Package 'GWAS.BAYES'

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Type Package

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R topics documented:

`aggregate_SNPs` *aggregate_SNPs*

Description

Aggregate SNPs and Y by Species

Usage

```
aggregate_SNPs(SNPs,Y,na.rm)
```

Arguments

`SNPs`	Standardized SNP data set where the values of each column are either 0 or 1
`Y`	The phenotype response of interest
`na.rm`	Logical value where TRUE removes NA's in response vector as well corresponding rows in SNP matrix.

Value

SNPs	reduced SNP dataset
Y	reduced Y vector

Examples

```
data("vignette_lm_dat")
Y <- vignette_lm_dat$Phenotype
SNPs <- vignette_lm_dat[,-1]
SNPs <- standardize(SNPs = SNPs,method = "major-minor",number_cores = 1)

aggregate_SNPs(SNPs = SNPs, Y = Y)
```

---

cor_plot *cor_plot(SNPs,significant,info = FALSE)*

Description

A function that creates correlation heatmaps for given significant SNPs from a SNP dataframe.

Usage

```
cor_plot(SNPs,significant,info = FALSE)
```

Arguments

SNPs	A standardized SNP matrix where the columns take on the values of 0 or 1.
significant	A vector of 0's or 1's that contain which significant SNP's to look at.
info	Default is FALSE. If information such as the chromosome and the position is known, then that can be entered here and will return a correlation heatmap with the labels chromosome - position. The format for this entry is the 2 row dataframe or matrix, where the first row is the chromosome and the second row is the position.

Value

A correlation heatmap with the axis labels either SNP1 ... or chromosome - position

Examples

```
data("vignette_lm_dat")
Y <- vignette_lm_dat$Phenotype
SNPs <- vignette_lm_dat[,-1]
fullPreprocess <- preprocess_SNPs(SNPs = SNPs,Y = Y,MAF = 0.01,number_cores = 1)
SNPs <- fullPreprocess$SNPs
Y <- fullPreprocess$Y
```

```
fullPreprocess$SNPs_Dropped
principal_comp <- pca_function(SNPs = SNPs,number_components = 1,plot_it = FALSE)
Significant_SNPs <- preselection(Y = Y, SNPs = SNPs,number_cores = 1, principal_components = principal_comp,freque

cor_plot(SNPs = SNPs,significant = Significant_SNPs$Significant,info = FALSE)
```

`eigenMapMatMult2` *eigenMapMatMult2*

Description

Matrix multiplication in C++ between two matrices.

Usage

```
eigenMapMatMult2(A, B)
```

Arguments

A	First Matrix
B	Second Matrix

Value

Returns the matrix multiplication of A*B

`eigenMapMatMult3` *eigenMapMatMult3*

Description

Matrix multiplication between 3 matrices (A * B * C)

Usage

```
eigenMapMatMult3(A, B, C)
```

Arguments

A	First Matrix
B	Second Matrix
C	Third Matrix

Value

The result of A * B * C

ga_modelselection_nopc

ga_modelselection_nopc

Description

Performs GA model selection to identify the best model when no principal components are involved

Usage

```
ga_modelselection_nopc(Y,X,significant,number_cores,maxiterations,runs_til_stop,kinship = FALSE)
```

Arguments

Y	The phenotype response on the reduced scale (aggregating phenotype by ecotype/taxa), this should be a matrix with 1 column.
X	The SNP matrix on the reduced scale (aggregating phenotype by ecotype/taxa).
significant	A vector of 0 and 1's where the 1's indicate what SNP's were found to be significant in the preselection function.
number_cores	Number of cores to be passed on to the genetic algorithm to increase computational speed.
maxiterations	This is the maximum number of iterations the Genetic Search algorithm will run.
runs_til_stop	This is the numebr of consectutive iterations where the BIC is not improved before the genetic algorithm is stopped.
kinship	Default is set at FALSE. If kinship model is desired, input a kinship matrix and this will search models with the kinship component.

Details

This function will print out lines correpsonding to the convergence of the genetic search algorithm.

Value

A named matrix where the names corespond to the significant SNP's. This will usually out a matrix with a singular row, where the values of this row is 0 or 1 where 1 indicates significance in the final model and 0 indicates non significance in the final model. Sometimes this will output a matrix with mulitple columns. This is because there is a SNP or multiple SNPs that when added to the model create rank deficiency issues in the model. Naturally rank deficient columns are forced out but the genetic algoritm is not smart enough to sort these.

ga_modelselection_nopc_new

ga_modelselection_nopc_new

Description

Performs GA model selection to identify the best model when no principal components are involved. Internal function for modelselection_new().

Usage

```
ga_modelselection_nopc_new(Y,X,regions,regionsnames,significant,number_cores,maxiterations,runs_til
```

Arguments

Y	The phenotype response on the reduced scale (aggregating phenotype by ecotype/taxa), this should be a matrix with 1 column.
X	The SNP matrix on the reduced scale (aggregating phenotype by ecotype/taxa).
significant	A vector of 0 and 1's where the 1's indicate what SNP's were found to be significant in the preselection function.
regions	A matrix where each column represents a principal component for each region.
regionsnames	A named list which highlights which SNPs fall into which region.
number_cores	Number of cores to be passed on to the genetic algorithm to increase computational speed.
maxiterations	This is the maximum number of iterations the Genetic Search algorithm will run.
runs_til_stop	This is the number of consecutive iterations where the BIC is not improved before the genetic algorithm is stopped.
kinship	The kinship matrix associated with the SNPs in this analysis.

Details

This function will print out lines corresponding to the convergence of the genetic search algorithm.

Value

A named matrix where the names correspond to the significant SNP's. This will usually out a matrix with a singular row, where the values of this row is 0 or 1 where 1 indicates significance in the final model and 0 indicates non significance in the final model. Sometimes this will output a matrix with multiple columns. This is because there is a SNP or multiple SNPs that when added to the model create rank deficiency issues in the model. Naturally rank deficient columns are forced out but the genetic algorithm is not smart enough to sort these.

ga_modelselection_pcs *ga_modelselection_pcs*

Description

Performs GA model selection to identify the best model when principal components are involved

Usage

```
ga_modelselection_pcs(Y,X,significant,number_cores,principal_components,maxiterations,runs_til_stop
```

Arguments

Y	The phenotype response on the reduced scale (aggregating phenotype by ecotype/taxa), this should be a matrix with 1 column.
X	The SNP matrix on the reduced scale (aggregating phenotype by ecotype/taxa).
significant	A vector of 0 and 1's where the 1's indicate what SNP's were found to be significant in the preselection function.
number_cores	Number of cores to be passed on to the genetic algorithm to increase computational speed.
principal_components	The principal component matrix on the reduced scale (aggregating phenotype by ecotype/taxa).
maxiterations	This is the maximum number of iterations the Genetic Search algorithm will run.
runs_til_stop	This is the numebr of consectutive iterations where the BIC is not improved before the genetic algorithm is stopped.
kinship	Default is set at FALSE. If kinship model is desired, input a kinship matrix and this will search models with the kinship component.

Details

This function will print out lines correpsonding to the convergence of the genetic search algorithm.

Value

A named matrix where the names corespond to the significant SNP's. This will usually out a matrix with a singular row, where the values of this row is 0 or 1 where 1 indicates significance in the final model and 0 indicates non significance in the final model. Sometimes this will output a matrix with mulitple columns. This is because there is a SNP or multiple SNPs that when added to the model create rank deficiency issues in the model. Naturally rank deficient columns are forced out but the genetic algoritm is not smart enough to sort these.

ga_modelselection_pcs_new
ga_modelselection_pcs_new

Description

Performs GA model selection to identify the best model when principal components are involved

Usage

```
ga_modelselection_pcs_new(Y,X,regions,regionsnames,significant,number_cores,principal_components,ma
```

Arguments

Y	The phenotype response on the reduced scale (aggregating phenotype by ecotype/taxa), this should be a matrix with 1 column.
X	The SNP matrix on the reduced scale (aggregating phenotype by ecotype/taxa).
significant	A vector of 0 and 1's where the 1's indicate what SNP's were found to be significant in the preselection function.
regions	A matrix where each column represents a principal component for each region.
regionsnames	A named list which highlights which SNPs fall into which region.
number_cores	Number of cores to be passed on to the genetic algorithm to increase computational speed.
principal_components	The principal component matrix on the reduced scale (aggregating phenotype by ecotype/taxa).
maxiterations	This is the maximum number of iterations the Genetic Search algorithm will run.
runs_til_stop	This is the numebr of consectutive iterations where the BIC is not improved before the genetic algorithm is stopped.
kinship	Default is set at FALSE. If kinship model is desired, input a kinship matrix and this will search models with the kinship component.

Details

This function will print out lines correpsonding to the convergence of the genetic search algorithm.

Value

A named matrix where the names corespond to the significant SNP's. This will usually out a matrix with a singular row, where the values of this row is 0 or 1 where 1 indicates significance in the final model and 0 indicates non significance in the final model. Sometimes this will output a matrix with mulitple columns. This is because there is a SNP or multiple SNPs that when added to the model create rank deficiency issues in the model. Naturally rank deficient columns are forced out but the genetic algoritm is not smart enough to sort these.

level_function *level_function*

Description

Removes all SNPs that only have one level in it

Usage

```
level_function(SNPs,MAF = 0.01)
```

Arguments

SNPs	The standardized SNP data where the columns take on the values of 0 or 1
MAF	The minor allele frequency at which to drop SNPs. Default is set to 0.01, meaning if the minor allele occurs less than 1 percent of the time in a given SNP, that given SNP will be dropped from the dataset.

Value

SNPs	The SNP matrix where columns that were either all 1's or all 0's are removed
SNPs_Dropped	A true/false vector with length ncol(SNPs), where the TRUE's indicate that the column was not dropped and the FALSE's indicate that the column was dropped

Examples

```
data("vignette_lm_dat")
Y <- vignette_lm_dat$Phenotype
SNPs <- vignette_lm_dat[,-1]
SNPs <- standardize(SNPs = SNPs,method = "major-minor",number_cores = 1)
list1 <- aggregate_SNPs(SNPs = SNPs, Y = Y)
SNPs <- list1[[1]]
Y <- list1[[2]]

level_function(SNPs, MAF = .01)
```

log_profile_likelihood_REML *log_profile_likelihood_REML*

Description

The log likelihood that needs to be optimized for the full kinship model.

Usage

```
log_profile_likelihood_REML(x,t,y,d)
```

Arguments

x	The reduced design matrix with principal components, intercept and SNP of interest
t	Tau value for the random effect term
y	The reduced matrix for the response value of interest
d	The spectral decomposition diagonal matrix of eigen values

Value

This returns the REML value

---

optim_llik_RE_BIC *optim_llik_RE_BIC*

Description

Calculates the BIC in the full kinship model scenario

Usage

```
optim_llik_RE_BIC(x,y,d)
```

Arguments

x	The reduced design matrix with principal components, intercept and SNP of interest
y	The reduced response matrix.
d	The spectral decomposition diagonal matrix of eigen values

Value

Returns the BIC for the model with this SNP

`optim_llik_RE_p` *optim_llik_RE_p*

Description

This will calculate the p-value and perform the optimization in the full kinship model case

Usage

```
optim_llik_RE_p(x,y,d)
```

Arguments

x	Reduced design matrix with principal components, intercept and SNP of interest
y	The reduced matrix of the response value of interest
d	The spectral decomposition diagonal matrix of eigen values

Value

Returns a p-value for the specified data

`optim_llik_SLR_BIC` *optim_llik_SLR_BIC*

Description

Calculates the BIC in the SLR scenario

Usage

```
optim_llik_SLR_BIC(x,y)
```

Arguments

x	The reduced design matrix that includes intercept, SNP, and principal components
y	The reduced response matrix

Value

The BIC for the given data

optim_llik_SLR_p *optim_llik_SLR_p*

Description

This calculates the p-value in the simple linear regression scenario

Usage

```
optim_llik_SLR_p(x,y)
```

Arguments

x	Design Matrix for a single SNP.
y	Phenotype Response

pca_function *pca_function*

Description

Create Principal Components from Standardized Set of SNPs.

Usage

```
pca_function(SNPs,number_components,plot_it)
```

Arguments

SNPs	The SNP matrix where the columns consist of 0 and 1's.
number_components	The number of principal components desired, if you don't know put a random value and use plot_it = TRUE.
plot_it	A TRUE FALSE logical equality, if TRUE will plot the percent variation explained by the components, if FALSE will not create a plot. In both scenarios this function will return a matrix of principal components.

Details

This will work with both the full SNP matrix and the reduced SNP matrix. If you use the full SNP matrix you will have to reduce it yourself and this is at a higher computational burden. If you use the reduced SNP matrix you will get the same values as if you aggregated the principal components from the full SNP matrix, but this will be much faster.

Value

Plot	A plot of the percent variation explained by the components when plot_it = TRUE
Matrix	A matrix that the number of columns is the number of principal components and the number of rows is the same number of rows as the inputted data matrix.

Examples

```
data("vignette_lm_dat")
Y <- vignette_lm_dat$Phenotype
SNPs <- vignette_lm_dat[,-1]
fullPreprocess <- preprocess_SNPs(SNPs = SNPs,Y = Y,MAF = 0.01,number_cores = 1)
SNPs <- fullPreprocess$SNPs
Y <- fullPreprocess$Y
fullPreprocess$SNPs_Dropped

pca_function(SNPs = SNPs,number_components = 3,plot_it = TRUE)
```

---

postGWAS *postGWAS*

Description

Performs GA model selection to identify the best model

Usage

```
postGWAS(Y,SNPs,significant,number_cores,principal_components,maxiterations,runs_til_stop,kinship =
```

Arguments

Y	The phenotype response on the reduced scale (aggregating phenotype by ecotype/taxa), this should be a matrix with 1 column.
SNPs	The SNP matrix on the reduced scale (aggregating phenotype by ecotype/taxa).
significant	A vector of 0 and 1's where the 1's indicate what SNP's were found to be significant in the preselection function.
number_cores	Number of cores to be passed on to the genetic algorithm to increase computational speed.
principal_components	The principal component matrix on the reduced scale (aggregating phenotype by ecotype/taxa).
maxiterations	This is the maximum number of iterations the Genetic Search algorithm will run.
runs_til_stop	This is the number of consecutive iterations where the BIC is not improved before the genetic algorithm is stopped.

kinship	Default is set at FALSE. If kinship model is desired, input a kinship matrix and this will search models with the kinship component.
info	Default is set at FALSE. An information matrix where the first row is the chromosomes and the second row is the position information

Details

This function will print out lines corresponding to the convergence of the genetic search algorithm.

Value

A named matrix where the names correspond to the significant SNP's. This will usually out a matrix with a singular row, where the values of this row is 0 or 1 where 1 indicates significance in the final model and 0 indicates non significance in the final model. Sometimes this will output a matrix with multiple columns. This is because there is a SNP or multiple SNPs that when added to the model create rank deficiency issues in the model. Naturally rank deficient columns are forced out but the genetic algorithm is not smart enough to sort these.

Examples

```
data("vignette_lm_dat")
Y <- vignette_lm_dat$Phenotype
SNPs <- vignette_lm_dat[,-1]
fullPreprocess <- preprocess_SNPs(SNPs = SNPs,Y = Y,MAF = 0.01,number_cores = 1)
SNPs <- fullPreprocess$SNPs
Y <- fullPreprocess$Y
fullPreprocess$SNPs_Dropped
principal_comp <- pca_function(SNPs = SNPs,number_components = 1,plot_it = FALSE)
Significant_SNPs <- preselection(Y = Y, SNPs = SNPs,number_cores = 1, principal_components = principal_comp,freque

postGWAS(Y = Y,SNPs = SNPs,number_cores = 1, significant = Significant_SNPs$Significant,principal_components = pri
```

---

postGWAS_Haplotype *postGWAS_Haplotype*

Description

Performs GA model selection to identify the best model

Usage

```
postGWAS_Haplotype(Y,SNPs,info,size = 10,significant,number_cores,principal_components,maxiterations
```

Arguments

Y	The phenotype response on the reduced scale (aggregating phenotype by ecotype/taxa), this should be a matrix with 1 column.
SNPs	The SNP matrix on the reduced scale (aggregating phenotype by ecotype/taxa).
info	A dataframe where the first row is the chromosome info for the SNP's and the second is the location of each SNP represented by its base pair.
size	The number of kilobase pairs to search for regions.
significant	A vector of 0 and 1's where the 1's indicate what SNP's were found to be significant in the preselection function.
number_cores	Number of cores to be passed on to the genetic algorithm to increase computational speed.
principal_components	The principal component matrix on the reduced scale (aggregating phenotype by ecotype/taxa).
maxiterations	This is the maximum number of iterations the Genetic Search algorithm will run.
runs_til_stop	This is the number of consecutive iterations where the BIC is not improved before the genetic algorithm is stopped.
kinship	Default is set at FALSE. If kinship model is desired, input a kinship matrix and this will search models with the kinship component.

Details

This function will print out lines corresponding to the convergence of the genetic search algorithm.

Value

A named matrix where the names correspond to the significant SNP's. This will usually out a matrix with a singular row, where the values of this row is 0 or 1 where 1 indicates significance in the final model and 0 indicates non significance in the final model. Sometimes this will output a matrix with multiple columns. This is because there is a SNP or multiple SNPs that when added to the model create rank deficiency issues in the model. Naturally rank deficient columns are forced out but the genetic algorithm is not smart enough to sort these.

Examples

```
data("RealDataSNPs_Y")
Y <- RealDataSNPs_Y$Phenotype
SNPs <- subset(RealDataSNPs_Y,select = -c(Phenotype))
fullPreprocess <- preprocess_SNPs(SNPs = SNPs,Y = Y,MAF = 0.01,number_cores = 1,na.rm = FALSE)
SNPs <- fullPreprocess$SNPs
Y <- fullPreprocess$Y
data("RealDataInfo")
RealDataInfo <- RealDataInfo[,-fullPreprocess$SNPs_Dropped]
data("RealDataKinship")
kinship <- as.matrix(RealDataKinship)
Significant_SNPs <- preselection(Y = log(Y), SNPs = SNPs,number_cores = 1, principal_components = FALSE,frequentis
```

```
#postGWAS_Haplotype(Y = log(Y),SNPs = SNPs,info = RealDataInfo,size = 10,number_cores = 1, significant = Significar
```

---

preprocess_SNPs *preprocess_SNPs*

Description

This functions takes raw SNP data and the associated phenotype response and returns a SNP dataset and phenotype response variable that can be used in the preselection function.

Usage

```
preprocess_SNPs(SNPs,Y,MAF = 0.01,number_cores,na.rm)
```

Arguments

SNPs	SNP data where each column is a SNP and the SNP column takes on the values A, C, T, or G.
Y	The phenotype response of interest. Should be a numeric vector.
MAF	The minor allele frequency at which to drop SNPs. Default is set to 0.01, meaning if the minor allele occurs less than 1 percent of the time in a given SNP, that given SNP will be dropped from the dataset.
number_cores	The number of cores one would wish to parallelize over.
na.rm	If there is NA's in the vector Y, set na.rm = TRUE and the Y values that are NA will be removed as well as the corresponding rows of the SNP matrix.

Value

SNPs	A new SNP matrix. The matrix will be formatted so the minor allele's are coded as 0's and the major allele's are coded as 1's. This matrix will have columns dropped that have minor allele frequency less than the specified value. It will also aggregate over replications, so SNP's and the vector Y will be aggregated according to replications in the SNP matrix.
Y	The new aggregated response vector Y. If you did not have any replications then this vector will be the exact same as the one entered.
SNPs_Dropped	This will tell you which SNPs were dropped if the had minor allele frequency less than the specified value, it will be in the form of column index number. If no SNPs were dropped this will be the character string "None".

Examples

```
data("vignette_lm_dat")
Y <- vignette_lm_dat$Phenotype
SNPs <- vignette_lm_dat[,-1]

preprocess_SNPs(SNPs = SNPs,Y = Y,MAF = 0.01,number_cores = 1,na.rm = FALSE)
```

preselection *preselection*

Description

Finds significant SNP's

Usage

```
preselection(Y,SNPs,number_cores,principal_components,frequentist,controlrate,threshold,nullprob,al
```

Arguments

Y	The reduced matrix of response values
SNPs	The reduced SNP matrix where the columns are either 1's or 0's.
number_cores	The number of cores on which you would like to parallize this procedure
principal_components	The reduced matrix of the principal components.
frequentist	A logical value to see whether one would like to use a frequentist multiple comparison test or Bayesian False Discovery based on BIC's. The value of this affects whether values of the next parameters are needed.
controlrate	Only used when frequentist = TRUE. This is for which multiple comparison method you would like to use. Examples are "bonferroni" and "BH". See p.adjust for a full list of methods.
threshold	The value at which type 1 error rate is held at. .05 in most common literature. Used when frequentist is TRUE or FALSE
nullprob	Used when frequentist = FALSE, the probability that is assigned to the null hypothesis.
alterprob	Used when frequentist = FALSE, the probability that is assigned to the alternate hypothesis.
kinship	The kinship matrix if a model with a kinship component is desired. If not set kinship = FALSE.
info	An information matrix where the first row is the chromosome information and the second row in the position information for the SNP's.

Value

Frequentist Matrix	The matrix of results when Frequentist = TRUE. The results are formatted as a data.frame with the column Significant being 1 or 0 depending on if the SNP was significant (1 for significant). The P_values column will be the p-values that were calculated for each SNP.
Bayesian Matrix	The matrix of results when Frequentist = FALSE. The results are formatted as a data.frame with the column Significant being 1 or 0 depending on if the SNP was significant (1 for significant). The ApprPosteriorProbs column will be the Approximate Posterior Probabilities that were calculated for each SNP.

Examples

```
data("vignette_lm_dat")
Y <- vignette_lm_dat$Phenotype
SNPs <- vignette_lm_dat[,-1]
fullPreprocess <- preprocess_SNPs(SNPs = SNPs,Y = Y,MAF = 0.01,number_cores = 1)
SNPs <- fullPreprocess$SNPs
Y <- fullPreprocess$Y
fullPreprocess$SNPs_Dropped
principal_comp <- pca_function(SNPs = SNPs,number_components = 1,plot_it = FALSE)

preselection(Y = Y, SNPs = SNPs,number_cores = 1, principal_components = principal_comp,frequentist = TRUE,control
```

`preselection_nopc` *preselection_nopc*

Description

Finds significant SNP's when no principal components are present.

Usage

```
preselection_nopc(Y,X,number_cores,frequentist,controlrate,threshold,nullprob,alterprob,kinship = FA
```

Arguments

`Y`	The reduced matrix of response values
`X`	The reduced SNP matrix where th columns are either 1's or 0's.
`number_cores`	The number of cores on which you would like to parallize this procedure
`frequentist`	A logical value to see whether one would like to use a frequentist multiple comparison test or Bayesian False Discovery based on BIC's. The value of this affects whether values of the next parameters are needed.
`controlrate`	Only used when frequentist = TRUE. This is for which multiple comparison method you would like to use. Examples are "bonferroni" and "BH". See p.adjust for a full list of methods.
`threshold`	The value at which type 1 error rate is held at. .05 in most common literature. Used when frequentist is TRUE or FALSE
`nullprob`	Used when frequentist = FALSE, the probability that is assigned to the null hypothesis.
`alterprob`	Used when frequentist = FALSE, the probability that is assigned to the alternate hypothesis.
`kinship`	The kinship matrix if a model with a kinship component is desired. If not set kinship = FALSE.

Value

`Frequentist Matrix`
: The matrix of results when Frequentist = TRUE. The results are formated as a data.frame with the column Significant being 1 or 0 depending on if the SNP was significant (1 for significant). The P_values column will be the p-values that were calculated for each SNP.

`Bayesian Matrix`
: The matrix of results when Frequentist = FALSE. The results are formated as a data.frame with the column Significant being 1 or 0 depending on if the SNP was significant (1 for significant). The ApprPosteriorProbs column will be the Approximate Posterior Probabilities that were calculated for each SNP.

`preselection_pc` *preselection_pc*

Description

Finds significant SNP's when principal components are present

Usage

```
preselection_pc(Y,X,number_cores,principal_components,frequentist,controlrate,threshold,nullprob,al
```

Arguments

`Y`	The reduced matrix of response values
`X`	The reduced SNP matrix where th columns are either 1's or 0's.
`number_cores`	The number of cores on which you would like to parallize this procedure
`principal_components`	The reduced matrix of the principal components.
`frequentist`	A logical value to see whether one would like to use a frequentist multiple comparison test or Bayesian False Discovery based on BIC's. The value of this affects whether values of the next parameters are needed.
`controlrate`	Only used when frequentist = TRUE. This is for which multiple comparison method you would like to use. Examples are "bonferroni" and "BH". See p.adjust for a full list of methods.
`threshold`	The value at which type 1 error rate is held at. .05 in most common literature. Used when frequentist is TRUE or FALSE
`nullprob`	Used when frequentist = FALSE, the probability that is assigned to the null hypothesis.
`alterprob`	Used when frequentist = FALSE, the probability that is assigned to the alternate hypothesis.
`kinship`	The kinship matrix if a model with a kinship component is desired. If not set kinship = FALSE.

Value

`Frequentist Matrix`

The matrix of results when Frequentist = TRUE. The results are formated as a data.frame with the column Significant being 1 or 0 depending on if the SNP was significant (1 for significant). The P_values column will be the p-values that were calculated for each SNP.

`Bayesian Matrix`

The matrix of results when Frequentist = FALSE. The results are formated as a data.frame with the column Significant being 1 or 0 depending on if the SNP was significant (1 for significant). The ApprPosteriorProbs column will be the Approximate Posterior Probabilities that were calculated for each SNP.

`Pval_function` *Pval_function*

Description

Performs multiple comparison corrections on p-values and returns significant SNP's. This is used internally for the preselection function.

Usage

```
Pval_function(p_vals,n,thresh,control)
```

Arguments

`p_vals`	A vector of p-values calculated by the preselection function.
`n`	The original number of SNPs
`thresh`	The type 1 error rate
`control`	The multiple comparison correction one would like to apply.

Value

The results are formated as a data.frame with the column Significant being 1 or 0 depending on if the SNP was significant (1 for significant). The P_values column will be the p-values that were calculated for each SNP.

RealDataInfo *RealDataInfo*

Description

A information matrix, where the first row is the chromosome information and the second row is the position information.

Usage

```
data("RealDataInfo")
```

Format

A data frame with 2 observations on the following 1500 variables.

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Examples

```
data(RealDataInfo)
```

RealDataKinship *RealDataKinship*

Description

A kinship matrix for a section of the vignette for GWAS.BAYES.

Usage

```
data("RealDataKinship")
```

Format

A data frame with 328 observations on the following 328 variables.

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V328 a numeric vector

Examples

```
data(RealDataKinship)
```

RealDataSNPs_Y *RealDataSNPs_Y*

Description

A dataset associated with the Vignette for GWAS.BAYES.

Usage

```
data("RealDataSNPs_Y")
```

Format

A data frame with 328 observations on the following 1501 variables.

Phenotype a numeric vector

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SNP1466 a character vector
SNP1467 a character vector
SNP1468 a character vector
SNP1469 a character vector
SNP1470 a character vector
SNP1471 a character vector
SNP1472 a character vector
SNP1473 a character vector
SNP1474 a character vector
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SNP1476 a character vector
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SNP1494 a character vector

SNP1495 a character vector

SNP1496 a character vector

SNP1497 a character vector

SNP1498 a character vector

SNP1499 a character vector

SNP1500 a character vector

Examples

```
data(RealDataSNPs_Y)
```

---

resids_diag *resids_diag*

Description

Tests residuals to see if they are normal. This looks at the model with all significant SNPs from the preselection phase.

Usage

```
resids_diag(Y,SNPs,significant,kinship = FALSE,principal_components = FALSE,plot_it = TRUE)
```

Arguments

Y	The phenotype response of interest
SNPs	Standardized SNP data set where the values of each column are either 0 or 1
significant	A vector of 0's and 1's where the 1's indicate a significant SNP. This is returned in the output of the preselection function.
kinship	A kinship matrix, can be calculated from the rrBLUP package.
principal_components	A matrix or vector of the principal components one would like to include in the analysis.
plot_it	If TRUE a histogram of the residuals is returned.

Value

value 1	The output of a Shapiro-Wilk test for the residuals. If the p-value is above .05, there is no evidence that the residuals are not normal. If the p-value is below .05 there is evidence that the residuals are not normal, and some transformation is suggested.
value 2	A histogram of the residuals when plot_it = TRUE

Examples

```
data("vignette_lm_dat")
Y <- vignette_lm_dat$Phenotype
SNPs <- vignette_lm_dat[,-1]
fullPreprocess <- preprocess_SNPs(SNPs = SNPs,Y = Y,MAF = 0.01,number_cores = 1)
SNPs <- fullPreprocess$SNPs
Y <- fullPreprocess$Y
fullPreprocess$SNPs_Dropped
principal_comp <- pca_function(SNPs = SNPs,number_components = 1,plot_it = FALSE)
Significant_SNPs <- preselection(Y = Y, SNPs = SNPs,number_cores = 1, principal_components = principal_comp,freque

resids_diag(Y = Y,SNPs = SNPs,significant = Significant_SNPs$Significant,kinship = FALSE,principal_components = pr
```

SNP_data_function_nopcp *SNP_data_function_nopcp*

Description

This is used internally in the preselection function to sort the SNPs into datasets

Usage

```
SNP_data_function_nopcp(x,int)
```

Arguments

x	The SNP of interest.
int	The intercept.

Value

Returns a dataframe combining all three entries using cbind.

SNP_data_function_pcp *SNP_data_function_pcp*

Description

This is used internally in the preselection function to sort the SNPs into datasets

Usage

```
SNP_data_function_pcp(x,pcp,int)
```

Arguments

x	The SNP of interest.
pcp	The principal components.
int	The intercept.

Value

Returns a dataframe combining all three entries using cbind.

---

standardize *standardize*

Description

Standardize the SNPs to the 0-1 scale

Usage

```
standardize(SNPs,method=c("major-minor","alphabetical"),number_cores)
```

Arguments

SNPs	The SNP dataset with columns of the values A, C, T, and G
method	The method in which to standarize. If "major-minor" is selected then the major allele gets the value 1 and the minor allele gets the value 0. If "alphabetical" is selected the first allele alphabetically gets a value of 0 and the second allele alphabetically gets the value of 1.
number_cores	The number of cores on which to parallize over.

Value

Returns a matrix of SNPs with the same dimension as th input, the columns are now defined as 0 and 1's.

Examples

```
data("vignette_lm_dat")
Y <- vignette_lm_dat$Phenotype
SNPs <- vignette_lm_dat[,-1]

standardize(SNPs = SNPs,method = "major-minor",number_cores = 1)
```

vignette_kinship_dat *vignette_kinship_dat*

Description

Dataset associated with the Vignette for the GWAS.BAYES package.

Usage

```
data("vignette_kinship_dat")
```

Format

A data frame with 4075 observations on the following 1001 variables.

`Phenotype` a numeric vector

`SNP1` a factor with levels `G` `T`

`SNP2` a factor with levels `C` `T`

`SNP3` a factor with levels `C` `T`

`SNP4` a factor with levels `C` `T`

`SNP5` a factor with levels `A` `C`

`SNP6` a factor with levels `C` `T`

`SNP7` a factor with levels `C` `T`

`SNP8` a factor with levels `A` `C`

`SNP9` a factor with levels `A` `G`

`SNP10` a factor with levels `C` `G`

`SNP11` a factor with levels `A` `T`

`SNP12` a factor with levels `A` `T`

`SNP13` a factor with levels `C` `T`

`SNP14` a factor with levels `A` `G`

`SNP15` a factor with levels `A` `C`

`SNP16` a factor with levels `C` `T`

`SNP17` a factor with levels `C` `T`

`SNP18` a factor with levels `C` `T`

`SNP19` a factor with levels `A` `T`

`SNP20` a factor with levels `C` `T`

`SNP21` a factor with levels `A` `G`

`SNP22` a factor with levels `C` `T`

`SNP23` a factor with levels `C` `T`

`SNP24` a factor with levels `A` `T`

SNP25 a factor with levels C G
SNP26 a factor with levels A T
SNP27 a factor with levels C T
SNP28 a factor with levels C G
SNP29 a factor with levels G T
SNP30 a factor with levels C G
SNP31 a factor with levels G T
SNP32 a factor with levels A G
SNP33 a factor with levels A G
SNP34 a factor with levels C G
SNP35 a factor with levels A C
SNP36 a factor with levels A G
SNP37 a factor with levels A C
SNP38 a factor with levels A G
SNP39 a factor with levels A T
SNP40 a factor with levels C G
SNP41 a factor with levels A G
SNP42 a factor with levels C G
SNP43 a factor with levels G T
SNP44 a factor with levels A C
SNP45 a factor with levels C T
SNP46 a factor with levels C G
SNP47 a factor with levels G T
SNP48 a factor with levels A C
SNP49 a factor with levels G T
SNP50 a factor with levels A T
SNP51 a factor with levels A T
SNP52 a factor with levels C G
SNP53 a factor with levels G T
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SNP113 a factor with levels C T
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SNP521 a factor with levels C T
SNP522 a factor with levels C G
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SNP996 a factor with levels C G

SNP997 a factor with levels A G

SNP998 a factor with levels A T

SNP999 a factor with levels A T

SNP1000 a factor with levels A C

Examples

```
data(vignette_kinship_dat)
```

---

vignette_lm_dat *vignette_lm_dat*

Description

Dataset associated with the Vignette for the GWAS.BAYES package.

Usage

```
data("vignette_lm_dat")
```

Format

A data frame with 4075 observations on the following 1001 variables.

Phenotype a numeric vector

SNP1 a factor with levels A G

SNP2 a factor with levels G T

SNP3 a factor with levels A G

SNP4 a factor with levels A T

SNP5 a factor with levels A T

SNP6 a factor with levels C T

SNP7 a factor with levels C G

SNP8 a factor with levels A C
SNP9 a factor with levels C G
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SNP525 a factor with levels A C

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SNP528 a factor with levels C G
SNP529 a factor with levels G T
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SNP531 a factor with levels C G
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SNP533 a factor with levels A C
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SNP997 a factor with levels A G

SNP998 a factor with levels A C

SNP999 a factor with levels A T

SNP1000 a factor with levels A C

Examples

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data(vignette_lm_dat)
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Index