

Package ‘Ravages’

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Description Rare variant association tests: burden tests (Bocher et al. 2019 <[doi:10.1002/gepi.22210](https://doi.org/10.1002/gepi.22210)>) and the Sequence Kernel Association Test (Bocher et al. 2021 <[doi:10.1038/s41431-020-00792-8](https://doi.org/10.1038/s41431-020-00792-8)>) in the whole genome using the RAVA-FIRST approach (Bocher et al. 2022 <[doi:10.1371/journal.pgen.1009923](https://doi.org/10.1371/journal.pgen.1009923)>). Ravages also enables to perform genetic simulations (Bocher et al. 2023 <[doi:10.1002/gepi.22529](https://doi.org/10.1002/gepi.22529)>).

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adjustedCADD.annotation

SNVs and Indels annotation with adjusted CADD scores

Description

Annotate SNVs and Indels with the adjusted CADD scores (CADD PHRED scores for coding, regulatory and intergenic regions)

Usage

```
adjustedCADD.annotation(x, SNVs.scores = NULL, indels.scores = NULL,
cores = 10, verbose = T, path.data,
                        build = c("b37", "b38"))
```

Arguments

| | |
|---------------|---|
| x | A bed.matrix annotated with CADD regions using set.CADDregions |
| SNVs.scores | A dataframe with the columns 'chr', 'pos', 'A1', 'A2' and 'adjCADD' containing the ADJUSTED CADD scores of the SNVs (Optional, useful to gain in computation time if the adjusted CADD scores of variants in the study are available) |
| indels.scores | A dataframe with the columns 'chr', 'pos', 'A1', 'A2' and 'PHRED_1.4' (or 'PHRED_1.6' if build 38) containing the CADD PHREDv1.4 (of PHREDv1.6) scores of the indels - Compulsory if indels are present in x |
| cores | How many cores to use, set at 10 by default |
| verbose | Whether to display information about the function actions |
| path.data | The repository where data for RAVA-FIRST are or will be downloaded from https://lysine.univ-brest.fr/RAVA-FIRST/ |
| build | The build of the data, either "b37" or "b38". The CADD Regions in the corresponding build will be considered |

Details

bedtools need to be installed on the system to run this function if indels are present are if scores are not provided for SNVs.

This function calls adjustedCADD.annotation.SNVs and adjustedCADD.annotation.indels. See the help of those two functions for more details.

Value

The bed matrix x with adjusted CADD scores in adjCADD.

Source

<https://lysine.univ-brest.fr/RAVA-FIRST/>

See Also

[adjustedCADD.annotation.SNVs](#), [adjustedCADD.annotation.indels](#), [RAVA.FIRST](#), [filter.adjustedCADD](#)

Examples

```
####Build37
#Import 1000Genome data from region around LCT gene
#x37 <- read.bed.matrix( system.file("extdata", "LCT.EUR.b37.bed", package="Ravages") )

#Annotate variants with adjusted CADD score
#x37 <- adjustedCADD.annotation(x37, build = "b37")

####Build38
#Import 1000Genome data from region around LCT gene
#x38 <- read.bed.matrix( system.file("extdata", "LCT.EUR.b38.bed", package="Ravages") )

#Annotate variants with adjusted CADD score
#x38 <- adjustedCADD.annotation(x38, build = "b38")
```

adjustedCADD.annotation.indels

Indels annotation with adjusted CADD scores

Description

Annotate Indels with the adjusted CADD scores (CADD PHRED scores for coding, regulatory and intergenic regions)

Usage

```
adjustedCADD.annotation.indels(x, variant.scores = NULL,
                               cores = 10, verbose = T, path.data,
                               build = c("b37", "b38"))
```

Arguments

| | |
|----------------|---|
| x | A bed.matrix annotated with CADD regions using set.CADDregions |
| variant.scores | A dataframe with the columns 'chr', 'pos', 'A1', 'A2' and 'PHRED_1.4' (or 'PHRED_1.6 if build 38) containing the CADD PHREDv1.4 (or PHREDv1.6) scores of the indels |
| cores | How many cores to use, set at 10 by default |
| verbose | Whether to display information about the function actions |
| path.data | The repository where data for RAVA-FIRST are or will be downloaded from https://lysine.univ-brest.fr/RAVA-FIRST/ |
| build | The build of the data, either "b37" or "b38". The CADD Regions in the corresponding build will be considered |

Details

bedtools need to be installed on the system to run this function.

Indels are directly annotated with the adjusted CADD scores in the function using the file "Adjusted-CADD_v1.4_202204_indels.tsv.gz" or "AdjustedCADD_v1.6_202602_indels.tsv.gz" downloaded from <https://lysine.univ-brest.fr/RAVA-FIRST/> in the repository of the package Ravages.

The adjusted CADD scores in "AdjustedCADD_v1.4_202204_indels.tsv.gz" have been computed using a set of 48M indels already annotated in the CADD website. The adjusted CADD scores in "AdjustedCADD_v1.6_202602_indels.tsv.gz" have been computed on the indels observed in GnomAD v1.3.2. If indels not present in this set are to be annotated, they will be given the same adjusted score as the indel with the nearest PHRED score provided in `variant.scores` which should contain the chromosome (`'chr'`), position (`'pos'`), reference allele (`'A1'`), alternative allele (`'A2'`) and PHRED CADD scores v1.4 (`'PHRED_1.4'`).

Those adjusted scores are used in the `RAVA.FIRST()` pipeline to filter rare variants.

As this function can take time when a large number of SNVs are present, it is recommended to use this function chromosome by chromosome for large datasets or to filter the bed matrix before the annotation.

Value

The bed matrix `x` with adjusted CADD scores in `adjCADD`.

Source

<https://lysine.univ-brest.fr/RAVA-FIRST/>

See Also

[adjustedCADD.annotation](#), [adjustedCADD.annotation.SNVs](#), [RAVA.FIRST](#), [filter.adjustedCADD](#)

adjustedCADD.annotation.SNVs

SNVs annotation with adjusted CADD scores

Description

Annotate SNVs with the adjusted CADD scores (CADD PHRED scores for coding, regulatory and intergenic regions)

Usage

```
adjustedCADD.annotation.SNVs(x, variant.scores = NULL,  
                             cores = 10, verbose = T, path.data,  
                             build = c("b37", "b38"))
```

Arguments

| | |
|-----------------------------|---|
| <code>x</code> | A bed.matrix annotated with CADD regions using <code>set.CADDregions</code> |
| <code>variant.scores</code> | A dataframe with the columns 'chr', 'pos', 'A1', 'A2' and 'adjCADD' containing the ADJUSTED CADD scores of the SNVs (Optional, useful to gain in computation time if the adjusted CADD scores of variants in the study are available) |
| <code>cores</code> | How many cores to use, set at 10 by default |
| <code>verbose</code> | Whether to display information about the function actions |
| <code>path.data</code> | The repository where data for RAVA-FIRST are or will be downloaded from https://lysine.univ-brest.fr/RAVA-FIRST/ |
| <code>build</code> | The build of the data, either "b37" or "b38". The CADD Regions in the corresponding build will be considered |

Details

bedtools need to be installed on the system if scores are not in `variants.scores` and need to be provided by Ravages.

SNVs are directly annotated with the adjusted CADD scores in the function using the file "AdjustedCADD_v1.4_202108.tsv.gz" or "AdjustedCADD_v1.6_202602.tsv.gz" (depending on the build) downloaded from <https://lysine.univ-brest.fr/RAVA-FIRST/> in the repository of the package Ravages or the scores of variants can be provided to `variant.scores` to gain in computation time (this file should contain 5 columns: the chromosome ('chr'), position ('pos'), reference allele ('A1'), alternative allele ('A2') and adjusted CADD scores ('adjCADD')).

Those adjusted scores are used in the `RAVA.FIRST()` pipeline to filter rare variants.

As this function can take time when a large number of SNVs are present, it is recommended to use this function chromosome by chromosome for large datasets or to filter the bed matrix before the annotation.

Value

The bed matrix `x` with adjusted CADD scores in `adjCADD`.

Source

<https://lysine.univ-brest.fr/RAVA-FIRST/>

See Also

[adjustedCADD.annotation](#), [adjustedCADD.annotation.indels](#), [RAVA.FIRST](#), [filter.adjustedCADD](#)

Examples

```
####Build37
#Import 1000Genome data from region around LCT gene
#x37 <- read.bed.matrix( system.file("extdata", "LCT.EUR.b37.bed", package="Ravages") )

#Annotate variants with adjusted CADD score
```

```
#x37 <- adjustedCADD.annotation.SNVs(x37, build = "b37")

####Build38
#Import 1000Genome data from region around LCT gene
#x38 <- read.bed.matrix( system.file("extdata", "LCT.EUR.b38.bed", package="Ravages") )

#Annotate variants with adjusted CADD score
#x38 <- adjustedCADD.annotation.SNVs(x38, build = "b38")
```

```
bed.matrix.split.genomic.region
```

Bed matrix for variants associated to multiple genomic regions

Description

Creates a new bed matrix with variants associated to multiple genomic regions being duplicated

Usage

```
bed.matrix.split.genomic.region(x, changeID=TRUE, genomic.region=NULL,
                               split.pattern=",")
```

Arguments

| | |
|----------------|--|
| x | A bed.matrix |
| changeID | TRUE/FALSE: whether to change the variants ID by including the gene name |
| genomic.region | A vector containing the genomic region of each variant |
| split.pattern | The character separating the genomic regions |

Details

If changeID=TRUE, variants will have new IDs being CHR:POS:A1:A2:genomic.region.

The genomic region(s) associated to each variant should be in x@snps\$genomic.region or given as a vector to genomic.region. If both are present, genomic.region is used.

Value

A bed matrix with variants assigned to multiple genomic regions being duplicated and the corresponding genomic regions separated and transformed into factors.

Examples

```
#Example bed matrix with 4 variants
x.ex <- as.bed.matrix(x=matrix(0, ncol=4, nrow=10),
                    bim=data.frame(chr=1:4, id=paste("rs", 1:4, sep=""), dist = rep(0,4),
                                   pos=c(150,150,200,250), A1=rep("A", 4), A2=rep("T", 4)))

#Example genes dataframe
```

```
genes.ex <- data.frame(Chr=c(1,1,3,4), Start=c(10,110,190,220), End=c(170,180,250,260),
  Gene_Name=factor(letters[1:4]))

#Attribute genomic regions
x.ex <- set.genomic.region(x.ex, regions = genes.ex)

#Split genomic regions
x.ex.split <- bed.matrix.split.genomic.region(x.ex, split.pattern = ",")
```

burden

*Linear, logistic or multinomial regression on a genetic score***Description**

Performs burden tests on categorical or continuous phenotypes

Usage

```
burden(x, NullObject, genomic.region = x@snps$genomic.region, burden,
  maf.threshold = 0.5, get.effect.size = FALSE, alpha = 0.05, cores = 10,
  verbose = TRUE)
```

Arguments

| | |
|------------------------------|---|
| <code>x</code> | A bed matrix, only needed if <code>burden="CAST"</code> or <code>burden="WSS"</code> |
| <code>NullObject</code> | A list returned from <code>NullObject.parameters</code> |
| <code>genomic.region</code> | A factor containing the genomic region of each SNP, <code>x@snps\$genomic.region</code> by default, only needed if <code>burden="CAST"</code> or <code>burden="WSS"</code> |
| <code>burden</code> | "CAST" or "WSS" to directly compute the CAST or the WSS genetic score, or a matrix with one row per individual and one column per <code>genomic.region</code> if another genetic score is wanted. |
| <code>maf.threshold</code> | The MAF threshold to use for the definition of a rare variant in the CAST score. Set at 0.5 by default |
| <code>get.effect.size</code> | TRUE/FALSE: whether to return effect sizes of the tested <code>genomic.region</code> (OR for categorical phenotypes, betas for continuous phenotypes) |
| <code>alpha</code> | The alpha threshold to use for the OR confidence interval |
| <code>cores</code> | How many cores to use, set at 10 by default. |
| <code>verbose</code> | Whether to display information about the function actions |

Details

This function will return results from the regression of the phenotype on the genetic score for each genomic region.

If only two groups of individuals are present, a classical logistic regression is performed. If more than two groups of individuals are present, a non-ordinal multinomial regression is performed, comparing each group of individuals to the reference group indicated by the argument `ref.level` in `NullObject.parameters`. The choice of the reference group won't affect the p-values, but only the Odds Ratios. In both types of regression, the p-value is estimated using the Likelihood Ratio test and the function `burden.mlogit`.

If the phenotype is continuous, a linear regression is performed using the function `burden.continuous`.

The type of phenotype is determined from `NullObject$pheno.type`.

If another genetic score than CAST or WSS is wanted, a matrix with one row per individual and one column per genomic region containing this score should be given to `burden`. In this situation, no bed matrix `x` is needed.

Value

A dataframe with one row per genomic region and at least two columns:

| | |
|----------------------|--|
| <code>p.value</code> | The p.value of the regression |
| <code>is.err</code> | 0/1: whether there was a convergence problem with the regression |

If `NullObject$pheno.type = "categorical"` and `get.OR.value=TRUE`, additional columns are present:

| | |
|----------------------|--|
| <code>OR/beta</code> | The OR/beta value(s) associated to the regression. For categorical phenotypes, if there are more than two groups, there will be one OR value per group compared to the reference group |
| <code>l.lower</code> | The lower bound of the confidence interval of each OR/beta |
| <code>l.upper</code> | The upper bound of the confidence interval of each OR/beta |

References

Bocher O, et al. DOI: 10.1002/gepi.22210. *Rare variant association testing for multicategory phenotype*. Genet.Epidemiol. 2019;43:646–656.

See Also

[NullObject.parameters](#), [burden.continuous](#), [burden.mlogit](#), [CAST](#), [WSS](#), [burden.weighted.matrix](#)

Examples

```
#Import data in a bed matrix
x <- read.bed.matrix( system.file("extdata", "LCT.EUR.b37.bed", package="Ravages") )

#Group variants within known genes
x <- set.genomic.region(x)
```

```

#Filter of rare variants: only non-monomorphic variants with
#a MAF lower than 2.5%
#keeping only genomic regions with at least 200 SNP
x1 <- filter.rare.variants(x, filter = "whole", maf.threshold = 0.025, min.nb.snps = 200)

#run null model, using the 1000Genome population as "outcome"
x1.H0 <- NullObject.parameters(pheno = x1@ped$population, ref.level = "CEU",
                              RVAT = "burden", pheno.type = "categorical")

#run burden test WSS
burden(x1, NullObject = x1.H0, burden = "WSS", get.effect.size=TRUE, cores = 1)

```

burden.continuous *Linear regression on a genetic score*

Description

Performs a linear regression on a genetic score

Usage

```

burden.continuous(x, NullObject, genomic.region = x@snps$genomic.region,
                 burden, maf.threshold = 0.5, get.effect.size = F,
                 alpha = 0.05, cores = 10)

```

Arguments

| | |
|-----------------|--|
| x | A bed matrix, only needed if burden="CAST" or burden="WSS" |
| NullObject | A list returned from NullObject.parameters |
| genomic.region | A factor containing the genomic region of each SNP, x@snps\$genomic.region by default, only needed if burden="CAST" or burden="WSS" |
| burden | "CAST" or "WSS" to directly compute the CAST or the WSS genetic score, or a matrix with one row per individual and one column per genomic.region if another genetic score is wanted. |
| maf.threshold | The MAF threshold to use for the definition of a rare variant in the CAST score. Set at 0.5 by default |
| get.effect.size | TRUE/FALSE: whether to return the beta value |
| alpha | The alpha threshold to use for the OR confidence interval |
| cores | How many cores to use for moments computation, set at 10 by default |

Details

This function will return results from the regression of the continuous phenotype on the genetic score for each genomic region.

If another genetic score than CAST or WSS is wanted, a matrix with one row per individual and one column per genomic region containing this score should be given to burden. In this situation, no bed matrix x is needed.

Value

A dataframe with one row per genomic region and at least two columns:

| | |
|---------|--|
| p.value | The p.value of the regression |
| is.err | 0/1: whether there was a convergence problem with the regression |
| beta | The beta coefficient associated to the tested genomic region |
| l.lower | The lower bound of the confidence interval of beta |
| l.upper | The upper bound of the confidence interval of beta |

See Also

[CAST](#), [WSS](#), [burden.weighted.matrix](#)

Examples

```
#Import data in a bed matrix
x <- read.bed.matrix( system.file("extdata", "LCT.EUR.b37.bed", package="Ravages") )

#Group variants within known genes
x <- set.genomic.region(x)

#Filter of rare variants: only non-monomorphic variants with
#a MAF lower than 2.5%
#keeping only genomic regions with at least 200 SNP
x1 <- filter.rare.variants(x, filter = "whole", maf.threshold = 0.025, min.nb.snps = 200)

#run burden test WSS, using a random continuous variable as phenotype
x1@ped$pheno <- rnorm(nrow(x1))
#Null model
x1.H0 <- NullObject.parameters(pheno = x1@ped$pheno,
                              RVAT = "burden", pheno.type = "continuous")

#Get the beta value
burden.continuous(x1, NullObject = x1.H0, burden = "WSS",
                 get.effect.size = TRUE, cores = 1)
```

burden.continuous.subscores

Linear regression on a multiple genetic scores within a genomic region

Description

Performs burden tests with subscores in the regression on continuous phenotypes

Usage

```
burden.continuous.subscores(x, NullObject, genomic.region = x@snps$genomic.region,
                           SubRegion = x@snps$SubRegion, burden.function = WSS,
                           maf.threshold = 0.5, get.effect.size = FALSE,
                           alpha = 0.05, cores = 10)
```

Arguments

| | |
|-----------------|--|
| x | A bed matrix, only needed if burden="CAST" or burden="WSS" |
| NullObject | A list returned from NullObject.parameters |
| genomic.region | A factor containing the genomic region of each SNP, x@snps\$genomic.region by default, for example the CADD regions |
| SubRegion | A vector containing subregions within each genomic.region, x@snps\$SubRegion by default, for example genomic categories |
| burden.function | A function to compute the genetic score, WSS by default. |
| maf.threshold | The MAF threshold to use for the definition of a rare variant in the CAST score. Set at 0.5 by default |
| get.effect.size | TRUE/FALSE: whether to return effect sizes of the tested genomic.region (OR for categorical phenotypes, betas for continuous phenotypes) |
| alpha | The alpha threshold to use for the OR confidence interval |
| cores | How many cores to use, set at 10 by default. Only needed if NullObject\$pheno.type = "categorical" |

Details

This function will return results from the regression of the phenotype on the genetic score(s) for each genomic region. Within each genomic region, a subscore will be computed for each SubRegion and one test will be performed for each genomic.region.

Value

A dataframe with one row per genomic region and two columns:

p.value The p.value of the regression
is.err 0/1: whether there was a convergence problem with the regression

If `get.effect.size=TRUE`, a list is returned with the previous dataframe in `$Asso` and with `effect`, a list containing matrices with three columns:

beta The beta value(s) associated to the subscores in the regression
l.lower The lower bound of the confidence interval of each beta
l.upper The upper bound of the confidence interval of each beta

See Also

[NullObject.parameters](#), [burden.subscores](#), [CAST](#), [WSS](#)

Examples

```
#Import data in a bed matrix
#x <- read.bed.matrix( system.file("extdata", "LCT.EUR.b37.bed", package="Ravages") )

#Group variants within CADD regions and genomic categories
#x <- set.CADDregions(x, build = "b37")

#Filter of rare variants: only non-monomorphic variants with
#a MAF lower than 2.5%
#keeping only genomic regions with at least 200 SNP
#x1 <- filter.rare.variants(x, filter = "whole", maf.threshold = 0.025, min.nb.snps = 200)

#Simulation of a continuous and a binary covariate
#set.seed(1) ; sex <- sample(0:1, nrow(x1), replace = T) ; u <- runif(nrow(x1))
#covar <- cbind(sex, u)

#Null model with the covariate sex and a continuous phenotype
#x1.H0.covar <- NullObject.parameters(pheno = x1@ped$pheno <- rnorm(nrow(x1)),
#                                   RVAT = "burden", pheno.type = "continuous",
#                                   data = covar, formula = ~ sex)

#WSS test
#res.subscores <-burden.continuous.subscores(x1, NullObject = x1.H0.covar,
#                                           burden = WSS, get.effect.size=TRUE, cores = 1)
#res.subscores$Asso # p-values
#res.subscores$effect #beta values
```

burden.mlogit

*Logistic or multinomial regression on a genetic score***Description**

Performs a logistical or a non-ordinal multinomial regression on a genetic score

Usage

```
burden.mlogit(x, NullObject, genomic.region = x@snps$genomic.region, burden,
             maf.threshold = 0.5, get.effect.size = FALSE, alpha = 0.05, cores = 10)
```

Arguments

| | |
|-----------------|--|
| x | A bed matrix, only needed if burden="CAST" or burden="WSS" |
| NullObject | A list returned from NullObject.parameters |
| genomic.region | A factor containing the genomic region of each SNP, x@snps\$genomic.region by default, only needed if burden="CAST" or burden="WSS" |
| burden | "CAST" or "WSS" to directly compute the CAST or the WSS genetic score; or a matrix with one row per individual and one column per genomic.region if another genetic score is wanted. |
| maf.threshold | The MAF threshold to use for the definition of a rare variant in the CAST score. Set at 0.5 by default |
| get.effect.size | TRUE/FALSE: whether to return OR values |
| alpha | The alpha threshold to use for the OR confidence interval |
| cores | How many cores to use for moments computation, set at 10 by default |

Details

This function will return results from the regression of the phenotype on the genetic score for each genomic region.

If only two groups of individuals are present, a classical logistic regression is performed. If more than two groups of individuals are present, a non-ordinal multinomial regression is performed, comparing each group of individuals to the reference group indicated by the argument `ref.level` in `NullObject.parameters`. The choice of the reference group won't affect the p-values, but only the Odds Ratios. In both types of regression, the p-value is estimated using the Likelihood Ratio test.

If another genetic score than CAST or WSS is wanted, a matrix with one row per individual and one column per `genomic.region` containing this score should be given to `burden`. In this situation, no bed matrix `x` is needed.

Value

A dataframe with one row per genomic region and at least two columns:

p.value The p.value of the regression
is.err 0/1: whether there was a convergence problem with the regression

If `get.effect.size=TRUE`, additional columns are present:

OR The OR value(s) associated to the regression. If there are more than two groups, there will be one OR value per group compared to the reference group
l.lower The lower bound of the confidence interval of each OR
l.upper The upper bound of the confidence interval of each OR

References

Bocher O, et al. DOI: 10.1002/gepi.22210. *Rare variant association testing for multicategory phenotype*. Genet.Epidemiol. 2019;43:646–656.

See Also

[NullObject.parameters](#), [CAST](#), [WSS](#), [burden.weighted.matrix](#)

Examples

```
#Import data in a bed matrix
x <- read.bed.matrix( system.file("extdata", "LCT.EUR.b37.bed", package="Ravages") )

#Group variants within known genes
x <- set.genomic.region(x)

#Filter of rare variants: only non-monomorphic variants with
#a MAF lower than 2.5%
#keeping only genomic regions with at least 200 SNP
x1 <- filter.rare.variants(x, filter = "whole", maf.threshold = 0.025, min.nb.snps = 200)

#Simulation of a continuous and a binary covariate
set.seed(1) ; sex <- sample(0:1, nrow(x1), replace = TRUE) ; u <- runif(nrow(x1))
covar <- cbind(sex, u)

#run null model, using the 1000Genome population as "outcome"
#Null model with the covariate sex
x1.H0.covar <- NullObject.parameters(pheno = x1@ped$population, ref.level = "CEU",
                                   RVAT = "burden", pheno.type = "categorical",
                                   data = covar, formula = ~ sex)

#WSS test
burden.mlogit(x1, NullObject = x1.H0.covar, burden = "WSS", get.effect.size=TRUE, cores = 1)
```

burden.mlogit.subscores

Logistic or multinomial regression on a multiple genetic scores within a genomic region

Description

Performs burden tests with subscores in the regression on categorical phenotypes

Usage

```
burden.mlogit.subscores(x, NullObject, genomic.region = x@snps$genomic.region,
                        SubRegion = x@snps$SubRegion, burden.function = WSS,
                        maf.threshold = 0.5, get.effect.size = FALSE,
                        alpha = 0.05, cores = 10)
```

Arguments

| | |
|-----------------|--|
| x | A bed matrix, only needed if burden="CAST" or burden="WSS" |
| NullObject | A list returned from NullObject.parameters |
| genomic.region | A factor containing the genomic region of each SNP, x@snps\$genomic.region by default, for example the CADD regions |
| SubRegion | A vector containing subregions within each genomic.region, x@snps\$SubRegion by default, for example genomic categories |
| burden.function | A function to compute the genetic score, WSS by default. |
| maf.threshold | The MAF threshold to use for the definition of a rare variant in the CAST score. Set at 0.5 by default |
| get.effect.size | TRUE/FALSE: whether to return effect sizes of the tested genomic.region (OR for categorical phenotypes, betas for continuous phenotypes) |
| alpha | The alpha threshold to use for the OR confidence interval |
| cores | How many cores to use, set at 10 by default. Only needed if NullObject\$pheno.type = "categorical" |

Details

This function will return results from the regression of the phenotype on the genetic score(s) for each genomic region. Within each genomic region, a subscore will be computed for each SubRegion and one test will be performed for each genomic.region.

If only two groups of individuals are present, a classical logistic regression is performed. If more than two groups of individuals are present, a non-ordinal multinomial regression is performed, comparing each group of individuals to the reference group indicated by the argument ref.level in NullObject.parameters. The choice of the reference group won't affect the p-values, but only the Odds Ratios. In both types of regression, the p-value is estimated using the Likelihood Ratio test and the function burden.mlogit.

Value

A dataframe with one row per genomic region and two columns:

| | |
|---------|--|
| p.value | The p.value of the regression |
| is.err | 0/1: whether there was a convergence problem with the regression |

If `get.effect.size=TRUE`, a list is returned with the previous dataframe in `$Asso` and with `effect`, a list containing matrices with three columns:

| | |
|---------|--|
| OR | The OR value(s) associated to the subscores in the regression. If there are more than two groups, there will be one OR value per group compared to the reference group |
| l.lower | The lower bound of the confidence interval of each OR |
| l.upper | The upper bound of the confidence interval of each OR |

See Also

[NullObject.parameters](#), [burden.subscores](#), [CAST](#), [WSS](#)

Examples

```
#Import data in a bed matrix
#x <- read.bed.matrix( system.file("extdata", "LCT.EUR.b37.bed", package="Ravages") )

#Group variants within CADD regions and genomic categories
#x <- set.CADDregions(x, build = "b37")

#Filter of rare variants: only non-monomorphic variants with
#a MAF lower than 2.5%
#keeping only genomic regions with at least 200 SNP
#x1 <- filter.rare.variants(x, filter = "whole", maf.threshold = 0.025, min.nb.snps = 200)

#run null model, using the 1000Genome population as "outcome"
#x1.H0 <- NullObject.parameters(pheno = x1@ped$population, ref.level = "CEU",
#                               RVAT = "burden", pheno.type = "categorical")

#run burden test WSS
#res.subscores <- burden.subscores(x1, NullObject = x1.H0, burden = WSS,
#                                  get.effect.size=TRUE, cores = 1)
#res.subscores$Asso # p-values
#res.subscores$effect #OR values
```

| | |
|------------------|--|
| burden.subscores | <i>Linear, logistic or multinomial regression on a multiple genetic scores within a genomic region</i> |
|------------------|--|

Description

Performs burden tests with subscores in the regression on categorical or continuous phenotypes

Usage

```
burden.subscores(x, NULLobject, genomic.region = x@snps$genomic.region,
                SubRegion = x@snps$SubRegion, burden.function = WSS,
                maf.threshold = 0.5, get.effect.size = FALSE,
                alpha = 0.05, cores = 10, verbose = TRUE)
```

Arguments

| | |
|-----------------|--|
| x | A bed matrix |
| NULLobject | A list returned from NULLobject.parameters |
| genomic.region | A factor containing the genomic region of each SNP, x@snps\$genomic.region by default, for example the CADD regions |
| SubRegion | A vector containing subregions within each genomic.region, x@snps\$SubRegion by default, for example genomic categories |
| burden.function | A function to compute the genetic score, WSS by default. |
| maf.threshold | The MAF threshold to use for the definition of a rare variant in the CAST score. Set at 0.5 by default |
| get.effect.size | TRUE/FALSE: whether to return effect sizes of the tested genomic.region (OR for categorical phenotypes, betas for continuous phenotypes) |
| alpha | The alpha threshold to use for the OR confidence interval |
| cores | How many cores to use, set at 10 by default. Only needed if NULLobject\$pheno.type = "categorical" |
| verbose | Whether to display information about the function actions |

Details

This function will return results from the regression of the phenotype on the genetic score(s) for each genomic region. Within each genomic region, a subscore will be computed for each SubRegion and one test will be performed for each genomic.region.

When used after set.CADDregions, it will perform a test by CADD region with one subscore by genomic category (coding, regulatory, intergenic) as in the RAVA.FIRST() strategy.

If only two groups of individuals are present, a classical logistic regression is performed. If more than two groups of individuals are present, a non-ordinal multinomial regression is performed,

comparing each group of individuals to the reference group indicated by the argument `ref.level` in `NullObject.parameters`. The choice of the reference group won't affect the p-values, but only the Odds Ratios. In both types of regression, the p-value is estimated using the Likelihood Ratio test and the function `burden.mlogit`.

If the phenotype is continuous, a linear regression is performed using the function `burden.continuous`. The type of phenotype is determined from `NullObject$pheno.type`.

Value

A dataframe with one row per genomic region and two columns:

| | |
|----------------------|--|
| <code>p.value</code> | The p.value of the regression |
| <code>is.err</code> | 0/1: whether there was a convergence problem with the regression |

If `get.effect.size=TRUE`, a list is returned with the previous dataframe in `$Asso` and with `effect`, a list containing matrices with three columns:

| | |
|----------------------|---|
| <code>OR/beta</code> | The OR/beta value(s) associated to the subscores in the regression. For categorical phenotypes, if there are more than two groups, there will be one OR value per group compared to the reference group |
| <code>l.lower</code> | The lower bound of the confidence interval of each OR/beta |
| <code>l.upper</code> | The upper bound of the confidence interval of each OR/beta |

See Also

[RAVA.FIRST](#), [NullObject.parameters](#), [burden.continuous.subscores](#), [burden.mlogit.subscores](#), [CAST](#), [WSS](#)

Examples

```
#Import data in a bed matrix
x <- read.bed.matrix( system.file("extdata", "LCT.EUR.b37.bed", package="Ravages") )

#Group variants within known genes and
#Within coding and regulatory regions
x <- set.genomic.region.subregion(x, regions = genes.b37,
                                subregions = subregions.LCT)

#Keep only variants with a MAF lower than 1%
x1 <- filter.rare.variants(x, filter = "whole", maf.threshold = 0.01)

#run null model, using the 1000Genome population as "outcome"
x1.H0 <- NullObject.parameters(pheno = x1@ped$population, ref.level = "CEU",
                              RVAT = "burden", pheno.type = "categorical")

#run functionally-informed burden test WSS in LCT
burden.subscores(select.snps(x1, genomic.region == "LCT"),
                 NullObject = x1.H0, burden.function = WSS,
                 get.effect.size=FALSE, cores = 1)
```

```
####Using the RAVA-FIRST approach with CADD regions (example on b37)
#Group variants within CADD regions and genomic categories
#x <- set.CADDregions(x, build = "b37")

#Filter of rare variants: only non-monomorphic variants with
#a MAF lower than 2.5%
#and with a adjusted CADD score greater than the median
#x1 <- filter.adjustedCADD(x, filter = "whole", maf.threshold = 0.025)

#run functionally-informed burden test WSS
#burden.subscores(x1, NullObject = x1.H0, burden.function = WSS,
#                 get.effect.size=FALSE, cores = 1)
```

burden.weighted.matrix

Score matrix for burden tests

Description

Computes the score matrix for burden tests based on variants' weights

Usage

```
burden.weighted.matrix(x, weights, genomic.region = x@snps$genomic.region)
```

Arguments

| | |
|-----------------------------|---|
| <code>x</code> | A bed.matrix |
| <code>weights</code> | A vector containing the weight of each variant |
| <code>genomic.region</code> | A factorcontaining the genomic region of each variant |

Details

For variant i and individual j , the genetic score will be computed as weight of variant i * number of minor alleles for individual j . This function returns a weighted score of rare alleles in the genomic region: if the reference allele is rare, it will be counted in the score instead of the alternative allele.

Value

A matrix containing the computed genetic score with one row per individual and one column per genomic.region.

See Also

[CAST](#), [WSS](#), [burden.mlogit](#)

Examples

```
#Import data in a bed matrix
x <- read.bed.matrix( system.file("extdata", "LCT.EUR.b37.bed", package="Ravages") )

#Group variants within known genes
x <- set.genomic.region(x)

#Filter of rare variants: only non-monomorphic variants with
#a MAF lower than 2.5%
#keeping only genomic regions with at least 200 SNP
x1 <- filter.rare.variants(x, filter = "whole", maf.threshold = 0.025, min.nb.snps = 200)

#Compute burden score with weights = 1-maf
score.burden <- burden.weighted.matrix(x1, weights=1-x1@snps$maf)
```

CAST

*Cohort Allelic Sum Test***Description**

Calculates the CAST genetic score

Usage

```
CAST(x, genomic.region = x@snps$genomic.region, maf.threshold = 0.5,
     flip.rare.alleles = T)
```

Arguments

| | |
|--------------------------------|--|
| <code>x</code> | A bed.matrix |
| <code>genomic.region</code> | A factor defining the genomic region of each variant |
| <code>maf.threshold</code> | The MAF used for the definition of a rare variant, set at 0.5 by default, i.e. all variants are kept |
| <code>flip.rare.alleles</code> | Whether to flip the A1/A2 alleles if the A1 allele is rare, set at T by default |

Details

By default, CAST counts if an individual carries at least one rare allele in the genomic region. If `flip.rare.alleles = F` and the reference allele A1 is rare, the alleles A1 and A2 won't be flipped and CAST will count the number of alternative alleles A2.

Value

A matrix containing the CAST genetic score with one row per individual and one column per `genomic.region`

References

Morgenthaler S and Thilly WG. *A strategy to discover genes that carry multi-allelic or mono-allelic risk for common diseases: a cohort allelic sums test (CAST)*. Mutat Res. 2007

See Also

[WSS](#), [burden.weighted.matrix](#), [burden.mlogit](#)

Examples

```
#Import data in a bed matrix
x <- read.bed.matrix( system.file("extdata", "LCT.EUR.b37.bed", package="Ravages") )

#Group variants within known genes
x <- set.genomic.region(x)

#Filter of rare variants: only non-monomorphic variants with
#a MAF lower than 2.5%
#keeping only genomic regions with at least 10 SNP
x1 <- filter.rare.variants(x, filter = "whole", maf.threshold = 0.025, min.nb.snps = 10)

# Compute burden score CAST
score.CAST <- CAST(x1, maf.threshold=0.025)
```

| | |
|---------------------|--|
| filter.adjustedCADD | <i>Variant filtering based on frequency and median adjusted CADD by CADD regions</i> |
|---------------------|--|

Description

Filter rare variants based on a MAF threshold, a given number of SNP or a given cumulative MAF per genomic region and the median of adjusted CADD score for each CADD region

Usage

```
filter.adjustedCADD(x, SNVs.scores = NULL, indels.scores = NULL,
  ref.level = NULL,
  filter=c("whole", "controls", "any"),
  maf.threshold=0.01, min.nb.snps = 2,
  min.cumulative.maf = NULL,
  group = NULL, cores = 10, path.data, verbose = T,
  build = c("b37", "b38"))
```

Arguments

x A bed.matrix annotated with CADD regions using set.CADDregions

| | |
|--------------------|---|
| SNVs.scores | A dataframe containing the ADJUSTED CADD scores of the SNVs (Optional, useful to gain in computation time if the adjusted CADD scores of variants in the study are available) |
| indels.scores | A dataframe containing the CADD PHREDv1.4 scores of the indels - Compulsory if indels are present in x |
| ref.level | The level corresponding to the controls group, only needed if filter=="controls" |
| filter | On which group the filter will be applied |
| maf.threshold | The MAF threshold used to define a rare variant, set at 0.01 by default |
| min.nb.snps | The minimum number of variants needed to keep a CADD region, set at 2 by default |
| min.cumulative.maf | The minimum cumulative maf of variants needed to keep a CADD region |
| group | A factor indicating the group of each individual, only needed if filter = "controls" or filter = "any". If missing, x@ped\$pheno is taken |
| cores | How many cores to use, set at 10 by default |
| path.data | The repository where data for RAVA-FIRST are or will be downloaded from https://lysine.univ-brest.fr/RAVA-FIRST/ |
| verbose | Whether to display information about the function actions |
| build | The build of the data, either "b37" or "b38". The CADD Regions in the corresponding build will be considered |

Details

Variants are directly annotated with the adjusted CADD scores in the function using the file "AdjustedCADD_v1.4_202108.tsv.gz" downloaded from <https://lysine.univ-brest.fr/RAVA-FIRST/> in the repository of the package Ravages or the scores of variants can be provided to `variant.scores` to gain in computation time (this file should contain 5 columns: the chromosome ('chr'), position ('pos'), reference allele ('A1'), alternative allele ('A2') and adjusted CADD scores ('adjCADD')). As CADD scores are only available for SNVs, only those ones will be kept in the analysis.

If a column 'adjCADD' is already present in `x@snps`, no annotation will be performed and filtering will be directly on this column.

To use this function, a factor 'genomic.region' corresponding to the CADD regions and a vector 'adjCADD.Median' should be present in the slot `x@snps`. To obtain those two, use the function `set.CADDregions`.

Only variants with an adjusted CADD score upper than the median value are kept in the analysis. It is the filtering strategy applied in the `RAVA.FIRST()` pipeline.

If `filter="whole"`, only the variants having a MAF lower than the threshold in the entire sample are kept.

If `filter="controls"`, only the variants having a MAF lower than the threshold in the controls group are kept.

If `filter="any"`, only the variants having a MAF lower than the threshold in any of the groups are kept.

It is recommended to use this function chromosome by chromosome for large datasets.

Value

A bed.matrix with filtered variants

Source

<https://lysine.univ-brest.fr/RAVA-FIRST/>

See Also

[RAVA.FIRST](#), [set.CADDregions](#), [burden.subscores](#), [filter.rare.variants](#)

Examples

```
#Import 1000Genome data from region around LCT gene (b37)
#x37 <- read.bed.matrix( system.file("extdata", "LCT.EUR.b37.bed", package="Ravages") )

#Group variants within CADD regions and genomic categories
#x <- set.CADDregions(x, build = "b37")

#Annotate variants with adjusted CADD score
#and filter on frequency and median
#x.median <- filter.adjustedCADD(x, maf.threshold = 0.025,
#                               #                               min.nb.snps = 2, build = "b37")
```

filter.rare.variants *Rare variants filtering*

Description

Filter rare variants based on a MAF threshold and a given number of SNP or a given cumulative MAF per genomic region

Usage

```
filter.rare.variants(x, ref.level = NULL, filter=c("whole", "controls", "any"),
                    maf.threshold=0.01, min.nb.snps = 2, min.cumulative.maf = NULL,
                    group = NULL, genomic.region = NULL)
```

Arguments

| | |
|---------------|---|
| x | A bed.matrix |
| ref.level | The level corresponding to the controls group, only needed if filter=="controls" |
| filter | On which group the filter will be applied |
| maf.threshold | The MAF threshold used to define a rare variant, set at 0.01 by default |
| min.nb.snps | The minimum number of variants needed to keep a genomic region, set at 2 by default |

| | |
|---------------------------------|--|
| <code>min.cumulative.maf</code> | The minimum cumulative maf of variants needed to keep a genomic region |
| <code>group</code> | A factor indicating the group of each individual, only needed if <code>filter = "controls"</code> or <code>filter = "any"</code> . If missing, <code>x@ped\$pheno</code> is taken |
| <code>genomic.region</code> | An optional factor containing the genomic region of each variant, only needed if <code>min.nb.snps</code> or <code>min.cumulative.maf</code> is specified and if <code>x@snps\$genomic.region</code> doesn't exist |

Details

To use this function, a factor 'genomic.region' should be present in the slot `x@snps`.

If `filter="whole"`, only the variants having a MAF lower than the threshold in the entire sample are kept.

If `filter="controls"`, only the variants having a MAF lower than the threshold in the controls group are kept.

If `filter="any"`, only the variants having a MAF lower than the threshold in any of the groups are kept.

Value

A `bed.matrix` with filtered variants

Examples

```
#Import 1000Genome data from region around LCT gene
x <- as.bed.matrix(LCT.gen, LCT.fam, LCT.bim)

#Group variants within known genes
x <- set.genomic.region(x)
table(x@snps$genomic.region, useNA="ifany")

#Filter of rare variants: only non-monomorphic variants with
#a MAF lower than 2.5%
#keeping only genomic regions with at least 10 SNPs
x1 <- filter.rare.variants(x, filter = "whole", maf.threshold = 0.025, min.nb.snps = 10)
table(x1@snps$genomic.region, useNA="ifany")

#Keep only variants with a MAF<2%
#and regions with a cumulative MAF>10%
filter.rare.variants(x, filter = "whole", maf.threshold = 0.02, min.nb.snps = 1,
                    min.cumulative.maf=0.2)
```

| | |
|-----------------|------------------------|
| genes.positions | <i>Genes positions</i> |
|-----------------|------------------------|

Description

Positions of human genes in bed format (Start is 0-based and End is 1-based). These data were downloaded from Biomart on the Ensembl website with the GRCh37 and GRCh38 versions. Only genes present in GnomAD were kept.

Data contain the Chr, the Start position, the End position and the Name of all the genes in chromosomes 1 to 22 representing 19375 and 18278 genes in the two GRCh versions respectively.

Usage

```
data(genes.b37)
data(genes.b38)
```

Format

The data contain one dataframe with four columns:

Chr The chromosome of the gene

Start The start position of the gene (0-based)

End The end position of the gene (1-based)

Name The name of the gene

Source

The data were obtained from the Ensembl website.

References

RJ Kinsella et al, 2011, *Ensembl BioMart: a hub for data retrieval across taxonomic space*, Database. doi:10.1093/database/bar030;

AD Yates et al, 2020, *Ensembl 2020*, Nucleic Acide Research. doi:10.1093/nar/gkz966

See Also

[set.genomic.region](#)

| | |
|----------------|---|
| genotypic.freq | <i>Genotypic frequencies calculation for data simulations</i> |
|----------------|---|

Description

Calculates the three genotypic frequencies in the controls group and each group of cases based on MAF in the general population and GRR values

Usage

```
genotypic.freq(genes.maf = Kryukov, GRR.het, GRR.homo.alt, prev,
              genetic.model = c("general", "multiplicative",
                               "dominant", "recessive"), select.gene,
              selected.controls = T)
```

Arguments

| | |
|-------------------|--|
| genes.maf | A file containing the MAF in the general population (column maf) for variants with their associated gene (column gene), by default the file Kryukov is used |
| GRR.het | A matrix giving the GRR of the heterozygous genotype compared to the homozygous reference genotype with one row per cases group and one column per variant |
| GRR.homo.alt | A matrix giving the GRR of the homozygous alternative genotype compared to the homozygous reference genotype with one row per cases group and one column per variant, only need if genetic.model="general" |
| prev | A vector containing the prevalence of each group of cases |
| genetic.model | The genetic model of the disease |
| select.gene | Which gene to choose from genes.maf\$gene if multiple genes are present. If missing, only the first level is kept. |
| selected.controls | Whether controls are selected controls (by default) or controls from the general population |

Details

This function is used to simulate genetic data.

The genetic model of the disease needs to be specified to genetic.model:

If genetic.model="general", there is no link between the GRR associated to the heterozygous genotype and the GRR associated to the homozygous alternative genotype. Therefore, the user has to give two matrices of GRR, one for each of these genotypes.

If genetic.model="multiplicative", we assume that the GRR associated to the homozygous alternative genotype is the square of the GRR associated to the heterozygous genotype.

If genetic.model="dominant", we assume that the GRR associated to the heterozygous genotype and the GRR associated to the homozygous alternative genotype are equal.

If `genetic.model="recessive"`, we assume that the GRR associated to the heterozygous genotype is equal to 1: the GRR given is the one associated to the homozygous alternative genotype.

`prev` corresponds to the proportion of each sub-group of cases in the population. It is used only to calculate the MAF in the controls group.

If `selected.controls = T`, genotypic frequencies in the control group are computed from genotypic frequencies in the cases groups and the prevalence of the disease. If `FALSE`, genotypic frequencies in the control group are computed from allelic frequencies under Hardy-Weinberg equilibrium.

The dataframes `Kryukov` or `GnomADgenes` available with the package `Ravages` can be used for the argument `genes.maf`.

Value

A matrix of MAF values with one column per variant and one row per group (the first one being the controls group)

See Also

[GRR.matrix](#), [rbm.GRR](#), [GnomADgenes](#), [Kryukov](#)

Examples

```
#Construction of the GRR matrix using the formula from SKAT
#to compute the GRR (higher weights to rarer variants)
#GRR in the second group are twice as high as in the first group
GRR.del <- GRR.matrix(GRR = "SKAT", GRR.multiplicative.factor=2,
                    select.gene="R1")

#Calculation of frequency in the three groups of individuals
#under a multiplicative model of the disease
geno.freq.groups <- genotypic.freq(genes.maf = Kryukov, GRR.het = GRR.del,
                                   prev = c(0.001, 0.001), select.gene="R1",
                                   genetic.model = "multiplicative")
```

GnomADgenes

GnomADgenes dataset

Description

This dataframe contains variants from the GnomAD database with MAF values in the Non-Finnish European (NFE) and their consequences from VEP with each associated gene in build version 37.

Usage

```
data(GnomADgenes)
```

Format

GnomADgenes is a dataframe with five columns:

chr The chromosome of the variant

pos The position of the variant

consequence The functional consequence of the variant predicted by Variant Effect Predictor (VEP)

gene The gene associated to each variant predicted by VEP

maf The MAF of the variant in the NFE population

Source

The data were obtained from the GnomAD website (see <http://gnomad.broadinstitute.org/>) and the VEP website (see <https://www.ensembl.org/info/docs/tools/vep/>).

GRR.matrix

GRR matrix for genetic data simulation

Description

Computes a GRR matrix based on a simulation model

Usage

```
GRR.matrix(genes.maf = Kryukov, n.case.groups = 2,
           GRR = c("SKAT", "constant", "variable"),
           GRR.value, GRR.function, GRR.multiplicative.factor, select.gene)
```

Arguments

| | |
|---------------------------|---|
| genes.maf | A dataframe containing at least the MAF in the general population (column maf) with their associated gene (column gene). By default, maf from the file Kryukov are used |
| n.case.groups | The number of cases groups (set at 2 by default), i.e. the number of groups where variants will have a GRR greater than 1 |
| GRR | How to calculate the GRR |
| GRR.value | GRR value if GRR="constant" |
| GRR.function | A function indicating how to calculate the GRR depending on MAF in the general population, only needed if GRR="variable" |
| GRR.multiplicative.factor | A vector of size (n.case.groups-1) containing the multiplicative factor for the GRR for each group of cases compared to the first group of cases |
| select.gene | The gene(s) to be selected from the file genes.maf if multiple genes are present. If missing, the first level of genes.maf\$gene is kept. |

Details

The GRR can be computed in three ways using the argument GRR.

If GRR="constant", the same GRR is given to all the variants, its value being specified to GRR.value. If GRR="SKAT", the GRR are calculating using the formula from the paper presenting the SKAT method and thus depend on MAF. If GRR="variable", the GRR are calculating using a function given by the user to GRR.function depending only on the MAF in the general population.

The argument multiplicative.factor contains n.case.groups-1 values; if multiplicative.factor=1, GRR will be the same between the different groups of cases.

The two dataframes Kryukov (used by default) and GnomADgenes (containing MAF in the NFE population) can be used as genes.maf.

GRR.matrix returns a matrix that can be used in other simulation functions such as rbm.GRR.

Value

A matrix containing the GRR values with one column per variant and one line per cases group

See Also

[rbm.GRR](#), [GnomADgenes](#), [Kryukov](#)

Examples

```
#GRR calculated on the MAF from the first unit of the file Kryukov
#using the formula from the SKAT paper, with the second group of cases
#having GRR values twice as high as the first one
GRR.del <- GRR.matrix(GRR = "SKAT", genes.maf = Kryukov,
                     GRR.multiplicative.factor=2, select.gene = "R1")
```

Jaccard

Jaccard index

Description

Calculates the Jaccard index for each pair of individuals using a bed.matrix

Usage

```
Jaccard(x, maf.threshold = 0.01)
```

Arguments

x A bed.matrix

maf.threshold The MAF used for the definition of a rare variant, set at 0.01 by default

Details

The individuals carrying no rare variants will have a null Jaccard index with all the individuals including themselves.

Value

A squared matrix giving the Jaccard index for each pair of individuals

References

Jaccard, P. (1908) *Nouvelles recherches sur la distribution florale*, Bulletin de la Société vaudoise des sciences naturelles, **44**, 223-270

Examples

```
#Simulation of genetic data with GRR values according to the SKAT formula
GRR.del <- GRR.matrix(GRR = "SKAT", genes.maf = Kryukov,
                     n.case.groups = 2, select.gene = "R1",
                     GRR.multiplicative.factor=2)

#Simulation of one group of 1,000 controls and two groups of 500 cases,
#50% of causal variants, 5 genomic regions are simulated.
x <- rbm.GRR(genes.maf=Kryukov, size = c(1000, 500, 500),
            prev = c(0.001, 0.001), select.gene = "R1",
            GRR.matrix.del = GRR.del, p.causal = 0.5,
            genetic.model = "multiplicative", replicates = 5)

#Calculate the Jaccard matrix
J <- Jaccard(x, maf.threshold = 0.01)
```

Kryukov

Kryukov data set

Description

The data from *Kryukov et al, 2009*, contain simulated site frequency spectrum data using European demographic models with purifying selection.

Usage

```
data(Kryukov)
```

Format

Kryukov is a dataframe with four columns:

gene The unit of each variant

maf The maf of each variant in the European population

selection.coefficient The selection coefficient of each variant in the European population

position The position of each variant

Details

200 units are present corresponding to 200 genes. For each unit, the data set contains the maf in the European population, the selection coefficient and the position of each variant.

Source

The data were obtained from the SeqPower software (see also http://www.bioinformatics.org/spower/input#data_download).

References

Kryukov et al, 2009, *Power of deep, all-exon resequencing for discovery of human trait genes*, Proceedings of the National Academy of Sciences, DOI:10.1073/pnas.0812824106

LCT.EUR

LCT genotypes matrix

Description

These data contain the genotype matrix from the 1000 Genomes EUR ancestry individuals in the Lactase gene (positions retrieved from GeneCards. Information about individuals is present in LCT.EUR.b37/b38.fam, including the subpopulation, in a format needed to generate a bedmatrix. Two set of files are available: one set in build 37, and one set in build 38. Data have been anonymized by randomly sampling the genotype positions.

Format

LCT.EUR.b37/b38.bed Binary genotype file

LCT.EUR.b37/b38.bim Variant information file

LCT.EUR.b37/b38.fam Sample information file

Source

Data were obtained from the 1000 Genomes Project.

References

McVean et al, 2012, *An integrated map of genetic variation from 1,092 human genomes*, Nature **491**, 56-65 doi:10.1038/nature11632

Examples

```
#Import data in a bed matrix
x <- read.bed.matrix( system.file("extdata", "LCT.EUR.b37.bed", package="Ravages") )
```

| | |
|----------------|--------------------------------|
| LCT.haplotypes | <i>LCT haplotypes data set</i> |
|----------------|--------------------------------|

Description

These data contain the haplotype matrix LCT.hap (5008 haplotypes) of the 2004 individuals from the 1000 Genomes data for a ~300kb segment containing the Lactase gene. Information about individuals (sex, population and super population) is present in LCT.sample, and information about snps is available in LCT.snps.

Usage

```
data(LCT.haplotypes)
```

Format

Three data objects are present in LCT.haplotypes:

LCT.hap A matrix of haplotypes

LCT.sample A data frame with information on individuals (sex, population, super.population)

LCT.snps A data frame with information on snps (chr, id, dist, pos, A1, A2)

Source

Data were obtained from the 1000 Genomes Project.

References

McVean et al, 2012, *An integrated map of genetic variation from 1,092 human genomes*, Nature **491**, 56-65 doi:10.1038/nature11632

multinomial.asso.freq *Single variant association test with categorical phenotype*

Description

Performs an association test between categorical phenotypes and single variants

Usage

```
multinomial.asso.freq(x, pheno = x@ped$pheno, ref.level,
                     test = c("Genotypic", "Allelic"), get.effect.size = F,
                     min.maf.threshold = 0.05)
```

Arguments

| | |
|-------------------|---|
| x | A bed matrix, only needed if burden="CAST" or burden="WSS" |
| pheno | The phenotype of each individual: a factor if pheno.type = "categorical", and a numeric vector if pheno.type = "continuous" |
| ref.level | The reference group of individuals for the estimation of the effect size, only needed if get.effect.size = T |
| test | Whether to perform the test on the three genotypes ("Genotypic") or on the two alleles ("Allelic") |
| get.effect.size | TRUE/FALSE: whether to return effect sizes of the variants (OR) |
| min.maf.threshold | MAF threshold used to define a frequent variant to apply single-variant test |

Details

This association test is based on a chi-square with the following number of df: If test = "Genotypic", (number of groups of individuals - 1)* 2 If test = "Allelic", (number of groups of individuals - 1)

Value

A dataframe with one row per variant and three columns: the chromosome, position and p-value of each variant. If get.effect.size = T, a list with Asso containing the previous dataframe and OR containing the OR in each group for each variant.

Examples

```
#Import data in a bed matrix
x <- read.bed.matrix( system.file("extdata", "LCT.EUR.b37.bed", package="Ravages") )

#Group variants within known genes
x <- set.genomic.region(x)
```

```
#Perform association test
x.freq.asso <- multinomial.asso.freq(x, test = "Genotypic",
                                     pheno = x@ped$population)
```

NullObject.parameters *Null Model for SKAT and burden tests*

Description

Get the parameters under the null model to performs burden tests or SKAT

Usage

```
NullObject.parameters(pheno, RVAT, pheno.type = c("categorical", "continuous"),
                     ref.level, data, formula)
```

Arguments

| | |
|------------|--|
| pheno | The phenotype of each individual: a factor if pheno.type = "categorical", and a numeric vector if pheno.type = "continuous" |
| RVAT | The type of Rare Variant Association Test (RVAT) to perform: should be "burden" or "SKAT" |
| pheno.type | The type of phenotype: "categorical" for binary or multinomial traits, or "continuous" |
| ref.level | The reference group of individuals for the regression, only needed if RVAT = "burden" and pheno.type = "categorical" |
| data | Optional, a matrix containing the covariates with one column per covariate and one row per individual |
| formula | Optional, an R formula corresponding to the regression model indicating which covariates from data to include in the model if only some of them are to be included |

Details

Warning: individuals in pheno and data should be in the same order.

This function gets the parameters under the null model for SKAT or the burden tests.

For burden tests, it computes the Log-Likelihood under the null model used to perform the Likelihood Ratio Test.

For SKAT, it computes the probabilities for each individual of belonging to each group based on the group sizes and the potential covariates.

If formula is missing, all columns from data will be included as covariates.

Value

A list containing different elements depending on the RVAT performed and the pheno.type.

- if RVAT = "burden" and pheno.type = "categorical":

| | |
|-----------------|--|
| group | A factor containing the group of each individual as given |
| ref.level | The reference group of individuals for the regression as given |
| H0.LogLik | The Log-Likelihood of the null model |
| covar.toinclude | Which covariates to include in the regression, depends on the argument formula |
| data | The data argument containing covariates, NULL if it was missing |

- if RVAT = "burden" and pheno.type = "continuous":

| | |
|-----------------|--|
| pheno | A numeric vector containing the phenotype value for each individual as given |
| covar.toinclude | Which covariates to include in the regression, depends on the argument formula |
| data | The data argument containing covariates, NULL if it was missing |

- if RVAT = "SKAT" and pheno.type = "categorical":

| | |
|-------------|--|
| Pi.data | A matrix n.individuals x n.groups containing the probabilities that each individual belong to each group |
| X | A matrix containing 1 in the first column for the intercept, and covariates from data and formula |
| group | A factor containing the group of each individual as given |
| get.moments | How to compute moments based on sample size for p-value calculations (only used if get.moments = "size.based" for a categorical phenotype in SKAT. |
| P1 | The vairance-covariance matrix of (Y - Pi_hat) |

- if RVAT = "SKAT" and pheno.type = "continuous":

| | |
|-------|--|
| ymp | A matrix n.individuals x 1 containing the (y - pi_hat) values, i.e. the residuals from the regression of the phenotype on the potential covariates |
| X | A matrix containing 1 in the first column for the intercept, and covariates from data and formula |
| pheno | The phenotype of each individual as given |
| P1 | The variance matrix of ymp |

See Also

[SKAT](#), [burden](#)

Examples

```
#Random phenotype of 100 individuals
random.multi.pheno <- sample(1:3, 100, replace = TRUE)
#Random continuous phenotype
random.continuous.pheno <- rnorm(100)
#Random sex covariate
random.covar <- matrix( sample(1:2, prob = c(0.4, 0.6), size = 100, replace = TRUE),
                        ncol = 1 )

#Null Model for burden with a multinomi-category phenotype
#Controls as reference group, no covariates
H0.burden.multi <- NullObject.parameters(pheno = as.factor(random.multi.pheno),
                                       RVAT = "burden", pheno.type = "categorical", ref.level = 1)
#Null Model for SKAT with a continuous phenotype and a covariate
H0.SKAT.continuous <- NullObject.parameters(pheno = random.continuous.pheno,
                                           RVAT = "SKAT", pheno.type = "continuous",
                                           data = random.covar)
```

| | |
|------------|---|
| RAVA.FIRST | <i>RAVA-FIRST: RAre Variant Association using Functionally-InfoRmed Steps</i> |
|------------|---|

Description

Analyse rare variants using the RAVA-FIRST approach based on CADD scores to group and filter rare variants

Usage

```
RAVA.FIRST(x, SNVs.scores = NULL, indels.scores = NULL, ref.level,
           filter=c("whole", "controls", "any"),
           maf.threshold=0.01, min.nb.snps = 2,
           min.cumulative.maf = NULL, group = NULL,
           cores = 10, burden = TRUE, H0.burden, burden.parameters,
           SKAT = TRUE, H0.SKAT, SKAT.parameters, verbose = TRUE,
           path.data, build = c("b37", "b38"))
```

Arguments

| | |
|---------------|---|
| x | A bed.matrix |
| SNVs.scores | A dataframe with the columns 'chr', 'pos', 'A1', 'A2' and 'adjCADD' containing the ADJUSTED CADD scores of the SNVs (Optional, useful to gain in computation time if the adjusted CADD scores of variants in the study are available) |
| indels.scores | A dataframe with the columns 'chr', 'pos', 'A1', 'A2' and 'PHRED_1.4' containing the CADD PHREDv1.4 scores of the indels - Compulsory if indels are present in x |

| | |
|---------------------------------|---|
| <code>ref.level</code> | The level corresponding to the controls group, only needed if <code>filter=="controls"</code> |
| <code>filter</code> | On which group the MAF filter will be applied |
| <code>maf.threshold</code> | The MAF threshold used to define a rare variant, set at 0.01 by default |
| <code>min.nb.snps</code> | The minimum number of variants needed to keep a CADD region, set at 2 by default |
| <code>min.cumulative.maf</code> | The minimum cumulative maf of variants needed to keep a CADD region |
| <code>group</code> | A factor indicating the group of each individual, only needed if <code>filter = "controls"</code> or <code>filter = "any"</code> . If missing, <code>x@ped\$pheno</code> is taken |
| <code>cores</code> | How many cores to use, set at 10 by default |
| <code>burden</code> | Whether to compute the burden test |
| <code>H0.burden</code> | A list returned from <code>NullObject.parameters</code> with <code>RVAT="burden"</code> |
| <code>burden.parameters</code> | A list containing the parameters to use by <code>burden.subscores</code> for the burden analysis ('burden.function' and 'get.effect.size') |
| <code>SKAT</code> | Whether to compute SKAT |
| <code>H0.SKAT</code> | A list returned from <code>NullObject.parameters</code> with <code>RVAT="SKAT"</code> |
| <code>SKAT.parameters</code> | A list containing the parameters to use by SKAT ('get.moments', 'estimation.pvalue', 'params.sampling', 'debug') |
| <code>verbose</code> | Whether to display information about the function actions |
| <code>path.data</code> | The repository where data for RAVA-FIRST are or will be downloaded from https://lysine.univ-brest.fr/RAVA-FIRST/ |
| <code>build</code> | The build of the data, either "b37" or "b38". The CADD Regions in the corresponding build will be considered |

Details

Rare variants are analysed using the 'RAVA-FIRST' strategy composed of three steps: - Rare variants are grouped in 'CADD regions' defined from the CADD scores of variants observed in GnomAD. - Rare variant are selected within each CADD region based on an adjusted CADD score using a region-specific threshold corresponding to the median of scores observed in GnomAD in each region. - Burden analysis is performed by integrating sub-scores for the coding, regulatory and intergenic categories within each CADD region. For SKAT analysis, a test for each CADD region is performed.

RAVA.FIRST() is based on the functions `set.CADDregions`, `filter.adjustedCADD`, `burden.subscores` and `SKAT`. Please refer to these functions for more information. Especially, refer to the functions `burden.subscores` and `SKAT` to get more information about what is need in `burden.parameters` and `SKAT.parameters`.

bedtools need to be installed on the system if indels are present or if scores are not provided for SNVs.

It is recommended to use this function chromosome by chromosome for large datasets.

Value

A list containing the results for the burden analysis ('burden') and the results for the SKAT analysis ('SKAT'), along with information about CADD regions (positions, type of genomic categories overlapped by each region and median of adjusted CADD scores).

Source

<https://lysine.univ-brest.fr/RAVA-FIRST/>

See Also

set.CADDregions, filter.adjustedCADD, burden.subscores, SKAT

Examples

```
##This example takes a few minutes to run.
##To run it quickly, we advise the user to decrease
##the number of variants or to increase the number of cores used
#Import data in a bed matrix (example in build 37)
#x <- read.bed.matrix( system.file("extdata", "LCT.EUR.b37.bed", package="Ravages") )

#Remove the multi-allelic variants
#x <- select.snps(x, !grepl(A2, pattern = ",") & !grepl(A1, pattern = ","))

#Keep only the rare variants
#x <- select.snps(x, maf <= 0.01 & maf > 0)

#Select the indels and make a dataframe to be used for annotation
#x.vcf <- subset(x@snps, nchar(A1)>1 | nchar(A2)>1)[,c("chr", "pos", "id", "A1", "A2")]
#Export the file for annotation
#write.table(x.vcf, file = "indels.toannotate.vcf",
#           col.names = F, row.names = F, quote = F, sep = "\t")

#####
#Annotate the file in on CADD website (https://cadd.gs.washington.edu/score)
#Please be careful here about which CADD version to use for annotation, here is v1.4 for b37
#####

#Download the results file, unzip it and load it in R
#x.indels <- read.table("indels.annotated.tsv")
#colnames(x.indels) <- c("chr", "pos", "A1", "A2", "CADD1.4", "PHRED_1.4")

#Set the NULL model for burden testing
#H0.burden <- NullObject.parameters(pheno = x@ped$population, ref.level = "CEU",
#                                RVAT = "burden", pheno.type = "categorical")

#Run RAVA-FIRST
#x.RAVAFIRST = RAVA.FIRST(x, indels.scores = x.indels, H0.burden = H0.burden, SKAT = F, cores = 1,
#                        path.data = "RAVA-FIRST/Package", maf.threshold = 1, build = "b37")
```

rbm.GRR

*Simulation of genetic data using GRR values***Description**

Generates a simulated bed.matrix with genotypes for cases and controls based on GRR values

Usage

```
rbm.GRR(genes.maf = Kryukov, size, prev, replicates,
        GRR.matrix.del, GRR.matrix.pro = NULL,
        p.causal = 0.5, p.protect = 0, same.variant = FALSE,
        genetic.model=c("general", "multiplicative", "dominant", "recessive"),
        select.gene, selected.controls = T, max.maf.causal = 0.01)
```

Arguments

| | |
|-------------------|--|
| genes.maf | A dataframe containing at least the MAF in the general population (column maf) for variants with their associated gene (column gene), by default the file Kryukov is used |
| size | A vector containing the size of each group (the first one being the control group) |
| prev | A vector containing the prevalence of each group of cases |
| replicates | The number of simulations to perform |
| GRR.matrix.del | A list containing the GRR matrix associated to the heterozygous genotype compared to the homozygous reference genotype as if all variants are deleterious. An additional GRR matrix associated to the homozygous for the alternate allele is needed if genetic.genetic.model="general" |
| GRR.matrix.pro | The same argument as GRR.matrix.del but for protective variants |
| p.causal | The proportion of causal variants in cases |
| p.protect | The proportion of protective variants in cases among causal variants |
| same.variant | TRUE/FALSE: whether the causal variants are the same in the different groups of cases |
| genetic.model | The genetic model of the disease |
| select.gene | Which gene to choose from genes.maf\$gene if multiple genes are present. If missing, only the first level is kept. |
| selected.controls | Whether controls are selected controls (by default) or controls from the general population |
| max.maf.causal | Only variants with a MAF lower than this threshold can be sampled as causal variants. |

Details

The genetic model of the disease needs to be specified in this function.

If `genetic.model="general"`, there is no link between the GRR for the heterozygous genotype and the GRR for the homozygous alternative genotype. Therefore, the user has to give two matrices of GRR, one for the heterozygous genotype, the other for the homozygous alternative genotype.

If `genetic.model="multiplicative"`, we assume that the the GRR for the homozygous alternative genotype is the square of the GRR for the heterozygous genotype.

If `genetic.model="dominant"`, we assume that the GRR for the heterozygous genotype and the GRR for the homozygous alternative genotype are equal.

If `genetic.model="recessive"`, we assume that the GRR for the heterozygous genotype is equal to 1: the GRR given is the one associated to the homozygous alternative genotype.

`GRR.matrix.del` contains GRR values as if all variants are deleterious. These values will be used only for the proportion `p.causal` of variants that will be sampled as causal.

If `selected.controls = T`, genotypic frequencies in the control group are computed from genotypic frequencies in the cases groups and the prevalence of the disease. If `FALSE`, genotypic frequencies in the control group are computed from allelic frequencies under Hardy-Weinberg equilibrium.

The files `Kryukov` or `GnomADgenes` available with the package `Ravages` can be used as the argument `genes.maf`.

If `GRR.matrix.del` (or `GRR.matrix.pro`) has been generated using the function `GRR.matrix`, the arguments `genes.maf` and `select.gene` should have the same value as in `GRR.matrix`.

Only non-monomorphic variants are kept for the simulations.

Causal variants that have been sampled in each group of individuals are indicated in `x@ped$Causal`.

Value

A `bed.matrix` with as much columns (variants) as `replicates*number of variants`. The field `x@snps$genomic.region` contains the replicate number and the field `x@ped$pheno` contains the group of each individual, "0" being the controls group.

See Also

[GRR.matrix](#), [Kryukov](#), [GnomADgenes](#), [rbm.GRR.power](#)

Examples

```
#GRR values calculated with the SKAT formula
GRR.del <- GRR.matrix(GRR = "SKAT", genes.maf = Kryukov,
                     n.case.groups = 2, select.gene = "R1",
                     GRR.multiplicative.factor=2)

#Simulation of one group of 1,000 controls and two groups of 500 cases,
#each one with a prevalence of 0.001
#with 50% of causal variants, 5 genomic regions are simulated.
x <- rbm.GRR(genes.maf = Kryukov, size = c(1000, 500, 500),
            prev = c(0.001, 0.001), GRR.matrix.del = GRR.del,
```

```
p.causal = 0.5, p.protect = 0, select.gene="R1",
same.variant = FALSE,
genetic.model = "multiplicative", replicates = 5)
```

| | |
|---------------|--|
| rbm.GRR.power | <i>Power of RVAT based on simulations and theoretical calculations (CAST) with GRR</i> |
|---------------|--|

Description

Computes the power of the tests CAST, WSS and SKAT based on simulations with GRR and based on theoretical calculations for CAST

Usage

```
rbm.GRR.power(genes.maf = Kryukov, size = c(500, 500), prev = 0.01,
  GRR.matrix.del, GRR.matrix.pro = NULL,
  p.causal = 0.5, p.protect = 0, same.variant = FALSE,
  genetic.model=c("multiplicative", "general", "dominant", "recessive"),
  select.gene, alpha = 2.5e-6, selected.controls = TRUE,
  power.type = c("simulations", "theoretical"), verbose = TRUE,
  RVAT = c("CAST", "WSS", "SKAT"),
  SKAT.method = c("permutations", "theoretical"),
  max.maf.causal = 0.01, maf.filter = max.maf.causal,
  replicates = 1000, cores = 10)
```

Arguments

| | |
|----------------|--|
| genes.maf | A dataframe containing at least the MAF in the general population (column maf) for variants with their associated gene (column gene), by default the file Kryukov is used |
| size | A vector containing the size of each group (the first one being the control group) |
| prev | A vector containing the prevalence of each group of cases |
| GRR.matrix.del | A list containing the GRR matrix associated to the heterozygous genotype compared to the homozygous reference genotype as if all variants are deleterious. An additional GRR matrix associated to the homozygous for the alternate allele is needed if genetic.genetic.model="general" |
| GRR.matrix.pro | The same argument as GRR.matrix.del but for protective variants |
| p.causal | The proportion of causal variants in cases |
| p.protect | The proportion of protective variants in cases among causal variants |
| same.variant | TRUE/FALSE: whether the causal variants are the same in the different groups of cases |
| genetic.model | The genetic model of the disease |
| select.gene | Which gene to choose from genes.maf\$gene if multiple genes are present. If missing, only the first level is kept. |

| | |
|-------------------|---|
| alpha | The significance level to compute the power |
| selected.controls | Whether controls are selected controls (by default) or controls from the general population |
| power.type | Whether to compute the power based on 'simulations' (by default) or 'theoretical' calculations (only for CAST) |
| verbose | Whether to print details about the running function |
| RVAT | On which RVAT among 'CAST', 'WSS' and 'SKAT' to compute power (only needed if power.type="simulations") |
| SKAT.method | Which method to use to compute SKAT power, i.e. permutations or theoretical moments (cf SKAT documentation) |
| max.maf.causal | The maf threshold to consider a causal variant (set at 0.01 by default) |
| maf.filter | The MAF filter to apply after the simulations to select rare variants to keep for RVAT power analysis. By default corresponds to max.maf.causal |
| replicates | On how many replicates the power should be computed |
| cores | How many cores to use for moments computation, set at 10 by default |

Details

Simulations are performed in the same way as in `rbm.GRR`. Please refer to the documentation of this function.

Theoretical power is only available for CAST for which a non-central Chi-squared is used.

Variants are filtered after the simulations to keep only the rare ones, defined by `maf.filter`. By default, it corresponds to `max.maf.causal` is used. To disable this filter, set `maf.filter` at 0.5.

Value

A single value giving the power of CAST if `power.type="theoretical"` or the power of RVAT if `power.type="simulations"`.

See Also

[GRR.matrix](#), [Kryukov](#), [GnomADgenes](#), [rbm.GRR](#)

Examples

```
#GRR values calculated with the SKAT formula
GRR.del <- GRR.matrix(GRR = "SKAT", genes.maf = Kryukov,
                     n.case.groups = 2, select.gene = "R1",
                     GRR.multiplicative.factor=2)

#Simulation of one group of 1,000 controls and two groups of 500 cases,
#each one with a prevalence of 0.001
#with 50% of causal variants, 5 genomic regions are simulated.
rbm.GRR.power(genes.maf = Kryukov, size = c(1000, 500, 500),
              prev = c(0.001, 0.001), GRR.matrix.del = GRR.del,
              p.causal = 0.5, p.protect = 0, select.gene="R1",
```



```

1/table(LCT.sample.EUR$population)[z], 0))

#Simulation of genetic data for five groups of 50 individuals
x <- rbm.haplos.freqs(haplos=LCT.gene.hap, freqs=LCT.freqs, size=rep(50,5), replicates=5)

```

rbm.haplos.power *Power of RVAT based on simulations with haplotypes*

Description

Computes the power of the tests CAST, WSS and SKAT based on simulations with haplotypes

Usage

```

rbm.haplos.power(haplos, freqs, weights = "SKAT",
                 max.maf.causal = 0.01, maf.filter = max.maf.causal, p.causal = 0.5,
                 p.protect = 0, h2 = c(0.01, 0.01), prev = c(1, 0.01),
                 normal.approx = TRUE, size = c(500, 500), verbose = TRUE,
                 alpha = 2.5e-6, RVAT = c("CAST", "WSS", "SKAT"),
                 SKAT.method = c("permutations", "theoretical"),
                 simus.haplos = c("freqs", "liability"),
                 replicates = 1000, rep.by.causal = 50, cores = 10)

```

Arguments

| | |
|----------------|---|
| haplos | A matrix of haplotypes with one row per haplotype and one column per variant |
| freqs | A matrix of haplotypes frequencies in each group of individuals, only needed if simus.haplos = "freqs" |
| weights | How to weight rare variants (if "constant", all variants have the same weight, if "SKAT", the rarest variants have the highest weights: weights = -0.4*log10(MAF)) |
| max.maf.causal | The maf threshold to consider a rare variant (set at 0.01 by default). Only variants with a MAF upper than this threshold will be kept to compute RVAT power. If simus.haplos="liability", variants with a MAF upper this threshold will have a weight of 0 |
| maf.filter | The MAF filter to apply after the simulations to select rare variants to keep for RVAT power analysis. By default corresponds to max.maf.causal |
| p.causal | The percentage of causal variants, only needed if simus.haplos = "liability" |
| p.protect | The proportion of protective variants among causal variants, only needed if simus.haplos = "liability" |
| h2 | The variance explained by the gene, only needed if simus.haplos = "liability" |
| prev | A vector with the prevalence in each group of individuals, only needed if simus.haplos = "liability" |
| normal.approx | TRUE/FALSE: whether to use the normal approximation to compute thresholds. Set at TRUE by default, only needed if simus.haplos = "liability" |

| | |
|---------------|--|
| size | The sizes of each group of individuals |
| verbose | Whether to display information about the function actions |
| alpha | The significance level to compute the power |
| RVAT | On which RVAT among 'CAST', 'WSS' and 'SKAT' to compute power (only needed if power.type="simulations") |
| SKAT.method | Which method to use to compute SKAT ppower, i.e. permutations or theoretical moments (cf SKAT documentation) |
| simus.haplos | Which method to simulate the data, if simus.haplos="freqs", rbm.haplos.freqs() is used, otherwise rbm.haplos.thresholds() is used. |
| replicates | The number of simulations to perform to estimate the power |
| rep.by.causal | The number of time causal variants will be sampled |
| cores | How many cores to use for moments computation, set at 10 by default |

Details

Simulations are performed accordingly to `rbm.haplos.thresholds()` or `rbm.haplos.freqs()`. Please refer to the corresponding manuals for more details on the simulation procedures. Variants are filtered after the simulations to keep only the rare ones, defined by `maf.filter`. By default, it corresponds to `max.maf.causal` is used. To disable this filter, set `maf.filter` at 0.5.

Value

Power values of RVAT

Examples

```
#Simulations of 5 groups of individuals with haplotypes frequencies
#from the 5 EUR populations

#Load LCT dataset for haplotype matrix
data(LCT.haplotypes)
#Haplotypes for the variants in the LCT gene in the EUR population
LCT.gene.hap <- LCT.hap[which(LCT.sample$super.population=="EUR"),
  which(LCT.snps$pos>=136545410 & LCT.snps$pos<=136594750)]

#Individuals from EUR
LCT.sample.EUR <- subset(LCT.sample, super.population=="EUR")
#Matrix of haplotypic frequencies
LCT.freqs <- sapply(unique(LCT.sample.EUR$population), function(z)
  ifelse(LCT.sample.EUR$population==z,
    1/table(LCT.sample.EUR$population)[z], 0))

#Simulation of genetic data for five groups of 50 individuals
rbm.haplos.power(haplos=LCT.gene.hap, freqs=LCT.freqs, size=rep(50,5),
  replicates=5, rep.by.causal = 5, RVAT = "CAST",
  alpha = c(0.001,2.5e-6), cores = 1)
```

 rbm.haplos.thresholds *Simulation of genetic data based on haplotypes and a liability model*

Description

Simulates genetic data with respect to allele frequency spectrum and linkage disequilibrium pattern observed on given haplotype data under a liability model

Usage

```
rbm.haplos.thresholds(haplos, weights = c("SKAT", "constant"),
                      max.maf.causal = 0.01, p.causal = 0.5, p.protect = 0,
                      h2, prev, normal.approx = TRUE, size,
                      replicates, rep.by.causal, verbose = TRUE)
```

Arguments

| | |
|----------------|--|
| haplos | A matrix of haplotypes with one row per haplotype and one column per variant |
| weights | How to weight rare variants (if "constant", all variants have the same weight, if "SKAT", the rarest variants have the highest weights as in the SKAT paper: $weights = -0.4 * \log_{10}(MAF)$) |
| max.maf.causal | The maf threshold to consider a rare variant (set at 0.01 by default), variants with a MAF upper this threshold will have a weight of 0 |
| p.causal | The proportion of causal variants |
| p.protect | The proportion of protective variants among causal variants |
| h2 | The variance explained by the gene |
| prev | A vector with the prevalence in each group of individuals |
| normal.approx | TRUE/FALSE: whether to use the normal approximation to compute thresholds. Set at TRUE by default |
| size | The sizes of each group of individuals |
| replicates | The number of simulations to perform |
| rep.by.causal | The number of time causal variants will be sampled |
| verbose | Whether to display information about the function actions |

Details

nb.causal, p.protect, h2 and prev should be vectors of length corresponding to the number of groups to simulate. If they are of size 1, values will be duplicated.

All monomorphic variants and variants with a MAF higher than max.maf.causal will have a weight of 0. Causal variants are sampled among variants having weights greater than 0. Causal variants in each group of individuals are indicated in `x@ped$Causal`.

A liability model is built on haplotypes' burden computed on sampled causal variants using each variant's weights, and adjusted on the desired h2. Thresholds from this liability are then chosen

to respect the given prev (from a standard normal distribution if `normal.approx=TRUE`, or using a distribution from $1e6$ sampled burdens if `normal.approx=FALSE`). Please be careful when using the normal approximation with high h^2 values or low prev values. Haplotypes' probabilities in each group of individuals are then computed and two haplotypes are then sampled for each individual based on these probabilities.

To simulate a group of controls, prev needs to be set at 1, regardless of the other arguments.

`N` replicates will be performed, and to gain in computation time, the same causal variants can be used for multiple replicates as different haplotypes will be sampled for each individual. `rep.by.causal` indicates the number of replicates to perform for each set of causal variants. To ensure a variability in the simulations, we yet recommend to resample causal variants a few times when many replicates are to be performed. For example, if 1000 replicates are to be performed, we recommend to resample causal variants 20 times.

The phenotype will be stored in `@ped$pheno`, and the simulation number is `@snps$genomic.region`.

Value

`x` A bed matrix with simulated genotypes

Examples

```
#Load LCT dataset for haplotype matrix
data(LCT.haplotypes)
#LCT gene in the EUR population
LCT.gene.hap <- LCT.hap[which(LCT.sample$super.population=="EUR"),
                      which(LCT.snps$pos>=136545410 & LCT.snps$pos<=136594750)]

#Simulation of 100 controls, and two groups of 50 cases with 30% causal variants
#and with the second group having half h2 and twice the prevalence
#compared to the first one
#5 replicates are performed and causal variants are sampled once
x <- rbm.haplos.thresholds(haplos=LCT.gene.hap, max.maf.causal = 0.01, p.causal=0.3,
                          p.protect=0, h2=c(0.01, 0.01, 0.02), prev=c(1, 0.01, 0.005),
                          size=c(100, 50, 50), replicates = 5, rep.by.causal = 5)
```

| | |
|-----------------|---|
| set.CADDregions | <i>Variants annotation based on 'CADD regions' and genomic categories</i> |
|-----------------|---|

Description

Attributes CADD regions and genomic categories to variants based on their positions

Usage

```
set.CADDregions(x, verbose = T, path.data, build = c("b37", "b38"))
```

Arguments

| | |
|-----------|---|
| x | A bed.matrix |
| verbose | Whether to display information about the function actions |
| path.data | The repository where data for RAVA-FIRST are or will be downloaded from https://lysine.univ-brest.fr/RAVA-FIRST/ |
| build | The build of the data, either "b37" or "b38". The CADD Regions in the corresponding build will be considered |

Details

To attribute variants to CADD regions and genomic categories, the files "CADDRegions.2021.hg19.bed.gz" and "FunctionalAreas.hg19.bed.gz" will be downloaded from <https://lysine.univ-brest.fr/RAVA-FIRST/> in the repository of the package Ravages. CADD regions are non-overlapping regions that have been defined in the whole genome to perform rare variant association tests in the RAVA.FIRST() pipeline. It is recommended to use this function chromosome by chromosome for large datasets for time and memory management.

Value

The same bed matrix as x with three additional columns :

| | |
|----------------|---|
| genomic.region | The CADD region of each variant |
| SubRegion | The genomic category of each variant among 'Coding', 'Regulatory' or 'Intergenic' |
| adjCADD.Median | The median of adjusted CADD of variants observed at least to times in GnomAD genomes r2.0.1 |

Source

<https://lysine.univ-brest.fr/RAVA-FIRST/>

See Also

[RAVA.FIRST](#), [filter.adjustedCADD](#), [burden.subscores](#)

Examples

```
#Import data in a bed matrix (example in build 37)
#x <- read.bed.matrix( system.file("extdata", "LCT.EUR.b37.bed", package="Ravages") )

#Group variants within CADD regions and genomic categories
#x <- set.CADDregions(x, build = "b37")
#table(x@snps$genomic.region) #CADD regions
#table(x@snps$SubRegion) #Genomic categories
```

set.genomic.region *Variants annotation based on gene positions*

Description

Attributes regions to variants based on given region positions

Usage

```
set.genomic.region(x, regions = genes.b37, flank.width = 0L, split = TRUE)
```

Arguments

| | |
|-------------|---|
| x | A bed.matrix |
| regions | A dataframe in bed format (start is 0-based and end is 1-based) containing the fields : Chr (the chromosome of the gene), Start (the start position of the gene, 0-based), End (the end position of the gene, 1-based), and Name (the name of the gene - a factor), |
| flank.width | An integer: width of the flanking regions in base pairs downstream and upstream the regions. |
| split | Whether to split variants attributed to multiple regions by duplicating this variants, set at TRUE by default |

Details

Warnings: regions\$Name should be a factor containing UNIQUE names of the regions, ORDERED in the genome order.

We provide two data sets of autosomal human genes, genes.b37 and genes.b38.

If x@snps\$chr is not a vector of integers, it should be a factor with same levels as regions\$Chr.

If flank.width is null, only the variants having their position between the regions\$Start and the regions\$End of a gene will be attributed to the corresponding gene. When two regions overlap, variants in the overlapping zone will be assigned to those two regions, separated by a comma.

If flank.width is a positive number, variants flank.width downstream or upstream a gene will be annotated annotated to this gene. You can use flank.width = Inf to have each variant attributed to the nearest gene.

If a variant is attributed to multiple genomic regions, it will be duplicated in the bed matrix with one row per genomic region if split = TRUE. Variants will have new IDs being CHR:POS:A1:A2:genomic.region.

Value

The same bed matrix as x with an additional column x@snps\$genomic.region containing the annotation of each variant.

See Also

[genes.b37](#), [genes.b38](#)

Examples

```
#Import 1000Genome data from region around LCT gene
x <- as.bed.matrix(LCT.gen, LCT.fam, LCT.bim)

#Group variants within known genes
x <- set.genomic.region(x)

#Group variants within know genes +/- 500bp
x <- set.genomic.region(x, flank.width=500)
```

```
set.genomic.region.subregion
```

Variants annotation based on regions and subregions positions

Description

Attributes regions and subregions to variants based on given positions

Usage

```
set.genomic.region.subregion(x, regions, subregions, split = TRUE)
```

Arguments

| | |
|------------|--|
| x | A bed.matrix |
| regions | A dataframe in bed format (start is 0-based and end is 1-based) containing the regions with the fields : Chr (the chromosome of the gene), Start (the start position of the gene, 0-based), End (the end position of the gene, 1-based), and Name (the name of the gene - a factor), |
| subregions | A dataframe containing the subregions in the same format as regions |
| split | Whether to split variants attributed to multiple regions by duplicating this variants, set at TRUE by default |

Details

Warnings: regions\$Name and subregions\$Name should be factors containing UNIQUE names of the regions, ORDERED in the genome order.

If x@snps\$chr is not a vector of integers, it should be a factor with same levels as regions\$Chr.

If a variant is attributed to multiple genomic regions, it will be duplicated in the bed matrix with one row per genomic region if split = TRUE.

This function can be applied before using burden.subscores to perform a functionally-informed burden tests with sub-scores for each SubRegion within each genomic.region.

Value

The same bed matrix as x with two additional columns: x@snps\$genomic.region containing the annotation of the regions and x@snps\$SubRegion containing the annotation of the subregions.

See Also

[set.genomic.region, burden.subscores](#)

Examples

```
#Import data in a bed matrix
x <- read.bed.matrix( system.file("extdata", "LCT.EUR.b37.bed", package="Ravages") )

#Group variants within known genes and
#Within coding and regulatory regions
x <- set.genomic.region.subregion(x,
  regions = genes.b37, subregions = subregions.LCT)
```

 SKAT

SKAT test

Description

Performs SKAT on categorical or binary phenotypes

Usage

```
SKAT(x, NullObject, genomic.region = x@snp$genomic.region,
  weights = (1 - x@snp$maf)**24, maf.threshold = 0.5,
  get.moments = "size.based", estimation.pvalue = "kurtosis",
  params.sampling, cores = 10, debug = FALSE, verbose = TRUE)
```

Arguments

| | |
|-------------------|--|
| x | A bed.matrix |
| NullObject | A list returned from NullObject.parameters |
| genomic.region | A factor defining the genomic region of each variant |
| weights | A vector with the weight of each variant. By default, the weight of each variant is inversely proportionnal to its MAF, as it was computed in the original SKAT method |
| maf.threshold | The MAF above which variants are removed (default is to keep all variants) |
| get.moments | How to estimate the moments to compute the p-values among "size.based", "bootstrap", "permutations", or "theoretical" for categorical phenotypes (2 or more groups of individuals). By default "size.based" that will choose the method depending on sample size (see details) |
| estimation.pvalue | Whether to use the skewness ("skewness") or the kurtosis ("kurtosis") for the chi-square approximation |
| params.sampling | A list containing the elements "perm.target", "perm.max", "debug". Only needed if get.moments = "bootstrap" or get.moments = "permutations" |

| | |
|---------|--|
| cores | How many cores to use for moments computation, set at 10 by default. Only needed if <code>get.moments = "theoretical"</code> |
| debug | Whether to return the mean, standard deviation, skewness and kurtosis of the statistics |
| verbose | Whether to display information about the function actions |

Details

For categorical phenotypes, the p-value is calculated using a chi-square approximation based on the statistics' moments. The user has to choose how to compute these moments (argument `get.moments`), and which moments to use for the chi-square approximation (argument `estimation.pvalue`).

The moments can be computed either using a sampling procedure ("`permutations`" if there are no covariates, or "`bootstrap`" otherwise), or using theoretical moments computed as in Liu et al. 2008 ("`theoretical`").

If `get.moments = "size.based"`, the sampling procedure will be used for sample sizes lower than 2000, and the theoretical calculations otherwise.

To estimate the p-values, either the first three moments are used (`estimation.pvalue = "skewness"`), or the moments 1, 2 and 4 are used (`estimation.pvalue = "kurtosis"`).

If `get.moments = "theoretical"` and `estimation.pvalue = "skewness"`, it corresponds to `method = "liu"` in the SKAT package. If `get.moments = "theoretical"` and `estimation.pvalue = "kurtosis"`, it corresponds to `method = "liu.mod"` in the SKAT package.

For small samples, p-values estimation is based on sampling and a sequential procedure: permuted statistics are computed and each one is compared to the observed statistics. This method requires `perm.target` and `perm.max` that should be given as a list to `params.bootstrap`. If `params.bootstrap` is not specified, `perm.target` will be set at 100, `perm.max` at $5e4$. The bootstrap program stops when either `perm.target` or `perm.max` is reached. P-values are then computed using a mixed procedure:

if `perm.target` is reached, the p-value is computed as : `perm.target` divided by the number of permutations used to reach `perm.target`;

if `perm.max` is reached, the SKAT small sample procedure is used, and p-values are approximated using a chi-square distributions based on statistics' moments 1, 2 and 4 computed from the permuted values.

If `NullObject$pheno.type = "continuous"`, the method from Liu et al. will be used to compute the p-value for the continuous phenotype, but `estimation.pvalue` can be set at "`skewness`" or "`kurtosis`".

If `debug=TRUE`, more informations about the estimated statistics moments are given.

All missing genotypes are imputed by the mean genotype.

Value

A data frame containing for each genomic region:

| | |
|----------------------|-------------------------|
| <code>stat</code> | The observed statistics |
| <code>p.value</code> | The p-value of the test |

If `get.moments = "bootstrap"` or `get.moments = "permutations"`, additional fields are present:

| | |
|--------|--|
| p.perm | The p-value computed by permutations: number of times permuted is greater than observed statistics divided by the total number of permutations performed |
| p.chi2 | The p-value computed by the chi-square approximation using the SKAT small sample procedure |

If debug = TRUE, the mean, standard deviation, skewness and kurtosis are also returned, as well as for the sampling procedure:

| | |
|----------|---|
| nb.gcp | The number of times a permuted statistics is equal or greater than the observed statistics stat |
| nb.eq | The number of times a permuted statistics is equal to the observed statistics stat |
| nb.perms | The total number of simulations performed |

References

Wu et al. 2011, *Rare-variant association testing for sequencing data with the sequence kernel association test*, American Journal of Human Genetics **82-93** doi:10.1016/j.ajhg.2011.05.029;

Lee et al. 2012, *Optimal Unified Approach for Rare-Variant Association Testing with Application to Small-Sample Case-Control Whole-Exome Sequencing Studies*, American Journal of Human Genetics, doi:10.1016/j.ajhg.2012.06.007;

Liu et al. 2008, *A new chi-square approximation to the distribution of non-negative definite quadratic forms in non-central normal variables*, Computational Statistics & Data Analysis, doi:10.1016/j.csda.2008.11.025

See Also

[NullObject.parameters](#), [SKAT.theoretical](#), [SKAT.bootstrap](#), [SKAT.permutations](#)

Examples

```
#Example on simulated data from Ravages with
#One group of 50 controls and
#two groups of 25 cases, each one with a prevalence of 0.01
#with 50% of causal variants, 5 genomic regions are simulated
GRR.del <- GRR.matrix(GRR = "SKAT", genes.maf = Kryukov,
                     n.case.groups = 2, select.gene = "R1",
                     GRR.multiplicative.factor=2)

x.sim <- rbm.GRR(genes.maf = Kryukov, size = c(50, 25, 25),
               prev = c(0.001, 0.001), GRR.matrix.del = GRR.del,
               p.causal = 0.5, p.protect = 0, select.gene="R1",
               same.variant = FALSE, genetic.model = "multiplicative", replicates = 5)

#Null Model
x.sim.H0 <- NullObject.parameters(x.sim@ped$pheno, RVAT = "SKAT", pheno.type = "categorical")

#Run SKAT (here permutations as n<2000 and no covariates)
#Parameters for the sampling procedure: target = 5, max = 100
#Please increase the number of permutations for a more accurate estimation of the p-values
params.sampling = list(perm.target = 5, perm.max = 100)
SKAT(x.sim, x.sim.H0, params.sampling = params.sampling)
```

```

#Run SKAT with a random continuous phenotype
#Null Model
x.sim.H0.c <- NullObject.parameters(rnorm(100), RVAT = "SKAT", pheno.type = "continuous")
SKAT(x.sim, x.sim.H0.c, cores = 1)

#Example on 1000Genome data
#Import data in a bed matrix
x <- read.bed.matrix( system.file("extdata", "LCT.EUR.b37.bed", package="Ravages") )

#Group variants within known genes
x <- set.genomic.region(x)

#Filter of rare variants: only non-monomorphic variants with
#a MAF lower than 2.5%
#keeping only genomic regions with at least 10 SNP
x1 <- filter.rare.variants(x, filter = "whole", maf.threshold = 0.025, min.nb.snps = 10)

#Simulation of a continuous and a binary covariate
set.seed(1) ; sex <- sample(0:1, nrow(x1), replace = TRUE) ; u <- runif(nrow(x1))
covar <- cbind(sex, u)

#run SKAT using the 1000 genome EUR populations as "outcome"
#with very few permutations
#Please increase the permutations for a more accurate estimation of the p-values
#Fit Null model with covariate sex
x1.H0.covar <- NullObject.parameters(x1@ped$population, RVAT = "SKAT", pheno.type = "categorical",
                                   data = covar, formula = ~ sex)

#Run SKAT with the covariates: use bootstrap as n<2000
SKAT(x1, x1.H0.covar, params.sampling = params.sampling, get.moments = "bootstrap")

#Run SKAT using theoretical moments (discourage here as n<2000) and 1 core
#SKAT(x1, x1.H0.covar, get.moments = "theoretical", cores = 1)

```

SKAT.bootstrap

Multi group SKAT test using bootstrap sampling

Description

Performs SKAT on two or more groups of individuals using bootstrap sampling

Usage

```

SKAT.bootstrap(x, NullObject, genomic.region = x@snps$genomic.region,
              weights = (1-x@snps$maf)**24, maf.threshold = 0.5,

```

```
perm.target = 100, perm.max = 5e4, debug = FALSE,
estimation.pvalue = "kurtosis")
```

Arguments

| | |
|-------------------|--|
| x | A bed.matrix |
| NullObject | A list returned from NullObject.parameters |
| genomic.region | A factor defining the genomic region of each variant |
| weights | A vector with the weight of each variant. By default, the weight of each variant is inversely proportionnal to its MAF, as it was computed in the original SKAT method |
| maf.threshold | The MAF above which variants are removed (default is to keep all variants) |
| perm.target | The number of times to exceed the observed statistics. If not reached, perm.max permutations will be used |
| perm.max | The maximum number of permutations to perform to estimate the p-value, will be used if perm.target is not reached |
| debug | Whether to print details about the permutations (mean, standard deviation, skewness, kurtosis), FALSE by default |
| estimation.pvalue | Whether to use the skewness ("skewness") or the kurtosis ("kurtosis") for the chi-square approximation |

Details

P-values estimation is based on bootstrap sampling and a sequential procedure: permuted statistics are computed and each one is compared to the observed statistics. The bootstrap program stops when either perm.target or perm.max is reached. P-values are then computed using a mixed procedure: if perm.target is reached, the p-value is computed as : perm.target divided by the number of permutations used to reach perm.target;

if perm.max is reached, p-values are approximated using a chi-square distributions based on the first three moments if estimation.pvalue = "skewness", or on statistics' moments 1, 2 and 4 if estimation.pvalue = "kurtosis".

If debug=TRUE, more informations about the estimated statistics moments are given.

This function is used by SKAT when the sample size is smaller than 2000 and covariates are present.

All missing genotypes are imputed by the mean genotype.

Value

A data frame containing for each genomic:

| | |
|---------|--|
| stat | The observed statistics |
| p.value | p.perm if perm.target is reached, p.chi2 if perm.max is reached. |
| p.perm | The p-value computed by permutations: number of times permuted is greater than observed statistics divided by the total number of permutations performed |

p.chi2 The p-value computed by the chi-square approximation using the SKAT small sample procedure

If debug=TRUE, other informations are given about the moments estimation:

nb.gep The number of times a permuted statistics is equal or greater than the observed statistics stat

nb.eq The number of times a permuted statistics is equal to the observed statistics stat

nb.perms The total number of simulations performed

mean The mean of the permuted statistics

sigma The standard deviation of the permuted statistics

skewness The skewness of the permuted statistics

kurtosis The kurtosis of the permuted statistics

References

Wu et al. 2011, *Rare-variant association testing for sequencing data with the sequence kernel association test*, American Journal of Human Genetics **82-93** doi:10.1016/j.ajhg.2011.05.029;

Lee et al. 2012, *Optimal Unified Approach for Rare-Variant Association Testing with Application to Small-Sample Case-Control Whole-Exome Sequencing Studies*, American Journal of Human Genetics, doi:10.1016/j.ajhg.2012.06.007;

See Also

[NullObject.parameters, SKAT](#)

Examples

```
#Import data in a bed matrix
x <- read.bed.matrix( system.file("extdata", "LCT.EUR.b37.bed", package="Ravages") )

#Group variants within known genes
x <- set.genomic.region(x)

#Filter of rare variants: only non-monomorphic variants with
#a MAF lower than 2.5%
#keeping only genomic regions with at least 10 SNP
x1 <- filter.rare.variants(x, filter = "whole", maf.threshold = 0.025, min.nb.snps = 10)

#Simulation of a continuous and a binary covariate
set.seed(1) ; sex <- sample(0:1, nrow(x1), replace = TRUE) ; u <- runif(nrow(x1))
covar <- cbind(sex, u)

#run SKAT using the 1000 genome EUR populations as "outcome"
#The maximum number of permutations used is 100,
#and the target number is 10, please increase
#both values for a more accurate estimation of the p-values
#Fit Null model with covariates
```

```
x1.H0 <- NullObject.parameters(x1@ped$population, data = covar,
  RVAT = "SKAT", pheno.type = "categorical")

SKAT.bootstrap(x1, x1.H0, perm.target = 10, perm.max = 100)
```

SKAT.continuous *Multi group SKAT test using Liu et al. approximation*

Description

Performs SKAT on a continuous phenotype using Liu et al. approximation

Usage

```
SKAT.continuous(x, NullObject, genomic.region = x@snps$genomic.region,
  weights = (1 - x@snps$maf)**24, maf.threshold = 0.5,
  estimation.pvalue = "kurtosis", cores = 10, debug = FALSE )
```

Arguments

| | |
|-------------------|--|
| x | A bed.matrix |
| NullObject | A list returned from NullObject.parameters |
| genomic.region | A factor defining the genomic region of each variant |
| weights | A vector with the weight of each variant. By default, the weight of each variant is inversely proportionnal to its MAF, as it was computed in the original SKAT method |
| maf.threshold | The MAF above which variants are removed (default is to keep all variants) |
| estimation.pvalue | Whether to use the skewness ("skewness") or the kurtosis ("kurtosis") for the chi-square approximation |
| cores | How many cores to use for moments computation, set at 10 by default |
| debug | Whether to return the mean, standard deviation, skewness and kurtosis of the statistics. Set at FALSE by default |

Details

The method from Liu et al. 2008 is used where p-values are estimated using a chi-square approximation from moment's

If estimation.pvalue = "kurtosis", the kurtosis is used instead of skewness in the chi-square approximation. This is equivalent to "liu.mod" in SKAT package.

Value

A data frame containing for each genomic region:

| | |
|---------|-------------------------|
| stat | The observed statistics |
| p.value | The p-value of the test |

If debug = TRUE, the mean, standard deviation, skewness and kurtosis used to compute the p-value are returned

References

Wu et al. 2011, *Rare-variant association testing for sequencing data with the sequence kernel association test*, American Journal of Human Genetics **82-93** doi:10.1016/j.ajhg.2011.05.029;

Liu et al. 2008, *A new chi-square approximation to the distribution of non-negative definite quadratic forms in non-central normal variables*, Computational Statistics & Data Analysis, doi:10.1016/j.csda.2008.11.025

See Also

[NullObject.parameters](#), [SKAT](#)

Examples

```
#Import data in a bed matrix
x <- read.bed.matrix( system.file("extdata", "LCT.EUR.b37.bed", package="Ravages") )

#Group variants within known genes
x <- set.genomic.region(x)

#Filter of rare variants: only non-monomorphic variants with
#a MAF lower than 2.5%
#keeping only genomic regions with at least 10 SNP
x1 <- filter.rare.variants(x, filter = "whole", maf.threshold = 0.025, min.nb.snps = 10)

#run SKAT using a random continuous phenotype
#Fit Null model
x1.H0 <- NullObject.parameters(rnorm(nrow(x1)), RVAT = "SKAT", pheno.type = "continuous")

SKAT.continuous(x1, x1.H0, cores = 1)
```

SKAT.permutations

Multi group SKAT test using bootstrap sampling

Description

Performs SKAT on two or more groups of individuals using bootstrap sampling

Usage

```
SKAT.permutations(x, NullObject, genomic.region = x@snps$genomic.region,
                 weights = (1-x@snps$maf)**24, maf.threshold = 0.5,
                 perm.target = 100, perm.max = 5e4, debug = FALSE,
                 estimation.pvalue = "kurtosis")
```

Arguments

| | |
|-------------------|--|
| x | A bed.matrix |
| NullObject | A list returned from NullObject.parameters |
| genomic.region | A factor defining the genomic region of each variant |
| weights | A vector with the weight of each variant. By default, the weight of each variant is inversely proportionnal to its MAF, as it was computed in the original SKAT method |
| maf.threshold | The MAF above which variants are removed (default is to keep all variants) |
| perm.target | The number of times to exceed the observed statistics. If not reached, perm.max permutations will be used |
| perm.max | The maximum number of permutations to perform to estimate the p-value, will be used if perm.target is not reached |
| debug | Whether to print details about the permutations (mean, standard deviation, skewness, kurtosis), FALSE by default |
| estimation.pvalue | Whether to use the skewness ("skewness") or the kurtosis ("kurtosis") for the chi-square approximation |

Details

P-values estimation is based on permutations sampling and a sequential procedure: permuted statistics are computed and each one is compared to the observed statistics. The bootstrap program stops when either perm.target or perm.max is reached. P-values are then computed using a mixed procedure:

if perm.target is reached, the p-value is computed as : perm.target divided by the number of permutations used to reach perm.target;

if perm.max is reached, p-values are approximated using a chi-square distributions based on the first three moments if estimation.pvalue = "skewness", or on statistics' moments 1, 2 and 4 if estimation.pvalue = "kurtosis".

If debug=TRUE, more informations about the estimated statistics moments are given.

This function is used by SKAT when the sample size is smaller than 2000 and no covariates are present.

All missing genotypes are imputed by the mean genotype.

Value

A data frame containing for each genomic:

| | |
|---------|--|
| stat | The observed statistics |
| p.value | p.perm if perm.target is reached, p.chi2 if perm.max is reached. |
| p.perm | The p-value computed by permutations: number of times permuted is greater than observed statistics divided by the total number of permutations performed |
| p.chi2 | The p-value computed by the chi-square approximation using the SKAT small sample procedure |

If debug=TRUE, other informations are given about the moments estimation:

| | |
|----------|---|
| nb.grep | The number of times a permuted statistics is equal or greater than the observed statistics stat |
| nb.eq | The number of times a permuted statistics is equal to the observed statistics stat |
| nb.perms | The total number of simulations performed |
| mean | The mean of the permuted statistics |
| sigma | The standard deviation of the permuted statistics |
| skewness | The skewness of the permuted statistics |
| kurtosis | The kurtosis of the permuted statistics |

References

Wu et al. 2011, *Rare-variant association testing for sequencing data with the sequence kernel association test*, American Journal of Human Genetics **82-93** doi:10.1016/j.ajhg.2011.05.029;

Lee et al. 2012, *Optimal Unified Approach for Rare-Variant Association Testing with Application to Small-Sample Case-Control Whole-Exome Sequencing Studies*, American Journal of Human Genetics, doi:10.1016/j.ajhg.2012.06.007;

See Also

[NullObject.parameters](#), [SKAT](#)

Examples

```
#Import data in a bed matrix
x <- read.bed.matrix( system.file("extdata", "LCT.EUR.b37.bed", package="Ravages") )

#Group variants within known genes
x <- set.genomic.region(x)

#Filter of rare variants: only non-monomorphic variants with
#a MAF lower than 1%
#keeping only genomic regions with at least 10 SNP
x1 <- filter.rare.variants(x, filter = "whole", maf.threshold = 0.01, min.nb.snps = 10)

#Simulation of a continuous and a binary covariate
```

```

set.seed(1) ; sex <- sample(0:1, nrow(x1), replace = TRUE) ; u <- runif(nrow(x1))
covar <- cbind(sex, u)

#run SKAT using the 1000 genome EUR populations as "outcome"
#The maximum number of permutations used is 100,
#and the target number is 10, please increase
#both values for a more accurate estimation of the p-values
#Fit Null model
x1.H0 <- NullObject.parameters(x1@ped$population, RVAT = "SKAT", pheno.type = "categorical")
SKAT.permutations(x1, x1.H0, perm.target = 10, perm.max=100)

```

SKAT.theoretical

Multi group SKAT test using Liu et al. approximation

Description

Performs SKAT on two or more groups of individuals using Liu et al. approximation

Usage

```

SKAT.theoretical(x, NullObject, genomic.region = x@snp$genomic.region,
                weights = (1 - x@snp$maf)**24, maf.threshold = 0.5,
                estimation.pvalue = "kurtosis", cores = 10, debug = FALSE )

```

Arguments

| | |
|--------------------------------|--|
| <code>x</code> | A bed.matrix |
| <code>NullObject</code> | A list returned from <code>NullObject.parameters</code> |
| <code>genomic.region</code> | A factor defining the genomic region of each variant |
| <code>weights</code> | A vector with the weight of each variant. By default, the weight of each variant is inversely proportionnal to its MAF, as it was computed in the original SKAT method |
| <code>maf.threshold</code> | The MAF above which variants are removed (default is to keep all variants) |
| <code>estimation.pvalue</code> | Whether to use the skewness ("skewness") or the kurtosis ("kurtosis") for the chi-square approximation |
| <code>cores</code> | How many cores to use for moments computation, set at 10 by default |
| <code>debug</code> | Whether to return the mean, standard deviation, skewness and kurtosis of the statistics. Set at FALSE by default |

Details

The method from Liu et al. 2008 is used where p-values are estimated using a chi-square approximation from moment's statistics

If `estimation.pvalue = "kurtosis"`, the kurtosis is used instead of skewness in the chi-square approximation. This is equivalent to "liu.mod" in SKAT package.

This function is used by SKAT when the sample size is larger than 2000.

All missing genotypes are imputed by the mean genotype.

Value

A data frame containing for each genomic region:

| | |
|----------------------|-------------------------|
| <code>stat</code> | The observed statistics |
| <code>p.value</code> | The p-value of the test |

If `debug = TRUE`, the mean, standard deviation, skewness and kurtosis used to compute the p-value are returned

References

Wu et al. 2011, *Rare-variant association testing for sequencing data with the sequence kernel association test*, American Journal of Human Genetics **82-93** doi:10.1016/j.ajhg.2011.05.029;

Liu et al. 2008, *A new chi-square approximation to the distribution of non-negative definite quadratic forms in non-central normal variables*, Computational Statistics & Data Analysis, doi:10.1016/j.csda.2008.11.025

See Also

[NullObject.parameters](#), SKAT

Examples

```
#Import data in a bed matrix
x <- read.bed.matrix( system.file("extdata", "LCT.EUR.b37.bed", package="Ravages") )

#Group variants within known genes
x <- set.genomic.region(x)

#Filter of rare variants: only non-monomorphic variants with
#a MAF lower than 2.5%
#keeping only genomic regions with at least 10 SNP
x1 <- filter.rare.variants(x, filter = "whole", maf.threshold = 0.025, min.nb.snps = 10)

#Simulation of a continuous and a binary covariate
set.seed(1) ; sex <- sample(0:1, nrow(x1), replace = TRUE) ; u <- runif(nrow(x1))
covar <- cbind(sex, u)

#run SKAT using the 1000 genome EUR populations as "outcome" using one core
#Fit Null model
x1.H0 <- NullObject.parameters(x1@ped$population, RVAT = "SKAT", pheno.type = "categorical")
```

```
SKAT.theoretical(x1, x1.H0, cores = 1)
```

subregions.LCT *Exemple of functional categories*

Description

Example of arbitrary functional categories (coding or regulatory) in the LCT locus (bed format, GRCH37). "Coding" corresponds to coding parts of the exons and "Regulatory" corresponds to everything that falls outside these coding regions.

Data contain the Chr, the Start position, the End position and the Name of all functional regions in the LCT locus.

Format

The data contain one dataframe with four columns:

Chr The chromosome of the gene

Start The start position of the functional region (0-based)

End The end position of the functional region (1-based)

Name The name of the gene

See Also

[set.genomic.region.subregion](#), [burden.subscores](#)

WSS *WSS genetic score*

Description

Calculates the WSS genetic score

Usage

```
WSS(x, genomic.region = x@snps$genomic.region)
```

Arguments

x A bed.matrix

genomic.region A factor containing the genomic region of each variant

Value

A matrix containing the WSS genetic score with one row per individual and one column per genomic.region

References

Madsen E and Browning S. *A Groupwise Association Test for Rare Mutations Using a Weighted Sum Statistic*. PLoS Genet. 2009

See Also

[CAST](#), [burden.weighted.matrix](#), [burden.mlogit](#)

Examples

```
#Import data in a bed matrix
x <- read.bed.matrix( system.file("extdata", "LCT.EUR.b37.bed", package="Ravages") )

#Group variants within known genes
x <- set.genomic.region(x)

#Filter of rare variants: only non-monomorphic variants with
#a MAF lower than 2.5%
#keeping only genomic regions with at least 10 SNP
x1 <- filter.rare.variants(x, filter = "whole", maf.threshold = 0.025, min.nb.snps = 10)

# Compute burden score WSS
score.WSS <- WSS(x1)
```

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