Package 'rareMETALS'

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Type Package

Title Meta-Analysis of Gene-level Rare Variant Association Test

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Description rareMETALS implements our methodologies for performing rare variant associations using summary level statistics. By sharing information on the single variant score statistics, and their variance-covariance matrix, a variety of rare variant association test can be performed centrally. The set of gene-level rare variant tests include simple or weighted burden test, sequence kernel association test, and variable threshold test. The user can also determine the set of variants they want to include in the gene-level test centrally.Additional features for rareMETALS package include 1.) A monte-carlo method for evaluating statistical significance empirically 2.) methods for performing conditional association analysis and dissecting independent association signals.

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Depends seqminer,mvtnorm,CompQuadForm,getopt,MASS

R topics documented:

`binary.rareMETALS.single.group`
Single variant meta-analysis

Description

Single variant meta-analysis

Usage

```
binary.rareMETALS.single.group(score.stat.file, cov.file, range, refaltList,
  alternative = c("two.sided", "greater", "less"), callrate.cutoff = 0,
  hwe.cutoff = 0, correctFlip = TRUE, analyzeRefAltListOnly = TRUE)
```

Arguments

`score.stat.file`	files of score statistics
`cov.file`	covariance matrix files
`range`	tabix range of variants to be analyzed
`refaltList`	A list of reference alternative and positions of variants to be analyzed; Each variant in the dataset will be match against ref/alt alleles specified in refaltList; Only variants with matched ref and alt alleles can be included; we also need AF and af.diff.max to determine if the flips are due to strand issues or due to ref/alt alleles flips;
`alternative`	alternative hypothesis to be specified

`callrate.cutoff`
: Cutoffs of call rate, lower than which will NOT be analyzed (labelled as missing)

`hwe.cutoff`
: Cutoffs of HWE p-values

`refaltList`
: A list that contains pos, ref and alt for calibrating variant sites to have the right ref and alt alleles;

`correctFlip`
: Correcting for flipped alleles; Default is TRUE; If FALSE, studies with incorrect REF/ALT alleles will be labelled as missing, and dropped from meta-analyses

`analyzeRefAltListOnly`
: Only analyze variants that are included in the refaltList; Default is TRUE; If FALSE, variant sites in the dataset but not specified in the refaltList will be labelled as missing and dropped from studies;

Value

a list consisting of results

`ColSums` *Safe colSums*

Description

Safe colSums

Usage

```
ColSums(a)
```

Arguments

`a`
: Input vector, matrix etc.

Value

Return the sum of the elements in a;

`conditional.rareMETALS.range` *Perform conditional analysis for gene-level tests*

Description

Perform conditional analysis for gene-level tests

Usage

```
conditional.rareMETALS.range(range.name = NULL, score.stat.file, cov.file,
  candidate.variant.vec, known.variant.vec, test = "GRANVIL", maf.cutoff,
  alternative = c("two.sided", "greater", "less"), ix.gold = 1,
  out.digits = 4, callrate.cutoff = 0, hwe.cutoff = 0, max.VT = NULL)
```

Arguments

`range.name`	name of the range to be analyzed (for example, it can be a gene name e.g. APOE)
`score.stat.file`	files of score statistics
`cov.file`	covariance matrix files
`candidate.variant.vec`	Vectors of candidate variants: e.g. c("1:123","1:1234"). The quotation is necessary!!
`known.variant.vec`	Vectors of known variants: e.g. c("1:123","1:1234"). The quotation is necessary!!
`test`	test of rare variant tests
`maf.cutoff`	Cutoffs of MAF used for determining rare variants
`alternative`	Alternative hypothesis to be tested
`ix.gold`	Index of the gold standard population: Used for flipping alleles
`out.digits`	The number of digits used in the output
`callrate.cutoff`	Cutoff of call rates. Sites with callrates lower than the cutoff will be labeled as missing
`hwe.cutoff`	Cutoff of HWE p-values. Sites with HWE pvalues lower than the cutoff will be labeled as missing
`max.VT`	The maximum number of thresholds used in VT; Setting max.VT to 10 can improve the speed for calculation without affecting the power too much. The default parameter is NULL, which does not set upper limit on the number of variable frequency threhsold.

`conditional.rareMETALS.range.group` *Perform conditional analysis for gene-level tests and correcting for allele flips with*

Description

Perform conditional analysis for gene-level tests and correcting for allele flips with

Usage

```
conditional.rareMETALS.range.group(range.name = NULL, score.stat.file,
  cov.file, candidate.variant.vec, known.variant.vec, test = "GRANVIL",
  maf.cutoff, alternative = c("two.sided", "greater", "less"), refaltList,
  out.digits = 4, callrate.cutoff = 0, hwe.cutoff = 0, max.VT = NULL,
  correctFlip = TRUE, analyzeRefAltListOnly = TRUE)
```

Arguments

`range.name`	name of the range to be analyzed (for example, it can be a gene name e.g. APOE)
`score.stat.file`	files of score statistics
`cov.file`	covariance matrix files
`candidate.variant.vec`	Vectors of candidate variants: e.g. c("1:123","1:1234"). The quotation is necessary!!
`known.variant.vec`	Vectors of known variants: e.g. c("1:123","1:1234"). The quotation is necessary!!
`test`	test of rare variant tests
`maf.cutoff`	Cutoffs of MAF used for determining rare variants
`alternative`	Alternative hypothesis to be tested
`ix.gold`	Index of the gold standard population: Used for flipping alleles
`out.digits`	The number of digits used in the output
`callrate.cutoff`	Cutoff of call rates. Sites with callrates lower than the cutoff will be labeled as missing
`hwe.cutoff`	Cutoff of HWE p-values. Sites with HWE pvalues lower than the cutoff will be labeled as missing
`max.VT`	The maximum number of thresholds used in VT; Setting max.VT to 10 can improve the speed for calculation without affecting the power too much. The default parameter is NULL, which does not set upper limit on the number of variable frequency threhsold.

`correctFlip` Correcting for flipped alleles; Default is TRUE; If FALSE, studies with incorrect REF/ALT alleles will be labelled as missing, and dropped from meta-analyses

`analyzeRefAltListOnly` Only analyze variants that are included in the refaltList; Default is TRUE; If FALSE, variant sites in the dataset but not specified in the refaltList will be labelled as missing and dropped from studies;

`conditional.rareMETALS.single` *Perform conditional analysis for single variant tests*

Description

Perform conditional analysis for single variant tests

Usage

```
conditional.rareMETALS.single(candidate.variant.vec, score.stat.file, cov.file,
  known.variant.vec, maf.cutoff, no.boot = 10000,
  alternative = c("two.sided", "greater", "less"), ix.gold = 1,
  out.digits = 4, callrate.cutoff = 0, hwe.cutoff = 0,
  p.value.known.variant.vec = NA, anno.known.variant.vec = NA,
  anno.candidate.variant.vec = NA)
```

Arguments

`candidate.variant` name of the range to be analyzed (for example, it can be a gene name e.g. APOE)

`score.stat.file` files of score statistics

`cov.file` covariance matrix files

`known.variant.vec` range of candidate variant, expressed in a vector, e.g. c("1:12345","1:234567");

`known.variant.range` range of known variant, expressed in tabix format, e.g. c("1:123456","1:2345678");

`test` test of rare variant tests

`maf.cutoff` Cutoffs of MAF used for determining rare variants

`alternative` Alternative hypothesis to be tested

`out.digits` The number of digits used in the output

`callrate.cutoff` Cutoff of call rates. Sites with callrates lower than the cutoff will be labeled as missing

`hwe.cutoff` Cutoff of HWE p-values. Sites with HWE pvalues lower than the cutoff will be labeled as missing

Value

return a list of meta-analysis results

`conditional.rareMETALS.single.group`
Perform conditional analysis for single variant tests

Description

Perform conditional analysis for single variant tests

Usage

```
conditional.rareMETALS.single.group(candidate.variant, score.stat.file,
  cov.file, known.variant.vec, refaltList, maf.cutoff,
  alternative = c("two.sided", "greater", "less"), out.digits = 4,
  callrate.cutoff = 0, hwe.cutoff = 0, approxCov = TRUE,
  correctFlip = TRUE)
```

Arguments

`candidate.variant`	Candidate variant position;
`score.stat.file`	files of score statistics
`cov.file`	covariance matrix files
`known.variant.vec`	range of candidate variant, expressed in a vector, e.g. c("1:12345","1:234567");
`refaltList`	A list of ref, alt alleles, as well as variant frequencies, whether it needs to check AF as for flipping alleles;
`test`	test of rare variant tests
`maf.cutoff`	Cutoffs of MAF used for determining rare variants
`alternative`	Alternative hypothesis to be tested
`out.digits`	The number of digits used in the output
`callrate.cutoff`	Cutoff of call rates. Sites with callrates lower than the cutoff will be labeled as missing
`hwe.cutoff`	Cutoff of HWE p-values. Sites with HWE pvalues lower than the cutoff will be labeled as missing

Value

return a list of meta-analysis results

`conditional.rareMETALS.single.group.core` *Perform conditional analysis for single variant tests*

Description

Perform conditional analysis for single variant tests

Usage

```
conditional.rareMETALS.single.group.core(candidate.variant, score.stat.file,
  cov.file, known.variant.vec, refaltList, maf.cutoff,
  alternative = c("two.sided", "greater", "less"), out.digits = 4,
  callrate.cutoff = 0, hwe.cutoff = 0, approxCov = TRUE,
  correctFlip = TRUE)
```

Arguments

`candidate.variant`	Candidate variant position;
`score.stat.file`	files of score statistics
`cov.file`	covariance matrix files
`known.variant.vec`	range of candidate variant, expressed in a vector, e.g. c("1:12345","1:234567");
`refaltList`	A list of ref, alt alleles, as well as variant frequencies, whether it needs to check AF as for flipping alleles;
`test`	test of rare variant tests
`maf.cutoff`	Cutoffs of MAF used for determining rare variants
`alternative`	Alternative hypothesis to be tested
`out.digits`	The number of digits used in the output
`callrate.cutoff`	Cutoff of call rates. Sites with callrates lower than the cutoff will be labeled as missing
`hwe.cutoff`	Cutoff of HWE p-values. Sites with HWE pvalues lower than the cutoff will be labeled as missing

Value

return a list of meta-analysis results

find.gene.chrpos *Find the chromosomal position for genes;*

Description

Find the chromosomal position for genes;

Usage

```
find.gene.chrpos(candidate.gene)
```

Arguments

candidate.gene	Name of candidate genes;

Value

a list consisiting of tabix, pos.start and pos.end;

find.top.variant *Find top variants in a gene region that satisfy a MAF cutoff;*

Description

Find top variants in a gene region that satisfy a MAF cutoff;

Usage

```
find.top.variant(candidate.variant.vec, window.size, singlevar.result,
  pval.cutoff = 3.1e-07)
```

Arguments

candidate.vairant.vec	The vector of candidate variant;
window.size	The size of window, default is 1e6
singlevar.result	Single varinat association results;
pval.cutoff	The cutoffs of p-values;

`flipAllele` *This is the function for flipping alleles*

Description

This is the function for flipping alleles

Usage

```
flipAllele(raw.data, raw.data.ori, refaltList, ix.pop, ix.var, log.mat.var,
  correctFlip = TRUE, analyzeRefAltListOnly = TRUE)
```

Arguments

`raw.data`	The input datasets to be considered flipped
`raw.data.ori`	The input datasets to be considered flipped
`refaltList`	The list consists of ref, alt, pos, af and af.diff.max, as well as the option of whether throw away sites with large af.differences checkAF;
`ix.pop`	index of the population
`ix.var`	index of the variant;
`log.mat.var`	The log for QC procedure;
`correctFlip`	Correct for score and covariance matrices for flipped alleles;

Value

A list consist of modified raw.data, ix.include and log.mat.var

---

`genomic.dist` *Get genomic distance between two variant positions;*

Description

Get genomic distance between two variant positions;

Usage

```
genomic.dist(pos1, pos2)
```

Arguments

`pos1`	Position for variant 1;
`pos2`	Position for variant 2;

Value

Return variant positions;

get.gene.inWindow *Find nearby genes for a sigificant SNP*

Description

Find nearby genes for a sigificant SNP

Usage

```
get.gene.inWindow(known.variant.vec, window.size = 1e+06)
```

Arguments

known.variant.vec	Positions of known variants, in the format of 1:12345
window.size	The window size. Genes within the window are extracted. Default size is 1e6

Value

A vector of genes;

get.tabix.range *change position to tabix range;*

Description

change position to tabix range;

Usage

```
get.tabix.range(variant.vec)
```

Arguments

variant.vec	The vector of variants of the format "1:12345";

Value

A vector of tabix ranges;

Mean *Safe mean*

Description

Safe mean

Usage

```
Mean(a)
```

Arguments

a	Input vector, matrix etc.

Value

Return the sum of the elements in a;

rareMETALS.cleanScore *Single variant meta-analysis*

Description

Single variant meta-analysis

Usage

```
rareMETALS.cleanScore(score.stat.file, refaltList, hwe.cutoff, callrate.cutoff,
  af.diff.max = 0.7, checkAF = TRUE)
```

Arguments

score.stat.file	files of score statistics
callrate.cutoff	Cutoffs of call rate, lower than which will NOT be analyzed (labelled as missing)
hwe.cutoff	Cutoffs of HWE p-values
refaltList	A list that contains pos, ref and alt for calibrating variant sites to have the right ref and alt alleles;

Value

a list consisting of results

`rareMETALS.gene` *Meta-analysis of gene-level tests;*

Description

Meta-analysis of gene-level tests;

Usage

```
rareMETALS.gene(ANNO, score.stat.file, cov.file, gene, test = "GRANVIL",
  maf.cutoff, no.boot = 10000, alternative = c("two.sided", "greater",
  "less"), alpha = 0.05, ix.gold = 1, out.digits = 4,
  callrate.cutoff = 0, hwe.cutoff = 0, gene.file = "refFlat_hg19.txt.gz",
  max.VT = NULL)
```

Arguments

`ANNO`	type of variants to be analyzed;
`score.stat.file`	files of score statistics
`cov.file`	covariance matrix files
`test`	rare variant tests to be used
`maf.cutoff`	MAF cutoff used to analyze variants
`no.boot`	Number of bootstraps to be used. No need if asymptotics are used
`alternative`	alternative hypothesis to be specified
`alpha`	Significance threshold to determine the number of resampling. Set to 0 if analytic p-values are calculated.
`ix.gold`	Gold standard population to align reference allele to
`out.digits`	Number of digits used in the output
`callrate.cutoff`	Cutoffs of call rate, lower than which will NOT be analyzed (labelled as missing)
`hwe.cutoff`	Cutoffs of HWE p-values, lower than which will NOT be analyzed (labelled as missing)
`max.VT`	The maximum number of thresholds used in VT; Setting max.VT to 10 can improve the speed for calculation without affecting the power too much. The default parameter is NULL, which does not set upper limit on the number of variable frequency threhsold.

Value

a list consisting of results

`rareMETALS.gene.group` *Meta-analysis of gene-level tests by range;*

Description

Meta-analysis of gene-level tests by range;

Usage

```
rareMETALS.gene.group(score.stat.file, cov.file, range, range.name,
  test = "GRANVIL", refaltList, maf.cutoff = 1, no.boot = 10000,
  alternative = c("two.sided", "greater", "less"), alpha = 0.05,
  ix.gold = 1, out.digits = 4, callrate.cutoff = 0, hwe.cutoff = 0,
  max.VT = NULL)
```

Arguments

`score.stat.file`	files of score statistics
`cov.file`	covariance matrix files
`range`	tabix range for each gene/region
`range.name`	The name of the range,e.g. gene names can be used
`test`	rare variant tests to be used
`maf.cutoff`	MAF cutoff used to analyze variants
`refaltList`	List of reference, alternative and variant positions;
`no.boot`	Number of bootstraps to be used. No need if asymptotics are used
`alternative`	alternative hypothesis to be specified
`alpha`	Significance threshold to determine the number of resampling. Set to 0 if analytic p-values are calculated.
`ix.gold`	Gold standard population to align reference allele to
`out.digits`	Number of digits used in the output
`callrate.cutoff`	Cutoffs of call rate, lower than which will NOT be analyzed (labelled as missing)
`hwe.cutoff`	Cutoffs of HWE p-values
`max.VT`	The maximum number of thresholds used in VT; Setting max.VT to 10 can improve the speed for calculation without affecting the power too much. The default parameter is NULL, which does not set upper limit on the number of variable frequency threhsold.

Value

a list consisting of results

`rareMETALS.range` *Meta-analysis of gene-level tests by range;*

Description

Meta-analysis of gene-level tests by range;

Usage

```
rareMETALS.range(score.stat.file, cov.file, range, range.name,
  test = "GRANVIL", maf.cutoff = 1, alternative = c("two.sided",
  "greater", "less"), ix.gold = 1, out.digits = 4, callrate.cutoff = 0,
  hwe.cutoff = 0, max.VT = NULL)
```

Arguments

`score.stat.file`	files of score statistics
`cov.file`	covariance matrix files
`range`	tabix range for each gene/region
`range.name`	The name of the range,e.g. gene names can be used
`test`	rare variant tests to be used
`maf.cutoff`	MAF cutoff used to analyze variants
`alternative`	alternative hypothesis to be specified
`ix.gold`	Gold standard population to align reference allele to
`out.digits`	Number of digits used in the output
`callrate.cutoff`	Cutoffs of call rate, lower than which will NOT be analyzed (labelled as missing)
`hwe.cutoff`	Cutoffs of HWE p-values
`max.VT`	The maximum number of thresholds used in VT; Setting max.VT to 10 can improve the speed for calculation without affecting the power too much. The default parameter is NULL, which does not set upper limit on the number of variable frequency threhsold.

Value

a list consisting of results

`rareMETALS.range.core` *#' Meta-analysis of gene-level tests by range;*

Description

#' Meta-analysis of gene-level tests by range;

Usage

```
rareMETALS.range.core(score.stat.file, cov.file, range, range.name,
  test = "GRANVIL", maf.cutoff = 1, alternative = c("two.sided",
  "greater", "less"), ix.gold = 1, out.digits = 4, callrate.cutoff = 0,
  hwe.cutoff = 0, max.VT = NULL)
```

Arguments

`score.stat.file`	files of score statistics
`cov.file`	covariance matrix files
`range`	tabix range for each gene/region
`range.name`	The name of the range,e.g. gene names can be used
`test`	rare variant tests to be used
`maf.cutoff`	MAF cutoff used to analyze variants
`alternative`	alternative hypothesis to be specified
`ix.gold`	Gold standard population to align reference allele to
`out.digits`	Number of digits used in the output
`callrate.cutoff`	Cutoffs of call rate, lower than which will NOT be analyzed (labelled as missing)
`hwe.cutoff`	Cutoffs of HWE p-values
`max.VT`	The maximum number of thresholds used in VT; Setting max.VT to 10 can improve the speed for calculation without affecting the power too much. The default parameter is NULL, which does not set upper limit on the number of variable frequency threhsold.

Value

a list consisting of results

`rareMETALS.range.group`
Meta-analysis of gene-level tests by range;

Description

Meta-analysis of gene-level tests by range;

Usage

```
rareMETALS.range.group(score.stat.file, cov.file, range, range.name,
  test = "GRANVIL", refaltList, maf.cutoff = 1,
  alternative = c("two.sided", "greater", "less"), out.digits = 4,
  callrate.cutoff = 0, hwe.cutoff = 0, max.VT = NULL,
  correctFlip = TRUE, analyzeRefAltListOnly = TRUE)
```

Arguments

`score.stat.file`	files of score statistics
`cov.file`	Covariance matrix files
`range`	tabix range for each gene/region; Tabix range needs to be in the format of "1:123-1234". Quotation marks are necessary.
`range.name`	The name of the range,e.g. gene names can be used;
`refaltList`	A list of reference, alternative allele, a vector of alternative allele frequencies; Specifically, the list should consist of
`test`	rare variant tests to be used
`maf.cutoff`	MAF cutoff used to analyze variants; Default value is 1, i.e. no cutoffs are applied. MAFs are based upon the sample MAFs.
`alternative`	alternative hypothesis to be specified; Only applicable to GRANVIL test;
`out.digits`	Number of digits used in the output
`callrate.cutoff`	Cutoffs of call rate, lower than which will NOT be analyzed (labelled as missing)
`hwe.cutoff`	Cutoffs of HWE p-values
`max.VT`	The maximum number of thresholds used in VT; For small p-values, the calculation of VT p-values can be very slow. Setting max.VT to 10 can improve the speed for calculation without affecting the power too much. The default parameter is NULL, which does not set upper limit on the number of variable frequency threhsold.
`correctFlip`	Correct for flipped sites for score statistics and their covariance matrices

Value

a list consisting of results;

`rareMETALS.range.group.core` *Meta-analysis of gene-level tests by range;*

Description

Meta-analysis of gene-level tests by range;

Usage

```
rareMETALS.range.group.core(score.stat.file, cov.file, range, range.name,
  test = "GRANVIL", refaltList, maf.cutoff = 1,
  alternative = c("two.sided", "greater", "less"), out.digits = 4,
  callrate.cutoff = 0, hwe.cutoff = 0, max.VT = NULL,
  correctFlip = TRUE, analyzeRefAltListOnly = TRUE)
```

Arguments

`score.stat.file`	files of score statistics
`cov.file`	Covariance matrix files
`range`	tabix range for each gene/region; Tabix range needs to be in the format of "1:123-1234". Quotation marks are necessary.
`range.name`	The name of the range,e.g. gene names can be used;
`refaltList`	A list of reference, alternative allele, a vector of alternative allele frequencies; Specifically, the list should consist of
`test`	rare variant tests to be used
`maf.cutoff`	MAF cutoff used to analyze variants; Default value is 1, i.e. no cutoffs are applied. MAFs are based upon the sample MAFs.
`alternative`	alternative hypothesis to be specified; Only applicable to GRANVIL test;
`out.digits`	Number of digits used in the output
`callrate.cutoff`	Cutoffs of call rate, lower than which will NOT be analyzed (labelled as missing)
`hwe.cutoff`	Cutoffs of HWE p-values
`max.VT`	The maximum number of thresholds used in VT; For small p-values, the calculation of VT p-values can be very slow. Setting max.VT to 10 can improve the speed for calculation without affecting the power too much. The default parameter is NULL, which does not set upper limit on the number of variable frequency threhsold.

Value

a list consisting of results;

rareMETALS.single *Single variant meta-analysis*

Description

Single variant meta-analysis

Usage

```
rareMETALS.single(score.stat.file, cov.file, range,
  alternative = c("two.sided", "greater", "less"), ix.gold = 1,
  callrate.cutoff = 0, hwe.cutoff = 0)
```

Arguments

score.stat.file	files of score statistics
cov.file	covariance matrix files
range	tabix range of variants to be analyzed
alternative	alternative hypothesis to be specified
ix.gold	Gold standard population to align reference allele to
callrate.cutoff	Cutoffs of call rate, lower than which will NOT be analyzed (labelled as missing)
hwe.cutoff	Cutoffs of HWE p-values

Value

a list consisting of results

rareMETALS.single.correctRefAlt *Single variant meta-analysis*

Description

Single variant meta-analysis

Usage

```
rareMETALS.single.correctRefAlt(score.stat.file, cov.file, range, refaltList,
  alternative = c("two.sided", "greater", "less"), callrate.cutoff = 0,
  hwe.cutoff = 0)
```

Arguments

score.stat.file	files of score statistics
cov.file	covariance matrix files
range	tabix range of variants to be analyzed
refaltList	A list of reference alternative and positions of variants to be analyzed; Each variant in the dataset will be match against ref/alt alleles specified in refaltList; Only variants with matched ref and alt alleles can be included;
alternative	alternative hypothesis to be specified
callrate.cutoff	Cutoffs of call rate, lower than which will NOT be analyzed (labelled as missing)
hwe.cutoff	Cutoffs of HWE p-values
refaltList	A list that contains pos, ref and alt for calibrating variant sites to have the right ref and alt alleles;

Value

a list consisting of results

---

rareMETALS.single.group

Single variant meta-analysis

Description

Single variant meta-analysis

Usage

```
rareMETALS.single.group(score.stat.file, cov.file, range, refaltList,
  alternative = c("two.sided", "greater", "less"), callrate.cutoff = 0,
  hwe.cutoff = 0, correctFlip = TRUE, analyzeRefAltListOnly = TRUE)
```

Arguments

score.stat.file	files of score statistics
cov.file	covariance matrix files
range	tabix range of variants to be analyzed
refaltList	A list of reference alternative and positions of variants to be analyzed; Each variant in the dataset will be match against ref/alt alleles specified in refaltList; Only variants with matched ref and alt alleles can be included; we also need AF and af.diff.max to determine if the flips are due to strand issues or due to ref/alt alleles flips;

`alternative` alternative hypothesis to be specified

`callrate.cutoff`
Cutoffs of call rate, lower than which will NOT be analyzed (labelled as missing)

`hwe.cutoff` Cutoffs of HWE p-values

`refaltList` A list that contains pos, ref and alt for calibrating variant sites to have the right ref and alt alleles;

`correctFlip` Correcting for flipped alleles; Default is TRUE; If FALSE, studies with incorrect REF/ALT alleles will be labelled as missing, and dropped from meta-analyses

`analyzeRefAltListOnly`
Only analyze variants that are included in the refaltList; Default is TRUE; If FALSE, variant sites in the dataset but not specified in the refaltList will be labelled as missing and dropped from studies;

Value

a list consisting of results

`rm.na` *Remove nas*

Description

Remove nas

Usage

```
rm.na(x)
```

Arguments

`x` input;

`RowSums` *Safe rowSums*

Description

Safe rowSums

Usage

```
RowSums(a)
```

Arguments

a	Input vector, matrix etc.

Value

Return the sum of the elements in a;

---

set.intersect *Intersection of two sets;*

Description

Intersection of two sets;

Usage

```
set.intersect(set1, set2)
```

Arguments

set1	The set 1
set2	The set 2

Value

The intersection of set1 and set2;

---

sortPos *Sort genomic positions;*

Description

Sort genomic positions;

Usage

```
sortPos(pos)
```

Arguments

pos	Genomic positions in the form of 1:12345;

Value

Return sorted genomic positions;

`Sum` *Safe sum*

Description

Safe sum

Usage

```
Sum(a)
```

Arguments

`a`	Input vector, matrix etc.

Value

Return the sum of the elements in a;

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