Package 'EHPGS'

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Type Package

Title Evaluation of hybrid performance in plant breeding via genomic selection

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Description

We propose a GS-based approach to identify potential parental lines and superior hybrid combinations from a breeding population composed of hybrids produced by a half diallel mating scheme.

License GPL (>= 3)

Depends R (>= 3.5.0)

Imports MASS,stats,utils,BGLR,sommer

Encoding UTF-8

LazyData true

RoxygenNote 7.2.2

R topics documented:

BGS   *The Bayesian Gibbs sampling algorithm*

Description

The Bayesian Gibbs sampling algorithm

Usage

```
BGS(
  pheno,
  KA,
  KD,
  mu.ini = 0,
  ga.ini = 0,
  gd.ini = 0,
  vE.ini = 1,
  vA.ini = 0,
  vD.ini = 0,
  iter = 5000,
  m = 1,
  S_star,
  nu_star = 5,
  cat.itr = TRUE
)
```

Arguments

pheno	A numeric vector of phenotype which include all the lines in relationship matrix.
KA	Additive relationship matrix.
KD	Dominance relationship matrix.
mu.ini	Initial values for the constant term.
ga.ini	Initial values for the additive genotypic value.
gd.ini	Initial values for the dominance genotypic value
vE.ini	Initial values for the error variance.
vA.ini	Initial values for the additive variance.
vD.ini	Initial values for the dominance variance.
iter	Number of iteration in each chain.
m	Number of independent chain.
S_star	The shape of freedom of the variance components for the prior distribution of a scaled inverse Chi square.
nu_star	The degree of freedom of the variance components for the prior distribution of a scaled inverse Chi square.
cat.itr	A boolean variable determines whether to print out the iteration number.

Value

This function will return the MCMC value of additive genotypic value (g_A;ga), dominance genotypic value (g_D;gd), constant term (mu;mu), and variance components(additive variance;vA, dominance variance;vD, error variance;vE)

Examples

```
KA <- kinship(train.geno)
Xd <- replace(train.geno,train.geno==0,99)
Xd <- replace(Xd,Xd==1,0)
Xd <- replace(Xd,Xd==-1,0)
```

```
Xd <- replace(Xd,Xd==99,1)

KD <- kinship(Xd)
KA <- KA +diag(10^(-9),nrow = nrow(KA), ncol = ncol(KA))
KD <- KD +diag(10^(-9),nrow = nrow(KD), ncol = ncol(KD))

result <- BGS(pheno =train.pheno$F1.weight,KA = KA,KD = KD,mu.ini = 0,ga.ini = 0,gd.ini = 0,
vE.ini = 1,vA.ini = 0.5,vD.ini = 0.5,iter = 100,m = 1,S_star = 0.5*var(train.pheno$F1.weight),nu_star = 5)
```

EHPGS	*Evaluation of hybrid performance in plant breeding via genomic selection*

Description

Evaluation of hybrid performance in plant breeding via genomic selection

Usage

```
EHPGS(
  num.F1,
  num.P,
  train.pheno,
  train.geno,
  parent.geno,
  train.in.test = NULL,
  method = "BGS",
  mu.ini = NULL,
  ga.ini = 0,
  gd.ini = 0,
  vE.ini = 1,
  vA.ini = 0.5,
  vD.ini = 0.5,
  iter = 10000,
  m = 5,
  burnIn = 500,
  thin = 5
)
```

Arguments

num.F1	An integer number of superior hybrid combinations are select.
num.P	An integer number of potential parental lines are select.
train.pheno	A numeric vector of training set's phenotype.
train.geno	A numerical matrix of training set's genotype. Matrix is coded as -1,0 and 1 for Minor, Hetero, and Major, respectively.
parent.geno	A numerical matrix of parental lines' genotype. Matrix is coded as -1,0 and 1 for Minor, Hetero, and Major, respectively.
train.in.test	A character vector of lines' names which are both in training set and half-diallel design.

method	Select the method used to build the model, including BGS, BGLR, and sommer.
mu.ini	Initial values for the constant term for BGS method.
ga.ini	Initial values for the additive genotypic value for BGS method.
gd.ini	Initial values for the dominance genotypic value for BGS method.
vE.ini	Initial values for the error variance for BGS method.
vA.ini	Initial values for the additive variance for BGS method.
vD.ini	Initial values for the dominance variance for BGS method.
iter	Number of iteration in each chain for BGS or BGLR method.
m	Number of independent chain for BGS method.
burnIn	An integer number of burn-in for BGLR method.
thin	An integer number of thinning for BGLR method.

Value

This function will return 3 data frames, F1.out includes the top n GEBV F1s (n=num.F1) and its GEBV,SCA,MPH, and BPH. P.out includes the top m GEBV parents (m=num.P) and its GEBV,GCA. V.out includes the estimate of constant term and variance components (additive variance,dominance variance,and error variance)

Examples

```
EHPGS(num.F1=15,num.P=5,train.pheno=train.pheno$F1.weight,train.geno,parent.geno[1:10,],
train.in.test=rownames(train.geno),mu.ini=NULL,
ga.ini = 0,gd.ini = 0,vE.ini = 1,vA.ini = 0.5,vD.ini = 0.5,iter = 100,m = 1)
```

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kinship	*Relationship matrix*

Description

This function calculate additive and dominance relationship matrix.

Usage

```
kinship(X)
```

Arguments

X	A numerical matrix of genotype. If is additive relationship matrix can be coded as -1,0,and 1.If is dominance relationship matrix can be coded as 0,1,and 0 (row: sample; column: marker).

Value

K A numerical matrix (relationship matrix)

Examples

```
KA <- kinship(train.geno)
```

parent.geno	*Genotype information of parental lines*

Description

Genotype information of parental lines. This data was published by Wu et al. (2019) <doi.org/10.3835/plantgenome2018.

Usage

```
parent.geno
```

Format

A numeric matrix with 142 rows (parental lines) and 4,521 columns (SNPs).

Examples

```
data(parent.geno)
```

train.geno	*Genotype information of training set.*

Description

Genotype information of hybrids used to construct a prediction model. This data was published by Wu et al. (2019) <doi.org/10.3835/plantgenome2018.10.0082>

Usage

```
train.geno
```

Format

A numeric matrix with 119 rows (Hybrid of half diallel design) and 4,512 columns (SNPs).

Examples

```
data(train.geno)
```

train.pheno	*Phenotype*

Description

Fruit weight (kg) of samples. This data was published by Wu et al. (2019) <doi.org/10.3835/plantgenome2018.10.0082>

Usage

```
train.pheno
```

Format

A numeric data frame with four columns representing the hybrids, parent names, and their corresponding phenotypes.

Examples

```
data(train.pheno)
```

Index