HIBLUP User Manual

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v1.2.0

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_1.2.0.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: 1.2.0 #
#      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
 Deriving GA matrix from genotype...Done within 2s
 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!
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 1s
HE Prior derived: A:0.06936 e:2.342; Done within 0s
HE adopted: TRUE
Variance components estimation:
[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 1s
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: 6s
HIBLUP ACCOMPLISHED SUCCESSFULLY!
```

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

```r
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 three BLUP methods in HIBLUP:
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 and K model, `vc=c(`V_g, V_e`)`; (g: genetic variance, e: residual variance)
for pairs of correlated traits, `vc=c(`$V_g^{(1)}, V_g^{(2)}, COV_g^{(12)}, V_e^{(1)}, V_e^{(2)}, COV_e^{(12)}$`)`;
for multiple K model, `vc=c(`$V_g^{(1)}, V_g^{(2)} \ldots V_g^{(n)}, V_e$`)`;
if R (Random effects) is added in the model, V_R should be added in the beginning of `vc` vector.

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
X1	NULL	Users	Fixed effects for the first trait
X2	NULL	Users	Fixed effects for the second trait
R	NULL	Users	Random effects
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", and "HI"	methods for variance components estimation
nAIiter	20	Positive integer	Maximum iteration number for "AI"
nEMiter	1	Positive integer	Maximum iteration number for "EM"
mme.method	"sor"	"solve" and "sor"	methods for solving mixed model equation when vc is known
reliability	FALSE	TRUE or FALSE	if TRUE, the reliability of individual genetic value will be calculated
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 1s

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, phe_ind = phe_ind, A = A_PA,
    G = A_GA, Ainv = A_PAinv, alpha = 0.05, tag = "a")

 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 1s
```

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 1s
 Deriving the inverse of both A and D matrix from pedigree...Done within 2s

AD_PAinv <- ADcal$PA
AD_PDinv <- ADcal$PD

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, phe_ind = phe_ind, A = AD_PA,
    G = AD_GA, Ainv = AD_PAinv, alpha = 0.05, tag = "a")
```

```
 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 1s
```

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

```
 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 1s
```

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:
 [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 0s

# 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:
 [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 0s


# 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 Pairs of correlated traits

Variance and co-variance for pairs of correlated traits can be estimated using following codes. X1 and X2 are the fixed effects of trait1 and trait2, respectively.

```
# No K (BLUP)
vc <- hiblup.bivar.vc(y1 = pheno$t1, y2 = pheno$t2, X1 = X, X2 = X, R = R,
    method = "AI", blup.solution = FALSE, verbose = TRUE)
```

```
# 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$order.id
index <- match(pheno[, 1], id)
vc <- hiblup.bivar.vc(y1 = pheno$t1, y2 = pheno$t2, X1 = X, X2 = X, K = A_PA[index,
    index], method = "AI", blup.solution = FALSE, verbose = TRUE)


 Variance components estimation:
 Number of components: 6
```

```
Dimension of V: 1600 * 1600
Bivariate GREML analysis:  V(G1)_tr1 V(G1)_tr2 CoV(G1)_tr12 V(e)_tr1 V(e)_tr2 CoV(e)_tr12
[AI] Iter 1 of Max Iter 25: 0.842372 0.732004 0.697899 1.210966 0.814299 0.837582
[AI] Iter 2 of Max Iter 25: 0.856506 0.964980 0.867441 2.032594 1.234730 1.307332
[AI] Iter 3 of Max Iter 25: 0.871486 1.075397 0.957126 2.617028 1.529934 1.630738
[AI] Iter 4 of Max Iter 25: 0.884284 1.092801 0.975311 2.781225 1.605165 1.713651
[AI] Iter 5 of Max Iter 25: 0.885506 1.094709 0.977313 2.791538 1.607339 1.716704
[AI] Iter 6 of Max Iter 25: 0.885448 1.094653 0.977276 2.791650 1.607388 1.716749
[AI] Iter 7 of Max Iter 25: 0.885452 1.094658 0.977281 2.791647 1.607385 1.716746
[AI] Iter 8 of Max Iter 25: 0.885451 1.094658 0.977280 2.791648 1.607385 1.716746
[Convergence] YES
Done within 8s
```

```
# multiple K model
vc <- hiblup.bivar.vc(y1 = pheno$t1, y2 = pheno$t2, X1 = X, X2 = X, R = R,
    K = list(AD_PA[index, index], AD_PD[index, index]), method = "AI",
    blup.solution = FALSE, verbose = TRUE)

vc <- hiblup.bivar.vc(y1 = pheno$t1, y2 = pheno$t2, X1 = X, X2 = X, R = R,
    K = list(AD_PA[index, index], AD_PD[index, index]), method = "HE",
    blup.solution = FALSE, verbose = TRUE)

# X1 and X2 could be different. 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 0.7526 0.4497 5.3819 4.1848 4.2729
```

```r
# 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")

# Pairs of correlated traits
vc <- hiblup.bivar.vc(y1 = pheno$t1[index], y2 = pheno$t2[index], X1 = X[index,
    ], X2 = X[index, ], start = start5, K = A_GA, method = "AI")
```

4.4 BLUP

4.4.1 Single trait with random effects only

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

```
#-------------------------Welcome to HIBLUP-------------------------#
#  He-aI BLUP    _     _ _____ ____  _      _    _ _____             #
#               | |   | |_   _|  _ \| |    | |  | |  __ \            #
#               | |__| | | | | |_) | |    | |  | | |__) |           #
#               |  __  | | | |  _ <| |    | |  | |  ___/            #
#               | |  | |_| |_| |_) | |___| |__| | |                  #
#               |_|  |_|_____|____/|______\____/|_|    Version: 1.2.0 #
#      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:
 [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 1s
 Estimating random effect...Done within 0s
 Estimated Vr and Ve: 0.3735 2.355
 Estimated beta: 11.51 0.8485
 HIBLUP IS DONE WITHIN: 1s
 HIBLUP ACCOMPLISHED SUCCESSFULLY!
```

4.4.2 Pairs of correlated traits

```
X <- model.matrix(~Sex, data = pheno)  # fixed effects
R <- as.matrix(pheno$Sire)  # random effects
gebv <- hiblup(pheno = pheno, bivar.pos = c(4, 5), X1 = X, X2 = X, R = R)


#-------------------------Welcome to HIBLUP--------------------------#
#  He-aI BLUP   _    _ _____ ____  _     _    _ _____                #
#              | |  | |_   _|  _ \| |   | |  | |  __ \               #
#              | |__| | | | | |_) | |   | |  | | |__) |              #
#              |  __  | | | |  _ <| |   | |  | |  ___/               #
#              | |  | |_| |_| |_) | |___| |__| | |                   #
#              |_|  |_|_____|____/|______\____/|_|    Version: 1.2.0 #
#      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)
 Number of random effects: 1
 Number of phenotypic observations for trait1: 800
 Number of phenotypic observations for trait2: 800
 Number of individuals for analysis: 800
 HE prior derived... Done within 1s
 Updated prior values: 0.273579 0.316413 0.292155 3.415972 2.399766 2.415241
 Variance components estimation:
 Number of components: 6
 Dimension of V: 1600 * 1600
 Bivariate GREML analysis:  V(R1)_tr1 V(R1)_tr2 CoV(R1)_tr12 V(e)_tr1 V(e)_tr2 CoV(e)_tr12
 [AI] Iter 1 of Max Iter 20: 0.311005 0.370418 0.336561 3.384740 2.352924 2.377483
 [AI] Iter 2 of Max Iter 20: 0.313605 0.375816 0.340203 3.385889 2.354442 2.378953
 [AI] Iter 3 of Max Iter 20: 0.313420 0.375673 0.339980 3.385888 2.354495 2.379018
 [AI] Iter 4 of Max Iter 20: 0.313428 0.375678 0.339977 3.385872 2.354494 2.379016
 [AI] Iter 5 of Max Iter 20: 0.313428 0.375677 0.339975 3.385869 2.354494 2.379016
 [AI] Iter 6 of Max Iter 20: 0.313428 0.375677 0.339974 3.385869 2.354494 2.379016
 [Convergence] YES
 Done within 5s
 Estimating random effect...Done within 0s
 Estimated Vr and Ve of trait1: 0.3134 3.386
 Estimated Vr and Ve of trait2: 0.3757 2.354
 Estimated COVr of trait1 and trait2: 0.34
 Estimated COVe of trait1 and trait2: 2.379
 Estimated genetic correlation: 0.9908
 Estimated beta1: 161.3 0.9206
 Estimated beta2: 11.51 0.8513
 HIBLUP IS DONE WITHIN: 6s
 HIBLUP ACCOMPLISHED SUCCESSFULLY!
```

4.5 Pedigree BLUP(PBLUP)

4.5.1 Additive effect based model

if variance components are unknown:

```
# 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: 1.2.0 #
#      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 0s
 HE adopted: TRUE
 Variance components estimation:
 [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 1s
 Estimating random effect...Done within 0s
 Estimated beta: 11.52 0.8442
 Estimated Vg and Ve: 0.5824 1.92
 HIBLUP IS DONE WITHIN: 2s
 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: 1.2.0 #
#      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 0s
HE adopted: TRUE
Variance components estimation:
[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 1s
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: 3s
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 `mme.method` parameter. The options are "solve" and "sor".

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


#-------------------------Welcome to HIBLUP--------------------------#
#  He-aI BLUP   _     _ _____ ____  _     _    _ _____                #
#              | |   | |_   _|  _ \| |   | |  | | __ \               #
#              | |__| | | | | |_) | |   | |  | | |__) |              #
#              |  __  | | | |  _ <| |   | |  | |  ___/               #
#              | |  | |_| |_| |_) | |___| |__| | |                   #
#              |_|  |_|_____|____/|______\____/|_|    Version: 1.2.0 #
#      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 the inverse of 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!
 Solving MME...
 Done within 3s
 Estimated beta: 10.94 1.085
 Estimated Vg and Ve: 0.03995 3.61
 HIBLUP IS DONE WITHIN: 3s
 HIBLUP ACCOMPLISHED SUCCESSFULLY!


# Solve mixed model equation using SOR method
```

```
gebv.a <- hiblup(pheno = pheno[, c(1, 5)], pedigree = pedigree, CV = X,
    R = R, vc = start2, mme.method = "sor", mode = "A")


#-------------------------Welcome to HIBLUP-------------------------#
#  He-aI BLUP   _     _ _____ ____  _     _    _ _____               #
#              | |   | |_   _|  _ \| |   | |  | |  __ \              #
#              | |__| | | | | |_) | |   | |  | | |__) |             #
#              |  __  | | | |  _ <| |   | |  | |  ___/              #
#              | |  | |_| |_| |_) | |___| |__| | |                  #
#              |_|  |_|_____|____/|______\____/|_|    Version: 1.2.0 #
#      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 the inverse of 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!
 Solving MME...
 using SOR method...
 Final solution achieved after the 398 th iteration Done within 49s
 Estimated beta: 10.93 1.117
 Estimated Vg and Ve: 0.03995 3.61
 HIBLUP IS DONE WITHIN: 49s
 HIBLUP ACCOMPLISHED SUCCESSFULLY!
```

4.5.4 Pairs of correlated traits

HIBLUP supports the estimation of individual genetic values for pairs of correlated 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), X1 = X, X2 = X, R = R,
    pedigree = pedigree)


#-------------------------Welcome to HIBLUP-------------------------#
#  He-aI BLUP   _     _ _____ ____  _     _    _ _____               #
#              | |   | |_   _|  _ \| |   | |  | |  __ \              #
#              | |__| | | | | |_) | |   | |  | | |__) |             #
#              |  __  | | | |  _ <| |   | |  | |  ___/              #
#              | |  | |_| |_| |_) | |___| |__| | |                  #
#              |_|  |_|_____|____/|______\____/|_|    Version: 1.2.0 #
#      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)
 Number of random effects: 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!
HE prior derived... Done within 2s
Updated prior values: 0.119432 0.618292 0.085878 0.923566 0.101275 0.755667 2.961051 1.718203 1.854219
Variance components estimation:
Number of components: 9
Dimension of V: 5048 * 5048
Bivariate GREML analysis:  V(R1)_tr1 V(G1)_tr1 V(R1)_tr2 V(G1)_tr2 CoV(R1)_tr12 CoV(G1)_tr12 V(e)_tr1 V(e)_tr2 C
[AI] Iter 1 of Max Iter 20: 0.201674 0.411720 0.216823 0.579612 0.205231 0.488506 3.077824 1.918597 2.008901
[AI] Iter 2 of Max Iter 20: 0.215900 0.429363 0.236983 0.605330 0.221741 0.509810 3.066440 1.902956 1.994534
[AI] Iter 3 of Max Iter 20: 0.217506 0.429114 0.239169 0.604673 0.223426 0.509386 3.066680 1.903258 1.994429
[AI] Iter 4 of Max Iter 20: 0.217634 0.428813 0.239206 0.604714 0.223468 0.509224 3.066877 1.903193 1.994409
[AI] Iter 5 of Max Iter 20: 0.217643 0.428756 0.239198 0.604709 0.223461 0.509188 3.066913 1.903190 1.994405
[AI] Iter 6 of Max Iter 20: 0.217646 0.428741 0.239197 0.604709 0.223459 0.509179 3.066923 1.903189 1.994405
[AI] Iter 7 of Max Iter 20: 0.217647 0.428738 0.239196 0.604709 0.223459 0.509177 3.066925 1.903189 1.994405
[AI] Iter 8 of Max Iter 20: 0.217647 0.428737 0.239196 0.604709 0.223459 0.509177 3.066925 1.903189 1.994405
[Convergence] YES
Done within 19s
Estimating random effect...Done within 0s
Estimated beta1: 161.3 0.9178
Estimated beta2: 11.51 0.8493
Estimated Vg and Ve of trait1: 0.2176 0.4287 3.067
Estimated Vg and Ve of trait2: 0.2392 0.6047 1.903
Estimated COVg of trait1 and trait2: 0.2235 0.5092
Estimated COVe of trait1 and trait2: 1.994
Estimated genetic correlation: 0.9794 1
HIBLUP IS DONE WITHIN: 22s
HIBLUP ACCOMPLISHED SUCCESSFULLY!
```

4.5.5 Reliability of individual genetic value

The boolean parameter `reliability` is used to specify whether to calculate the reliability of each individual's genetic value.

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

# get the reliability of individual genetic value
gebv.a.hi <- hiblup(pheno = pheno[, c(1, 5)], pedigree = pedigree, CV = X,
    R = R, vc.method = c("HI"), nAIiter = 5, mode = "A", reliability = TRUE)
```

```
#-------------------------Welcome to HIBLUP--------------------------#
#  He-aI BLUP    _     _ _____ ____  _      _    _ _____              #
#               | |   | |_   _|  _ \| |    | |  | |  __ \             #
#               | |__| | | | | |_) | |    | |  | | |__) |            #
#               |  __  | | | |  _ <| |    | |  | |  ___/             #
#               | |  | |_| |_| |_) | |___| |__| | |                  #
#               |_|  |_|_____|____/|______\____/|_|    Version: 1.2.0 #
#      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 0s
 HE adopted: TRUE
```

```
Variance components estimation:
[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 2s
Estimating random effect...Done within 0s
Estimated beta: 11.52 0.8442
Estimated Vg and Ve: 0.5824 1.92
Calculating SEP and reliability... Done!
HIBLUP IS DONE WITHIN: 9s
HIBLUP ACCOMPLISHED SUCCESSFULLY!
```

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: 1.2.0 #
#      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
 Deriving GA matrix from genotype...Done within 1s
 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:
 [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 1s
Estimating random effect...Done within 0s
Estimated beta: 12.4 0.4291
Estimated Vg and Ve: 0.7644 4.196
HIBLUP IS DONE WITHIN: 3s
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: 1.2.0 #
#      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
 Deriving GA and GD matrix from genotype...Done within 4s
 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:
 [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)
 [Convergence] YES
 Done within 0s
 Estimating random effect...Done within 0s
 Estimated beta: 13.25
 Estimated additive genetic variacne: 1.061
 Estimated Dominance genetic variacne: 0
 Estimated Ve: 5.923
 HIBLUP IS DONE WITHIN: 5s
 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 `mme.method` parameter. The options are "solve" and "sor".

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


#-------------------------Welcome to HIBLUP--------------------------#
#  He-aI BLUP   _    _ _____ ____  _     _    _ _____                #
#              | |  | |_   _|  _ \| |   | |  | |  __ \               #
#              | |__| | | | | |_) | |   | |  | | |__) |              #
#              |  __  | | | |  _ <| |   | |  | |  ___/               #
#              | |  | |_| |_| |_) | |___| |__| | |                   #
#              |_|  |_|_____|____/|______\____/|_|    Version: 1.2.0 #
#      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
 Deriving GA matrix from genotype...Done within 2s
 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!
 Solving MME...
 Done within 0s
 Estimated beta: 0.000000000000000000000000000015 0.00000000000000000000000000004906
 Estimated Vg and Ve: 0.03995 3.61
 HIBLUP IS DONE WITHIN: 2s
 HIBLUP ACCOMPLISHED SUCCESSFULLY!



# Solve mixed model equation using SOR method
gebv.a <- hiblup(pheno = pheno[, c(1, 5)], mme.method = "sor", 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: 1.2.0 #
#      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
 Deriving GA matrix from genotype...Done within 2s
 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!
 Solving MME...
 using SOR method...
 Final solution achieved after the 2 th iteration Done within 0s
```

```
Estimated beta: 12.41 13.23
Estimated Vg and Ve: 0.03995 3.61
HIBLUP IS DONE WITHIN: 2s
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: 1.2.0 #
#      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
 Deriving GA matrix from genotype...Done within 1s
 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:
 [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 1s
 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: 3s
 HIBLUP ACCOMPLISHED SUCCESSFULLY!
```

4.6.5 Pairs of correlated traits

HIBLUP supports the estimation of individual genetic values for pairs of 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), X1 = X, X2 = X, R = R,
    map = map, geno = geno, geno.id = geno.id)


#-------------------------Welcome to HIBLUP--------------------------#
#  He-aI BLUP   _     _ _____ ____  _     _    _ _____               #
#              | |   | |_   _|  _ \| |   | |  | |  __ \              #
#              | |__| | | | | |_) | |   | |  | | |__) |             #
#              |  __  | | | |  _ <| |   | |  | |  ___/              #
#              | |  | |_| |_| |_) | |___| |__| | |                  #
#              |_|  |_|_____|____/|______\____/|_|    Version: 1.2.0 #
#      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)
 Number of random effects: 1 + 1
 Number of phenotypic observations for trait1: 800
 Number of phenotypic observations for trait2: 800
 Number of individuals for analysis: 800
 Deriving GA matrix from genotype...Done within 1s
 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!
 HE prior derived... Done within 0s
 Updated prior values: 1.033684 0.073084 1.462147 0.237988 1.229389 0.131883 4.584752 3.265501 3.404069
 Variance components estimation:
 Number of components: 9
 Dimension of V: 1146 * 1146
 Bivariate GREML analysis:  V(R1)_tr1 V(G1)_tr1 V(R1)_tr2 V(G1)_tr2 CoV(R1)_tr12 CoV(G1)_tr12 V(e)_tr1 V(e)_tr2 C
 [AI] Iter 1 of Max Iter 20: 0.939028 0.041647 1.338462 0.147407 1.121095 0.078352 4.670016 3.413353 3.510560
 [AI] Iter 2 of Max Iter 20: 0.901519 0.026046 1.291364 0.098720 1.078976 0.050707 4.715444 3.491412 3.564615
 [AI] Iter 3 of Max Iter 20: 0.893339 0.021675 1.281669 0.084748 1.070030 0.042859 4.727599 3.512031 3.578173
 [AI] Iter 4 of Max Iter 20: 0.887444 0.018277 1.274849 0.073461 1.063653 0.036642 4.736969 3.527835 3.588346
 [AI] Iter 5 of Max Iter 20: 0.883195 0.015598 1.270074 0.064259 1.059114 0.031659 4.744228 3.539979 3.595990
 [AI] Iter 6 of Max Iter 20: 0.880134 0.013459 1.266758 0.056691 1.055896 0.027623 4.749884 3.549343 3.601745
 [AI] Iter 7 of Max Iter 20: 0.879034 0.012570 1.265619 0.053577 1.054762 0.025952 4.752101 3.552967 3.603916
 [AI] Iter 8 of Max Iter 20: 0.878091 0.011771 1.264665 0.050716 1.053798 0.024433 4.754082 3.556186 3.605824
 [AI] Iter 9 of Max Iter 20: 0.877283 0.011050 1.263869 0.048082 1.052981 0.023050 4.755856 3.559048 3.607500
 [AI] Iter 10 of Max Iter 20: 0.876591 0.010397 1.263207 0.045656 1.052290 0.021787 4.757446 3.561596 3.608975
 [AI] Iter 11 of Max Iter 20: 0.875999 0.009803 1.262660 0.043417 1.051708 0.020631 4.758873 3.563867 3.610273
 [AI] Iter 12 of Max Iter 20: 0.875494 0.009262 1.262210 0.041349 1.051217 0.019570 4.760157 3.565894 3.611417
 [AI] Iter 13 of Max Iter 20: 0.875063 0.008768 1.261845 0.039436 1.050806 0.018595 4.761314 3.567704 3.612426
 [AI] Iter 14 of Max Iter 20: 0.874696 0.008315 1.261550 0.037664 1.050463 0.017697 4.762357 3.569324 3.613316
 [AI] Iter 15 of Max Iter 20: 0.874384 0.007900 1.261316 0.036021 1.050178 0.016869 4.763300 3.570774 3.614103
 [AI] Iter 16 of Max Iter 20: 0.874120 0.007517 1.261132 0.034495 1.049943 0.016103 4.764154 3.572075 3.614800
 [AI] Iter 17 of Max Iter 20: 0.873896 0.007165 1.260991 0.033077 1.049750 0.015395 4.764927 3.573244 3.615417
 [AI] Iter 18 of Max Iter 20: 0.873708 0.006841 1.260887 0.031758 1.049593 0.014739 4.765630 3.574294 3.615964
 [AI] Iter 19 of Max Iter 20: 0.873628 0.006687 1.260850 0.031146 1.049530 0.014432 4.765950 3.574768 3.616207
 [AI] Iter 20 of Max Iter 20: 0.873556 0.006541 1.260819 0.030555 1.049474 0.014137 4.766255 3.575218 3.616436
 [Convergence] NO(More iteration number is needed!)
 Done within 2s
 Estimating random effect...Done within 0s
```

```
Estimated beta1: 162.7 0.2151
Estimated beta2: 13.37 -0.04621
Estimated Vg and Ve of trait1: 0.8736 0.006541 4.766
Estimated Vg and Ve of trait2: 1.261 0.03056 3.575
Estimated COVg of trait1 and trait2: 1.049 0.01414
Estimated COVe of trait1 and trait2: 3.616
Estimated genetic correlation: 1 1
HIBLUP IS DONE WITHIN: 4s
HIBLUP ACCOMPLISHED SUCCESSFULLY!
```

4.6.6 Reliability of individual genetic value

The boolean parameter `reliability` is used to specify whether to calculate the reliability of each individual's genetic value.

```
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", reliability = TRUE)


#-------------------------Welcome to HIBLUP-------------------------#
#  He-aI BLUP    _     _ _____ ____  _     _    _ _____              #
#               | |   | |_   _|  _ \| |   | |  | |  __ \             #
#               | |__| | | | | |_) | |   | |  | | |__) |            #
#               |  __  | | | |  _ <| |   | |  | |  ___/             #
#               | |  | |_| |_| |_) | |___| |__| | |                  #
#               |_|  |_|_____|____/|______\____/|_|    Version: 1.2.0 #
#      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
 Deriving GA matrix from genotype...Done within 1s
 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:
 [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 1s
 Estimating random effect...Done within 0s
 Estimated beta: 12.4 0.4291
 Estimated Vg and Ve: 0.7644 4.196
 Calculating SEP and reliability... Done!
```

```
HIBLUP IS DONE WITHIN: 2s
HIBLUP ACCOMPLISHED SUCCESSFULLY!
```

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: 1.2.0 #
#      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
 Deriving GA matrix from genotype...Done within 1s
 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!
 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 1s
 Variance components estimation:
 [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 2s
 Estimating random effect...Done within 0s
 Estimated beta: 13.09
 Estimated Vg and Ve: 1.261 1.625
 HIBLUP IS DONE WITHIN: 5s
 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: 1.2.0 #
#      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
 Deriving GA and GD matrix from genotype...Done within 4s
 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!
 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 1s
 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 1s
 HE Prior derived: A:1.407 D:0 e:2.843; Done within 0s
 HE adopted: TRUE
 Variance components estimation:
 [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)
 [Convergence] YES
 Done within 0s
 Estimating random effect...Done within 0s
 Estimated beta: 13.07
 Estimated additive genetic variacne: 1.407
 Estimated Dominance genetic variacne: 0
 Estimated Ve: 2.843
 HIBLUP IS DONE WITHIN: 7s
 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 `mme.method` parameter. The options are “solve” and “sor”.

```
# Solve mixed model equation directly
gebv.a <- hiblup(pheno = pheno[, c(1, 5)], mme.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: 1.2.0 #
#      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
 Deriving GA matrix from genotype...Done within 1s
 Number of genotyped individuals: 573
 Number of genotyped individuals with phenotypic observations: 175
 Number of genotyped individuals without phenotypic observations: 398
 Deriving the inverse of A matrix from pedigree...Done within 0s
 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!
 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
 Solving MME...
 Done within 3s
 Estimated beta: 11.5 0.8719
 Estimated Vg and Ve: 0.0686 0.0008
 HIBLUP IS DONE WITHIN: 5s
 HIBLUP ACCOMPLISHED SUCCESSFULLY!



# Solve mixed model equation using SOR method
gebv.a <- hiblup(pheno = pheno[, c(1, 5)], mme.method = "sor", 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: 1.2.0 #
#      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
Deriving GA matrix from genotype...Done within 1s
Number of genotyped individuals: 573
Number of genotyped individuals with phenotypic observations: 175
Number of genotyped individuals without phenotypic observations: 398
Deriving the inverse of A matrix from pedigree...Done within 0s
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!
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
Solving MME...
using SOR method...
Final solution achieved after the 26 th iteration Done within 4s
Estimated beta: 10.21 12.86
Estimated Vg and Ve: 0.0686 0.0008
HIBLUP IS DONE WITHIN: 7s
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: 1.2.0 #
#      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
 Deriving GA matrix from genotype...Done within 1s
 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!
 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 1s
Variance components estimation:
[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 2s
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: 5s
HIBLUP ACCOMPLISHED SUCCESSFULLY!
```

4.7.5 Pairs of correlated traits

HIBLUP also supports the estimation of individual genetic values for pairs of 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), X1 = X, X2 = X, R = R,
    pedigree = pedigree, map = map, geno = geno, geno.id = geno.id)


#-------------------------Welcome to HIBLUP-------------------------#
#  He-aI BLUP   _    _ _____ ____  _     _    _ _____               #
#              | |  | |_   _|  _ \| |   | |  | |  __ \              #
#              | |__| | | | | |_) | |   | |  | | |__) |             #
#              |  __  | | | |  _ <| |   | |  | |  ___/              #
#              | |  | |_| |_| |_) | |___| |__| | |                  #
#              |_|  |_|_____|____/|______\____/|_|    Version: 1.2.0 #
#      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)
 Number of random effects: 1 + 1
 Number of phenotypic observations for trait1: 800
 Number of phenotypic observations for trait2: 800
 Number of individuals for analysis: 800
 Deriving GA matrix from genotype...Done within 1s
 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!
 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 1s
HE prior derived... Done within 1s
Updated prior values: 0.292929 0.020659 0.310201 0.045313 0.299864 -0.030596 2.852033 0.744657 1.457322
Variance components estimation:
Number of components: 9
Dimension of V: 5048 * 5048
Bivariate GREML analysis:  V(R1)_tr1 V(G1)_tr1 V(R1)_tr2 V(G1)_tr2 CoV(R1)_tr12 CoV(G1)_tr12 V(e)_tr1 V(e)_tr2 C
[AI] Iter 1 of Max Iter 20: 0.314532 0.006545 0.351282 0.106699 0.328711 -0.004902 2.839191 0.745565 1.451889
[AI] Iter 2 of Max Iter 20: 0.336166 0.022349 0.417366 0.265689 0.367122 0.077058 2.849506 0.762850 1.457985
[AI] Iter 3 of Max Iter 20: 0.339794 0.093213 0.441242 0.498565 0.377495 0.215576 2.892024 0.830904 1.490466
[AI] Iter 4 of Max Iter 20: 0.328565 0.196305 0.401980 0.694339 0.355349 0.369191 2.937613 1.040063 1.574955
[AI] Iter 5 of Max Iter 20: 0.311583 0.232132 0.359121 0.566661 0.329010 0.362685 3.047359 1.528793 1.814571
[AI] Iter 6 of Max Iter 20: 0.307266 0.133700 0.356792 0.283856 0.326320 0.194812 3.229783 2.023159 2.129840
[AI] Iter 7 of Max Iter 20: 0.306971 0.102973 0.354516 0.265595 0.325659 0.165376 3.300825 2.119110 2.218308
[AI] Iter 8 of Max Iter 20: 0.306740 0.103021 0.353706 0.264169 0.325110 0.164970 3.305566 2.123586 2.221641
[AI] Iter 9 of Max Iter 20: 0.306761 0.102764 0.353764 0.264267 0.325157 0.164794 3.305749 2.123490 2.221799
[AI] Iter 10 of Max Iter 20: 0.306757 0.102787 0.353753 0.264225 0.325147 0.164799 3.305743 2.123517 2.221776
[AI] Iter 11 of Max Iter 20: 0.306757 0.102780 0.353754 0.264231 0.325149 0.164796 3.305746 2.123511 2.221779
[AI] Iter 12 of Max Iter 20: 0.306757 0.102781 0.353754 0.264230 0.325148 0.164796 3.305746 2.123512 2.221779
[AI] Iter 13 of Max Iter 20: 0.306757 0.102781 0.353754 0.264230 0.325148 0.164796 3.305746 2.123512 2.221779
[Convergence] YES
Done within 39s
Estimating random effect...Done within 0s
Estimated beta1: 161.4 0.9167
Estimated beta2: 11.53 0.8464
Estimated Vg and Ve of trait1: 0.3068 0.1028 3.306
Estimated Vg and Ve of trait2: 0.3538 0.2642 2.124
Estimated COVg of trait1 and trait2: 0.3251 0.1648
Estimated COVe of trait1 and trait2: 2.222
Estimated genetic correlation: 0.987 1
HIBLUP IS DONE WITHIN: 43s
HIBLUP ACCOMPLISHED SUCCESSFULLY!
```

4.7.6 Reliability of individual genetic value

The boolean parameter **reliability** is used to specify whether to calculate the reliability of each individual's genetic value.

```
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", reliability = TRUE)


#-------------------------Welcome to HIBLUP-------------------------#
#  He-aI BLUP   _    _ _____ ____  _     _    _ _____               #
#              | |  | |_   _|  _ \| |   | |  | |  __ \              #
#              | |__| | | | | |_) | |   | |  | | |__) |             #
#              |  __  | | | |  _ <| |   | |  | |  ___/              #
#              | |  | |_| |_| |_) | |___| |__| | |                  #
#              |_|  |_|_____|____/|______\____/|_|    Version: 1.2.0 #
#      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
 Deriving GA matrix from genotype...Done within 1s
 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!
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 1s
Variance components estimation:
[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 2s
Estimating random effect...Done within 0s
Estimated beta: 13.09
Estimated Vg and Ve: 1.261 1.625
Calculating SEP and reliability... Done!
HIBLUP IS DONE WITHIN: 10s
HIBLUP ACCOMPLISHED SUCCESSFULLY!
```

5 Function support list of HIBLUP

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

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