Package 'GEXCIS'

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Type Package

Title What the Package Does (Title Case)

Version 0.1.0

Author Who wrote it

Maintainer The package maintainer <yourself@somewhere.net>

Description More about what it does (maybe more than one line)
Use four spaces when indenting paragraphs within the Description.

License What license is it under?

Encoding UTF-8

LazyData true

RoxygenNote 7.1.2

R topics documented:

genotype1 *A gene containing 50 SNPs without missing values*

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

```
genotype1
```

Format

a data for 1000 individuals and 55 variables.

pid pedigree ID.

iid individual ID.

fid father ID.

mid mother ID.

sex the genetic sex of individuals.

genotype2 *A gene containing 50 SNPs 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

```
genotype2
```

Format

a data for 1000 individuals and 55 variables.

pid pedigree ID.

iid individual ID.

fid father ID.

mid mother ID.

sex the genetic sex of individuals.

genotype3 *A gene containing 50 SNPs 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

```
genotype3
```

Format

a data for 1000 individuals and 55 variables.

pid pedigree ID.

iid individual ID.

fid father ID.

mid mother ID.

sex the genetic sex of individuals.

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

Description

This code contains the gene-based Bayesian method for measuring the degree of the skewness of X chromosome inactivation for either quantitative phenotype or qualitative phenotype, with or without covariates using unrelated female individuals.

Usage

```
G_Bayes_XCI(phenotype,genotype,phenotype_type,phenotype_missing=NA,
       allele_missing=NA,prior,model_customize=NULL,chains_num=4,
       iter_num=5000,warmup_num=2500,acceptance_rate=0.99)
```

Arguments

phenotype	A data frame containing 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 mother ID of founders are both set to 0.The numerical codes for sex are 0=unknown, 1=male, 2=female.The phenotype is in the last column of the data frame. For quality phenotypes, the numerical codes are 0=unaffected, 1=affected.

`genotype` A data frame containing pedigree information and genotypes. The pedigree information in the first five columns is consistent with that in the phenotype. The genotype includes the codes for all the loci contained in the gene on X chromosome. Numerical coding 0=dd, 1=Dd, 2=DD, where d represents the normal allele and D represents the mutant allele.

`phenotype_type` A character string either being "quantitative" or "qualitative".

`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.

`allele_missing` The input variable "allele_missing" represents that the allele contained in the gene is 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 the prior distribution of gamma is the normal distribution specified in the paper, that is, gamma~N(1,1), and the prior distribution of other unknown parameters is also consistent with that in the paper; prior="uniform" represents the prior distribution of gamma is the uniform distribution specified in the paper, that is, gamma~U(0,2), and the prior distribution of other unknown parameters is also consistent with that in the paper; prior="customize" indicates that the user should specify the prior distribution of gamma and other unknown parameters according to the research needs.

`chains_num` A positive integer specifying the number of Markov chains. The default is 4.

`iter_num` A positive integer specifying the number of iterations for each chain (including warmup). The default is 5000.

`warmup_num` A positive integer specifying the number of warmup (also known as burnin) iterations per chain. The number of warmup iterations should be smaller than the number of iterations and the default is 2500.

`acceptance_rate`
A value between 0 and 1 that represents the target acceptance rate, the default is 0.99.

Details

Please install the rstan package and make sure it can work before using this function.Note that we measure 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, seed number should be set before running the function. 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.

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 estimated interval

`HPDI_Upper` The upper bound of the estimated interval.

Note

The interval not containing 1 indicates skewed X chromosome inactivation (XCI), otherwise it suggests random XCI or escapes from XCI.

Author(s)

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

References

Meng-Kai Li, Yu-Xin Yuan, Bin Zhu, Kai-Wen Wang, Wing Kam Fung and Ji-Yuan Zhou.Gene-based methods for estimating the degree of the skewness of X chromosome inactivation. 2022

Annis J, Miller BJ, Palmeri TJ. Bayesian inference with Stan: a tutorial on adding custom distributions. Behav Res Methods 2017;49:863-86.

Examples

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

##example 1:
##quantitative phenotype with covariate
##the prior distribution of gamma is a normal distribution specified in the paper
##the prior distribution of other unknown parameters is consistent with that in the paper
set.seed(123456)
G_Bayes_XCI(phenotype=phenotype1,genotype=genotype1,phenotype_type="quantitative",
            phenotype_missing=NA,allele_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 phenotype with covariate
##the prior distribution of gamma is a uniform distribution specified in the paper
##the prior distribution of other unknown parameters is consistent with that in the paper
set.seed(123456)
G_Bayes_XCI(phenotype=phenotype1,genotype=genotype1,phenotype_type="quantitative",
            phenotype_missing=NA,allele_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 phenotype with covariate
##the prior distribution of gamma or other unknown parameters is customize.
##Users are required to define the prior distribution of each parameter
according to the 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,phenotype_type="quantitative",
            phenotype_missing=NA,allele_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 phenotype without covariate
##the prior distribution of gamma is a normal distribution specified in the paper
##the prior distribution of other unknown parameters is consistent with that in the paper
set.seed(123456)
G_Bayes_XCI(phenotype=phenotype2,genotype=genotype1,phenotype_type="quantitative",
            phenotype_missing=NA,allele_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 phenotype with covariate
##the prior distribution of gamma is a normal distribution specified in the paper
##the prior distribution of other unknown parameters is consistent with that in the paper
set.seed(123456)
G_Bayes_XCI(phenotype=phenotype5,genotype=genotype1,phenotype_type="qualitative",
            phenotype_missing=NA,allele_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 phenotype without covariate
##the prior distribution of gamma is a uniform distribution specified in the paper
##the prior distribution of other unknown parameters is consistent with that in the paper
set.seed(123456)
G_Bayes_XCI(phenotype=phenotype6,genotype=genotype1,phenotype_type="qualitative",
            phenotype_missing=NA,allele_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 phenotype without covariate
##the prior distribution of gamma or other unknown parameters is customize.
##Users are required to define the prior distribution of each parameter
according to the 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,phenotype_type="qualitative",
            phenotype_missing=NA,allele_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 phenotype with covariate and missing values. Both phenotype
and genotype contain the missing value (denoted by NA)
##the prior distribution of gamma is a uniform distribution specified in the paper
##the prior distribution of other unknown parameters is consistent with that in the paper
set.seed(123456)
G_Bayes_XCI(phenotype=phenotype3,genotype=genotype2,phenotype_type="quantitative",
            phenotype_missing=NA,allele_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 phenotype with covariate and missing values. Both phenotype
and genotype contain the missing value (denoted by NA)
##the prior distribution of gamma is a uniform distribution specified in the paper
##the prior distribution of other unknown parameters is consistent with that in the paper
set.seed(123456)
G_Bayes_XCI(phenotype=phenotype7,genotype=genotype2,phenotype_type="qualitative",
            phenotype_missing=NA,allele_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 phenotype with covariate and missing values. Both phenotype
and genotype contain the missing value (denoted by 9)
##the prior distribution of gamma is a normal distribution specified in the paper
##the prior distribution of other unknown parameters is consistent with that in the paper
set.seed(123456)
G_Bayes_XCI(phenotype=phenotype4,genotype=genotype3,phenotype_type="quantitative",
            phenotype_missing=9,allele_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 measuring the degree of the skewness of X chromosome inactivation for genes.*

Description

This code contains two gene-based methods, the penalized Fieller's method and the Fieller's method, for measureing the degree of the skewness of X chromosome inactivation for either quantitative phenotype or qualitative phenotype, with or with covariates using unrelated females subjects.

Usage

```
G_Frequen_XCI(phenotype,genotype,phenotype_type,phenotype_missing=NA,
                    allele_missing=NA,alpha=0.05)
```

Arguments

phenotype	A data frame containing 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 mother ID of founders are both set to 0.The numerical codes for sex are 0=unknown, 1=male, 2=female.The phenotype is in the last column of the data frame. For quality phenotypes, the numerical codes are 0=unaffected, 1=affected.
genotype	A data frame containing pedigree information and genotypes. The pedigree information in the first five columns is consistent with that in the phenotype. The genotype includes the codes for all the loci contained in the gene on X chromosome. Numerical coding 0=dd, 1=Dd, 2=DD, where d represents the normal allele and D represents the mutant allele.
phenotype_type	A character string either being "quantitative" or "qualitative".
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.
allele_missing	The input variable "allele_missing" represents that the allele contained in the gene is missing, and the default value is NA. It may be 9 in some data files; or other numeric value.
alpha	The significant level, the default value is 0.05.

Details

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

Value

PF	Point estimate of gamma by the penalized Fieller method
PF_lower	Lower bound of confidence interval obtained by the penalized Fieller method
PF_upper	Upper bound of confidence interval obtained by the penalized Fieller method
PF_length	Length of confidence interval obtained by the penalized Fieller method
Fieller	Point estimate of gamma by the Fieller's method
F_lower	Lower bound of confidence interval obtained by the Fieller's method
F_upper	Upper bound of confidence interval obtained by the Fieller's method
F_length	Length of confidence interval obtained by the Fieller's method
F_D	Indicates whether 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 skewed X chromosome inactivation (XCI), otherwise it suggests random XCI or escapes from XCI.

Author(s)

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

References

Meng-Kai Li, Yu-Xin Yuan, Bin Zhu, Kai-Wen Wang, Wing Kam Fung and Ji-Yuan Zhou.Gene-based methods for estimating the degree of the skewness of X chromosome inactivation. 2022

Wang P , Xu SQ, Wang YX, et al. Penalized Fieller's confidence interval for the ratio of bivariate normal means. Biometrics 2020;1-14.

Wang P, Zhang Y, Wang BQ, et al. A statistical measure for the skewness of X chromosome inactivation based on case-control design. BMC Bioinformatics 2019;20(1):11.

Li BH, Yu WY, Zhou JY. A statistical measure for the skewness of X chromosome inactivation for quantitative traits and its application to the MCTFR data. BMC Genomic Data 2021;22(1):24.

Examples

```
##example 11:
##quantitative phenotype with covariate
G_Frequen_XCI(phenotype=phenotype1,genotype=genotype1,phenotype_type="quantitative",
              phenotype_missing=NA,allele_missing=NA,alpha=0.05)
#result:
$PF
[1] 0.4763586
$PF_lower
[1] 0.06569505
$PF_upper
[1] 1.23757
$PF_length
```

```
[1] 1.171875
$Fieller
[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 phenotype without covariate
G_Frequen_XCI(phenotype=phenotype2,genotype=genotype1,phenotype_type="quantitative",
              phenotype_missing=NA,allele_missing=NA,alpha=0.05)
#result:
$PF
[1] 0.4862892
$PF_lower
[1] 0.06740264
$PF_upper
[1] 1.277344
$PF_length
[1] 1.209942
$Fieller
[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 phenotype with covariate
G_Frequen_XCI(phenotype=phenotype5,genotype=genotype1,phenotype_type="qualitative",
              phenotype_missing=NA,allele_missing=NA,alpha=0.05)
#result:
$PF
[1] 0.2934478
$PF_lower
[1] 0
$PF_upper
[1] 0.9289332
$PF_length
[1] 0.9289332
$Fieller
[1] 0.2950001
$F_lower
[1] 0
$F_upper
[1] 1.013214
$F_length
[1] 1.013214
```

```
$F_D
[1] 0

##example 14:
##qualitative phenotype without covariate
G_Frequen_XCI(phenotype=phenotype6,genotype=genotype1,phenotype_type="qualitative",
              phenotype_missing=NA,allele_missing=NA,alpha=0.05)
#result:
$PF
[1] 0.6241968
$PF_lower
[1] 0
$PF_upper
[1] 2
$PF_length
[1] 2
$Fieller
[1] 0.6431983
$F_lower
[1] 0
$F_upper
[1] 2
$F_length
[1] 2
$F_D
[1] 0

##example 15:
##quantitative phenotype with covariate and missing values.
##Both phenotype and genotype contain the missing value (denoted by NA)
G_Frequen_XCI(phenotype=phenotype3,genotype=genotype2,phenotype_type="quantitative",
              phenotype_missing=NA,allele_missing=NA,alpha=0.05)
#result:
$PF
[1] 0.5153325
$PF_lower
[1] 0.0797702
$PF_upper
[1] 1.383422
$PF_length
[1] 1.303651
$Fieller
[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 phenotype with covariate and missing values.
##Both phenotype and genotype contain the missing value (denoted by NA)
G_Frequen_XCI(phenotype=phenotype7,genotype=genotype2,phenotype_type="qualitative",
              phenotype_missing=NA,allele_missing=NA,alpha=0.05)
```

```
#result:
$PF
[1] 0.2896869
$PF_lower
[1] 0
$PF_upper
[1] 0.8723483
$PF_length
[1] 0.8723483
$Fieller
[1] 0.2909573
$F_lower
[1] 0
$F_upper
[1] 0.9343073
$F_length
[1] 0.9343073
$F_D
[1] 0

##example 17:
##quantitative phenotype with covariate and missing values.
##Both phenotype and genotype contain the missing value (denoted by 9)
G_Frequen_XCI(phenotype=phenotype4,genotype=genotype3,phenotype_type="quantitative",
              phenotype_missing=9,allele_missing=9,alpha=0.05)
#result:
PF
[1] 0.5153325
$PF_lower
[1] 0.0797702
$PF_upper
[1] 1.383422
$PF_length
[1] 1.303651
$Fieller
[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 that specifies the proportion of samples that should be included in an interval, the default is 0.95.

Value

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

Author(s)

Wen-Yi Yu and Ji-Yuan Zhou

References

Wen-Yi Yu, Yu Zhang, Meng-Kai Li, Zi-Ying Yang, Wing Kam Fung, Pei-Zhen Zhao and Ji-Yuan Zhou. BEXCIS: Bayesian 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)

Wen-Yi Yu and Ji-Yuan Zhou

References

Wen-Yi Yu, Yu Zhang, Meng-Kai Li, Zi-Ying Yang, Wing Kam Fung, Pei-Zhen Zhao and Ji-Yuan Zhou. BEXCIS: Bayesian 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 SQ, Wang YX, et al. Penalized Fieller's confidence interval for the ratio of bivariate normal means. Biometrics 2020;1-14.

phenotype1 *Quantitative phenotype with 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 data for 1000 individuals and 7 variables.

pid pedigree ID.

iid individual ID.

fid father ID.

mid mother ID.

sex the genetic sex of individuals.

x1 a numeric variable of covariate.

y a numeric variable of quantitative phenotype.

phenotype2 *Quantitative phenotype without 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

```
phenotype2
```

Format

a data for 1000 individuals and 6 variables.

pid pedigree ID.

iid individual ID.

fid father ID.

mid mother ID.

sex the genetic sex of individuals.

y a numeric variable of quantitative phenotype.

phenotype3 — *Quantitative phenotype with covariate and 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 data for 1000 individuals and 7 variables.

pid pedigree ID.

iid individual ID.

fid father ID.

mid mother ID.

sex the genetic sex of individuals.

x1 a numeric variable of covariate.

y a numeric variable of quantitative phenotype.

phenotype4 — *Quantitative phenotype with covariate and 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 data for 1000 individuals and 7 variables.

pid pedigree ID.

iid individual ID.

fid father ID.

mid mother ID.

sex the genetic sex of individuals.

x1 a numeric variable of covariate.

y a numeric variable of quantitative phenotype.

phenotype5 *Qualitative phenotype with 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 data for 1000 individuals and 7 variables.

pid pedigree ID.

iid individual ID.

fid father ID.

mid mother ID.

sex the genetic sex of individuals.

x1 a numeric variable of covariate.

y a numeric variable of qualitative phenotype: 0=unaffected, 1=affected.

phenotype6 *Qualitative phenotype without 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

```
phenotype6
```

Format

a data for 1000 individuals and 6 variables.

pid pedigree ID.

iid individual ID.

fid father ID.

mid mother ID.

sex the genetic sex of individuals.

y a numeric variable of qualitative phenotype: 0=unaffected, 1=affected.

phenotype7 *Qualitative phenotype with covariate and 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 data for 1000 individuals and 7 variables.

pid pedigree ID.

iid individual ID.

fid father ID.

mid mother ID.

sex the genetic sex of individuals.

x1 a numeric variable of covariate.

y a numeric variable of qualitative phenotype: 0=unaffected, 1=affected.

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