlation matrix in blocks as independent as possible. This finds the splitting in blocks that minimizes the sum of squared correlation between these blocks (i.e. everything outside these blocks). In case of equivalent splits, it then minimizes the sum of squared sizes of the blocks.

**Usage**

```
snp_ldsplit(
  corr,
  thr_r2,
  min_size,
  max_size,
  max_K = 500,
  max_r2 = 0.3,
  max_cost = ncol(corr)/200
)
```

**Arguments**

<code>corr</code>	Sparse correlation matrix. Usually, the output of <code>snp_cor()</code> .
<code>thr_r2</code>	Threshold under which squared correlations are ignored. This is useful to avoid counting noise, which should give clearer patterns of costs vs. number of blocks. It is therefore possible to have a splitting cost of 0. If this parameter is used, then <code>corr</code> can be computed using the same parameter in <code>snp_cor()</code> (to increase the sparsity of the resulting matrix).
<code>min_size</code>	Minimum number of variants in each block. This is used not to have a disproportionate number of small blocks.
<code>max_size</code>	Maximum number of variants in each block. This is used not to have blocks that are too large, e.g. to limit computational and memory requirements of applications that would use these blocks. For some long-range LD regions, it may be needed to allow for large blocks. You can now provide a vector of values to try.
<code>max_K</code>	Maximum number of blocks to consider. All optimal solutions for <code>K</code> from 1 to <code>max_K</code> will be returned. Some of these <code>K</code> might not have any corresponding solution due to the limitations in size of the blocks. For example, splitting 10,000 variants in blocks with at least 500 and at most 2000 variants implies that there are at least 5 and at most 20 blocks. Then, the choice of <code>K</code> depends on the application, but a simple solution is to choose the largest <code>K</code> for which the cost is lower than some threshold. Default is 500.
<code>max_r2</code>	Maximum squared correlation allowed for one pair of variants in two different blocks. This is used to make sure that strong correlations are not discarded and also to speed up the algorithm. Default is 0.3.
<code>max_cost</code>	Maximum cost reported. Default is <code>ncol(corr) / 200</code> .

**Value**

Either NULL when no block splitting satisfies the conditions, or a tibble with seven columns:

- `$max_size`: Input parameter, useful when providing a vector of values to try.
- `$n_block`: Number of blocks.
- `$cost`: The sum of squared correlations outside the blocks.
- `$cost2`: The sum of squared sizes of the blocks.
- `$perc_kept`: Percentage of initial non-zero values kept within the blocks defined.
- `$all_last`: Last index of each block.
- `$all_size`: Sizes of the blocks.
- `$block_num`: Resulting block numbers for each variant. This is not reported anymore, but can be computed with `rep(seq_along(all_size), all_size)`.

**Examples**

```
## Not run:

corr <- readRDS(url("https://www.dropbox.com/s/65u96jf7y32j2mj/spMat.rds?raw=1"))

# adjust `THR_R2` depending on sample size used to compute corr
```

```

# use e.g. 0.05 for small sample sizes, and 0.01 for large sample sizes
THR_R2 <- 0.02
m <- ncol(corr)
(SEQ <- round(seq_log(m / 30, m / 5, length.out = 10)))
# replace `min_size` by e.g. 100 for larger data
(res <- snp_ldsplit(corr, thr_r2 = THR_R2, min_size = 10, max_size = SEQ))

# add the variant block IDs corresponding to each split
res$block_num <- lapply(res$all_size, function(.) rep(seq_along(.), .))

library(ggplot2)
# trade-off cost / number of blocks
qplot(n_block, cost, color = factor(max_size, SEQ), data = res) +
  theme_bw(14) +
  scale_y_log10() +
  theme(legend.position = "top") +
  labs(x = "Number of blocks", color = "Maximum block size",
       y = "Sum of squared correlations outside blocks")

# trade-off cost / number of non-zero values
qplot(perc_kept, cost, color = factor(max_size, SEQ), data = res) +
  theme_bw(14) +
  # scale_y_log10() +
  theme(legend.position = "top") +
  labs(x = "Percentage of non-zero values kept", color = "Maximum block size",
       y = "Sum of squared correlations outside blocks")

# trade-off cost / sum of squared sizes
qplot(cost2, cost, color = factor(max_size, SEQ), data = res) +
  theme_bw(14) +
  scale_y_log10() +
  geom_vline(xintercept = 0) +
  theme(legend.position = "top") +
  labs(x = "Sum of squared blocks", color = "Maximum block size",
       y = "Sum of squared correlations outside blocks")

## Pick one solution and visualize blocks
library(dplyr)
all_ind <- res %>%
  arrange(cost2 * sqrt(5 + cost)) %>%
  print() %>%
  slice(1) %>%
  pull(all_last)

## Transform sparse representation into (i,j,x) triplets
corrT <- as(corr, "dgTMatrix")
upper <- (corrT@i <= corrT@j & corrT@x^2 >= THR_R2)
df <- data.frame(
  i = corrT@i[upper] + 1L,
  j = corrT@j[upper] + 1L,
  r2 = corrT@x[upper]^2
)

```

```

df$y <- (df$j - df$i) / 2

ggplot(df) +
  geom_point(aes(i + y, y, alpha = r2)) +
  theme_minimal() +
  theme(axis.text.y = element_blank(), axis.ticks.y = element_blank(),
        strip.background = element_blank(), strip.text.x = element_blank()) +
  scale_alpha_continuous(range = 0:1) +
  scale_x_continuous(expand = c(0.02, 0.02), minor_breaks = NULL,
                    breaks = head(all_ind[[1]], -1) + 0.5) +
  facet_wrap(~ cut(i + y, 4), scales = "free", ncol = 1) +
  labs(x = "Position", y = NULL)

## End(Not run)

```

---

snp\_ld\_scores

*LD scores*


---

## Description

LD scores

## Usage

```

snp_ld_scores(
  Gna,
  ind.row = rows_along(Gna),
  ind.col = cols_along(Gna),
  size = 500,
  infos.pos = NULL,
  ncores = 1
)

bed_ld_scores(
  obj.bed,
  ind.row = rows_along(obj.bed),
  ind.col = cols_along(obj.bed),
  size = 500,
  infos.pos = NULL,
  ncores = 1
)

```

## Arguments

Gna	A <a href="#">FBM.code256</a> (typically <bigSNP>\$genotypes). You can have missing values in these data.
ind.row	An optional vector of the row indices (individuals) that are used. If not specified, all rows are used. <b>Don't use negative indices.</b>



ind.col	An optional vector of the column indices (SNPs) that are used. If not specified, all columns are used. <b>Don't use negative indices.</b>
size	For one SNP, window size around this SNP to compute correlations. Default is 500. If not providing infos.pos (NULL, the default), this is a window in number of SNPs, otherwise it is a window in kb (genetic distance).
infos.pos	Vector of integers specifying the physical position on a chromosome (in base pairs) of each SNP. Typically <code>&lt;bigSNP&gt;\$map\$physical.pos</code> .
ncores	Number of cores used. Default doesn't use parallelism. You may use <code>nb_cores</code> .
obj.bed	Object of type <code>bed</code> , which is the mapping of some bed file. Use <code>obj.bed &lt;- bed.bedfile</code> to get this object.

**Value**

A vector of LD scores. For each variant, this is the sum of squared correlations with the neighboring variants (including itself).

**Examples**

```
test <- snp_attachExtdata()
G <- test$genotypes

(ld <- snp_ld_scores(G, ind.col = 1:1000))
```

---

snp\_MAF

*MAF*


---

**Description**

Minor Allele Frequency.

**Usage**

```
snp_MAF(
  G,
  ind.row = rows_along(G),
  ind.col = cols_along(G),
  nploidy = 2,
  ncores = 1
)
```

**Arguments**

G	A <a href="#">FBM.code256</a> (typically <code>&lt;bigSNP&gt;\$genotypes</code> ). <b>You shouldn't have missing values.</b> Also, remember to do quality control, e.g. some algorithms in this package won't work if you use SNPs with 0 MAF.
ind.row	An optional vector of the row indices (individuals) that are used. If not specified, all rows are used. <b>Don't use negative indices.</b>
ind.col	An optional vector of the column indices (SNPs) that are used. If not specified, all columns are used. <b>Don't use negative indices.</b>
nploidy	Number of trials, parameter of the binomial distribution. Default is 2, which corresponds to diploidy, such as for the human genome.
ncores	Number of cores used. Default doesn't use parallelism. You may use <a href="#">nb_cores</a> .

**Value**

A vector of MAFs, corresponding to `ind.col`.

**Examples**

```
obj.bigsnp <- snp_attachExtdata()
str(maf <- snp_MAF(obj.bigsnp$genotypes))
```

---

snp\_manhattan

*Manhattan plot*


---

**Description**

Creates a manhattan plot.

**Usage**

```
snp_manhattan(
  gwas,
  infos.chr,
  infos.pos,
  colors = c("black", "grey60"),
  dist.sep.chrs = 1e+07,
  ind.highlight = integer(0),
  col.highlight = "red",
  labels = NULL,
  npoints = NULL,
  coeff = 1
)
```

**Arguments**

gwas	A mhtest object with the p-values associated with each SNP. Typically, the output of <code>big_univLinReg</code> , <code>big_univLogReg</code> or <code>snp_pcadapt</code> .
infos.chr	Vector of integers specifying each SNP's chromosome. Typically <code>&lt;bigSNP&gt;\$map\$chromosome</code> .
infos.pos	Vector of integers specifying the physical position on a chromosome (in base pairs) of each SNP. Typically <code>&lt;bigSNP&gt;\$map\$physical.pos</code> .
colors	Colors used for each chromosome (they are recycled). Default is an alternation of black and gray.
dist.sep.chrs	"Physical" distance that separates two chromosomes. Default is 10 Mbp.
ind.highlight	Indices of SNPs you want to highlight (of interest). Default doesn't highlight any SNPs.
col.highlight	Color used for highlighting SNPs. Default uses red.
labels	Labels of the x axis. Default uses the number of the chromosome there are in <code>infos.chr(sort(unique(infos.chr)))</code> . This may be useful to restrict the number of labels so that they are not overlapping.
npoints	Number of points to keep (ranked by p-value) in order to get a lighter object (and plot). Default doesn't cut anything. If used, the resulting object will have an attribute called <code>subset</code> giving the indices of the kept points.
coeff	Relative size of text. Default is 1.

**Details**

If you don't have information of chromosome and position, you should simply use `plot` instead.

**Value**

A `ggplot2` object. You can plot it using the `print` method. You can modify it as you wish by adding layers. You might want to read [this chapter](#) to get more familiar with the package **ggplot2**.

**Examples**

```
set.seed(9)

test <- snp_attachExtdata()
G <- test$genotypes
y <- rnorm(nrow(G))

gwas <- big_univLinReg(G, y)
snp_qq(gwas)
gwas_gc <- snp_gc(gwas) # change attr(gwas_gc, "transfo")

snp_qq(gwas_gc)
# The next plot should be prettier with a real dataset
snp_manhattan(gwas_gc,
              infos.chr = test$map$chromosome,
```

```

infos.pos = test$map$physical.pos)

p <- snp_qq(gwas_gc) + ggplot2::aes(text = asPlotlyText(test$map))
## Not run: plotly::ggplotly(p, tooltip = "text")

```

---

snp\_match

*Match alleles*


---

### Description

Match alleles between summary statistics and SNP information. Match by ("chr", "a0", "a1") and ("pos" or "rsid"), accounting for possible strand flips and reverse reference alleles (opposite effects).

### Usage

```

snp_match(
  sumstats,
  info_snp,
  strand_flip = TRUE,
  join_by_pos = TRUE,
  remove_dups = TRUE,
  match.min.prop = 0.2,
  return_flip_and_rev = FALSE
)

```

### Arguments

sumstats	A data frame with columns "chr", "pos", "a0", "a1" and "beta".
info_snp	A data frame with columns "chr", "pos", "a0" and "a1".
strand_flip	Whether to try to flip strand? (default is TRUE) If so, ambiguous alleles A/T and C/G are removed.
join_by_pos	Whether to join by chromosome and position (default), or instead by rsid.
remove_dups	Whether to remove duplicates (same physical position)? Default is TRUE.
match.min.prop	Minimum proportion of variants in the smallest data to be matched, otherwise stops with an error. Default is 20%.
return_flip_and_rev	Whether to return internal boolean variables "_FLIP_" and "_REV_" (whether the alleles were flipped and/or reversed). Default is FALSE. Values in column \$beta are multiplied by -1 for variants with alleles reversed.

### Value

A single data frame with matched variants. Values in column \$beta are multiplied by -1 for variants with alleles reversed.

**See Also**[snp\\_modifyBuild](#)**Examples**

```

sumstats <- data.frame(
  chr = 1,
  pos = c(86303, 86331, 162463, 752566, 755890, 758144),
  a0 = c("T", "G", "C", "A", "T", "G"),
  a1 = c("G", "A", "T", "G", "A", "A"),
  beta = c(-1.868, 0.250, -0.671, 2.112, 0.239, 1.272),
  p = c(0.860, 0.346, 0.900, 0.456, 0.776, 0.383)
)

info_snp <- data.frame(
  id = c("rs2949417", "rs115209712", "rs143399298", "rs3094315", "rs3115858"),
  chr = 1,
  pos = c(86303, 86331, 162463, 752566, 755890),
  a0 = c("T", "A", "G", "A", "T"),
  a1 = c("G", "G", "A", "G", "A")
)

snp_match(sumstats, info_snp)
snp_match(sumstats, info_snp, strand_flip = FALSE)

```

snp\_MAX3

*MAX3 statistic***Description**

Compute the MAX3 statistic, which tests for three genetic models (additive, recessive and dominant).

**Usage**

```
snp_MAX3(Gna, y01.train, ind.train = rows_along(Gna), val = c(0, 0.5, 1))
```

**Arguments**

Gna	A <a href="#">FBM.code256</a> (typically <bigSNP>\$genotypes). You can have missing values in these data.
y01.train	Vector of responses, corresponding to ind.train. <b>Must be only 0s and 1s.</b>
ind.train	An optional vector of the row indices that are used, for the training part. If not specified, all rows are used. <b>Don't use negative indices.</b>
val	Computing $\max_{x \in \text{val}} Z_{CATT}^2(x)$ . <ul style="list-style-type: none"> <li>• Default is c(0, 0.5, 1) and corresponds to the <i>MAX3</i> statistic.</li> <li>• Only c(0, 1) corresponds to <i>MAX2</i>.</li> <li>• And only 0.5 corresponds to the Armitage trend test.</li> <li>• Finally, seq(0, 1, length.out = L) corresponds to <i>MAXL</i>.</li> </ul>

**Details**

**P-values associated with returned scores are in fact the minimum of the p-values of each test separately. Thus, they are biased downward.**

**Value**

An object of classes `mhtest` and `data.frame` returning one score by SNP. See `methods(class = "mhtest")`.

**References**

Zheng, G., Yang, Y., Zhu, X., & Elston, R. (2012). Robust Procedures. Analysis Of Genetic Association Studies, 151-206. doi:[10.1007/9781461422457\\_6](https://doi.org/10.1007/9781461422457_6).

**Examples**

```
set.seed(1)

# constructing a fake genotype big.matrix
N <- 50; M <- 1200
fake <- snp_fake(N, M)
G <- fake$genotypes
G[] <- sample(as.raw(0:3), size = length(G), replace = TRUE)
G[1:8, 1:10]

# Specify case/control phenotypes
fake$fam$affectation <- rep(1:2, each = N / 2)

# Get MAX3 statistics
y01 <- fake$fam$affectation - 1
str(test <- snp_MAX3(fake$genotypes, y01.train = y01))
# p-values are not well calibrated
snp_qq(test)
# genomic control is not of much help
snp_qq(snp_gc(test))

# Armitage trend test (well calibrated because only one test)
test2 <- snp_MAX3(fake$genotypes, y01.train = y01, val = 0.5)
snp_qq(test2)
```

---

snp\_modifyBuild

*Modify genome build*


---

**Description**

Modify the physical position information of a data frame when converting genome build using executable *liftOver*.

**Usage**

```
snp_modifyBuild(
  info_snp,
  liftOver,
  from = "hg18",
  to = "hg19",
  check_reverse = TRUE
)
```

**Arguments**

info_snp	A data frame with columns "chr" and "pos".
liftOver	Path to liftOver executable. Binaries can be downloaded at <a href="https://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/liftOver">https://hgdownload.cse.ucsc.edu/admin/exe/macOSX.x86_64/liftOver</a> for Mac and at <a href="https://hgdownload.cse.ucsc.edu/admin/exe/linux.x86_64/liftOver">https://hgdownload.cse.ucsc.edu/admin/exe/linux.x86_64/liftOver</a> for Linux.
from	Genome build to convert from. Default is hg18.
to	Genome build to convert to. Default is hg19.
check_reverse	Whether to discard positions for which we cannot go back to initial values by doing 'from -> to -> from'. Default is TRUE.

**Value**

Input data frame info\_snp with column "pos" in the new build.

**References**

Hinrichs, Angela S., et al. "The UCSC genome browser database: update 2006." *Nucleic acids research* 34.suppl\_1 (2006): D590-D598.

---

snp\_pcadapt

*Outlier detection*


---

**Description**

Method to detect genetic markers involved in biological adaptation. This provides a statistical tool for outlier detection based on Principal Component Analysis. This corresponds to the statistic based on mahalanobis distance, as implemented in package **pcadapt**.

**Usage**

```
snp_pcadapt(
  G,
  U.row,
  ind.row = rows_along(G),
  ind.col = cols_along(G),
  ncores = 1
)
```

```

)

bed_pcadapt(
  obj.bed,
  U.row,
  ind.row = rows_along(obj.bed),
  ind.col = cols_along(obj.bed),
  ncores = 1
)

```

### Arguments

G	A <a href="#">FBM.code256</a> (typically <code>&lt;bigSNP&gt;\$genotypes</code> ). <b>You shouldn't have missing values.</b> Also, remember to do quality control, e.g. some algorithms in this package won't work if you use SNPs with 0 MAF.
U.row	Left singular vectors (not scores, $U^T U = I$ ) corresponding to <code>ind.row</code> .
ind.row	An optional vector of the row indices (individuals) that are used. If not specified, all rows are used. <b>Don't use negative indices.</b>
ind.col	An optional vector of the column indices (SNPs) that are used. If not specified, all columns are used. <b>Don't use negative indices.</b>
ncores	Number of cores used. Default doesn't use parallelism. You may use <a href="#">nb_cores</a> .
obj.bed	Object of type <a href="#">bed</a> , which is the mapping of some bed file. Use <code>obj.bed &lt;- bed.bedfile</code> to get this object.

### Value

An object of classes `mhtest` and `data.frame` returning one score by SNP. See `methods(class = "mhtest")`.

### References

Luu, K., Bazin, E., & Blum, M. G. (2017). `pcadapt`: an R package to perform genome scans for selection based on principal component analysis. *Molecular ecology resources*, 17(1), 67-77.

### See Also

[snp\\_manhattan](#), [snp\\_qq](#) and [snp\\_gc](#).

### Examples

```

test <- snp_attachExtdata()
G <- test$genotypes
obj.svd <- big_SVD(G, fun.scaling = snp_scaleBinom(), k = 10)
plot(obj.svd) # there seems to be 3 "significant" components
pcadapt <- snp_pcadapt(G, obj.svd$u[, 1:3])
snp_qq(pcadapt)

```



---

snp\_plinkIBDQC      *Identity-by-descent*

---

### Description

Quality Control based on Identity-by-descent (IBD) computed by **PLINK 1.9** using its method-of-moments.

### Usage

```
snp_plinkIBDQC(
  plink.path,
  bedfile.in,
  bedfile.out = NULL,
  pi.hat = 0.08,
  ncores = 1,
  pruning.args = c(100, 0.2),
  do.blind.QC = TRUE,
  extra.options = "",
  verbose = TRUE
)
```

### Arguments

plink.path	Path to the executable of PLINK 1.9.
bedfile.in	Path to the input bedfile.
bedfile.out	Path to the output bedfile. Default is created by appending "_nore1" to prefix.in (bedfile.in without extension).
pi.hat	PI_HAT value threshold for individuals (first by pairs) to be excluded. Default is 0.08.
ncores	Number of cores used. Default doesn't use parallelism. You may use <a href="#">nb_cores</a> .
pruning.args	A vector of 2 pruning parameters, respectively the window size (in variant count) and the pairwise $r^2$ threshold (the step size is fixed to 1). Default is c(100, 0.2).
do.blind.QC	Whether to do QC with pi.hat without visual inspection. Default is TRUE. If FALSE, return the data.frame of the corresponding ".genome" file without doing QC. One could use <code>ggplot2::qplot(Z0, Z1, data = mydf, col = RT)</code> for visual inspection.
extra.options	Other options to be passed to PLINK as a string (for the IBD part). More options can be found at <a href="https://www.cog-genomics.org/plink/1.9/ibd">https://www.cog-genomics.org/plink/1.9/ibd</a> .
verbose	Whether to show PLINK log? Default is TRUE.

### Value

The path of the new bedfile. If no sample is filter, no new bed/bim/fam files are created and then the path of the input bedfile is returned.

## References

Chang, Christopher C, Carson C Chow, Laurent CAM Tellier, Shashaank Vattikuti, Shaun M Purcell, and James J Lee. 2015. *Second-generation PLINK: rising to the challenge of larger and richer datasets*. GigaScience 4 (1): 7. doi:10.1186/s1374201500478.

## See Also

[download\\_plink](#) [snp\\_plinkQC](#) [snp\\_plinkKINGQC](#)

## Examples

```
## Not run:

bedfile <- system.file("extdata", "example.bed", package = "bigsnpr")
plink <- download_plink()

bedfile <- snp_plinkIBDQC(plink, bedfile,
                        bedfile.out = tempfile(fileext = ".bed"),
                        ncores = 2)

df_rel <- snp_plinkIBDQC(plink, bedfile, do.blind.QC = FALSE, ncores = 2)
str(df_rel)

library(ggplot2)
qplot(Z0, Z1, data = df_rel, col = RT)
qplot(y = PI_HAT, data = df_rel) +
  geom_hline(yintercept = 0.2, color = "blue", linetype = 2)
snp_plinkRmSamples(plink, bedfile,
                  bedfile.out = tempfile(fileext = ".bed"),
                  df.or.files = subset(df_rel, PI_HAT > 0.2))

## End(Not run)
```

---

snp\_plinkKINGQC

*Relationship-based pruning*

---

## Description

Quality Control based on KING-robust kinship estimator. More information can be found at [https://www.cog-genomics.org/plink/2.0/distance#king\\_cutoff](https://www.cog-genomics.org/plink/2.0/distance#king_cutoff).

## Usage

```
snp_plinkKINGQC(
  plink2.path,
  bedfile.in,
  bedfile.out = NULL,
  thr.king = 2^-3.5,
```

```

    make.bed = TRUE,
    ncores = 1,
    extra.options = "",
    verbose = TRUE
  )

```

### Arguments

plink2.path	Path to the executable of PLINK 2.
bedfile.in	Path to the input bedfile.
bedfile.out	Path to the output bedfile. Default is created by appending "_norel" to prefix.in (bedfile.in without extension).
thr.king	Note that KING kinship coefficients are scaled such that duplicate samples have kinship 0.5, not 1. First-degree relations (parent-child, full siblings) correspond to ~0.25, second-degree relations correspond to ~0.125, etc. It is conventional to use a cutoff of ~0.354 ( $2^{-1.5}$ , the geometric mean of 0.5 and 0.25) to screen for monozygotic twins and duplicate samples, ~0.177 ( $2^{-2.5}$ ) to remove first-degree relations as well, and ~0.0884 ( $2^{-3.5}$ , <b>default</b> ) to remove second-degree relations as well, etc.
make.bed	Whether to create new bed/bim/fam files (default). Otherwise, returns a table with coefficients of related pairs.
ncores	Number of cores used. Default doesn't use parallelism. You may use <a href="#">nb_cores</a> .
extra.options	Other options to be passed to PLINK2 as a string.
verbose	Whether to show PLINK log? Default is TRUE.

### Value

See parameter `make-bed`.

### References

Manichaikul, Ani, Josyf C. Mychaleckyj, Stephen S. Rich, Kathy Daly, Michele Sale, and Wei-Min Chen. "Robust relationship inference in genome-wide association studies." *Bioinformatics* 26, no. 22 (2010): 2867-2873.

### See Also

[download\\_plink2](#) [snp\\_plinkQC](#)

### Examples

```

## Not run:

bedfile <- system.file("extdata", "example.bed", package = "bigsnpr")
plink2 <- download_plink2(AVX2 = FALSE)

bedfile2 <- snp_plinkKINGQC(plink2, bedfile,
                           bedfile.out = tempfile(fileext = ".bed"),

```

```

ncores = 2)

df_rel <- snp_plinkKINGQC(plink2, bedfile, make.bed = FALSE, ncores = 2)
str(df_rel)

## End(Not run)

```

---

snp\_plinkQC

*Quality Control*


---

## Description

Quality Control (QC) and possible conversion to *bed/bim/fam* files using **PLINK 1.9**.

## Usage

```

snp_plinkQC(
  plink.path,
  prefix.in,
  file.type = "--bfile",
  prefix.out = paste0(prefix.in, "_QC"),
  maf = 0.01,
  geno = 0.1,
  mind = 0.1,
  hwe = 1e-50,
  autosome.only = FALSE,
  extra.options = "",
  verbose = TRUE
)

```

## Arguments

plink.path	Path to the executable of PLINK 1.9.
prefix.in	Prefix (path without extension) of the dataset to be QCed.
file.type	Type of the dataset to be QCed. Default is "--bfile" and corresponds to bed/bim/fam files. You can also use "--file" for ped/map files, "--vcf" for a VCF file, or "--gzvcf" for a gzipped VCF. More information can be found at <a href="https://www.cog-genomics.org/plink/1.9/input">https://www.cog-genomics.org/plink/1.9/input</a> .
prefix.out	Prefix (path without extension) of the bed/bim/fam dataset to be created. Default is created by appending "_QC" to prefix.in.
maf	Minimum Minor Allele Frequency (MAF) for a SNP to be kept. Default is 0.01.
geno	Maximum proportion of missing values for a SNP to be kept. Default is 0.1.
mind	Maximum proportion of missing values for a sample to be kept. Default is 0.1.
hwe	Filters out all variants which have Hardy-Weinberg equilibrium exact test p-value below the provided threshold. Default is 1e-50.

autosome.only	Whether to exclude all unplaced and non-autosomal variants? Default is FALSE.
extra.options	Other options to be passed to PLINK as a string. More options can be found at <a href="https://www.cog-genomics.org/plink2/filter">https://www.cog-genomics.org/plink2/filter</a> . If using PLINK 2.0, you could e.g. use "--king-cutoff 0.0884" to remove some related samples at the same time of quality controls.
verbose	Whether to show PLINK log? Default is TRUE.

### Value

The path of the newly created bedfile.

### References

Chang, Christopher C, Carson C Chow, Laurent CAM Tellier, Shashaank Vattikuti, Shaun M Purcell, and James J Lee. 2015. *Second-generation PLINK: rising to the challenge of larger and richer datasets*. GigaScience 4 (1): 7. doi:10.1186/s1374201500478.

### See Also

[download\\_plink](#) [snp\\_plinkIBDQC](#)

### Examples

```
## Not run:

bedfile <- system.file("extdata", "example.bed", package = "bigsnpr")
prefix <- sub_bed(bedfile)
plink <- download_plink()
test <- snp_plinkQC(plink.path = plink,
                  prefix.in = prefix,
                  prefix.out = tempfile(),
                  file.type = "--bfile", # the default (for ".bed")
                  maf = 0.05,
                  geno = 0.05,
                  mind = 0.05,
                  hwe = 1e-10,
                  autosome.only = TRUE)

test

## End(Not run)
```

---

snp\_plinkRmSamples      *Remove samples*

---

### Description

Create new *bed/bim/fam* files by removing samples with PLINK.

**Usage**

```
snp_plinkRmSamples(
  plink.path,
  bedfile.in,
  bedfile.out,
  df.or.files,
  col.family.ID = 1,
  col.sample.ID = 2,
  ...,
  verbose = TRUE
)
```

**Arguments**

plink.path	Path to the executable of PLINK 1.9.
bedfile.in	Path to the input bedfile.
bedfile.out	Path to the output bedfile.
df.or.files	Either <ul style="list-style-type: none"> <li>• A data.frame,</li> <li>• A character vector of file names where to find at the information you want. You should have one column for family IDs and one for sample IDs.</li> </ul>
col.family.ID	Index of the column containing the family IDs to match with those of the study. Default is the second one.
col.sample.ID	Index of the column containing the sample IDs to match with those of the study. Default is the first one.
...	Any additional parameter to pass to <code>bigreadr::fread2()</code> . Particularly, option <code>header = FALSE</code> is sometimes needed.
verbose	Whether to show PLINK log? Default is TRUE.

**Value**

The path of the new bedfile.

**See Also**

[download\\_plink](#)

---

snp\_prodBGEN

*BGEN matrix product*

---

**Description**

Compute a matrix product between BGEN files and a matrix. This removes the need to read an intermediate FBM object with `snp_readBGEN()` to compute the product. Moreover, when using dosages, they are not rounded to two decimal places anymore.

**Usage**

```
snp_prodBGEN(
  bgenfiles,
  beta,
  list_snp_id,
  ind_row = NULL,
  bgi_dir = dirname(bgenfiles),
  read_as = c("dosage", "random"),
  block_size = 1000,
  ncores = 1
)
```

**Arguments**

bgenfiles	Character vector of paths to files with extension ".bgen". The corresponding ".bgen.bgi" index files must exist.
beta	A matrix (or a vector), with rows corresponding to list_snp_id.
list_snp_id	List (same length as the number of BGEN files) of character vector of SNP IDs to read. These should be in the form "<chr>_<pos>_<a1>_<a2>" (e.g. "1_88169_C_T" or "01_88169_C_T"). If you have one BGEN file only, just wrap your vector of IDs with list(). <b>This function assumes that these IDs are uniquely identifying variants.</b>
ind_row	An optional vector of the row indices (individuals) that are used. If not specified, all rows are used. <b>Don't use negative indices.</b>
bgi_dir	Directory of index files. Default is the same as bgenfiles.
read_as	How to read BGEN probabilities? Currently implemented: <ul style="list-style-type: none"> <li>• as dosages (rounded to two decimal places), the default,</li> <li>• as hard calls, randomly sampled based on those probabilities (similar to PLINK option '--hard-call-threshold random').</li> </ul>
block_size	Maximum size of temporary blocks (in number of variants). Default is 1000.
ncores	Number of cores used. Default doesn't use parallelism. You may use nb_cores().

**Value**

The product `bgen_data[ind_row, 'list_snp_id'] %*% beta`.

**See Also**

[snp\\_readBGEN\(\)](#)

snp\_PRS

PRS

## Description

Polygenic Risk Scores with possible clumping and thresholding.

## Usage

```
snp_PRS(
  G,
  betas.keep,
  ind.test = rows_along(G),
  ind.keep = cols_along(G),
  same.keep = rep(TRUE, length(ind.keep)),
  lpS.keep = NULL,
  thr.list = 0
)
```

## Arguments

G	A <a href="#">FBM.code256</a> (typically <code>&lt;bigSNP&gt;\$genotypes</code> ). <b>You shouldn't have missing values.</b> Also, remember to do quality control, e.g. some algorithms in this package won't work if you use SNPs with 0 MAF.
betas.keep	Numeric vector of weights associated with each SNP corresponding to <code>ind.keep</code> . You may want to see <a href="#">big_univLinReg</a> or <a href="#">big_univLogReg</a> .
ind.test	The individuals on whom to project the scores. Default uses all.
ind.keep	Column (SNP) indices to use (if using clumping, the output of <a href="#">snp_clumping</a> ). Default doesn't clump.
same.keep	A logical vector associated with <code>betas.keep</code> whether the reference allele is the same for G. Default is all TRUE (for example when you train the betas on the same dataset). Otherwise, use <a href="#">same_ref</a> .
lpS.keep	Numeric vector of $-\log_{10}(\text{p-value})$ associated with <code>betas.keep</code> . Default doesn't use thresholding.
thr.list	Threshold vector on <code>lpS.keep</code> at which SNPs are excluded if they are not significant enough. Default doesn't use thresholding.

## Value

A matrix of scores, where rows correspond to `ind.test` and columns correspond to `thr.list`.



**Examples**

```

test <- snp_attachExtdata()
G <- big_copy(test$genotypes, ind.col = 1:1000)
CHR <- test$map$chromosome[1:1000]
POS <- test$map$physical.position[1:1000]
y01 <- test$fam$affectation - 1

# PCA -> covariables
obj.svd <- snp_autoSVD(G, infos.chr = CHR, infos.pos = POS)

# train and test set
ind.train <- sort(sample(nrow(G), 400))
ind.test <- setdiff(rows_along(G), ind.train) # 117

# GWAS
gwas.train <- big_univLogReg(G, y01.train = y01[ind.train],
                             ind.train = ind.train,
                             covar.train = obj.svd$u[ind.train, ])

# clumping
ind.keep <- snp_clumping(G, infos.chr = CHR,
                        ind.row = ind.train,
                        S = abs(gwas.train$score))

# -log10(p-values) and thresholding
summary(lpS.keep <- -predict(gwas.train)[ind.keep])
thrs <- seq(0, 4, by = 0.5)
nb.pred <- sapply(thrs, function(thr) sum(lpS.keep > thr))

# PRS
prs <- snp_PRS(G, betas.keep = gwas.train$estim[ind.keep],
              ind.test = ind.test,
              ind.keep = ind.keep,
              lpS.keep = lpS.keep,
              thr.list = thrs)

# AUC as a function of the number of predictors
aucs <- apply(prs, 2, AUC, target = y01[ind.test])
library(ggplot2)
qplot(nb.pred, aucs) +
  geom_line() +
  scale_x_log10(breaks = nb.pred) +
  labs(x = "Number of predictors", y = "AUC") +
  theme_bigstatsr()

```

snp\_qq

*Q-Q plot***Description**

Creates a quantile-quantile plot from p-values from a GWAS study.

**Usage**

```
snp_qq(gwas, lambdaGC = TRUE, coeff = 1)
```

**Arguments**

gwas	A mhtest object with the p-values associated with each SNP. Typically, the output of <a href="#">big_univLinReg</a> , <a href="#">big_univLogReg</a> or <a href="#">snp_pcadapt</a> .
lambdaGC	Add the Genomic Control coefficient as subtitle to the plot?
coeff	Relative size of text. Default is 1.

**Value**

A ggplot2 object. You can plot it using the print method. You can modify it as you wish by adding layers. You might want to read [this chapter](#) to get more familiar with the package **ggplot2**.

**Examples**

```
set.seed(9)

test <- snp_attachExtdata()
G <- test$genotypes
y <- rnorm(nrow(G))

gwas <- big_univLinReg(G, y)
snp_qq(gwas)
gwas_gc <- snp_gc(gwas) # change attr(gwas_gc, "transfo")

snp_qq(gwas_gc)
# The next plot should be prettier with a real dataset
snp_manhattan(gwas_gc,
              infos.chr = test$map$chromosome,
              infos.pos = test$map$physical.pos)

p <- snp_qq(gwas_gc) + ggplot2::aes(text = asPlotlyText(test$map))
## Not run: plotly::ggplotly(p, tooltip = "text")
```

---

snp\_readBed

*Read PLINK files into a "bigSNP"*


---

**Description**

Functions to read bed/bim/fam files into a [bigSNP](#).

**Usage**

```
snp_readBed.bedfile, backingfile = sub_bed.bedfile))

snp_readBed2(
  bedfile,
  backingfile = sub_bed.bedfile),
  ind.row = rows_along.obj.bed),
  ind.col = cols_along.obj.bed),
  ncores = 1
)
```

**Arguments**

bedfile	Path to file with extension ".bed" to read. You need the corresponding ".bim" and ".fam" in the same directory.
backingfile	The path (without extension) for the backing files for the cache of the <a href="#">bigSNP</a> object. Default takes the bedfile without the ".bed" extension.
ind.row	An optional vector of the row indices (individuals) that are used. If not specified, all rows are used. <b>Don't use negative indices.</b>
ind.col	An optional vector of the column indices (SNPs) that are used. If not specified, all columns are used. <b>Don't use negative indices.</b>
ncores	Number of cores used. Default doesn't use parallelism. You may use <a href="#">nb_cores</a> .

**Details**

For more information on these formats, please visit [PLINK webpage](#). For other formats, please use PLINK to convert them in bedfiles, which require minimal space to store and are faster to read. For example, to convert from a VCF file, use the --vcf option. See [snp\\_plinkQC](#).

**Value**

The path to the RDS file that stores the bigSNP object. Note that this function creates one other file which stores the values of the Filebacked Big Matrix.

**You shouldn't read from PLINK files more than once.** Instead, use [snp\\_attach](#) to load the "bigSNP" object in any R session from backing files.

**Examples**

```
(bedfile <- system.file("extdata", "example.bed", package = "bigsnpr"))

# Reading the bedfile and storing the data in temporary directory
rds <- snp_readBed.bedfile, backingfile = tempfile())

# Loading the data from backing files
test <- snp_attach(rds)
```

```
str(test)
dim(G <- test$genotypes)
G[1:8, 1:8]
```

---

snp\_readBGEN                      *Read BGEN files into a "bigSNP"*

---

## Description

Function to read the UK Biobank BGEN files into a [bigSNP](#).

## Usage

```
snp_readBGEN(
  bgenfiles,
  backingfile,
  list_snp_id,
  ind_row = NULL,
  bgi_dir = dirname(bgenfiles),
  read_as = c("dosage", "random"),
  ncores = 1
)
```

## Arguments

bgenfiles	Character vector of paths to files with extension ".bgen". The corresponding ".bgen.bgi" index files must exist.
backingfile	The path (without extension) for the backing files (".bk" and ".rds") that are created by this function for storing the <a href="#">bigSNP</a> object.
list_snp_id	List (same length as the number of BGEN files) of character vector of SNP IDs to read. These should be in the form "<chr>_<pos>_<a1>_<a2>" (e.g. "1_88169_C_T" or "01_88169_C_T"). If you have one BGEN file only, just wrap your vector of IDs with <code>list()</code> . <b>This function assumes that these IDs are uniquely identifying variants.</b>
ind_row	An optional vector of the row indices (individuals) that are used. If not specified, all rows are used. <b>Don't use negative indices.</b>
bgi_dir	Directory of index files. Default is the same as bgenfiles.
read_as	How to read BGEN probabilities? Currently implemented: <ul style="list-style-type: none"> <li>• as dosages (rounded to two decimal places), the default,</li> <li>• as hard calls, randomly sampled based on those probabilities (similar to PLINK option '--hard-call-threshold random').</li> </ul>
ncores	Number of cores used. Default doesn't use parallelism. You may use <code>nb_cores()</code> .

## Details

For more information on this format, please visit [BGEN webpage](#).

This function is designed to read UK Biobank imputation files. This assumes that variants have been compressed with zlib, that there are only 2 possible alleles, and that each probability is stored on 8 bits. For example, if you use *qctool* to generate your own BGEN files, please make sure you are using options `'-ofiletype bgen_v1.2 -bgen-bits 8'`.

If the format is not the expected one, this will result in an error or even a crash of your R session. Another common source of error is due to corrupted files; e.g. if using UK Biobank files, compare the result of `tools::md5sum()` with the ones at <https://biobank.ndph.ox.ac.uk/ukb/refer.cgi?id=998>.

You can look at some example code from my papers on how to use this function:

- <https://github.com/privefl/paper-ldpred2/blob/master/code/prepare-genotypes.R#L1-L62>
- <https://github.com/privefl/paper4-bedpca/blob/master/code/missing-values-UKBB.R#L34-L75>
- <https://github.com/privefl/UKBiobank/blob/master/10-get-dosages.R>

## Value

The path to the RDS file `<backingfile>.rds` that stores the bigSNP object created by this function. Note that this function creates one other file which stores the values of the Filebacked Big Matrix.

**You shouldn't read from BGEN files more than once.** Instead, use [snp\\_attach](#) to load the "bigSNP" object in any R session from backing files.

---

snp_readBGI	<i>Read variant info from one BGI file</i>
-------------	--

---

## Description

Read variant info from one BGI file

## Usage

```
snp_readBGI(bgifile, snp_id = NULL)
```

## Arguments

bgifile	Path to one file with extension ".bgi".
snp_id	Character vector of SNP IDs. These should be in the form " <code>&lt;chr&gt;_&lt;pos&gt;_&lt;a1&gt;_&lt;a2&gt;</code> " (e.g. "1_88169_C_T" or "01_88169_C_T"). <b>This function assumes that these IDs are uniquely identifying variants.</b> Default is NULL, and returns information on all variants.

## Value

A data frame containing variant information.

---

snp_save	<i>Save modifications</i>
----------	---------------------------

---

### Description

Save a bigSNP after having made some modifications to it. As bigSNP is an S3 class, you can add any slot you want to an object of this class, then use `snp_save` to save these modifications in the corresponding ".rds" backing file.

### Usage

```
snp_save(x, version = NULL)
```

### Arguments

<code>x</code>	A <a href="#">bigSNP</a> .
<code>version</code>	the workspace format version to use. NULL specifies the current default version (3). The only other supported value is 2, the default from R 1.4.0 to R 3.5.0.

### Value

The (saved) bigSNP.

### Examples

```
set.seed(1)

# Reading example
test <- snp_attachExtdata()

# I can add whatever I want to an S3 class
test$map$`p-values` <- runif(nrow(test$map))
str(test$map)

# Reading again
rds <- test$genotypes$rds
test2 <- snp_attach(rds)
str(test2$map) # new slot wasn't saved

# Save it
snp_save(test)

# Reading again
test3 <- snp_attach(rds)
str(test3$map) # it is saved now

# The complicated code of this function
snp_save
```

---

snp_scaleAlpha	<i>Binomial(n, p) scaling</i>
----------------	-------------------------------

---

### Description

Binomial(n, p) scaling where n is fixed and p is estimated.

### Usage

```
snp_scaleAlpha(alpha = -1)
```

```
snp_scaleBinom(nploidy = 2)
```

### Arguments

alpha	Assumes that the average contribution (e.g. heritability) of a SNP of frequency $p$ is proportional to $[2p(1 - p)]^{1+\alpha}$ . The center is then $2p$ and the scale is $[2p(1 - p)]^{-\alpha/2}$ . Default is -1.
nploidy	Number of trials, parameter of the binomial distribution. Default is 2, which corresponds to diploidy, such as for the human genome.

### Details

You will probably not use this function as is but as the `fun.scaling` parameter of other functions of package `bigstatsr`.

### Value

A new **function** that returns a data.frame of two vectors "center" and "scale" which are of the length of `ind.col`.

### References

This scaling is widely used for SNP arrays. Patterson N, Price AL, Reich D (2006). Population Structure and Eigenanalysis. PLoS Genet 2(12): e190. [doi:10.1371/journal.pgen.0020190](https://doi.org/10.1371/journal.pgen.0020190).

### Examples

```
set.seed(1)

a <- matrix(0, 93, 170)
p <- 0.2
a[] <- rbinom(length(a), 2, p)
X <- add_code256(big_copy(a, type = "raw"), code = c(0, 1, 2, rep(NA, 253)))
X.svd <- big_SVD(X, fun.scaling = snp_scaleBinom())
str(X.svd)
plot(X.svd$center)
abline(h = 2 * p, col = "red")
```

```
plot(X.svd$scale)
abline(h = sqrt(2 * p * (1 - p)), col = "red")
```

snp\_simuPheno

*Simulate phenotypes***Description**

Simulate phenotypes using a linear model. When a prevalence is given, the liability threshold is used to convert liabilities to a binary outcome. The genetic and environmental liabilities are scaled such that the variance of the genetic liability is exactly equal to the requested heritability, and the variance of the total liability is equal to 1.

**Usage**

```
snp_simuPheno(
  G,
  h2,
  M,
  K = NULL,
  alpha = -1,
  ind.row = rows_along(G),
  ind.possible = cols_along(G),
  prob = NULL,
  effects.dist = c("gaussian", "laplace"),
  ncores = 1
)
```

**Arguments**

G	A <a href="#">FBM.code256</a> (typically <bigSNP>\$genotypes). <b>You shouldn't have missing values.</b> Also, remember to do quality control, e.g. some algorithms in this package won't work if you use SNPs with 0 MAF.
h2	Heritability.
M	Number of causal variants.
K	Prevalence. Default is NULL, giving a continuous trait.
alpha	Assumes that the average contribution (e.g. heritability) of a SNP of frequency $p$ is proportional to $[2p(1-p)]^{1+\alpha}$ . Default is -1.
ind.row	An optional vector of the row indices (individuals) that are used. If not specified, all rows are used. <b>Don't use negative indices.</b>
ind.possible	Indices of possible causal variants.
prob	Vector of probability weights for sampling causal indices. It can have 0s (discarded) and is automatically scaled to sum to 1. Default is NULL (all indices have the same probability).
effects.dist	Distribution of effects. Either "gaussian" (the default) or "laplace".
ncores	Number of cores used. Default doesn't use parallelism. You may use <a href="#">nb_cores</a> .



**Value**

A list with 3 elements:

- \$pheno: vector of phenotypes,
- \$set: indices of causal variants,
- \$effects: effect sizes (of scaled genotypes) corresponding to set.
- \$allelic\_effects: effect sizes, but on the allele scale (0|1|2).

---

snp\_split

*Split-parApply-Combine*


---

**Description**

A Split-Apply-Combine strategy to parallelize the evaluation of a function on each SNP, independently.

**Usage**

```
snp_split(infos.chr, FUN, combine, ncores = 1, ...)
```

**Arguments**

infos.chr	Vector of integers specifying each SNP's chromosome. Typically <code>&lt;bigSNP&gt;\$map\$chromosome</code> .
FUN	The function to be applied. It must take a <a href="#">FBM.code256</a> as first argument and <code>ind.chr</code> , an another argument to provide subsetting over SNPs. You can access the number of the chromosome by using <code>attr(ind.chr, "chr")</code> .
combine	function that is used by <a href="#">foreach</a> to process the tasks results as they generated. This can be specified as either a function or a non-empty character string naming the function. Specifying 'c' is useful for concatenating the results into a vector, for example. The values 'cbind' and 'rbind' can combine vectors into a matrix. The values '+' and '*' can be used to process numeric data. By default, the results are returned in a list.
ncores	Number of cores used. Default doesn't use parallelism. You may use <a href="#">nb_cores</a> .
...	Extra arguments to be passed to FUN.

**Details**

This function splits indices for each chromosome, then apply a given function to each part (chromosome) and finally combine the results.

**Value**

The result of [foreach](#).

**Examples**

```
# parallelize over chromosomes made easy
# examples of functions from this package
snp_pruning
snp_clumping
snp_fastImpute
```

---

snp\_subset

*Subset a bigSNP*


---

**Description**

Subset (copy) of a bigSNP, also stored on disk.

**Usage**

```
snp_subset(
  x,
  ind.row = rows_along(x$fam),
  ind.col = rows_along(x$map),
  backingfile = NULL
)

## S3 method for class 'bigSNP'
subset(
  x,
  ind.row = rows_along(x$fam),
  ind.col = rows_along(x$map),
  backingfile = NULL,
  ...
)
```

**Arguments**

x	A <a href="#">bigSNP</a> .
ind.row	Indices of the rows (individuals) to keep. Negative indices <b>can</b> be used to exclude row indices. Default: keep them all.
ind.col	Indices of the columns (SNPs) to keep. Negative indices <b>can</b> be used to exclude column indices. Default: keep them all.
backingfile	Prefix of the two new files created (".bk" and ".rds"). By default, it is automatically determined by appending "_sub" and a number to the prefix of the input bigSNP backing files.
...	Not used.

**Value**

The path to the RDS file that stores the bigSNP object.

**See Also**

[bigSNP](#)

**Examples**

```
str(test <- snp_attachExtdata())

# keep only first 50 samples and SNPs
rdsfile <- snp_subset(test, ind.row = 1:50, ind.col = 1:50)
str(snp_attach(rdsfile))

# remove only first 50 samples and SNPs
rdsfile2 <- snp_subset(test, ind.row = -(1:50), ind.col = -(1:50))
str(snp_attach(rdsfile2))
```

---

snp\_thr\_correct      *Thresholding and correction*

---

**Description**

P-value thresholding and correction of summary statistics for winner's curse.

**Usage**

```
snp_thr_correct(beta, beta_se, lpS, thr_lpS)
```

**Arguments**

beta	Vector of effect sizes.
beta_se	Vector of standard errors for beta. Either beta_se or lpS must be provided.
lpS	Vector of $-\log_{10}(\text{p-value})$ associated with beta. Either beta_se or lpS must be provided.
thr_lpS	Threshold on lpS ( $-\log_{10}(\text{p-value})$ ) at which variants are excluded if they not significant enough.

**Value**

beta after p-value thresholding and shrinkage.

**References**

Zhong, H., & Prentice, R. L. (2008). Bias-reduced estimators and confidence intervals for odds ratios in genome-wide association studies. *Biostatistics*, 9(4), 621-634.

**Examples**

```

beta <- rnorm(1000)
beta_se <- runif(1000, min = 0.3, max = 0.5)
new_beta <- snp_thr_correct(beta, beta_se = beta_se, thr_lpS = 1)
plot(beta / beta_se, new_beta / beta_se, pch = 20); abline(0, 1, col = "red")
plot(beta, new_beta, pch = 20); abline(0, 1, col = "red")

# Can provide -log10(p-values) instead of standard errors
lpval <- -log10(pchisq((beta / beta_se)^2, df = 1, lower.tail = FALSE))
new_beta2 <- snp_thr_correct(beta, lpS = lpval, thr_lpS = 1)
all.equal(new_beta2, new_beta)

```

---

snp\_writeBed

*Write PLINK files from a "bigSNP"*


---

**Description**

Function to write bed/bim/fam files from a [bigSNP](#). This will use the slot code **rounded** to write 0s, 1s, 2s or NAs.

**Usage**

```
snp_writeBed(x, bedfile, ind.row = rows_along(G), ind.col = cols_along(G))
```

**Arguments**

x	A <a href="#">bigSNP</a> .
bedfile	Path to file with extension ".bed" to create.
ind.row	An optional vector of the row indices (individuals) that are used. If not specified, all rows are used. <b>Don't use negative indices.</b>
ind.col	An optional vector of the column indices (SNPs) that are used. If not specified, all columns are used. <b>Don't use negative indices.</b>

**Value**

The input bedfile path.

**Examples**

```

N <- 17
M <- 911

fake <- snp_fake(N, M)
G <- fake$genotypes

```

```
G[] <- sample(as.raw(0:3), size = length(G), replace = TRUE)

# Write the object as a bed/bim/fam object
tmp <- tempfile(fileext = ".bed")
bed <- snp_writeBed(fake, tmp)

# Read this new file for the first time
rds <- snp_readBed(bed, backingfile = tempfile())
# Attach object in R session
fake2 <- snp_attach(rds)

# Same content
all.equal(fake$genotypes[], fake2$genotypes[])
all.equal(fake$fam, fake2$fam)
all.equal(fake$map, fake2$map)

# Two different backingfiles
fake$genotypes$backingfile
fake2$genotypes$backingfile
```

---

sub_bed	<i>Replace extension '.bed'</i>
---------	---------------------------------

---

## Description

Replace extension '.bed'

## Usage

```
sub_bed(path, replacement = "", stop_if_not_ext = TRUE)
```

## Arguments

path	String with extension '.bed'.
replacement	Replacement of '.bed'. Default replaces by nothing. Can be useful to replace e.g. by '.bim' or '.fam'.
stop_if_not_ext	If replacement != "", whether to error if replacement is not an extension (starting with a '.').

## Value

String with extension '.bed' replaced by replacement.

**Examples**

```
path <- "toto.bed"
sub_bed(path)
sub_bed(path, ".bim")
sub_bed(path, ".fam")
sub_bed(path, "_QC", stop_if_not_ext = FALSE)
```

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