HIBLUP User Manual

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v1.3.1

Disclaimer: While extensive tests have been performed by Zhao lab at Huazhong Agricultural University and Yuan lab at Wuhan University of Technology. Results are, in general, reliable, correct, and appropriate. However, results are not guaranteed for any specific data set. We strongly recommend that users validate the HIBLUP results with other software packages, such as lme4, GCTA, LDAK, and DMU.

Support documents: Extensive support documents, including the user manual, demo script, demo data and demo results, are available at the zip file.

Questions and comments: Users and developers are recommended to send questions to Lilin Yin (ylilin@163.com), Haohao Zhang (haohaozhang@whut.edu.cn), and Xiaolei Liu (xiaoleiliu@mail.hzau.edu.cn).

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1 Installing HIBLUP and a quick start

1.1 Installation

It is highly recommended to install Microsoft R Open (`https://mran.microsoft.com/download/`) to speed up the mathematical calculation of HIBLUP, but this is not required. HIBLUP can also work fine with base R. The latest Installation scripts, software packages and user manuals are available on the HIBLUP homepage (`https://hiblup.github.io`). It can be installed with the following code:

```
# Linux & macOS
chmod 755 ./hiblupInstaller.sh
./hiblupInstaller.sh
```

```
# Windows
install.packages(c("RcppArmadillo", "bigmemory"))
install.packages("hiblup_1.3.1.zip", repos = NULL)
```

1.2 Quick start

The data embedded in HIBLUP was derived from an animal breeding farm, it includes a total of 2934 genetic related individuals and 573 of them were genotyped with 50K SNP Chip. The genotype was coded as 0, 1, 2 for AA, AB, BB, respectively, and two traits(t1, t2) were recorded for 800 individuals. Sire information and sex information can be treated as random effect and fixed effect, respectively. A quick start of HIBLUP to fit above model is shown below:

```
suppressMessages(library("hiblup"))
data("hidata")
X <- model.matrix(~as.factor(Sex), data = pheno)  # fixed effects
# if 'Sex' is fitted as fixed effect, please convert the column to
# factor by 'as.factor(Sex)' if 'Sex' is fitted as covariates, please
# convert the column to numeric by 'as.numeric(as.character(Sex))'

R <- as.matrix(pheno$Sire)  # random effects
# R can be either character or numeric.  For interaction between two or
# more random effects, it can be fitted by pasting them together, for
# example, there are two random effects R1 and R2, we could fit their
# interaction in the model as: R=cbind(R1,R2,paste(R1,R2,sep='_')).

gebv <- hiblup(pheno = pheno[, c(1, 5)], geno = geno, map = map, geno.id = geno.id,
    pedigree = pedigree, vc.method = c("HI"), mode = "A", CV = X, R = R,
    snp.solution = TRUE)


#-------------------------Welcome to HIBLUP-------------------------#
#  He-aI BLUP   _     _ _____ ____  _     _    _ _____               #
#              | |   | |_   _|  _ \| |   | |  | |  __ \              #
#              | |__| | | | | |_) | |   | |  | | |__) |             #
#              |  __  | | | |  _ <| |   | |  | |  ___/              #
#              | |  | |_| |_| |_) | |___| |__| | |                  #
#              |_|  |_|_____|____/|______\____/|_|    Version: 1.3.1 #
#      Developed by Lilin Yin#, HaoHao Zhang#, and Xiaolei Liu       #
#-------------------------------------------------------------------#
 SSBLUP model is selected based on the provided data!
 Analyzed trait: t2
 Number of fixed effects: 2 (intercept included)
 Number of random effects: 1 + 1
 Number of individuals with phenotypic observations: 800
 Number of SNPs in genotype: 48353
 Deriving GA matrix from genotype...Done within 10s
```

```
Number of genotyped individuals: 573
Number of genotyped individuals with phenotypic observations: 175
Number of genotyped individuals without phenotypic observations: 398
Deriving A matrix from pedigree...Done within 0s
Number of total predicted individuals: 2524
Realign index of y...Done!
Realign index of X matrix...Done!
Realign index of R matrix...Done!
Constructing H matrix...
Extracting A11 matrix...Done!
Mean of diagonal and Off-diagonal of PA: 1.001 0.0285
Mean of diagonal and Off-diagonal of GA: 0.9886 -0.0017
Adjusting GA matrix: GA* = 0.98 * GA + 0.03
Weighting of A11 and GA matrix: 0.05
Calculating the inverse of A11 matrix...Done within 0s
Constructing HA matrix...Done within 6s
HE Prior derived: A:0.06936 e:2.342; Done within 2s
HE adopted: TRUE
Variance components estimation:
Dimension of V^(-1): 800 * 800
[Iter]  Var_R1(SE)       Var_K1(SE)       Var_e(SE)       h2_R1(SE)       h2_K1(SE)
[AI] 0.352395(0.1041) 0.243706(0.1761) 2.142499(0.1935) 0.1287(0.0341) 0.0890(0.0640)
[AI] 0.359233(0.1242) 0.282642(0.2281) 2.116745(0.2139) 0.1302(0.0402) 0.1025(0.0816)
[AI] 0.359961(0.1280) 0.281931(0.2393) 2.117400(0.2193) 0.1305(0.0414) 0.1022(0.0855)
[AI] 0.359910(0.1283) 0.282037(0.2392) 2.117324(0.2193) 0.1304(0.0415) 0.1022(0.0855)
[AI] 0.359915(0.1283) 0.282025(0.2392) 2.117332(0.2193) 0.1304(0.0415) 0.1022(0.0855)
[AI] 0.359914(0.1283) 0.282027(0.2392) 2.117331(0.2193) 0.1304(0.0415) 0.1022(0.0855)
[Convergence] YES
Done within 5s
Estimating random effect...Done within 0s
Estimating SNP effect...Done within 0s
Estimated beta: 12.37 0.8425
Estimated Vg and Ve: 0.282 2.117
HIBLUP IS DONE WITHIN: 24s
HIBLUP ACCOMPLISHED SUCCESSFULLY!
```

You can also load your own data with the following codes:

```
pheno <- read.table("phenotype.txt", header = F)
geno <- bigmemory::attach.big.matrix("genotype.desc")
geno.id <- read.table("geno.id", header = F)
pedigree <- read.table("pedigree.txt", header = T)
map <- read.table("map.txt", header = F)
```

Note that two result files will be generated. One is used for storing the estimated genetic values, and the other is used for storing marker effects if "snp.solution" is TRUE. The contents of these two files are displayed as follows:

Ind	hiblup.A.ebv	hiblup.D.ebv	hiblup.AD.ebv
P0322	-0.0805	-3.21e-04	-0.0808
P0323	-0.1635	-3.14e-04	-0.1638
P0324	-0.0830	1.04e-06	-0.0830
P0325	-0.0637	1.31e-06	-0.0636

Table 1: Estimated genetic values.

Marker	Chr	Pos	P.Freq	SNP.A.effect	SNP.D.effect
ASGA0000014	1	342481	0.355	-0.0304	0.01134
ASGA0000021	1	489855	0.407	-0.0473	-0.00152
H3GA0000026	1	509928	0.286	0.2445	0.09484
ALGA0000009	1	538161	0.139	-0.2514	-0.07195
ALGA0000014	1	565627	0.390	-0.1583	-0.00737

Table 2: Genetic marker effects.

2 Input of HIBLUP

The data requirements of methods in HIBLUP:
BLUP: Phenotypic observations, random effect
PBLUP: Phenotypic observations, Pedigree records
GBLUP: Phenotypic observations, Genotype data
SSBLUP: Phenotypic observations, Genotype data, and Pedigree records

2.1 Pedigree Data

The pedigree data file includes 3 columns (sample id, paternal id, and maternal id). Note that the individuals in the pedigree data file do not need to be sorted by the date of birth, and the missing value can be replaced by NA or 0.

```
pedigree[c(1:3, 501:503), ]

        ID  Sire    Dam
1     ind1  <NA>   <NA>
2     ind2  <NA>   <NA>
3     ind3  <NA>   <NA>
501 ind501 ind41 ind139
502 ind502 ind34 ind140
503 ind503 ind45 ind141
```

2.2 Genotype data

HIBLUP accepts both "big.matrix" format, which is from R bigmemory package and R standard "matrix" format. Each Column represents an individual and each row represents a marker. Here is an example that contains 573 individuals and each individual has 48,353 markers from the demo data. Genotype data in multiple popular formats such as vcf, hapmap, and plink binary format can be converted to "big.matrix" using "MVP.Data" function in the rMVP package (`https://github.com/XiaoleiLiuBio/rMVP`). Genotype ID list is a one-column matrix that includes the id list of genotyped individusls. The order of individuals in genotype id list should match the order of individuals in Genotype data file.

```
geno.id[1:3, ]

[1] ind799 ind800 ind801
573 Levels: ind1061 ind1063 ind1066 ind1067 ind1068 ... ind842

dim(geno)

[1] 48353   573

geno[1:3, 1:10]

  V1 V2 V3 V4 V5 V6 V7 V8 V9 V10
1  1  1  2  0  1  2  1  1  0   1
2  1  1  2  2  2  0  2  1  2   1
3  1  1  1  1  1  0  0  1  2   0
```

2.3 Genotypic map data

Genotypic map data includes three columns, which are marker id, Chromosome ID, and physical position. This information is only used for the output.

```
dim(map)

[1] 48353     3

map[1:3, ]

       SNP Chrom BP
1 10000345     0  0
2 10007117     0  0
3 12784072     0  0
```

2.4 Phenotype, Fixed effects, and Random effects

Individuals in Phenotype, fixed effects, and random effects must have the same order and the individual ID is only added in the first column of phenotype data. Above three information are always incorporated in a single file. Missing phenotype value should be marked with "NA".

```
dim(pheno)

[1] 800   5

pheno[1:3, ]

       ID   Sire Sex    t1    t2
1 ind2124 ind852   2 163.3 12.31
2 ind1107 ind855   2 162.2 12.87
3 ind1814 ind849   2 163.4 13.33
```

2.5 Variance components

for single trait or single random effect model, $vc = (V_g, V_e)$;
for multiple traits, $vc = (V_g^{(1)}, V_e^{(1)}, COV_g^{(12)}, COV_e^{(12)}, ..., COV_g^{(1n)}, COV_e^{(1n)}, V_g^{(2)}, V_e^{(2)}, COV_g^{(23)}, COV_e^{(23)}, ..., COV_g^{(2n)}, COV_e^{(2n)}, ..., V_g^{(n)}, V_e^{(n)})$;
for multiple K model, $vc = (V_g^{(1)}, V_g^{(2)} \dots V_g^{(n)}, V_e)$;
Note that if R (Random effect) is added in the model, V_r (representing the variance components of R) should be added at the beginning of vc vector for single trait. For multiple traits, it should be added to the head of corresponding chunk of each trait.

3 Gallery of HIBLUP input parameters

Parameter	Default	Options	Description
Pheno	NULL	Users	Phenotypic observations
bivar.pos	NULL	Users	The position in columns of phenotype for tow related traits
CV	NULL	Users	Fixed effects
bivar.CV	NULL	Users	list, Fixed effects for multiple traits, each list contains a matrix representing the fixed effect for each trait.
bivar.R	NULL	Users	list, Random effects for multiple traits, each list contains a matrix representing the random effect for each trait.
R	NULL	Users	Random effects for single trait or shared random effects for multiple traits.
geno	NULL	Users	Genotype data
pedigree	NULL	Users	Pedigree records
map	NULL	Users	Genotypic map
geno.id	NULL	Users	Genotype id list
val.id	NULL	Users	sample id list for prediction on individual genetic value
K	NULL	Users	a list of variance-covariance matrices for random effects
G	NULL	Users	Relationship matrix that derived from genotype data
A	NULL	Users	Relationship matrix that derived from pedigree records
A.id	NULL	Users	Sample id list of relationship matrix that derived from pedigree records
alpha	0.05	$0 \sim 1$	the weight of A matrix when merging A and G matrices
cpu	NULL	Positive integer	number of threads used for parallel computation, default is NULL and automatically assign the computational task to appropriate number of threads
vc	NULL	Users	A vector includes known variance components. See section 2.5
mode	"A"	"A" or "AD"	"A" and "AD" repsent Additive model and Additive plus Dominant model, respectively; it doesn't work when "K" is not NULL
vc.method	HI	"AI", "EM", "AIEM", "EMAI", "HE", "HI", "CG", "SOR", "JOR", "SOLVE"	methods for variance components estimation and MME solution
nAIiter	20	Positive integer	Maximum iteration number for "AI"
nEMiter	1	Positive integer	Maximum iteration number for "EM"
snp.solution	FALSE	TRUE or FALSE	if TRUE, the marker effects will be calculated
file.output	TRUE	TRUE or FALSE	if TRUE, gebv and marker effect will be written out
het.add	FALSE	TRUE or FALSE	if TRUE, the individual heterozygosity will be added as covariates in AD model

Table 3: Gallery of HIBLUP input parameters

4 Functions and scripts

In this section, we will provide some code snippets to show the HIBLUP functions. For the sake of brevity, output has been hidden. All code has been verified under the built-in data set.

```
suppressMessages(library("hiblup"))
data("hidata")
```

4.1 Load data

You can also load your own data with the following codes:

```
pheno <- read.table("phenotype.txt", header = F)
geno <- bigmemory::attach.big.matrix("genotype.desc")
geno.id <- read.table("geno.id", header = F)
pedigree <- read.table("pedigree.txt", header = T)
map <- read.table("map.txt", header = F)
```

4.2 Construct relationship matrix

4.2.1 Pedigree based relationship matrix(A matrix)

Construct pedigree based Additive relationship matrix:

```
Acal <- hiblup.AD(pedigree = pedigree, mode = "A")


 Deriving A matrix from pedigree...Done within 0s


A_PA <- Acal$PA
id <- Acal$order.id
```

Construct pedigree based Additive and Dominant relationship matrix:

```
ADcal <- hiblup.AD(pedigree = pedigree, mode = "AD")


 Deriving A and D matrix from pedigree...Done within 0s


AD_PA <- ADcal$PA
AD_PD <- ADcal$PD
id <- ADcal$order.id
```

4.2.2 Genome based relationship matrix(G matrix)

Construct genome based Additive relationship matrix:

```
Acal <- hiblup.K(M = geno, mode = "A")
A_GA <- Acal$GA
```

Construct genome based Additive and Dominant relationship matrix:

```
ADcal <- hiblup.K(M = geno, mode = "AD")
AD_GA <- ADcal$GA
AD_GD <- ADcal$GD
```

4.2.3 Pedigree and genome based relationship matrix(H matrix)

Construct pedigree and genome based Additive relationship matrix:

```
G_ind <- as.character(as.matrix(geno.id)[, 1])
phe_ind <- as.character(as.matrix(pheno)[, 1])

Acal <- hiblup.AD(pedigree = pedigree, mode = "A")


 Deriving A matrix from pedigree...Done within 0s
```

```
A_PA <- Acal$PA
A_ind <- Acal$order.id

Acal <- hiblup.AD(pedigree, mode = "A", inverse = TRUE)


 Deriving the inverse of A matrix from pedigree...Done within 0s


A_PAinv <- Acal$PA

Acal <- hiblup.K(M = geno, mode = "A")
A_GA <- Acal$GA

H <- hiblup.H(A_ind = A_ind, G_ind = G_ind, A = A_PA, G = A_GA, Ainv = NULL,
    alpha = 0.05, tag = "a")


 Constructing H matrix...
 Extracting A11 matrix...Done!
 Mean of diagonal and Off-diagonal of PA: 1.001 0.0285
 Mean of diagonal and Off-diagonal of GA: 0.9886 -0.0017
 Adjusting GA matrix: GA* = 0.98 * GA + 0.03
 Weighting of A11 and GA matrix: 0.05
 Calculating the inverse of A11 matrix...Done within 0s
 Constructing HA matrix...Done within 6s

Hinv <- hiblup.H(A_ind = A_ind, G_ind = G_ind, A = A_PA, G = A_GA, Ainv = A_PAinv,
    alpha = 0.05, tag = "a")


 Constructing H inverse matrix...
 Extracting A11 matrix...Done!
 Mean of diagonal and Off-diagonal of PA: 1.001 0.0285
 Mean of diagonal and Off-diagonal of GA: 0.9886 -0.0017
 Adjusting GA matrix: GA* = 0.98 * GA + 0.03
 Weighting of A11 and GA matrix: 0.05
 Calculating the inverse of A11 matrix...Done within 0s
 Calculating the inverse of Gw.A...Done within 0s
 Constructing the inverse of HA matrix...Done within 0s
```

Construct pedigree and genome based Additive and Dominant relationship matrix:

```
G_ind <- as.character(as.matrix(geno.id)[, 1])
phe_ind <- as.character(as.matrix(pheno)[, 1])

ADcal <- hiblup.AD(pedigree = pedigree, mode = "AD")


 Deriving A and D matrix from pedigree...Done within 0s


AD_PA <- ADcal$PA
AD_PD <- ADcal$PD
A_ind <- ADcal$order.id

ADcal <- hiblup.AD(pedigree, mode = "AD", inverse = TRUE)


 Deriving A and D matrix from pedigree...Done within 0s
 Deriving the inverse of both A and D matrix from pedigree...Done within 6s


AD_PAinv <- ADcal$PAINV
AD_PDinv <- ADcal$PDINV

ADcal <- hiblup.K(M = geno, mode = "AD")
AD_GA <- ADcal$GA
```

```
AD_GD <- ADcal$GD

HA <- hiblup.H(A_ind = A_ind, G_ind = G_ind, A = AD_PA, G = AD_GA, Ainv = NULL,
    alpha = 0.05, tag = "a")


 Constructing H matrix...
 Extracting A11 matrix...Done!
 Mean of diagonal and Off-diagonal of PA: 1.001 0.0285
 Mean of diagonal and Off-diagonal of GA: 0.9886 -0.0017
 Adjusting GA matrix: GA* = 0.98 * GA + 0.03
 Weighting of A11 and GA matrix: 0.05
 Calculating the inverse of A11 matrix...Done within 0s
 Constructing HA matrix...Done within 6s

HAinv <- hiblup.H(A_ind = A_ind, G_ind = G_ind, A = AD_PA, G = AD_GA, Ainv = AD_PAinv,
    alpha = 0.05, tag = "a")


 Constructing H inverse matrix...
 Extracting A11 matrix...Done!
 Mean of diagonal and Off-diagonal of PA: 1.001 0.0285
 Mean of diagonal and Off-diagonal of GA: 0.9886 -0.0017
 Adjusting GA matrix: GA* = 0.98 * GA + 0.03
 Weighting of A11 and GA matrix: 0.05
 Calculating the inverse of A11 matrix...Done within 0s
 Calculating the inverse of Gw.A...Done within 0s
 Constructing the inverse of HA matrix...Done within 0s

HD <- hiblup.H(A_ind = A_ind, G_ind = G_ind, A = AD_PD, G = AD_GD, Ainv = NULL,
    alpha = 0.05, tag = "d")


 Constructing H matrix...
 Extracting D11 matrix...Done!
 Mean of diagonal and Off-diagonal of PD: 1 0.001
 Mean of diagonal and Off-diagonal of GD: 0.5374 -0.0009
 Adjusting GD matrix: GD* = 1.86 * GD + 0
 Weighting of D11 and GD matrix: 0.05
 Calculating the inverse of D11 matrix...Done within 0s
 Constructing HD matrix...Done within 6s

HDinv <- hiblup.H(A_ind = A_ind, G_ind = G_ind, A = AD_PD, G = AD_GD, Ainv = AD_PDinv,
    alpha = 0.05, tag = "d")


 Constructing H inverse matrix...
 Extracting D11 matrix...Done!
 Mean of diagonal and Off-diagonal of PD: 1 0.001
 Mean of diagonal and Off-diagonal of GD: 0.5374 -0.0009
 Adjusting GD matrix: GD* = 1.86 * GD + 0
 Weighting of D11 and GD matrix: 0.05
 Calculating the inverse of D11 matrix...Done within 0s
 Calculating the inverse of Gw.D...Done within 0s
 Constructing the inverse of HD matrix...Done within 0s
```

4.3 Variance components estimation

Six variance components estimation methods were implemented in HIBLUP, including AI, EM, EMAI, AIEM, HE Regression, and HI. HE is the most efficient as no big matrix inverse calculation and iteration requirments, but not stable, we assign the estimation of HE as the prior values of AI, which could help to fast coverge for AI step, we call it as HI. For the genetic correlation estimation model, our HE algorithm fit all two traits together, instead of fitting separately as

GCTA implemented. All methods can be called by setting the `method` parameter of the `hiblup.vc` function. `nAIiter` and `nEMiter` are the maximum iteration number of "AI" and "EM", valid only in the variance components estimation with "AI" or "EM" method.

4.3.1 No K included (BLUP)

```
index <- match(geno.id[, 1], pheno[, 1])
X <- model.matrix(~Sex, data = pheno)  # fixed effects
R <- as.matrix(pheno$Sire)  # random effects
vc <- hiblup.vc(y = pheno$t2, R = R, blup.solution = FALSE, verbose = TRUE)
```

4.3.2 Singe K model

```
index <- match(geno.id[, 1], pheno[, 1])

# AI
vc <- hiblup.vc(y = pheno$t2[index], K = A_GA, nAIiter = 20, method = "AI",
    blup.solution = FALSE, verbose = TRUE)

# EM
vc <- hiblup.vc(y = pheno$t2[index], K = A_GA, nEMiter = 20, method = "EM",
    blup.solution = FALSE, verbose = TRUE)

# HI
vc <- hiblup.vc(y = pheno$t2[index], K = A_GA, nAIiter = 20, method = "HI",
    blup.solution = FALSE, verbose = TRUE)

# EMAI
vc <- hiblup.vc(y = pheno$t2[index], K = A_GA, nAIiter = 20, nEMiter = 1,
    method = "EMAI", blup.solution = FALSE, verbose = TRUE)

# AIEM
vc <- hiblup.vc(y = pheno$t2[index], K = A_GA, nAIiter = 5, nEMiter = 20,
    method = "AIEM", blup.solution = FALSE, verbose = TRUE)

# HE Regression
vc <- hiblup.vc(y = pheno$t2[index], K = A_GA, method = "HE", blup.solution = FALSE,
    verbose = TRUE)
```

If `blup.solution=TRUE`, random effect will be estimated, for `HE` algorithm, P and Vinv matrix need to be constructed additionally, therefor it takes a little long time than others.
Fixed effects and random effects can be added by parameters `X` and `R`:

```
index <- match(geno.id[, 1], pheno[, 1])
X <- model.matrix(~Sex, data = pheno)  # fixed effects
R <- as.matrix(pheno$Sire)  # random effects

# AI
vc <- hiblup.vc(y = pheno$t2[index], X = X[index, ], R = R[index, ], K = A_GA,
    nAIiter = 20, method = "AI", blup.solution = FALSE, verbose = TRUE)


 Variance components estimation:
 Dimension of V^(-1): 175 * 175
 [Iter]  Var_R1(SE)       Var_K1(SE)       Var_e(SE)       h2_R1(SE)       h2_K1(SE)
 [AI] 1.146199(0.6755) 0.018965(0.8592) 3.277526(0.5790) 0.2580(0.1181) 0.0043(0.1931)
 [AI] 1.262022(0.4568) 0.036802(0.3420) 3.578946(0.4950) 0.2587(0.0743) 0.0075(0.0701)
 [AI] 1.274311(0.5270) 0.040030(0.4036) 3.609913(0.5720) 0.2588(0.0849) 0.0081(0.0820)
 [AI] 1.274342(0.5347) 0.039942(0.4113) 3.610357(0.5808) 0.2588(0.0861) 0.0081(0.0835)
```

```
 [AI] 1.274347(0.5348) 0.039948(0.4113) 3.610349(0.5808) 0.2588(0.0861) 0.0081(0.0835)
 [AI] 1.274347(0.5348) 0.039948(0.4113) 3.610349(0.5808) 0.2588(0.0861) 0.0081(0.0835)
 [Convergence] YES
 Done within 1s
```

```
# HE Regression
vc <- hiblup.vc(y = pheno$t2[index], X = X[index, ], R = R[index, ], K = A_GA,
    nAIiter = 20, method = "HE", blup.solution = FALSE, verbose = TRUE)
```

```
 Variance components estimation:
 [Iter]  Var_R1(SE)       Var_K1(SE)       Var_e(SE)       h2_R1(SE)       h2_K1(SE)
 [HE] 1.478910 0.274269 3.245188 0.295879 0.054872
 Done within 0s
```

4.3.3 Multiple K model

Parameter `K` accepts a list of `K`s and execute a multiple random effects model:

```
index <- match(geno.id[, 1], pheno[, 1])

ADcal <- hiblup.K(M = geno, mode = "AD")
AD_GA <- ADcal$GA
AD_GD <- ADcal$GD

# AI, EM, EMAI, AIEM, and HI algorithm
vc <- hiblup.vc(y = pheno$t2[index], K = list(AD_GA, AD_GD), method = "AI",
    nAIiter = 5, blup.solution = FALSE, verbose = TRUE)
```

```
 Variance components estimation:
 Dimension of V^(-1): 175 * 175
 [Iter]  Var_K1(SE)       Var_K2(SE)       Var_e(SE)       h2_K1(SE)       h2_K2(SE)
 [AI] 1.693366(1.3788) 0.791422(2.4007) 2.403310(1.6515) 0.3464(0.2689) 0.1619(0.4863)
 [AI] 1.744592(1.3761) 0.030725(2.4384) 3.099038(1.7194) 0.3579(0.2688) 0.0063(0.5001)
 [AI] 1.746125(1.3661) 0.009845(2.4571) 3.118258(1.7663) 0.3582(0.2669) 0.0020(0.5041)
 [AI] 1.746508(1.3658) 0.004647(2.4575) 3.123044(1.7674) 0.3583(0.2668) 0.0010(0.5042)
 [AI] 1.746699(1.3657) 0.002050(2.4576) 3.125435(1.7677) 0.3584(0.2668) 0.0004(0.5042)
 [Convergence] NO(More iteration number is needed!)
 Done within 1s
```

```
# HE algorithm
vc <- hiblup.vc(y = pheno$t2[index], K = list(AD_GA, AD_GD), method = "HE",
    blup.solution = FALSE, verbose = TRUE)
```

```
 Variance components estimation:
 [Iter]  Var_K1(SE)       Var_K2(SE)       Var_e(SE)       h2_K1(SE)       h2_K2(SE)
 [HE] 1.061103 0.000000 5.923261 0.151926 0.000000
 Done within 0s
```

With fixed effects and random effects:

```
index <- match(geno.id[, 1], pheno[, 1])

ADcal <- hiblup.K(M = geno, mode = "AD")
AD_GA <- ADcal$GA
AD_GD <- ADcal$GD

X <- model.matrix(~Sex, data = pheno)  # fixed effects
R <- as.matrix(pheno$Sire)  # random effects

# AI, EM, EMAI, AIEM, and HI algorithm
```

```
vc <- hiblup.vc(y = pheno$t2[index], X = X[index, ], R = R[index, ], K = list(AD_GA,
    AD_GD), method = "AI", blup.solution = FALSE, verbose = TRUE)

# HE algorithm
vc <- hiblup.vc(y = pheno$t2[index], X = X[index, ], R = R[index, ], K = list(AD_GA,
    AD_GD), method = "HE", blup.solution = FALSE, verbose = TRUE)
```

4.3.4 Multiple traits model

Variance and co-variance for multiple traits can be estimated using following codes.

```
# No K (BLUP)
vc <- hiblup.bivar.vc(y = list(pheno$t1, pheno$t2), bivar.X = list(X, X),
    R = R, method = "AI", blup.solution = FALSE, verbose = TRUE)
# if there are others trait-spercific random effects for traits, please
# assign to 'bivar.R'.  if there is a trait with no fixed or random
# effects, please set NULL at corresponding postion in 'bivar.X' or
# 'bivar.R'.
```

```
# single K model
X <- model.matrix(~Sex, data = pheno)  # fixed effects
R <- as.matrix(pheno$Sire)  # random effects
ADcal <- hiblup.AD(pedigree = pedigree, mode = "AD")

 Deriving A and D matrix from pedigree...Done within 0s

AD_PA <- ADcal$PA
AD_PD <- ADcal$PD
id <- ADcal$order.id
index <- match(pheno[, 1], id)
vc <- hiblup.bivar.vc(y = list(pheno$t1, pheno$t2), bivar.X = list(X, X),
    K = A_PA[index, index], method = "AI", blup.solution = FALSE, verbose = TRUE)

 Variance components estimation:
 Number of components: 6
 Dimension of V^(-1): 1600 * 1600
 Bivariate GREML analysis:  Vgtr1_R1 Vetr1 CoVgtr1tr2_R1 CoVetr1tr2 Vgtr2_R1 Vetr2
 [AI] Iter 1 of Max Iter 25: 0.842372 1.210966 0.697899 0.837582 0.732004 0.814299
 [AI] Iter 2 of Max Iter 25: 0.856506 2.032594 0.867441 1.307332 0.964980 1.234730
 [AI] Iter 3 of Max Iter 25: 0.871486 2.617028 0.957126 1.630738 1.075397 1.529934
 [AI] Iter 4 of Max Iter 25: 0.884284 2.781225 0.975311 1.713651 1.092801 1.605165
 [AI] Iter 5 of Max Iter 25: 0.885506 2.791538 0.977313 1.716704 1.094709 1.607339
 [AI] Iter 6 of Max Iter 25: 0.885448 2.791650 0.977276 1.716749 1.094653 1.607388
 [AI] Iter 7 of Max Iter 25: 0.885452 2.791647 0.977281 1.716746 1.094658 1.607385
 [AI] Iter 8 of Max Iter 25: 0.885451 2.791648 0.977280 1.716746 1.094658 1.607385
 [Convergence] YES
 Done within 45s
```

```
# multiple K model
vc <- hiblup.bivar.vc(y = list(pheno$t1, pheno$t2), bivar.X = list(X, X),
    R = R, K = list(AD_PA[index, index], AD_PD[index, index]), method = "AI",
    blup.solution = FALSE, verbose = TRUE)

# if you do not want to calculate the genetic correlation in 'R', just
# take them into random effect for corresponding triat: if there are
# others trait-spercific random effects for traits, please assign to
# 'bivar.R'.  if there is a trait with no fixed or random effects,
# please set NULL at corresponding postion in 'bivar.X' or 'bivar.R'.
vc <- hiblup.bivar.vc(y = list(pheno$t1, pheno$t2), bivar.X = list(X, X),
```

```
    bivar.R = list(R, R), K = list(AD_PA[index, index], AD_PD[index, index]),
    method = "AI", blup.solution = FALSE, verbose = TRUE)

# each trait could be assigned different number of fixed or random
# effects. AI, EM, EMAI, AIEM, HE and HI algorithms are available.
```

4.3.5 With user-provided variance components

The `start` parameter is used to accept the initial value in the variance component calculation method containing AI or EM. The length of the start vector is equal to the number of K plus one. It should be noted that if R is specified, the value of V_R needs to be given in the first position in start. For pairs of correlated traits, the elements in start are $V_g^{(1)}$, $V_g^{(2)}$, $COV_g^{(12)}$, $V_e^{(1)}$, $V_e^{(2)}$, and $COV_e^{(12)}$;

```
print(start1)

[1] 0.755 4.180

print(start2)

[1] 1.27435 0.03995 3.61035

print(start3)

[1] 4.455 0.000 7.414

print(start4)

[1] 2.115 9.890 0.000 0.755

print(start5)

[1] 0.2687 5.3819 0.4497 4.2729 0.7526 4.1848
```

```
# Single K model
vc <- hiblup.vc(y = pheno$t2[index], K = A_GA, start = start1, method = "AI")

# Single K model with fixed effects and random effects
vc <- hiblup.vc(y = pheno$t2[index], X = X[index, ], R = R[index, ], K = A_GA,
    start = start2, method = "AI")

# Multiple K model
vc <- hiblup.vc(y = pheno$t2[index], K = list(AD_GA, AD_GD), start = start3,
    method = "AI")

# Multiple K model with fixed effects and random effects
vc <- hiblup.vc(y = pheno$t2[index], X = X[index, ], R = R[index, ], start = start4,
    K = list(AD_GA, AD_GD), method = "AI")

# multiple traits
vc <- hiblup.bivar.vc(y = list(pheno$t1[index], pheno$t2[index]), bivar.X = list(X[index,
    ], X[index, ]), start = start5, K = A_GA, method = "AI")
# if there are others trait-spercific random effects for traits, please
# assign to 'bivar.R'.  if there is a trait with no fixed or random
# effects, please set NULL at corresponding postion in 'bivar.X' or
# 'bivar.R'.
```

4.4 BLUP

4.4.1 Single trait with random effects only

```
# AI, EM, EMAI, AIEM, and HI algorithm
X <- model.matrix(~Sex, data = pheno)  # fixed effects
R <- as.matrix(pheno$Sire)  # random effects

# using HI algorithm
gebv.a.hi <- hiblup(pheno = pheno[, c(1, 5)], CV = X, R = R, vc.method = c("HI"))


#-------------------------Welcome to HIBLUP-------------------------#
#  He-aI BLUP   _     _ _____ ____  _     _    _ _____               #
#              | |   | |_   _|  _ \| |   | |  | |  __ \              #
#              | |__| | | | | |_) | |   | |  | | |__) |             #
#              |  __  | | | |  _ <| |   | |  | |  ___/              #
#              | |  | |_| |_| |_) | |___| |__| | |                  #
#              |_|  |_|_____|____/|______\____/|_|    Version: 1.3.1 #
#      Developed by Lilin Yin#, HaoHao Zhang#, and Xiaolei Liu       #
#-------------------------------------------------------------------#
 BLUP model is selected based on the provided data!
 Analyzed trait: t2
 Number of fixed effects: 2 (intercept included)
 Number of random effects: 1
 Number of individuals with phenotypic observations: 800
 HE prior derived...Done!
 Updated prior values: 0.316413 2.399766
 Variance components estimation:
 Dimension of V^(-1): 800 * 800
 [Iter]  Var_R1(SE)       Var_e(SE)       h2_R1(SE)
 [AI] 0.369552(0.1034) 2.353335(0.1237) 0.1357(0.0337)
 [AI] 0.373681(0.1227) 2.354706(0.1202) 0.1370(0.0396)
 [AI] 0.373533(0.1244) 2.354742(0.1203) 0.1369(0.0401)
 [AI] 0.373540(0.1243) 2.354741(0.1203) 0.1369(0.0401)
 [AI] 0.373540(0.1243) 2.354741(0.1203) 0.1369(0.0401)
 [Convergence] YES
 Done within 2s
 Estimating random effect...Done within 0s
 Estimated beta: 11.51 0.8485
 Estimated Vr and Ve: 0.3735 2.355
 HIBLUP IS DONE WITHIN: 2s
 HIBLUP ACCOMPLISHED SUCCESSFULLY!
```

4.4.2 Multiple traits model

```
X <- model.matrix(~Sex, data = pheno)  # fixed effects
R <- as.matrix(pheno$Sire)  # random effects
gebv <- hiblup(pheno = pheno, bivar.pos = c(4, 5), bivar.CV = list(X, X),
    R = R)


#-------------------------Welcome to HIBLUP-------------------------#
#  He-aI BLUP   _     _ _____ ____  _     _    _ _____               #
#              | |   | |_   _|  _ \| |   | |  | |  __ \              #
#              | |__| | | | | |_) | |   | |  | | |__) |             #
#              |  __  | | | |  _ <| |   | |  | |  ___/              #
#              | |  | |_| |_| |_) | |___| |__| | |                  #
#              |_|  |_|_____|____/|______\____/|_|    Version: 1.3.1 #
#      Developed by Lilin Yin#, HaoHao Zhang#, and Xiaolei Liu       #
#-------------------------------------------------------------------#
```

```
Bivariate GREML analysis started...
BLUP model is selected based on the provided data!
Analyzed trait: t1 & t2
Number of fixed effects for trait1: 3(intercept included)
Number of fixed effects for trait2: 3(intercept included)
No trait-specific random effects.
Number of random effects for correlation: 1
Number of phenotypic observations for trait1: 800
Number of phenotypic observations for trait2: 800
Number of individuals for analysis: 800
Variance components estimation:
Number of components: 6
HE prior derived... Done within 0s
Updated prior values: 0.266455 3.406646 0.264548 2.426824 0.308261 2.390834
Dimension of V^(-1): 1600 * 1600
Bivariate GREML analysis:  Vgtr1_R1 Vetr1 CoVgtr1tr2_R1 CoVetr1tr2 Vgtr2_R1 Vetr2
[AI] Iter 1 of Max Iter 20: 0.297919 3.381535 0.330331 2.377775 0.366268 2.353204
[AI] Iter 2 of Max Iter 20: 0.312250 3.387004 0.340472 2.379055 0.376054 2.354413
[AI] Iter 3 of Max Iter 20: 0.313303 3.386167 0.340123 2.379040 0.375712 2.354497
[AI] Iter 4 of Max Iter 20: 0.313416 3.385925 0.340008 2.379019 0.375685 2.354494
[AI] Iter 5 of Max Iter 20: 0.313426 3.385878 0.339980 2.379017 0.375678 2.354494
[AI] Iter 6 of Max Iter 20: 0.313428 3.385870 0.339975 2.379016 0.375677 2.354494
[AI] Iter 7 of Max Iter 20: 0.313428 3.385869 0.339974 2.379016 0.375677 2.354494
[AI] Iter 8 of Max Iter 20: 0.313428 3.385869 0.339974 2.379016 0.375677 2.354494
[Convergence] YES
Done within 13s
Estimating random effect...Done within 0s
Estimated beta for trait1: 161.3 0.9206
Estimated beta for trait2: 11.51 0.8513
Estimated (CO)Variance(upper.tri+diag) and correlation(lower.tri) at R1:
        trait1  trait2
trait1  0.3134  0.3400
trait2  0.9908  0.3757
Estimated (CO)Variance(upper.tri+diag) and correlation(lower.tri) at Residual:
        trait1  trait2
trait1  3.3859   2.379
trait2  0.8426   2.354
HIBLUP IS DONE WITHIN: 13s
HIBLUP ACCOMPLISHED SUCCESSFULLY!
```

4.5 Pedigree BLUP(PBLUP)

4.5.1 Additive effect based model

if variance components are unknown:

```r
# AI, EM, EMAI, AIEM, and HI algorithm
X <- model.matrix(~Sex, data = pheno)  # fixed effects
R <- as.matrix(pheno$Sire)  # random effects

# using HI algorithm if variance components are unknown
gebv.a.hi <- hiblup(pheno = pheno[, c(1, 5)], pedigree = pedigree, CV = X,
    R = R, vc.method = c("HI"), nAIiter = 5, mode = "A")


#-------------------------Welcome to HIBLUP--------------------------#
#  He-aI BLUP    _     _ _____ ____  _      _    _ _____              #
#               | |   | |_   _|  _ \| |    | |  | |  __ \             #
#               | |__| | | | | |_) | |    | |  | | |__) |            #
#               |  __  | | | |  _ <| |    | |  | |  ___/             #
#               | |  | |_| |_| |_) | |___| |__| | |                  #
#               |_|  |_|_____|____/|______\____/|_|    Version: 1.3.1 #
```

```
#      Developed by Lilin Yin#, HaoHao Zhang#, and Xiaolei Liu       #
#-----------------------------------------------------------------------#
 PBLUP model is selected based on the provided data!
 Analyzed trait: t2
 Number of fixed effects: 2 (intercept included)
 Number of random effects: 1 + 1
 Number of individuals with phenotypic observations: 800
 Deriving A matrix from pedigree...Done within 0s
 Number of total predicted individuals: 2524
 Realign index of y...Done!
 Realign index of X matrix...Done!
 Realign index of R matrix...Done!
 HE Prior derived: A:0.9245 e:1.718; Done within 2s
 HE adopted: TRUE
 Variance components estimation:
 Dimension of V^(-1): 800 * 800
 [Iter]  Var_R1(SE)       Var_K1(SE)       Var_e(SE)       h2_R1(SE)       h2_K1(SE)
 [AI] 0.229478(0.1225) 0.543020(0.4023) 1.943620(0.2858) 0.0845(0.0446) 0.1999(0.1437)
 [AI] 0.243490(0.1379) 0.584212(0.3297) 1.918467(0.2531) 0.0887(0.0479) 0.2127(0.1179)
 [AI] 0.245364(0.1462) 0.582225(0.3416) 1.919894(0.2592) 0.0893(0.0507) 0.2119(0.1219)
 [AI] 0.245362(0.1467) 0.582361(0.3412) 1.919794(0.2590) 0.0893(0.0508) 0.2120(0.1218)
 [AI] 0.245364(0.1467) 0.582351(0.3412) 1.919801(0.2590) 0.0893(0.0508) 0.2120(0.1218)
 [Convergence] NO(More iteration number is needed!)
 Done within 4s
 Estimating random effect...Done within 0s
 Estimated beta: 11.52 0.8442
 Estimated Vg and Ve: 0.5824 1.92
 HIBLUP IS DONE WITHIN: 6s
 HIBLUP ACCOMPLISHED SUCCESSFULLY!
```

4.5.2 Additive and Dominant effect based model

```
gebv.ad <- hiblup(pheno = pheno[, c(1, 5)], pedigree = pedigree, mode = "AD")


#-------------------------Welcome to HIBLUP-------------------------#
#  He-aI BLUP   _    _ _____ ____  _     _    _ _____                #
#              | |  | |_   _|  _ \| |   | |  | |  __ \               #
#              | |__| | | | | |_) | |   | |  | | |__) |              #
#              |  __  | | | |  _ <| |   | |  | |  ___/               #
#              | |  | |_| |_| |_) | |___| |__| | |                   #
#              |_|  |_|_____|____/|______\____/|_|    Version: 1.3.1 #
#      Developed by Lilin Yin#, HaoHao Zhang#, and Xiaolei Liu       #
#-----------------------------------------------------------------------#
 PBLUP model is selected based on the provided data!
 Analyzed trait: t2
 Number of fixed effects: 1 (intercept included)
 Number of random effects: 0 + 2
 Number of individuals with phenotypic observations: 800
 Deriving A and D matrix from pedigree...Done within 0s
 Number of total predicted individuals: 2524
 Realign index of y...Done!
 Realign index of X matrix...Done!
 HE Prior derived: A:1.485 D:0 e:1.756; Done within 2s
 HE adopted: TRUE
 Variance components estimation:
 Dimension of V^(-1): 800 * 800
 [Iter]  Var_K1(SE)       Var_K2(SE)       Var_e(SE)       h2_K1(SE)       h2_K2(SE)
 [AI] 1.108232(0.4496) 0.108023(0.7766) 1.498475(0.6901) 0.4082(0.1461) 0.0398(0.2865)
 [AI] 1.196619(0.3148) 0.060027(0.6080) 1.535628(0.5445) 0.4285(0.0998) 0.0215(0.2178)
 [AI] 1.193404(0.3412) 0.066128(0.6286) 1.533604(0.5613) 0.4273(0.1077) 0.0237(0.2252)
```

```
 [AI] 1.194005(0.3406) 0.065335(0.6294) 1.533935(0.5620) 0.4275(0.1075) 0.0234(0.2255)
 [AI] 1.193916(0.3407) 0.065447(0.6294) 1.533891(0.5620) 0.4274(0.1076) 0.0234(0.2255)
 [AI] 1.193929(0.3407) 0.065431(0.6294) 1.533897(0.5620) 0.4274(0.1076) 0.0234(0.2255)
 [AI] 1.193927(0.3407) 0.065433(0.6294) 1.533897(0.5620) 0.4274(0.1076) 0.0234(0.2255)
 [AI] 1.193928(0.3407) 0.065433(0.6294) 1.533897(0.5620) 0.4274(0.1076) 0.0234(0.2255)
 [Convergence] YES
 Done within 6s
 Estimating random effect...Done within 0s
 Estimated beta: 13.09
 Estimated additive genetic variacne: 1.194
 Estimated Dominance genetic variacne: 0.06543
 Estimated Ve: 1.534
 HIBLUP IS DONE WITHIN: 9s
 HIBLUP ACCOMPLISHED SUCCESSFULLY!
```

4.5.3 With user-provided variance components

If the variance components are known and provided by the users, the methods for solving mixed model equation can be controlled by the `vc.method` parameter. The options are "CG", "JOR", "SOLVE" and "SOR".

```
# Solve mixed model equation directly
gebv.a <- hiblup(pheno = pheno[, c(1, 5)], pedigree = pedigree, CV = X,
    R = R, vc = start2, vc.method = "SOLVE", mode = "A")


#-------------------------Welcome to HIBLUP-------------------------#
#  He-aI BLUP    _     _ _____ ____  _      _    _ _____              #
#               | |   | |_   _|  _ \| |    | |  | |  __ \             #
#               | |__| | | | | |_) | |    | |  | | |__) |            #
#               |  __  | | | |  _ <| |    | |  | |  ___/             #
#               | |  | |_| |_| |_) | |___| |__| | |                  #
#               |_|  |_|_____|____/|______\____/|_|    Version: 1.3.1 #
#      Developed by Lilin Yin#, HaoHao Zhang#, and Xiaolei Liu       #
#-------------------------------------------------------------------#
 PBLUP model is selected based on the provided data!
 Analyzed trait: t2
 Number of fixed effects: 2 (intercept included)
 Number of random effects: 1 + 1
 Number of individuals with phenotypic observations: 800
 Deriving A matrix from pedigree...Done within 0s
 Number of total predicted individuals: 2524
 Realign index of y...Done!
 Realign index of X matrix...Done!
 Realign index of R matrix...Done!
 No need for Variance components estimation
 Provided variance components:
 Var_R1  Var_K1  Var_e
 1.27434691100927  0.0399477490264859  3.61034937032618
 Done within 0s
 Estimating random effect...Done within 0s
 Estimated beta: 9.524 1.673
 Estimated Vg and Ve: 0.03995 3.61
 HIBLUP IS DONE WITHIN: 1s
 HIBLUP ACCOMPLISHED SUCCESSFULLY!



# Solve mixed model equation using CG method
gebv.a <- hiblup(pheno = pheno[, c(1, 5)], pedigree = pedigree, CV = X,
    R = R, vc = start2, vc.method = "CG", mode = "A")


#-------------------------Welcome to HIBLUP-------------------------#
```

```
#  He-aI BLUP    _     _ _____ ____  _      _    _ _____                  #
#               | |   | |_   _|  _ \| |    | |  | |  __ \                 #
#               | |__| | | | | |_) | |    | |  | | |__) |                #
#               |  __  | | | |  _ <| |    | |  | |  ___/                 #
#               | |  | |_| |_| |_) | |___| |__| | |                      #
#               |_|  |_|_____|____/|______\____/|_|    Version: 1.3.1 #
#      Developed by Lilin Yin#, HaoHao Zhang#, and Xiaolei Liu       #
#-----------------------------------------------------------------#
 PBLUP model is selected based on the provided data!
 Analyzed trait: t2
 Number of fixed effects: 2 (intercept included)
 Number of random effects: 1 + 1
 Number of individuals with phenotypic observations: 800
 Deriving A matrix from pedigree...Done within 0s
 Number of total predicted individuals: 2524
 Realign index of y...Done!
 Realign index of X matrix...Done!
 Realign index of R matrix...Done!
 No need for Variance components estimation
 Provided variance components:
 Var_R1  Var_K1  Var_e
 1.27434691100927  0.0399477490264859  3.61034937032618
 Iterative solve using method CG
 Iter No.1 with minimum diff = 0.7499883
 Iter No.2 with minimum diff = 0.9741137
 ...
 Iter No.34 with minimum diff = 0.0000021
 Done within 0s
 Estimating random effect...Done within 0s
 Estimated beta: 9.524 1.673
 Estimated Vg and Ve: 0.03995 3.61
 HIBLUP IS DONE WITHIN: 0s
 HIBLUP ACCOMPLISHED SUCCESSFULLY!
```

4.5.4 Multiple traits model

HIBLUP supports the estimation of individual genetic values for multiple traits. Users can specify the columns of the trait1 and trait2 in phenotype file by setting the bivar.pos parameter, for example:

```
gebv <- hiblup(pheno = pheno, bivar.pos = c(4, 5), bivar.CV = list(X, X),
    R = R, pedigree = pedigree)


#-------------------------Welcome to HIBLUP-------------------------#
#  He-aI BLUP    _     _ _____ ____  _      _    _ _____                  #
#               | |   | |_   _|  _ \| |    | |  | |  __ \                 #
#               | |__| | | | | |_) | |    | |  | | |__) |                #
#               |  __  | | | |  _ <| |    | |  | |  ___/                 #
#               | |  | |_| |_| |_) | |___| |__| | |                      #
#               |_|  |_|_____|____/|______\____/|_|    Version: 1.3.1 #
#      Developed by Lilin Yin#, HaoHao Zhang#, and Xiaolei Liu       #
#-----------------------------------------------------------------#
 Bivariate GREML analysis started...
 PBLUP model is selected based on the provided data!
 Analyzed trait: t1 & t2
 Number of fixed effects for trait1: 3(intercept included)
 Number of fixed effects for trait2: 3(intercept included)
 No trait-specific random effects.
 Number of random effects for correlation: 1 + 1
 Number of phenotypic observations for trait1: 800
 Number of phenotypic observations for trait2: 800
```

```
Number of individuals for analysis: 800
Deriving A matrix from pedigree...Done within 0s
Number of total predicted individuals: 2524
Realign index of y...Done!
Realign index of X matrix...Done!
Realign index of R matrix...Done!
Variance components estimation:
Number of components: 9
HE prior derived... Done within 0s
Updated prior values: 0.128032 0.558371 2.986698 0.096720 0.551711 2.042941 0.102726 0.829088 1.767281
Dimension of V^(-1): 1600 * 1600
Bivariate GREML analysis:  Vgtr1_R1 Vgtr1_R2 Vetr1 CoVgtr1tr2_R1 CoVgtr1tr2_R2 CoVetr1tr2 Vgtr2_R1 Vgtr2_R2 Vetr
[AI] Iter 1 of Max Iter 20: 0.198432 0.294966 3.182058 0.198572 0.417866 1.984285 0.198712 0.591972 1.876850
[AI] Iter 2 of Max Iter 20: 0.211904 0.426446 3.055171 0.217372 0.496677 2.000912 0.235414 0.578475 1.917609
[AI] Iter 3 of Max Iter 20: 0.218397 0.425097 3.069374 0.223577 0.507353 1.994944 0.238969 0.605527 1.902415
[AI] Iter 4 of Max Iter 20: 0.217601 0.428728 3.066909 0.223347 0.509139 1.994284 0.239114 0.604633 1.903211
[AI] Iter 5 of Max Iter 20: 0.217670 0.428630 3.066997 0.223460 0.509113 1.994419 0.239192 0.604709 1.903181
[AI] Iter 6 of Max Iter 20: 0.217648 0.428728 3.066931 0.223456 0.509171 1.994402 0.239193 0.604708 1.903188
[AI] Iter 7 of Max Iter 20: 0.217648 0.428733 3.066928 0.223458 0.509175 1.994405 0.239196 0.604709 1.903188
[AI] Iter 8 of Max Iter 20: 0.217647 0.428736 3.066926 0.223459 0.509176 1.994405 0.239196 0.604709 1.903188
[AI] Iter 9 of Max Iter 20: 0.217647 0.428737 3.066925 0.223459 0.509177 1.994405 0.239196 0.604709 1.903189
[Convergence] YES
Done within 57s
Estimating random effect...Done within 0s
Estimated beta for trait1: 161.3 0.9178
Estimated beta for trait2: 11.51 0.8493
Estimated (CO)Variance(upper.tri+diag) and correlation(lower.tri) at R1:
        trait1  trait2
trait1  0.2176  0.2235
trait2  0.9794  0.2392
Estimated (CO)Variance(upper.tri+diag) and correlation(lower.tri) at Additive:
        trait1  trait2
trait1  0.4287  0.5092
trait2  1.0000  0.6047
Estimated (CO)Variance(upper.tri+diag) and correlation(lower.tri) at Residual:
        trait1  trait2
trait1  3.0669   1.994
trait2  0.8255   1.903
HIBLUP IS DONE WITHIN: 59s
HIBLUP ACCOMPLISHED SUCCESSFULLY!


# if there are others trait-spercific random effects for traits, please
# assign to 'bivar.R'.  if there is a trait with no fixed or random
# effects, please set NULL at corresponding postion in 'bivar.CV' or
# 'bivar.R'.
```

4.6 Genomic BLUP(GBLUP)

4.6.1 Additive effect based model

```
# AI, EM, EMAI, AIEM, and HI algorithm
X <- model.matrix(~Sex, data = pheno)  # fixed effects

gebv.a.ai <- hiblup(pheno = pheno[, c(1, 5)], geno = geno, map = map, geno.id = geno.id,
    CV = X, vc.method = c("AI"), mode = "A")


#-------------------------Welcome to HIBLUP-------------------------#
#  He-aI BLUP    _     _ _____ ____  _      _     _ _____                #
#              | |   | |_   _|  _ \| |    | |   | |  __ \               #
#              | |__| | | | | |_) | |    | |   | | |__) |              #
#
```

```
#              |  __  | | | |  _ <| |   | |  | |  ___/              #
#              | |  | |_| |_| |_) | |___| |__| | |                   #
#              |_|  |_|_____|____/|______\____/|_|    Version: 1.3.1 #
#      Developed by Lilin Yin#, HaoHao Zhang#, and Xiaolei Liu       #
#--------------------------------------------------------------------#
 GBLUP model is selected based on the provided data!
 Analyzed trait: t2
 Number of fixed effects: 2 (intercept included)
 Number of random effects: 0 + 1
 Number of individuals with phenotypic observations: 800
 Number of SNPs in genotype: 48353
 Deriving GA matrix from genotype...Done within 9s
 Number of genotyped individuals: 573
 Number of genotyped individuals with phenotypic observations: 175
 Number of genotyped individuals without phenotypic observations: 398
 Number of total predicted individuals: 573
 Realign index of y...Done!
 Realign index of X matrix...Done!
 Variance components estimation:
 Dimension of V^(-1): 175 * 175
 [Iter]  Var_K1(SE)       Var_e(SE)       h2_K1(SE)
 [AI] 1.265440(1.1820) 3.659904(0.8541) 0.2569(0.2182)
 [AI] 0.908219(0.9788) 4.057931(0.8841) 0.1829(0.1889)
 [AI] 0.807857(0.8896) 4.156277(0.8818) 0.1627(0.1743)
 [AI] 0.778040(0.8578) 4.183374(0.8754) 0.1568(0.1688)
 [AI] 0.768762(0.8476) 4.191671(0.8728) 0.1550(0.1671)
 [AI] 0.765820(0.8443) 4.194291(0.8719) 0.1544(0.1665)
 [AI] 0.764881(0.8433) 4.195126(0.8716) 0.1542(0.1663)
 [AI] 0.764581(0.8430) 4.195393(0.8715) 0.1542(0.1662)
 [AI] 0.764485(0.8429) 4.195478(0.8715) 0.1541(0.1662)
 [AI] 0.764454(0.8428) 4.195506(0.8715) 0.1541(0.1662)
 [AI] 0.764444(0.8428) 4.195515(0.8715) 0.1541(0.1662)
 [AI] 0.764441(0.8428) 4.195517(0.8715) 0.1541(0.1662)
 [Convergence] YES
 Done within 2s
 Estimating random effect...Done within 0s
 Estimated beta: 12.4 0.4291
 Estimated Vg and Ve: 0.7644 4.196
 HIBLUP IS DONE WITHIN: 11s
 HIBLUP ACCOMPLISHED SUCCESSFULLY!
```

4.6.2 Additive and Dominant effect based model

```
gebv.ad <- hiblup(pheno = pheno[, c(1, 5)], geno = geno, map = map, geno.id = geno.id,
    mode = "AD")


#-------------------------Welcome to HIBLUP--------------------------#
#  He-aI BLUP   _     _ _____ ____  _     _    _ _____               #
#              | |   | |_   _|  _ \| |   | |  | | |  __ \             #
#              | |__| | | | | |_) | |   | |  | | |__) |              #
#              |  __  | | | |  _ <| |   | |  | |  ___/               #
#              | |  | |_| |_| |_) | |___| |__| | |                   #
#              |_|  |_|_____|____/|______\____/|_|    Version: 1.3.1 #
#      Developed by Lilin Yin#, HaoHao Zhang#, and Xiaolei Liu       #
#--------------------------------------------------------------------#
 GBLUP model is selected based on the provided data!
 Analyzed trait: t2
 Number of fixed effects: 1 (intercept included)
 Number of random effects: 0 + 2
 Number of individuals with phenotypic observations: 800
```

```
Number of SNPs in genotype: 48353
Deriving GA and GD matrix from genotype...Done within 19s
Number of genotyped individuals: 573
Number of genotyped individuals with phenotypic observations: 175
Number of genotyped individuals without phenotypic observations: 398
Number of total predicted individuals: 573
Realign index of y...Done!
Realign index of X matrix...Done!
HE Prior derived: A:1.061 D:0 e:5.923; Done within 0s
HE adopted: TRUE
Variance components estimation:
Dimension of V^(-1): 175 * 175
[Iter]  Var_K1(SE)       Var_K2(SE)       Var_e(SE)       h2_K1(SE)       h2_K2(SE)
[AI] 1.061103(2.0660) 0.000000(4.3700) 5.923261(3.0981) 0.1519(0.2947) 0.0000(0.6257)
[AI] 2.733217(2.0660) 0.000000(4.3700) 7.243067(3.0981) 0.2740(0.2064) 0.0000(0.4380)
[AI] 2.226256(3.8396) 0.000000(7.3793) 9.142943(5.2895) 0.1958(0.3312) 0.0000(0.6491)
[AI] 4.048457(4.4426) 0.000000(9.0780) 8.059124(6.4675) 0.3344(0.3624) 0.0000(0.7498)
[AI] 1.971854(5.2920) 0.000000(9.7025) 9.484035(6.9746) 0.1721(0.4512) 0.0000(0.8469)
[AI] 4.656163(4.4130) 0.000000(9.1870) 7.515872(6.5288) 0.3825(0.3603) 0.0000(0.7548)
[AI] 1.454268(5.4400) 0.000000(9.6089) 9.643977(6.9159) 0.1310(0.4796) 0.0000(0.8658)
[AI] 5.326424(4.0620) 0.000000(8.7343) 6.740183(6.1751) 0.4414(0.3394) 0.0000(0.7238)
[AI] 0.908113(5.4715) 0.000000(9.2373) 9.631263(6.6513) 0.0862(0.5104) 0.0000(0.8765)
[AI] 5.574607(3.5901) 0.000000(7.9999) 6.098029(5.6164) 0.4776(0.3160) 0.0000(0.6854)
[AI] 0.806720(5.2520) 0.000000(8.6256) 9.301821(6.2091) 0.0798(0.5107) 0.0000(0.8533)
[AI] 5.261499(3.3476) 0.000000(7.4978) 6.246724(5.2580) 0.4572(0.2989) 0.0000(0.6515)
[AI] 1.055185(5.1171) 0.000000(8.5356) 9.193947(6.1456) 0.1030(0.4889) 0.0000(0.8328)
[AI] 5.126892(3.5064) 0.000000(7.7092) 6.601281(5.4275) 0.4371(0.3042) 0.0000(0.6573)
[AI] 1.112367(5.2368) 0.000000(8.8699) 9.375287(6.3868) 0.1061(0.4891) 0.0000(0.8457)
[AI] 5.275911(3.6413) 0.000000(7.9860) 6.536378(5.6251) 0.4466(0.3136) 0.0000(0.6761)
[AI] 0.989208(5.3069) 0.000000(8.9237) 9.436838(6.4254) 0.0949(0.4994) 0.0000(0.8559)
[AI] 5.371163(3.5667) 0.000000(7.8924) 6.348089(5.5492) 0.4583(0.3111) 0.0000(0.6735)
[AI] 0.937490(5.2600) 0.000000(8.7664) 9.358432(6.3117) 0.0911(0.5014) 0.0000(0.8514)
[AI] 5.306592(3.4855) 0.000000(7.7363) 6.349417(5.4359) 0.4553(0.3060) 0.0000(0.6637)
[Convergence] NO(More iteration number is needed!)
Done within 3s
Estimating random effect...Done within 0s
Estimated beta: 13.24
Estimated additive genetic variacne: 5.307
Estimated Dominance genetic variacne: 0
Estimated Ve: 6.349
HIBLUP IS DONE WITHIN: 23s
HIBLUP ACCOMPLISHED SUCCESSFULLY!
```

4.6.3 With user-provided variance components

If the variance components are known and provided by the users, the methods for solving mixed model equation can be controlled by the `vc.method` parameter. The options are "CG", "JOR", "SOLVE" and "SOR".

```
# Solve mixed model equation directly
gebv.a <- hiblup(pheno = pheno[, c(1, 5)], vc.method = "SOLVE", CV = X,
    R = R, vc = start2, geno = geno, map = map, geno.id = geno.id)


#-------------------------Welcome to HIBLUP--------------------------#
#  He-aI BLUP    _     _ _____ ____  _      _    _ _____               #
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#               | |__| | | | | |_) | |    | |  | | |__) |             #
#               |  __  | | | |  _ <| |    | |  | |  ___/              #
#               | |  | |_| |_| |_) | |____| |__| | |                   #
#               |_|  |_|_____|____/|______\____/|_|    Version: 1.3.1 #
#      Developed by Lilin Yin#, HaoHao Zhang#, and Xiaolei Liu       #
```

```
#-----------------------------------------------------------------------#
 GBLUP model is selected based on the provided data!
 Analyzed trait: t2
 Number of fixed effects: 2 (intercept included)
 Number of random effects: 1 + 1
 Number of individuals with phenotypic observations: 800
 Number of SNPs in genotype: 48353
 Deriving GA matrix from genotype...Done within 9s
 Number of genotyped individuals: 573
 Number of genotyped individuals with phenotypic observations: 175
 Number of genotyped individuals without phenotypic observations: 398
 Number of total predicted individuals: 573
 Realign index of y...Done!
 Realign index of X matrix...Done!
 Realign index of R matrix...Done!
 No need for Variance components estimation
 Provided variance components:
 Var_R1  Var_K1  Var_e
 1.27434691100927  0.0399477490264859  3.61034937032618
 Done within 0s
 Estimating random effect...Done within 0s
 Estimated beta: 4.38 4.344
 Estimated Vg and Ve: 0.03995 3.61
 HIBLUP IS DONE WITHIN: 9s
 HIBLUP ACCOMPLISHED SUCCESSFULLY!


# Solve mixed model equation using CG method
gebv.a <- hiblup(pheno = pheno[, c(1, 5)], vc.method = "CG", CV = X, R = R,
    vc = start2, geno = geno, map = map, geno.id = geno.id)

#-------------------------Welcome to HIBLUP-------------------------#
#  He-aI BLUP   _     _ _____ ____  _      _    _ _____              #
#              | |   | |_   _|  _ \| |    | |  | |  __ \             #
#              | |__| | | | | |_) | |    | |  | | |__) |            #
#              |  __  | | | |  _ <| |    | |  | |  ___/             #
#              | |  | |_| |_| |_) | |___| |__| | |                  #
#              |_|  |_|_____|____/|______\____/|_|    Version: 1.3.1 #
#      Developed by Lilin Yin#, HaoHao Zhang#, and Xiaolei Liu       #
#-----------------------------------------------------------------------#
 GBLUP model is selected based on the provided data!
 Analyzed trait: t2
 Number of fixed effects: 2 (intercept included)
 Number of random effects: 1 + 1
 Number of individuals with phenotypic observations: 800
 Number of SNPs in genotype: 48353
 Deriving GA matrix from genotype...Done within 9s
 Number of genotyped individuals: 573
 Number of genotyped individuals with phenotypic observations: 175
 Number of genotyped individuals without phenotypic observations: 398
 Number of total predicted individuals: 573
 Realign index of y...Done!
 Realign index of X matrix...Done!
 Realign index of R matrix...Done!
 No need for Variance components estimation
 Provided variance components:
 Var_R1  Var_K1  Var_e
 1.27434691100927  0.0399477490264859  3.61034937032618
 Iterative solve using method CG
 Iter No.1 with minimum diff = 0.0507406
 Iter No.2 with minimum diff = 0.6778303
 Iter No.3 with minimum diff = 0.9132001
 Iter No.4 with minimum diff = 0.6176299
 Iter No.5 with minimum diff = 0.9175542
```

```
 Iter No.6 with minimum diff = 0.4937566
 Iter No.7 with minimum diff = 0.1807650
 Iter No.8 with minimum diff = 0.7547505
 Iter No.9 with minimum diff = 0.0722158
 Iter No.10 with minimum diff = 0.0197789
 Iter No.11 with minimum diff = 0.0057512
 Iter No.12 with minimum diff = 0.0023442
 Iter No.13 with minimum diff = 0.0010592
 Iter No.14 with minimum diff = 0.0005588
 Iter No.15 with minimum diff = 0.0002038
 Iter No.16 with minimum diff = 0.0002174
 Iter No.17 with minimum diff = 0.0000370
 Iter No.18 with minimum diff = 0.0000168
 Iter No.19 with minimum diff = 0.0000077
 Iter No.20 with minimum diff = 0.0000021
 Done within 0s
 Estimating random effect...Done within 0s
 Estimated beta: 4.38 4.344
 Estimated Vg and Ve: 0.03995 3.61
 HIBLUP IS DONE WITHIN: 9s
 HIBLUP ACCOMPLISHED SUCCESSFULLY!
```

4.6.4 Estimate the marker effects

HIBLUP will output the marker effects if `snp.solution` is `TRUE`. it only works with GBLUP model or SSBLUP model.

```
gebv.a.ai <- hiblup(pheno = pheno[, c(1, 5)], geno = geno, map = map, geno.id = geno.id,
    CV = X, vc.method = c("AI"), mode = "A", snp.solution = TRUE)


#-------------------------Welcome to HIBLUP--------------------------#
#  He-aI BLUP   _     _ _____ ____  _      _    _ _____               #
#              | |   | |_   _|  _ \| |    | |  | | __ \              #
#              | |__| | | | | |_) | |    | |  | | |__) |             #
#              |  __  | | | |  _ <| |    | |  | |  ___/              #
#              | |  | |_| |_| |_) | |___| |__| | |                   #
#              |_|  |_|_____|____/|______\____/|_|    Version: 1.3.1 #
#      Developed by Lilin Yin#, HaoHao Zhang#, and Xiaolei Liu       #
#--------------------------------------------------------------------#
 GBLUP model is selected based on the provided data!
 Analyzed trait: t2
 Number of fixed effects: 2 (intercept included)
 Number of random effects: 0 + 1
 Number of individuals with phenotypic observations: 800
 Number of SNPs in genotype: 48353
 Deriving GA matrix from genotype...Done within 9s
 Number of genotyped individuals: 573
 Number of genotyped individuals with phenotypic observations: 175
 Number of genotyped individuals without phenotypic observations: 398
 Number of total predicted individuals: 573
 Realign index of y...Done!
 Realign index of X matrix...Done!
 Variance components estimation:
 Dimension of V^(-1): 175 * 175
 [Iter]  Var_K1(SE)       Var_e(SE)       h2_K1(SE)
 [AI] 1.265440(1.1820) 3.659904(0.8541) 0.2569(0.2182)
 [AI] 0.908219(0.9788) 4.057931(0.8841) 0.1829(0.1889)
 [AI] 0.807857(0.8896) 4.156277(0.8818) 0.1627(0.1743)
 [AI] 0.778040(0.8578) 4.183374(0.8754) 0.1568(0.1688)
 [AI] 0.768762(0.8476) 4.191671(0.8728) 0.1550(0.1671)
 [AI] 0.765820(0.8443) 4.194291(0.8719) 0.1544(0.1665)
```

```
 [AI] 0.764881(0.8433) 4.195126(0.8716) 0.1542(0.1663)
 [AI] 0.764581(0.8430) 4.195393(0.8715) 0.1542(0.1662)
 [AI] 0.764485(0.8429) 4.195478(0.8715) 0.1541(0.1662)
 [AI] 0.764454(0.8428) 4.195506(0.8715) 0.1541(0.1662)
 [AI] 0.764444(0.8428) 4.195515(0.8715) 0.1541(0.1662)
 [AI] 0.764441(0.8428) 4.195517(0.8715) 0.1541(0.1662)
 [Convergence] YES
 Done within 2s
 Estimating random effect...Done within 0s
 Estimating SNP effect...Done within 0s
 Estimated beta: 12.4 0.4291
 Estimated Vg and Ve: 0.7644 4.196
 HIBLUP IS DONE WITHIN: 11s
 HIBLUP ACCOMPLISHED SUCCESSFULLY!
```

4.6.5 Multiple traits model

HIBLUP supports the estimation of individual genetic values for multiple correlated traits. Users can specify the position of the trait1 and trait2 in pheno by setting the `bivar.pos` parameter, for example:

```
gebv <- hiblup(pheno = pheno, bivar.pos = c(4, 5), bivar.CV = list(X, X),
    R = R, map = map, geno = geno, geno.id = geno.id)


#-------------------------Welcome to HIBLUP--------------------------#
#  He-aI BLUP   _    _ _____ ____  _     _    _ _____                #
#              | |  | |_   _|  _ \| |   | |  | |  __ \               #
#              | |__| | | | | |_) | |   | |  | | |__) |              #
#              |  __  | | | |  _ <| |   | |  | |  ___/               #
#              | |  | |_| |_| |_) | |___| |__| | |                   #
#              |_|  |_|_____|____/|______\____/|_|    Version: 1.3.1 #
#      Developed by Lilin Yin#, HaoHao Zhang#, and Xiaolei Liu       #
#--------------------------------------------------------------------#
 Bivariate GREML analysis started...
 GBLUP model is selected based on the provided data!
 Analyzed trait: t1 & t2
 Number of fixed effects for trait1: 3(intercept included)
 Number of fixed effects for trait2: 3(intercept included)
 No trait-specific random effects.
 Number of random effects for correlation: 1 + 1
 Number of phenotypic observations for trait1: 800
 Number of phenotypic observations for trait2: 800
 Number of individuals for analysis: 800
 Number of SNPs in genotype: 48353
 Deriving GA matrix from genotype...Done within 9s
 Number of genotyped individuals: 573
 Number of genotyped individuals with phenotypic observations: 175
 Number of genotyped individuals without phenotypic observations: 398
 Number of total predicted individuals: 573
 Realign index of y...Done!
 Realign index of X matrix...Done!
 Realign index of R matrix...Done!
 Variance components estimation:
 Number of components: 9
 HE prior derived... Done within 0s
 Updated prior values: 1.004781 0.097162 4.532133 1.187127 0.138985 3.287236 1.421399 0.198810 3.240213
 Dimension of V^(-1): 350 * 350
 Bivariate GREML analysis:  Vgtr1_R1 Vgtr1_R2 Vetr1 CoVgtr1tr2_R1 CoVgtr1tr2_R2 CoVetr1tr2 Vgtr2_R1 Vgtr2_R2 Vetr
 [AI] Iter 1 of Max Iter 20: 0.933060 0.043871 4.633946 1.112646 0.071726 3.447067 1.328258 0.117266 3.404325
 [AI] Iter 2 of Max Iter 20: 0.900450 0.023564 4.693997 1.077657 0.042643 3.530650 1.289737 0.077170 3.489641
 [AI] Iter 3 of Max Iter 20: 0.892957 0.018590 4.711101 1.069634 0.035172 3.552312 1.281269 0.066543 3.511679
```

```
 [AI] Iter 4 of Max Iter 20: 0.887491 0.015090 4.724405 1.063814 0.029568 3.568722 1.275170 0.057939 3.528383
 [AI] Iter 5 of Max Iter 20: 0.883497 0.012569 4.734765 1.059599 0.025300 3.581149 1.270801 0.050924 3.541075
 [AI] Iter 6 of Max Iter 20: 0.882037 0.011584 4.738804 1.058076 0.023605 3.585855 1.269248 0.048097 3.545913
 [AI] Iter 7 of Max Iter 20: 0.880775 0.010737 4.742399 1.056766 0.022103 3.589991 1.267923 0.045503 3.550179
 [AI] Iter 8 of Max Iter 20: 0.879683 0.010001 4.745601 1.055641 0.020766 3.593626 1.266796 0.043120 3.553946
 [AI] Iter 9 of Max Iter 20: 0.878738 0.009355 4.748454 1.054676 0.019568 3.596822 1.265839 0.040932 3.557274
 [AI] Iter 10 of Max Iter 20: 0.877921 0.008784 4.750999 1.053848 0.018490 3.599632 1.265029 0.038920 3.560218
 [AI] Iter 11 of Max Iter 20: 0.877215 0.008275 4.753270 1.053140 0.017514 3.602104 1.264345 0.037070 3.562825
 [AI] Iter 12 of Max Iter 20: 0.876605 0.007819 4.755299 1.052534 0.016629 3.604279 1.263771 0.035366 3.565136
 [AI] Iter 13 of Max Iter 20: 0.876078 0.007407 4.757112 1.052018 0.015822 3.606193 1.263291 0.033796 3.567186
 [AI] Iter 14 of Max Iter 20: 0.875624 0.007035 4.758733 1.051578 0.015085 3.607878 1.262890 0.032345 3.569007
 [AI] Iter 15 of Max Iter 20: 0.875428 0.006861 4.759459 1.051392 0.014743 3.608620 1.262725 0.031680 3.569817
 [AI] Iter 16 of Max Iter 20: 0.875245 0.006696 4.760147 1.051219 0.014416 3.609318 1.262574 0.031038 3.570582
 [AI] Iter 17 of Max Iter 20: 0.875076 0.006539 4.760799 1.051060 0.014103 3.609974 1.262436 0.030419 3.571305
 [AI] Iter 18 of Max Iter 20: 0.874918 0.006389 4.761417 1.050913 0.013804 3.610592 1.262311 0.029822 3.571989
 [AI] Iter 19 of Max Iter 20: 0.874771 0.006246 4.762003 1.050778 0.013516 3.611173 1.262198 0.029247 3.572636
 [AI] Iter 20 of Max Iter 20: 0.874635 0.006109 4.762559 1.050653 0.013240 3.611719 1.262095 0.028692 3.573247
 [Convergence] NO(More iteration number is needed!)
 Done within 7s
 Estimating random effect...Done within 0s
 Estimated beta for trait1: 162.7 0.2151
 Estimated beta for trait2: 13.37 -0.04649
 Estimated (CO)Variance(upper.tri+diag) and correlation(lower.tri) at R1:
        trait1  trait2
 trait1  0.8746   1.051
 trait2  1.0000   1.262
 Estimated (CO)Variance(upper.tri+diag) and correlation(lower.tri) at Additive:
         trait1  trait2
 trait1 0.006109 0.01324
 trait2 1.000000 0.02869
 Estimated (CO)Variance(upper.tri+diag) and correlation(lower.tri) at Residual:
        trait1  trait2
 trait1  4.7626   3.612
 trait2  0.8755   3.573
 HIBLUP IS DONE WITHIN: 17s
 HIBLUP ACCOMPLISHED SUCCESSFULLY!


# if there are others random effects for traits, please assign to
# 'bivar.R'.  if there is a trait with no fixed or random effects,
# please set NULL at corresponding postion in 'bivar.X' or 'bivar.R'.
```

4.7 Single step BLUP(SSBLUP)

4.7.1 Additive effect based model

```
gebv.a.ai <- hiblup(pheno = pheno[, c(1, 5)], geno = geno, map = map, geno.id = geno.id,
    pedigree = pedigree, vc.method = c("AI"), mode = "A")


#-------------------------Welcome to HIBLUP-------------------------#
#  He-aI BLUP    _     _ _____ ____  _     _    _ _____              #
#               | |   | |_   _|  _ \| |   | |  | |  __ \             #
#               | |__| | | | | |_) | |   | |  | | |__) |            #
#               |  __  | | | |  _ <| |   | |  | |  ___/             #
#               | |  | |_| |_| |_) | |___| |__| | |                  #
#               |_|  |_|_____|____/|______\____/|_|    Version: 1.3.1 #
#      Developed by Lilin Yin#, HaoHao Zhang#, and Xiaolei Liu       #
#-------------------------------------------------------------------#
 SSBLUP model is selected based on the provided data!
 Analyzed trait: t2
```

```
Number of fixed effects: 1 (intercept included)
Number of random effects: 0 + 1
Number of individuals with phenotypic observations: 800
Number of SNPs in genotype: 48353
Deriving GA matrix from genotype...Done within 9s
Number of genotyped individuals: 573
Number of genotyped individuals with phenotypic observations: 175
Number of genotyped individuals without phenotypic observations: 398
Deriving A matrix from pedigree...Done within 0s
Number of total predicted individuals: 2524
Realign index of y...Done!
Realign index of X matrix...Done!
Constructing H matrix...
Extracting A11 matrix...Done!
Mean of diagonal and Off-diagonal of PA: 1.001 0.0285
Mean of diagonal and Off-diagonal of GA: 0.9886 -0.0017
Adjusting GA matrix: GA* = 0.98 * GA + 0.03
Weighting of A11 and GA matrix: 0.05
Calculating the inverse of A11 matrix...Done within 0s
Constructing HA matrix...Done within 6s
Variance components estimation:
Dimension of V^(-1): 800 * 800
[Iter]  Var_K1(SE)       Var_e(SE)       h2_K1(SE)
[AI] 1.219009(0.3209) 1.648960(0.2440) 0.4250(0.0976)
[AI] 1.267629(0.3044) 1.619052(0.2463) 0.4391(0.0933)
[AI] 1.258991(0.3125) 1.625889(0.2497) 0.4364(0.0955)
[AI] 1.260852(0.3112) 1.624455(0.2493) 0.4370(0.0952)
[AI] 1.260460(0.3115) 1.624759(0.2494) 0.4369(0.0952)
[AI] 1.260543(0.3114) 1.624695(0.2494) 0.4369(0.0952)
[AI] 1.260525(0.3114) 1.624708(0.2494) 0.4369(0.0952)
[AI] 1.260529(0.3114) 1.624705(0.2494) 0.4369(0.0952)
[AI] 1.260528(0.3114) 1.624706(0.2494) 0.4369(0.0952)
[Convergence] YES
Done within 7s
Estimating random effect...Done within 0s
Estimated beta: 13.09
Estimated Vg and Ve: 1.261 1.625
HIBLUP IS DONE WITHIN: 23s
HIBLUP ACCOMPLISHED SUCCESSFULLY!
```

4.7.2 Additive and Dominant effect based model

```
gebv.ad <- hiblup(pheno = pheno[, c(1, 5)], geno = geno, map = map, geno.id = geno.id,
    pedigree = pedigree, mode = "AD")


#-------------------------Welcome to HIBLUP--------------------------#
#  He-aI BLUP   _     _ _____ ____  _     _    _ _____               #
#              | |   | |_   _|  _ \| |   | |  | |  __ \              #
#              | |__| | | | | |_) | |   | |  | | |__) |             #
#              |  __  | | | |  _ <| |   | |  | |  ___/              #
#              | |  | |_| |_| |_) | |___| |__| | |                   #
#              |_|  |_|_____|____/|______\____/|_|    Version: 1.3.1 #
#      Developed by Lilin Yin#, HaoHao Zhang#, and Xiaolei Liu       #
#--------------------------------------------------------------------#
 SSBLUP model is selected based on the provided data!
 Analyzed trait: t2
 Number of fixed effects: 1 (intercept included)
 Number of random effects: 0 + 2
 Number of individuals with phenotypic observations: 800
 Number of SNPs in genotype: 48353
```

```
Deriving GA and GD matrix from genotype...Done within 19s
Number of genotyped individuals: 573
Number of genotyped individuals with phenotypic observations: 175
Number of genotyped individuals without phenotypic observations: 398
Deriving A and D matrix from pedigree...Done within 0s
Number of total predicted individuals: 2524
Realign index of y...Done!
Realign index of X matrix...Done!
Constructing H matrix...
Extracting A11 matrix...Done!
Mean of diagonal and Off-diagonal of PA: 1.001 0.0285
Mean of diagonal and Off-diagonal of GA: 0.9886 -0.0017
Adjusting GA matrix: GA* = 0.98 * GA + 0.03
Weighting of A11 and GA matrix: 0.05
Calculating the inverse of A11 matrix...Done within 0s
Constructing HA matrix...Done within 6s
Constructing H matrix...
Extracting D11 matrix...Done!
Mean of diagonal and Off-diagonal of PD: 1 0.001
Mean of diagonal and Off-diagonal of GD: 0.5374 -0.0009
Adjusting GD matrix: GD* = 1.86 * GD + 0
Weighting of D11 and GD matrix: 0.05
Calculating the inverse of D11 matrix...Done within 0s
Constructing HD matrix...Done within 6s
HE Prior derived: A:1.407 D:0 e:2.843; Done within 2s
HE adopted: TRUE
Variance components estimation:
Dimension of V^(-1): 800 * 800
[Iter]  Var_K1(SE)       Var_K2(SE)       Var_e(SE)       h2_K1(SE)       h2_K2(SE)
[AI] 1.406641(0.5809) 0.000000(1.2213) 2.842876(0.9848) 0.3310(0.1305) 0.0000(0.2874)
[AI] 2.797209(0.5809) 0.000000(1.2213) 4.356817(0.9848) 0.3910(0.0771) 0.0000(0.1707)
[AI] 3.684319(1.3773) 0.000000(2.6534) 7.005685(2.1093) 0.3447(0.1214) 0.0000(0.2482)
[AI] 6.367286(2.3641) 0.000000(4.8695) 6.673149(3.9137) 0.4883(0.1700) 0.0000(0.3734)
[AI] 0.615793(3.7758) 0.000000(6.3993) 12.262318(4.9764) 0.0478(0.2900) 0.0000(0.4969)
[AI] 4.431285(1.5587) 0.000000(5.6864) 2.544621(5.0127) 0.6352(0.2694) 0.0000(0.8151)
[AI] 1.268275(1.6555) 0.000000(2.3722) 6.364887(1.7877) 0.1662(0.2072) 0.0000(0.3108)
[AI] 6.688385(1.0262) 0.000000(2.8660) 1.117263(2.4156) 0.8569(0.1430) 0.0000(0.3672)
[AI] 2.316112(2.1005) 0.000000(2.4470) 4.313660(1.7649) 0.3494(0.2817) 0.0000(0.3691)
[AI] 4.125301(1.1623) 0.000000(2.3776) 5.945416(1.9087) 0.4096(0.1089) 0.0000(0.2361)
[AI] 3.226544(2.3536) 0.000000(4.4191) 9.720441(3.4979) 0.2492(0.1734) 0.0000(0.3413)
[AI] 8.244656(2.6986) 0.000000(6.4719) 3.441556(5.3278) 0.7055(0.2268) 0.0000(0.5538)
[AI] 0.786994(3.7188) 0.000000(4.9631) 8.968052(3.6870) 0.0807(0.3723) 0.0000(0.5088)
[AI] 5.345874(1.1632) 0.000000(3.9074) 0.321428(3.3934) 0.9433(0.2628) 0.0000(0.6895)
[AI] 0.745494(1.2878) 0.000000(1.4016) 3.894539(0.9946) 0.1607(0.2622) 0.0000(0.3021)
[AI] 3.058624(0.4800) 0.000000(1.3551) 3.398126(1.1441) 0.4737(0.0757) 0.0000(0.2099)
[AI] 2.183498(1.2967) 0.000000(2.2381) 7.544157(1.7461) 0.2245(0.1269) 0.0000(0.2301)
[AI] 9.199674(1.6762) 0.000000(4.1972) 0.706829(3.4783) 0.9286(0.1745) 0.0000(0.4237)
[AI] 0.598678(2.9857) 0.000000(3.2856) 6.024832(2.3379) 0.0904(0.4368) 0.0000(0.4961)
[AI] 4.998289(0.6722) 0.000000(2.2070) 0.347346(1.9092) 0.9350(0.1574) 0.0000(0.4129)
[Convergence] NO(More iteration number is needed!)
Done within 16s
Estimating random effect...Done within 0s
Estimated beta: 13.02
Estimated additive genetic variacne: 4.998
Estimated Dominance genetic variacne: 0
Estimated Ve: 0.3473
HIBLUP IS DONE WITHIN: 51s
HIBLUP ACCOMPLISHED SUCCESSFULLY!
```

4.7.3 With user-provided variance components

If the variance components are known and provided by the users, the methods for solving mixed model equation can be controlled by the `vc.method` parameter. The options are "CG", "JOR", "SOLVE" and "SOR".

```
# Solve mixed model equation directly
gebv.a <- hiblup(pheno = pheno[, c(1, 5)], vc.method = "SOLVE", CV = X,
    R = R, vc = c(57.893, 0.0686, 0.0008), geno = geno, map = map, geno.id = geno.id,
    pedigree = pedigree)


#-------------------------Welcome to HIBLUP-------------------------#
#  He-aI BLUP   _    _ _____ ____  _     _    _ _____               #
#              | |  | |_   _|  _ \| |   | |  | |  __ \              #
#              | |__| | | | | |_) | |   | |  | | |__) |             #
#              |  __  | | | |  _ <| |   | |  | |  ___/              #
#              | |  | |_| |_| |_) | |___| |__| | |                  #
#              |_|  |_|_____|____/|______\____/|_|    Version: 1.3.1 #
#      Developed by Lilin Yin#, HaoHao Zhang#, and Xiaolei Liu       #
#-------------------------------------------------------------------#
 SSBLUP model is selected based on the provided data!
 Analyzed trait: t2
 Number of fixed effects: 2 (intercept included)
 Number of random effects: 1 + 1
 Number of individuals with phenotypic observations: 800
 Number of SNPs in genotype: 48353
 Deriving GA matrix from genotype...Done within 9s
 Number of genotyped individuals: 573
 Number of genotyped individuals with phenotypic observations: 175
 Number of genotyped individuals without phenotypic observations: 398
 Deriving A matrix from pedigree...Done within 0s
 Number of total predicted individuals: 2524
 Realign index of y...Done!
 Realign index of X matrix...Done!
 Realign index of R matrix...Done!
 Constructing H matrix...
 Extracting A11 matrix...Done!
 Mean of diagonal and Off-diagonal of PA: 1.001 0.0285
 Mean of diagonal and Off-diagonal of GA: 0.9886 -0.0017
 Adjusting GA matrix: GA* = 0.98 * GA + 0.03
 Weighting of A11 and GA matrix: 0.05
 Calculating the inverse of A11 matrix...Done within 0s
 Constructing HA matrix...Done within 6s
 No need for Variance components estimation
 Provided variance components:
 Var_R1  Var_K1  Var_e
 57.893  0.0686  0.0008
 Done within 0s
 Estimating random effect...Done within 0s
 Estimated beta: 4.824 0.8039
 Estimated Vg and Ve: 0.0686 0.0008
 HIBLUP IS DONE WITHIN: 16s
 HIBLUP ACCOMPLISHED SUCCESSFULLY!



# Solve mixed model equation using CG method
gebv.a <- hiblup(pheno = pheno[, c(1, 5)], vc.method = "CG", CV = X, R = R,
    vc = c(57.893, 0.0686, 0.0008), geno = geno, map = map, geno.id = geno.id,
    pedigree = pedigree)


#-------------------------Welcome to HIBLUP-------------------------#
#  He-aI BLUP   _    _ _____ ____  _     _    _ _____               #
#              | |  | |_   _|  _ \| |   | |  | |  __ \              #
#              | |__| | | | | |_) | |   | |  | | |__) |             #
```

```
#              |  __  | | | |  _ <| |   | |  | |  ___/              #
#              | |  | |_| |_| |_) | |___| |__| | |                   #
#              |_|  |_|_____|____/|______\____/|_|    Version: 1.3.1 #
#      Developed by Lilin Yin#, HaoHao Zhang#, and Xiaolei Liu       #
#--------------------------------------------------------------------#
 SSBLUP model is selected based on the provided data!
 Analyzed trait: t2
 Number of fixed effects: 2 (intercept included)
 Number of random effects: 1 + 1
 Number of individuals with phenotypic observations: 800
 Number of SNPs in genotype: 48353
 Deriving GA matrix from genotype...Done within 9s
 Number of genotyped individuals: 573
 Number of genotyped individuals with phenotypic observations: 175
 Number of genotyped individuals without phenotypic observations: 398
 Deriving A matrix from pedigree...Done within 0s
 Number of total predicted individuals: 2524
 Realign index of y...Done!
 Realign index of X matrix...Done!
 Realign index of R matrix...Done!
 Constructing H matrix...
 Extracting A11 matrix...Done!
 Mean of diagonal and Off-diagonal of PA: 1.001 0.0285
 Mean of diagonal and Off-diagonal of GA: 0.9886 -0.0017
 Adjusting GA matrix: GA* = 0.98 * GA + 0.03
 Weighting of A11 and GA matrix: 0.05
 Calculating the inverse of A11 matrix...Done within 0s
 Constructing HA matrix...Done within 6s
 No need for Variance components estimation
 Provided variance components:
 Var_R1  Var_K1  Var_e
 57.893  0.0686  0.0008
 Iterative solve using method CG
 Iter No.1 with minimum diff = 0.6904610
 Iter No.2 with minimum diff = 0.8615704
 Iter No.3 with minimum diff = 0.1224252
 ...
 Iter No.344 with minimum diff = 0.0000022
 Done within 0s
 Estimating random effect...Done within 0s
 Estimated beta: 4.824 0.8039
 Estimated Vg and Ve: 0.0686 0.0008
 HIBLUP IS DONE WITHIN: 16s
 HIBLUP ACCOMPLISHED SUCCESSFULLY!
```

4.7.4 Estimate the marker effects

```
gebv.a.ai <- hiblup(pheno = pheno[, c(1, 5)], geno = geno, map = map, geno.id = geno.id,
    pedigree = pedigree, vc.method = c("AI"), mode = "A", snp.solution = TRUE)


#-------------------------Welcome to HIBLUP--------------------------#
#  He-aI BLUP   _     _ _____ ____  _     _    _ _____               #
#              | |   | |_   _|  _ \| |   | |  | | |  __ \             #
#              | |__| | | | | |_) | |   | |  | | | |__) |            #
#              |  __  | | | |  _ <| |   | |  | |  ___/              #
#              | |  | |_| |_| |_) | |___| |__| | |                   #
#              |_|  |_|_____|____/|______\____/|_|    Version: 1.3.1 #
#      Developed by Lilin Yin#, HaoHao Zhang#, and Xiaolei Liu       #
#--------------------------------------------------------------------#
 SSBLUP model is selected based on the provided data!
```

```
Analyzed trait: t2
Number of fixed effects: 1 (intercept included)
Number of random effects: 0 + 1
Number of individuals with phenotypic observations: 800
Number of SNPs in genotype: 48353
Deriving GA matrix from genotype...Done within 9s
Number of genotyped individuals: 573
Number of genotyped individuals with phenotypic observations: 175
Number of genotyped individuals without phenotypic observations: 398
Deriving A matrix from pedigree...Done within 0s
Number of total predicted individuals: 2524
Realign index of y...Done!
Realign index of X matrix...Done!
Constructing H matrix...
Extracting A11 matrix...Done!
Mean of diagonal and Off-diagonal of PA: 1.001 0.0285
Mean of diagonal and Off-diagonal of GA: 0.9886 -0.0017
Adjusting GA matrix: GA* = 0.98 * GA + 0.03
Weighting of A11 and GA matrix: 0.05
Calculating the inverse of A11 matrix...Done within 0s
Constructing HA matrix...Done within 6s
Variance components estimation:
Dimension of V^(-1): 800 * 800
[Iter]  Var_K1(SE)       Var_e(SE)       h2_K1(SE)
[AI] 1.219009(0.3209) 1.648960(0.2440) 0.4250(0.0976)
[AI] 1.267629(0.3044) 1.619052(0.2463) 0.4391(0.0933)
[AI] 1.258991(0.3125) 1.625889(0.2497) 0.4364(0.0955)
[AI] 1.260852(0.3112) 1.624455(0.2493) 0.4370(0.0952)
[AI] 1.260460(0.3115) 1.624759(0.2494) 0.4369(0.0952)
[AI] 1.260543(0.3114) 1.624695(0.2494) 0.4369(0.0952)
[AI] 1.260525(0.3114) 1.624708(0.2494) 0.4369(0.0952)
[AI] 1.260529(0.3114) 1.624705(0.2494) 0.4369(0.0952)
[AI] 1.260528(0.3114) 1.624706(0.2494) 0.4369(0.0952)
[Convergence] YES
Done within 7s
Estimating random effect...Done within 0s
Estimating SNP effect...Done within 0s
Estimated beta: 13.09
Estimated Vg and Ve: 1.261 1.625
HIBLUP IS DONE WITHIN: 23s
HIBLUP ACCOMPLISHED SUCCESSFULLY!
```

4.7.5 Multiple traits model

HIBLUP also supports the estimation of individual genetic values for multiple correlated traits. Users can specify the position of the trait1 and trait2 in pheno by setting the `bivar.pos` parameter, for example:

```
gebv <- hiblup(pheno = pheno, bivar.pos = c(4, 5), bivar.CV = list(X1 = X,
    X2 = X), R = R, pedigree = pedigree, map = map, geno = geno, geno.id = geno.id)


#-------------------------Welcome to HIBLUP--------------------------#
#  He-aI BLUP   _     _ _____ ____  _     _    _ _____               #
#              | |   | |_   _|  _ \| |   | |  | |  __ \              #
#              | |__| | | | | |_) | |   | |  | | |__) |             #
#              |  __  | | | |  _ <| |   | |  | |  ___/              #
#              | |  | |_| |_| |_) | |___| |__| | |                  #
#              |_|  |_|_____|____/|______\____/|_|    Version: 1.3.1 #
#      Developed by Lilin Yin#, HaoHao Zhang#, and Xiaolei Liu       #
#--------------------------------------------------------------------#
 Bivariate GREML analysis started...
```

```
SSBLUP model is selected based on the provided data!
Analyzed trait: t1 & t2
Number of fixed effects for trait1: 3(intercept included)
Number of fixed effects for trait2: 3(intercept included)
No trait-specific random effects.
Number of random effects for correlation: 1 + 1
Number of phenotypic observations for trait1: 800
Number of phenotypic observations for trait2: 800
Number of individuals for analysis: 800
Number of SNPs in genotype: 48353
Deriving GA matrix from genotype...Done within 9s
Number of genotyped individuals: 573
Number of genotyped individuals with phenotypic observations: 175
Number of genotyped individuals without phenotypic observations: 398
Deriving A matrix from pedigree...Done within 0s
Number of total predicted individuals: 2524
Realign index of y...Done!
Realign index of X matrix...Done!
Realign index of R matrix...Done!
Constructing H matrix...
Extracting A11 matrix...Done!
Mean of diagonal and Off-diagonal of PA: 1.001 0.0285
Mean of diagonal and Off-diagonal of GA: 0.9886 -0.0017
Adjusting GA matrix: GA* = 0.98 * GA + 0.03
Weighting of A11 and GA matrix: 0.05
Calculating the inverse of A11 matrix...Done within 0s
Constructing HA matrix...Done within 6s
Variance components estimation:
Number of components: 9
HE prior derived... Done within 0s
Updated prior values: 0.292865 0.010000 3.660764 0.248892 0.010000 2.278902 0.311846 0.010000 2.425322
Dimension of V^(-1): 1600 * 1600
Bivariate GREML analysis:  Vgtr1_R1 Vgtr1_R2 Vetr1 CoVgtr1tr2_R1 CoVgtr1tr2_R2 CoVetr1tr2 Vgtr2_R1 Vgtr2_R2 Vetr
[AI] Iter 1 of Max Iter 20: 0.290261 0.005595 3.651463 0.252708 0.009138 2.282321 0.312319 0.014925 2.416211
[AI] Iter 2 of Max Iter 20: 0.288268 0.003539 3.642283 0.256138 0.008063 2.285180 0.312880 0.018369 2.407342
[AI] Iter 3 of Max Iter 20: 0.287507 0.002977 3.637824 0.257700 0.007689 2.286392 0.313194 0.019862 2.403057
[AI] Iter 4 of Max Iter 20: 0.286840 0.002616 3.633438 0.259197 0.007453 2.287511 0.313521 0.021238 2.398850
[AI] Iter 5 of Max Iter 20: 0.286259 0.002391 3.629123 0.260633 0.007342 2.288544 0.313861 0.022551 2.394721
[AI] Iter 6 of Max Iter 20: 0.285753 0.002260 3.624878 0.262015 0.007340 2.289496 0.314211 0.023836 2.390671
[AI] Iter 7 of Max Iter 20: 0.285317 0.002198 3.620702 0.263345 0.007430 2.290373 0.314572 0.025115 2.386698
[AI] Iter 8 of Max Iter 20: 0.284943 0.002187 3.616592 0.264627 0.007598 2.291178 0.314940 0.026401 2.382802
[AI] Iter 9 of Max Iter 20: 0.284625 0.002215 3.612546 0.265864 0.007834 2.291915 0.315316 0.027705 2.378980
[AI] Iter 10 of Max Iter 20: 0.284358 0.002275 3.608562 0.267059 0.008127 2.292588 0.315698 0.029032 2.375229
[AI] Iter 11 of Max Iter 20: 0.284137 0.002361 3.604638 0.268214 0.008470 2.293198 0.316086 0.030385 2.371548
[AI] Iter 12 of Max Iter 20: 0.283957 0.002471 3.600773 0.269333 0.008859 2.293750 0.316477 0.031765 2.367934
[AI] Iter 13 of Max Iter 20: 0.283816 0.002601 3.596965 0.270417 0.009288 2.294245 0.316872 0.033174 2.364385
[AI] Iter 14 of Max Iter 20: 0.283709 0.002749 3.593212 0.271469 0.009755 2.294686 0.317269 0.034611 2.360898
[AI] Iter 15 of Max Iter 20: 0.283557 0.003075 3.585815 0.273509 0.010746 2.295465 0.318067 0.037550 2.354046
[AI] Iter 16 of Max Iter 20: 0.283518 0.003467 3.578626 0.275433 0.011864 2.296047 0.318869 0.040599 2.347426
[AI] Iter 17 of Max Iter 20: 0.283572 0.003919 3.571638 0.277252 0.013094 2.296448 0.319671 0.043750 2.341024
[AI] Iter 18 of Max Iter 20: 0.283702 0.004430 3.564839 0.278977 0.014428 2.296685 0.320469 0.046995 2.334825
[AI] Iter 19 of Max Iter 20: 0.284087 0.005529 3.551608 0.282252 0.017228 2.296855 0.322053 0.053682 2.322811
[AI] Iter 20 of Max Iter 20: 0.284674 0.006857 3.539074 0.285214 0.020391 2.296480 0.323600 0.060637 2.311518
[Convergence] NO(More iteration number is needed!)
Done within 2m10s
Estimating random effect...Done within 0s
Estimated beta for trait1: 161.3 0.9205
Estimated beta for trait2: 11.5 0.8549
Estimated (CO)Variance(upper.tri+diag) and correlation(lower.tri) at R1:
        trait1  trait2
trait1  0.2847  0.2852
trait2  0.9397  0.3236
Estimated (CO)Variance(upper.tri+diag) and correlation(lower.tri) at Additive:
         trait1  trait2
```

```
 trait1 0.006857 0.02039
 trait2 1.000000 0.06064
 Estimated (CO)Variance(upper.tri+diag) and correlation(lower.tri) at Residual:
         trait1  trait2
 trait1  3.5391   2.296
 trait2  0.8029   2.312
 HIBLUP IS DONE WITHIN: 2m27s
 HIBLUP ACCOMPLISHED SUCCESSFULLY!


# if there are others trait-spercific random effects for traits, please
# assign to 'bivar.R'.  if there is a trait with no fixed or random
# effects, please set NULL at corresponding postion in 'bivar.CV' or
# 'bivar.R'.
```

5 Function support list of HIBLUP

		HIBLUP
Input	Genotype	√
	Pedigree	√
	Phenotype	√
	Fixed effects	√
	Random effects	√
	Relationship matrix	√
VC	AI	√
	EM	√
	EMAI	√
	HE Regression	√
	HI	√
	CG	√
	JOR	√
	SOR	√
	SOLVE	√
Variable	Fixed effects	√
	Random effects	√
	Multiple traits	√
	Repeated records	√
Model	BLUP	√
	PBLUP	√
	GBLUP	√
	SSBLUP	√
Output	GEBV	√
	SNP Effect	√
	Random Effect	√
	residuals	√

Table 4: Function support list of HIBLUP.

6 HIBLUP Biography

Date	Version	Event
Aug-2018	1.0	BLUP/PBLUP/GBLUP/SSBLUP
Sep-2018	1.01	Add function of calculating reliability
Oct-2018	1.02	Fixed some bugs
Jan-2019	1.1	Add Repeated Models
Jun-2019	1.2	Add multiple random effect model of correlated traits; Add HE regression for multiple random effect model of correlated traits
Nov-2019	1.3	Add multiple traits model with trait-spercific random effect
Apr-2020	1.3.1	solve MME using CG, JOR, SOR, SOLVE algorithms