Package 'GEXCIS'

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Type Package

Title Gene-based methods for estimating the degree of the skewness of X chromosome inactivation

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Description This code contains the Bayesian method, the penalized Fieller's method and the Fieller's method for estimating the degree of the skewness of X chromosome inactivation based on genes for either quantitative traits or qualitative traits, with or without covariates using unrelated female subjects.

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Encoding UTF-8

LazyData true

RoxygenNote 7.1.2

R topics documented:

genotype1 — *A numeric genotype dataset of a gene with 50 SNPs and no missing values*

Description

A dataset of simulated genotypes with each row as a female subject, and with 5+50 columns, where 50 is the number of the SNPs. The first five columns are: pedigree ID (pid), individual ID (iid), father ID (fid), mother ID (mid) and sex, respectively, which are followed by one column per SNP.

Usage

```
genotype1
```

Format

A dataset for 1,000 unrelated female subjects and 55 variables.

pid Pedigree ID.

iid Individual ID.

fid Father ID.

mid Mother ID.

sex The genetic sex of the individual, coded as 1 for males and 2 for females, following the PLINK default coding.

SNP Each genotype is coded as 0, 1 or 2, indicating the number of the minor alleles.

genotype2 — *A numeric genotype dataset of a gene with 50 SNPs and missing values (denoted by NA)*

Description

A dataset of simulated genotypes with each row as a female subject, and with 5+50 columns, where 50 is the number of the SNPs. The first five columns are: pedigree ID (pid), individual ID (iid), father ID (fid), mother ID (mid) and sex, respectively, which are followed by one column per SNP.

Usage

```
genotype2
```

Format

A dataset for 1,000 unrelated female subjects and 55 variables.

pid Pedigree ID.

iid Individual ID.

fid Father ID.

mid Mother ID.

sex The genetic sex of the individual, coded as 1 for males and 2 for females, following the PLINK default coding.

SNP Each genotype is coded as 0, 1 or 2, indicating the number of the minor alleles.

genotype3 *A numeric genotype dataset of a gene with 50 SNPs and missing values (denoted by 9)*

Description

A dataset of simulated genotypes with each row as a female subject, and with 5+50 columns, where 50 is the number of the SNPs. The first five columns are: pedigree ID (pid), individual ID (iid), father ID (fid), mother ID (mid) and sex, respectively, which are followed by one column per SNP.

Usage

```
genotype3
```

Format

A dataset for 1,000 unrelated female subjects and 55 variables.

pid Pedigree ID.

iid Individual ID.

fid Father ID.

mid Mother ID.

sex The genetic sex of the individual, coded as 1 for males and 2 for females, following the PLINK default coding.

SNP Each genotype is coded as 0, 1 or 2, indicating the number of the minor alleles.

G_Bayes_XCI *The Bayesian method for estimating the degree of the skewness of X chromosome inactivation for genes*

Description

This code contains the gene-based Bayesian method for estimating the degree of the skewness of X chromosome inactivation (denoted as γ) of genes for either quantitative traits or qualitative traits, with or without covariates using unrelated female subjects.

Usage

```
G_Bayes_XCI(phenotype,genotype,trait_type,phenotype_missing=NA,
       genotype_missing=NA,prior,model_customize=NULL,chains_num=8,
       iter_num=10000,warmup_num=5000,acceptance_rate=0.99)
```

Arguments

phenotype	A data frame containing the pedigree information, phenotype and covariates (if any). The pedigree information in the first five columns includes: pedigree ID (pid), individual ID (iid), father ID (fid), mother ID (mid) and sex. The father ID and the mother ID of a founder are both set to be 0. The numerical codes for sex are 0=unknown, 1=male, 2=female. The trait values are in the last column of the data frame. For qualitative traits, the numerical codes are 0=unaffected, 1=affected. If there are covariates, the covariates are located in the sixth to second-to-last columns.
genotype	A data frame containing the pedigree information and genotypes. The pedigree information in the first five columns is consistent with that in the input variable "phenotype". The input variable "genotype" includes the genotype codes for all the SNPs in a gene, which are included in the current dataset. Each genotype is coded as 0, 1 or 2, indicating the number of the minor alleles.
trait_type	A character string either being "quantitative" or "qualitative", indicating the type of the trait.
phenotype_missing	The input variable "phenotype_missing" is the missing value for the phenotype in the data file, and the default value is NA. It may be 9 in some data files; or other numeric value.
genotype_missing	The input variable "genotype_missing" represents that the codes for the SNPs in the gene are missing, and the default value is NA. It may be 9 in some data files; or other numeric value.
prior	A character string either being "normal", "uniform" or "customize". "prior"="normal" represents that the prior distribution of γ is a truncated normal distribution with both parameters being 1 and the values ranging from 0 to 2, and the prior distributions of other unknown parameters are consistent with those proposed in our paper; "prior"="uniform" represents that the prior distribution of γ is the uniform distribution specified in our paper, that is, γ~U(0, 2), and the prior distributions of other unknown parameters are consistent with those proposed in our paper; "prior"="customize" indicates that the users could specify the prior distributions of γ and other unknown parameters according to their own research background.
model_customize	Bayesian model that satisfies rstan requirements, activated only when the input variable "prior"="customize". The default is NULL. Please see the examples for the details and the following details.
chains_num	A positive integer specifying the number of the Markov chains. The default number is 8.
iter_num	A positive integer specifying the number of the iterations for each chain (including warmup). The default number is 10,000.
warmup_num	A positive integer specifying the number of the warmup (also known as burnin) iterations per chain. The number of the warmup iterations should be smaller than the number of the iterations and the default is 5,000.
acceptance_rate	A value between 0 and 1 which represents the target acceptance rate, and the default is 0.99.

Details

Please install the "rstan" package and make sure that it can work before using this function. Note that we estimate the degree of the skewness of X chromosome inactivation in the presence of association. The results may be different for different runs, because of the sampling randomness of the HMC algorithm. If the fixed results are wanted, the seed number should be set before running the function. Note that different version of R may lead to different results under the same seed number. The results of the examples given in this file are obtained under the R with version 4.1.1. When the Bayesian model is "customize", it should be noted that the covariates are named x1, x2, x3, and so on; the coefficients of the covariates are named beta_1, beta_2, beta_3, and so on. Meanwhile, we recommend using "chains_num"=8, "iter_num"=10,000, "warmup_num"=5,000 and "acceptance_rate"=0.99 in practical applications.

Value

`Point_Estimate`	The point estimate of the degree of the skewness of X chromosome inactivation for the gene based on the Bayesian method.
`HPDI_Lower`	The lower bound of the HPDI.
`HPDI_Upper`	The upper bound of the HPDI.

Note

The interval not containing 1 indicates the skewed X chromosome inactivation (XCI-S), otherwise it suggests the random X chromosome inactivation (XCI-R) or the escape from X chromosome inactivation (XCI-E).

Author(s)

Meng-Kai Li, Yu-Xin Yuan and Ji-Yuan Zhou

References

Li, M. K.; Yuan, Y. X.; Zhu, B.; Wang, K. W.; Fung, W. K.; Zhou, J. Y. Gene-based methods for estimating the degree of the skewness of X chromosome inactivation. 2022

Annis, J.; Miller, B. J.; Palmeri, T. J. Bayesian inference with Stan: A tutorial on adding custom distributions. Behav. Res. Methods 2017, 49, 863-886.

Examples

```
install.package("rstan")
library(rstan)
rstan_options(javascript=FALSE)
options(mc.cores = parallel::detectCores())
rstan_options(auto_write = TRUE)

##example 1:
##quantitative trait with covariate
##the prior distribution of gamma is a truncated normal distribution specified in our paper
##the prior distributions of other unknown parameters are consistent with those in our paper
set.seed(123456)
G_Bayes_XCI(phenotype=phenotype1,genotype=genotype1,trait_type="quantitative",
           phenotype_missing=NA,genotype_missing=NA,prior="normal",model_customize=NULL,
            chains_num=2,iter_num=1000,warmup_num=500,acceptance_rate=0.99)
#result:
```

```
#$Point_Estimate
#[1] 0.4687626
#$HPDI_Lower
#[1] 0.1133476
#$HPDI_Upper
#[1] 1.235775

##example 2:
##quantitative trait with covariate
##the prior distribution of gamma is a uniform distribution specified in our paper
##the prior distributions of other unknown parameters are consistent with those in our paper
set.seed(123456)
G_Bayes_XCI(phenotype=phenotype1,genotype=genotype1,trait_type="quantitative",
          phenotype_missing=NA,genotype_missing=NA,prior="uniform",model_customize=NULL,
            chains_num=2,iter_num=1000,warmup_num=500,acceptance_rate=0.99)
#result:
#$Point_Estimate
#[1] 0.4411592
#$HPDI_Lower
#[1] 0.002059202
#$HPDI_Upper
#[1] 1.261761

##example 3:
##quantitative trait with covariate
##the prior distributions of gamma and other unknown parameters are "customize"
##users are required to define the prior distribution of each parameter according to their
own research background, for example:
model_customize="
data {
  int<lower=0> N ;
  vector[N] y;
  vector[N] x1;
  vector[N] gg_1;
  vector[N] gg_2;
}
parameters {
  real beta_0;
  real beta_1;
  real beta_c;
  real<lower=0,upper=2> gamma;
  real<lower=0> sigma;
}
model {
  vector[N] theta;
  theta = beta_0 + beta_1*x1 + beta_c*gamma*gg_1 + beta_c*(2-gamma)*gg_2;
  target += normal_lpdf( beta_0 | 0, 100 );
  target += normal_lpdf( beta_1 | 0, 10 );
  target += normal_lpdf( beta_c | 0, 20 );
  target += normal_lpdf( gamma | 1, 2 );
  target += exponential_lpdf(sigma | 1);
  for(i in 1:N)
    target += normal_lpdf( y[i] | theta[i], sigma );
}"
set.seed(123456)
G_Bayes_XCI(phenotype=phenotype1,genotype=genotype1,trait_type="quantitative",
            phenotype_missing=NA,genotype_missing=NA,
```

```
            prior="customize",model_customize=model_customize,
            chains_num=2,iter_num=1000,warmup_num=500,acceptance_rate=0.99)
#result:
#$Point_Estimate
#[1] 0.4902301
#$HPDI_Lower
#[1] 0.05620893
#$HPDI_Upper
#[1] 1.320036

##example 4:
##quantitative trait without covariate
##the prior distribution of gamma is a truncated normal distribution specified in our paper
##the prior distributions of other unknown parameters are consistent with those in our paper
set.seed(123456)
G_Bayes_XCI(phenotype=phenotype2,genotype=genotype1,trait_type="quantitative",
           phenotype_missing=NA,genotype_missing=NA,prior="normal",model_customize=NULL,
            chains_num=2,iter_num=1000,warmup_num=500,acceptance_rate=0.99)
#result:
#$Point_Estimate
#[1] 0.5224464
#$HPDI_Lower
#[1] 0.04441401
#$HPDI_Upper
#[1] 1.35557

##example 5:
##qualitative trait with covariate
##the prior distribution of gamma is a truncated normal distribution specified in our paper
##the prior distributions of other unknown parameters are consistent with those in our paper
set.seed(123456)
G_Bayes_XCI(phenotype=phenotype5,genotype=genotype1,trait_type="qualitative",
           phenotype_missing=NA,genotype_missing=NA,prior="normal",model_customize=NULL,
            chains_num=2,iter_num=1000,warmup_num=500,acceptance_rate=0.99)
#result:
#$Point_Estimate
#[1] 0.3091504
#$HPDI_Lower
#[1] 0.002824296
$HPDI_Upper
#[1] 1.121509

##example 6:
##qualitative trait without covariate
##the prior distribution of gamma is a uniform distribution specified in our paper
##the prior distributions of other unknown parameters are consistent with those in our paper
set.seed(123456)
G_Bayes_XCI(phenotype=phenotype6,genotype=genotype1,trait_type="qualitative",
          phenotype_missing=NA,genotype_missing=NA,prior="uniform",model_customize=NULL,
            chains_num=2,iter_num=1000,warmup_num=500,acceptance_rate=0.99)
#result:
#$Point_Estimate
#[1] 0.5869038
#$HPDI_Lower
#[1] 4.107076e-05
#$HPDI_Upper
#[1] 1.735476
```

```
##example 7:
##qualitative trait without covariate
##the prior distributions of gamma or other unknown parameters are "customize"
##users are required to define the prior distribution of each parameter according to their
own research background, for example:
model_customize = "
data {
  int<lower=0> N;
  int y[N] ;
  vector[N] gg_1;
  vector[N] gg_2;
}
parameters {
  real beta_0;
  real beta_c;
  real<lower=0,upper=2> gamma;
}
model {
  vector[N] theta;
  theta = beta_0 + beta_c*gamma*gg_1 + beta_c*(2-gamma)*gg_2;
  target += normal_lpdf( beta_0 | 0, 1 );
  target += normal_lpdf( beta_c | 0, 20 );
  target += normal_lpdf( gamma | 0.5, 2 );
  target += bernoulli_logit_lpmf( y | theta );
}"
set.seed(123456)
G_Bayes_XCI(phenotype=phenotype6,genotype=genotype1,trait_type="qualitative",
            phenotype_missing=NA,genotype_missing=NA,
            prior="customize",model_customize=model_customize,
            chains_num=2,iter_num=1000,warmup_num=500,acceptance_rate=0.99)
#result:
#$Point_Estimate
#[1] 0.5340016
#$HPDI_Lower
#[1] 0.107194
#$HPDI_Upper
#[1] 1.705485

##example 8:
##quantitative trait with covariate and missing values
##both "phenotype" and "genotype" contain the missing values (denoted by NA)
##the prior distribution of gamma is a uniform distribution specified in our paper
##the prior distributions of other unknown parameters are consistent with those in our paper
set.seed(123456)
G_Bayes_XCI(phenotype=phenotype3,genotype=genotype2,trait_type="quantitative",
          phenotype_missing=NA,genotype_missing=NA,prior="uniform",model_customize=NULL,
            chains_num=2,iter_num=1000,warmup_num=500,acceptance_rate=0.99)
#result:
#$Point_Estimate
#[1] 0.5601698
#$HPDI_Lower
#[1] 0.03673035
#$HPDI_Upper
#[1] 1.261375

##example 9:
```

```
##qualitative trait with covariate and missing values
##both "phenotype" and "genotype" contain the missing values (denoted by NA)
##the prior distribution of gamma is a uniform distribution specified in our paper
##the prior distributions of other unknown parameters are consistent with those in our paper
set.seed(123456)
G_Bayes_XCI(phenotype=phenotype7,genotype=genotype2,trait_type="qualitative",
          phenotype_missing=NA,genotype_missing=NA,prior="uniform",model_customize=NULL,
            chains_num=2,iter_num=1000,warmup_num=500,acceptance_rate=0.99)
#result:
#$Point_Estimate
#[1] 0.280913
#$HPDI_Lower
#[1] 0.004132392
#$HPDI_Upper
#[1] 0.9235037

##example 10:
##quantitative trait with covariate and missing values
##both "phenotype" and "genotype" contain the missing values (denoted by 9)
##the prior distribution of gamma is a truncated normal distribution specified in our paper
##the prior distributions of other unknown parameters are consistent with those in our paper
set.seed(123456)
G_Bayes_XCI(phenotype=phenotype4,genotype=genotype3,trait_type="quantitative",
            phenotype_missing=9,genotype_missing=9,prior="normal",model_customize=NULL,
            chains_num=2,iter_num=1000,warmup_num=500,acceptance_rate=0.99)
#result:
#$Point_Estimate
#[1] 0.4528636
#$HPDI_Lower
#[1] 0.1132948
#$HPDI_Upper
#[1] 1.370303
```

`G_Frequen_XCI` *The penalized Fieller's method and the Fieller's method for estimating the degree of the skewness of X chromosome inactivation for genes*

Description

This code can get the point estimate and the penalized point estimate of the degree of the skewness of X chromosome inactivation (denoted as γ) of genes, and their confidence intervals based on the Fieller's and penalized Fieller's methods, respectively. Only female subjects are used, either for quantitative traits or qualitative traits, with or without covariates.

Usage

```
G_Frequen_XCI(phenotype,genotype,trait_type,phenotype_missing=NA,
                      genotype_missing=NA,alpha=0.05)
```

Arguments

phenotype	A data frame containing the pedigree information, phenotype and covariates (if any). The pedigree information in the first five columns includes: pedigree ID (pid), individual ID (iid), father ID (fid), mother ID (mid) and sex. The father ID and the mother ID of a founder are both set to be 0. The numerical codes for sex are 0=unknown, 1=male, 2=female. The trait values are in the last column of the data frame. For qualitative traits, the numerical codes are 0=unaffected, 1=affected. If there are covariates, the covariates are located in the sixth to second-to-last columns.
genotype	A data frame containing the pedigree information and genotypes. The pedigree information in the first five columns is consistent with that in the input variable "phenotype". The input variable "genotype" includes the genotype codes for all the SNPs in a gene, which are included in the current dataset. Each genotype is coded as 0, 1 or 2, indicating the number of the minor alleles.
trait_type	A character string either being "quantitative" or "qualitative", indicating the type of the trait.
phenotype_missing	The input variable "phenotype_missing" is the missing value for the phenotype in the data file, and the default value is NA. It may be 9 in some data files; or other numeric value.
genotype_missing	The input variable "genotype_missing" represents that the codes for the SNPs in the gene are missing, and the default value is NA. It may be 9 in some data files; or other numeric value.
alpha	The significance level, and the default value is 0.05.

Details

Note that we estimate the degree of the skewness of X chromosome inactivation in the presence of association.

Value

penalized_point_estimate	The penalized point estimate of the degree of the skewness of X chromosome inactivation for the gene.
PF_lower	The lower bound of the confidence interval obtained by the penalized Fieller's method.
PF_upper	The upper bound of the confidence interval obtained by the penalized Fieller's method.
PF_length	The length of the confidence interval obtained by the penalized Fieller's method.
point_estimate	The point estimate of the degree of the skewness of X chromosome inactivation for the gene.
F_lower	The lower bound of the confidence interval obtained by the Fieller's method.
F_upper	The upper bound of the confidence interval obtained by the Fieller's method.
F_length	The length of the confidence interval obtained by the Fieller's method.
F_D	Indicates whether or not the confidence interval obtained by the Fieller's method is a discontinuous interval, where 0=NO, 1=YES.

Note

The interval not containing 1 indicates the skewed X chromosome inactivation (XCI-S), otherwise it suggests the random X chromosome inactivation (XCI-R) or the escape from X chromosome inactivation (XCI-E).

Author(s)

Meng-Kai Li, Yu-Xin Yuan and Ji-Yuan Zhou

References

Li, M. K.; Yuan, Y. X.; Zhu, B.; Wang, K. W.; Fung, W. K.; Zhou, J. Y. Gene-based methods for estimating the degree of the skewness of X chromosome inactivation. 2022

Wang, P.; Xu, S.; Wang, Y. X.; et al. Penalized Fieller's confidence interval for the ratio of bivariate normal means. Biometrics 2021, 77, 1355-1368.

Wang, P; Zhang, Y.; Wang, B. Q.; et al. A statistical measure for the skewness of X chromosome inactivation based on case-control design. BMC Bioinformatics 2019, 20, 11.

Li, B. H.; Yu, W. Y.; Zhou, J. Y. A statistical measure for the skewness of X chromosome inactivation for quantitative traits and its application to the MCTFR data. BMC Genom. Data 2021, 22, 24.

Examples

```
##example 11:
##quantitative trait with covariate
G_Frequen_XCI(phenotype=phenotype1,genotype=genotype1,trait_type="quantitative",
              phenotype_missing=NA,genotype_missing=NA,alpha=0.05)
#result:
#$penalized_point_estimate
#[1] 0.4763586
#$PF_lower
#[1] 0.06569505
#$PF_upper
#[1] 1.23757
#$PF_length
#[1] 1.171875
#$point_estimate
#[1] 0.4786828
#$F_lower
#[1] 0.06919327
#$F_upper
#[1] 1.347783
#$F_length
#[1] 1.27859
#$F_D
#[1] 0

##example 12:
##quantitative trait without covariate
G_Frequen_XCI(phenotype=phenotype2,genotype=genotype1,trait_type="quantitative",
              phenotype_missing=NA,genotype_missing=NA,alpha=0.05)
#result:
#$penalized_point_estimate
#[1] 0.4862892
```

```
#$PF_lower
#[1] 0.06740264
#$PF_upper
#[1] 1.277344
#$PF_length
#[1] 1.209942
#$point_estimate
#[1] 0.4888167
#F_lower
#[1] 0.07121611
#$F_upper
#[1] 1.401534
#$F_length
#[1] 1.330318
#$F_D
#[1] 0

##example 13:
##qualitative trait with covariate
G_Frequen_XCI(phenotype=phenotype5,genotype=genotype1,trait_type="qualitative",
              phenotype_missing=NA,genotype_missing=NA,alpha=0.05)
#result:
#$penalized_point_estimate
#[1] 0.2934478
#$PF_lower
#[1] 0
#$PF_upper
#[1] 0.9289332
#$PF_length
#[1] 0.9289332
#$point_estimate
#[1] 0.2950001
#$F_lower
#[1] 0
#$F_upper
#[1] 1.013214
#$F_length
#[1] 1.013214
#$F_D
#[1] 0

##example 14:
##qualitative trait without covariate
G_Frequen_XCI(phenotype=phenotype6,genotype=genotype1,trait_type="qualitative",
              phenotype_missing=NA,genotype_missing=NA,alpha=0.05)
#result:
#$penalized_point_estimate
#[1] 0.6241968
#$PF_lower
#[1] 0
#$PF_upper
#[1] 2
#$PF_length
#[1] 2
#$point_estimate
#[1] 0.6431983
#$F_lower
```

```
#[1] 0
#$F_upper
#[1] 2
#$F_length
#[1] 2
#$F_D
#[1] 0

##example 15:
##quantitative trait with covariate and missing values.
##both "phenotype" and "genotype" contain the missing values (denoted by NA)
G_Frequen_XCI(phenotype=phenotype3,genotype=genotype2,trait_type="quantitative",
              phenotype_missing=NA,genotype_missing=NA,alpha=0.05)
#result:
#$penalized_point_estimate
#[1] 0.5153325
#$PF_lower
#[1] 0.0797702
#$PF_upper
#[1] 1.383422
#$PF_length
#[1] 1.303651
#$point_estimate
#[1] 0.5183941
#$F_lower
#[1] 0.08485905
#$F_upper
#[1] 1.547297
#$F_length
#[1] 1.462438
#$F_D
#[1] 0

##example 16:
##qualitative trait with covariate and missing values.
##both "phenotype" and "genotype" contain the missing values (denoted by NA)
G_Frequen_XCI(phenotype=phenotype7,genotype=genotype2,trait_type="qualitative",
              phenotype_missing=NA,genotype_missing=NA,alpha=0.05)
#result:
#$penalized_point_estimate
#[1] 0.2896869
#$PF_lower
#[1] 0
#$PF_upper
#[1] 0.8723483
#$PF_length
#[1] 0.8723483
#$point_estimate
#[1] 0.2909573
#$F_lower
#[1] 0
#$F_upper
#[1] 0.9343073
#$F_length
#[1] 0.9343073
#$F_D
#[1] 0
```

```
##example 17:
##quantitative trait with covariate and missing values.
##both "phenotype" and "genotype" contain the missing values (denoted by 9)
G_Frequen_XCI(phenotype=phenotype4,genotype=genotype3,trait_type="quantitative",
              phenotype_missing=9,genotype_missing=9,alpha=0.05)
#result:
#$penalized_point_estimate
#[1] 0.5153325
#$PF_lower
#[1] 0.0797702
#$PF_upper
#[1] 1.383422
#$PF_length
#[1] 1.303651
#$point_estimate
#[1] 0.5183941
#$F_lower
#[1] 0.08485905
#$F_upper
#[1] 1.547297
#$F_length
#[1] 1.462438
#$F_D
#[1] 0
```

`HPDIofHMC` *A function to obtain the highest posterior density interval of the samples*

Description

A function to obtain the highest posterior density interval of the samples.

Usage

```
HPDIofHMC(sampleVec,credMass=0.95)
```

Arguments

`sampleVec`	A vector contains the samples.
`credMass`	A value between 0 and 1 used to specify the probability of the samples which should be included in an interval, and the default is 0.95.

Value

A vector contains the lower bound and the upper bound of the highest posterior density interval.

Author(s)

Meng-Kai Li, Yu-Xin Yuan and Ji-Yuan Zhou

References

Li, M. K.; Yuan, Y. X.; Zhu, B.; Wang, K. W.; Fung, W. K.; Zhou, J. Y. Gene-based methods for estimating the degree of the skewness of X chromosome inactivation. 2022

Examples

```
HPDIofHMC(rnorm(100,1,1),credMass = 0.95)
```

`modeofHMC` *A function to obtain the mode of the samples*

Description

A function to obtain the mode of the samples.

Usage

```
modeofHMC(sam_chain)
```

Arguments

`sam_chain`	A vector contains the samples.

Value

The modeofHMC() returns a value.

Author(s)

Meng-Kai Li, Yu-Xin Yuan and Ji-Yuan Zhou

References

Li, M. K.; Yuan, Y. X.; Zhu, B.; Wang, K. W.; Fung, W. K.; Zhou, J. Y. Gene-based methods for estimating the degree of the skewness of X chromosome inactivation. 2022

Examples

```
modeofHMC(runif(100,5,50))
```

PenFieller *A function for obtaining the confidence interval of a ratio by the penalized Fieller's method*

Description

This function is used to calculate the upper and lower limits of the penalized Fieller's confidence interval for the ratio estimate.

Usage

```
PenFieller(mu_n,mu_d,var_n,var_d,rho=0,df_n=NULL,df_d=NULL,con_level=0.95)
```

Arguments

mu_n	The estimated mean of the numerator.
mu_d	The estimated mean of the denominator.
var_n	A positive value gives the estimated variance of the numerator.
var_d	A positive value gives the estimated variance of the denominator.
rho	A value between -1 and 1 that represents the estimated correlation coefficient of the numerator and the denominator.
df_n	The degree of freedom of the numerator. The default value is NULL.
df_d	The degree of freedom of the denominator. The default value is NULL.
con_level	The confidence level. Should be between 0 and 1. The default is 0.95.

Value

PenFieller_value
: The penalized point estimate of the ratio.

PenFieller_Lower
: The lower bound of the estimated interval of the penalized Fieller's method.

PenFieller_Upper
: The upper bound of the estimated interval of the penalized Fieller's method.

Author(s)

Peng Wang

References

Wang, P.; Xu, S.; Wang, Y. X.; et al. Penalized Fieller's confidence interval for the ratio of bivariate normal means. Biometrics 2021, 77, 1355-1368.

phenotype1 *A dataset of simulated quantitative trait and covariate*

Description

The pedigree information in the first five columns includes: pedigree ID (pid), individual ID (iid), father ID (fid), mother ID (mid) and sex.

Usage

```
phenotype1
```

Format

A dataset for 1,000 unrelated female subjects and seven variables.

pid Pedigree ID.

iid Individual ID.

fid Father ID.

mid Mother ID.

sex The genetic sex of the individual, coded as 1 for males and 2 for females, following the PLINK default coding.

x1 A numeric variable of the covariate.

y A numeric variable of the quantitative trait.

phenotype2 *A dataset of simulated quantitative trait*

Description

The pedigree information in the first five columns includes: pedigree ID (pid), individual ID (iid), father ID (fid), mother ID (mid) and sex.

Usage

```
phenotype2
```

Format

A dataset for 1,000 unrelated female subjects and six variables.

pid Pedigree ID.

iid Individual ID.

fid Father ID.

mid Mother ID.

sex The genetic sex of the individual, coded as 1 for males and 2 for females, following the PLINK default coding.

y A numeric variable of the quantitative trait.

phenotype3 *A dataset of simulated quantitative trait and covariate with missing values (denoted by NA)*

Description

The pedigree information in the first five columns includes: pedigree ID (pid), individual ID (iid), father ID (fid), mother ID (mid) and sex.

Usage

```
phenotype3
```

Format

A dataset for 1,000 unrelated female subjects and seven variables.

pid Pedigree ID.

iid Individual ID.

fid Father ID.

mid Mother ID.

sex The genetic sex of the individual, coded as 1 for males and 2 for females, following the PLINK default coding.

x1 A numeric variable of the covariate.

y A numeric variable of the quantitative trait.

phenotype4 *A dataset of simulated quantitative trait and covariate with missing values (denoted by 9)*

Description

The pedigree information in the first five columns includes: pedigree ID (pid), individual ID (iid), father ID (fid), mother ID (mid) and sex.

Usage

```
phenotype4
```

Format

A dataset for 1,000 unrelated female subjects and seven variables.

pid Pedigree ID.

iid Individual ID.

fid Father ID.

mid Mother ID.

sex The genetic sex of the individual, coded as 1 for males and 2 for females, following the PLINK default coding.

x1 A numeric variable of the covariate.

y A numeric variable of the quantitative trait.

`phenotype5` *A dataset of simulated qualitative trait and covariate*

Description

The pedigree information in the first five columns includes: pedigree ID (pid), individual ID (iid), father ID (fid), mother ID (mid) and sex.

Usage

```
phenotype5
```

Format

A dataset for 1,000 unrelated female subjects and seven variables.

pid Pedigree ID.

iid Individual ID.

fid Father ID.

mid Mother ID.

sex The genetic sex of the individual, coded as 1 for males and 2 for females, following the PLINK default coding.

x1 A numeric variable of the covariate.

y A numeric variable of the affection status: 0=unaffected, 1=affected.

`phenotype6` *A dataset of simulated qualitative trait*

Description

The pedigree information in the first five columns includes: pedigree ID (pid), individual ID (iid), father ID (fid), mother ID (mid) and sex.

Usage

```
phenotype6
```

Format

A dataset for 1,000 unrelated female subjects and six variables.

pid Pedigree ID.

iid Individual ID.

fid Father ID.

mid Mother ID.

sex The genetic sex of the individual, coded as 1 for males and 2 for females, following the PLINK default coding.

y A numeric variable of the affection status: 0=unaffected, 1=affected.

`phenotype7` *A dataset of simulated qualitative trait and covariate with missing values (denoted by NA)*

Description

The pedigree information in the first five columns includes: pedigree ID (pid), individual ID (iid), father ID (fid), mother ID (mid) and sex.

Usage

```
phenotype7
```

Format

A dataset for 1,000 unrelated female subjects and seven variables.

pid Pedigree ID.

iid Individual ID.

fid Father ID.

mid Mother ID.

sex The genetic sex of the individual, coded as 1 for males and 2 for females, following the PLINK default coding.

x1 A numeric variable of the covariate.

y A numeric variable of the affection status: 0=unaffected, 1=affected.

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