User manual for PIBLUP v1.1

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Introduction

PIBLUP is an application program for solving mixed model equations (MME), especially for very large ones. The core algorithm is preconditioned conjugate gradient (PCG) with preconditioner of block diagonal of MME, by iteration on data (IOD).

To take full advantage of modern multicore and multiprocessor systems, two parallel computing strategies are applied in PIBLUP. Firstly, Intel Math Kernel Library (MKL) is employed (https://software.intel.com/en-us/intel-mkl) to accelerate mathematical operations. Secondly, we used shared memory programming introduced in Message Passing Interface Standard (MPI) Version 3.0. In a practical application, users can control both the Intel MKL threading and the number of MPI processes to optimally utilize computational resources.

PIBLUP is written in C. The program will be actively maintained and new functions will be incorporated. If you have any questions and suggestions, please do not hesitate to contact us.

Dependencies

1. MPI

   Users should install one of MPI implementation. MPICH
   (http://www.mpich.org/downloads/) is suggested.

2. MKL

   Users do need to install MKL (https://software.intel.com/en-us/intel-mkl).

What is new?

Compared to version 1.0, PIBLUP v1.1 added nearpd option to compute the nearest
positive definite matrix of **G** in GBLUP and single-step GBLUP. This leads to a little
change of Syntax in parameter file (see Description of COVFILE) and the preparation
before running PIBLUP.

Parameter file for application

PIBLUP is driven by the parameter file. The parameter file consists of keywords that
are fixed and followed by values. Keywords underlined are mandatory.

Description of keywords used in the parameter file:

Keyword	Function (F)/Syntax (S)
DATAFILE	F: specifies name of the file with phenotypes S: DATAFILE fn where: fn = name of data file Full path name if the file is not in the current directory Format of data file see: Associated files
NVAR	F: specifies the number of variables in data file

	S: NVAR #var where: #var = number of variables, i.e., number of columns in data file
NTRAITS	F: specifies the number of traits to be analyzed S: NTRAITS #traits where: #traits = number of traits to be analyzed
TRAITS	F: specifies the position(s) of observations in data file, indicated by column number(s) S: TRAITS tr1 tr2 … where: tr1 = the column number of observations for the 1st trait tr2 = the column number of observations for the 2nd trait, if it exists
MISSING	F: specifies the value should be regarded as missing for real variables S: MISSING miss where: miss = reals equaling to this value are regarded as missing
NEFFECTS	F: specifies the number of effects, except for residual, in a model for each trait S: NEFFECTS #tr1 #tr2 … where: #tr1 = number of effects for the 1st trait #tr2 = number of effects for the 2nd trait
WEIGHT	F: specifies the position(s) of weight on observations for each trait, if used. More details see: Weighted analysis S: WEIGHT tr1 tr2 … where: tr1 = the column number of weight for the 1st trait tr2 = the column number of weight for the 2nd trait A zero (0) stands for weight is not applied for this trait

EFFECTS	F: specifies effects, except for residual, in the model for each trait
	S: EFFECTS
	Followed by lines with effects specified in a fixed format for traits
	Format of effects see: Description of effects
COV	F: specifies (co)variance matrix for each random effect, except for residual. If the model includes random effects, COV must be specified.
	S: COV #ran
	Followed by (co)variance matrix
	where: #ran = the unique CV number of the random effect, which is specified in EFFECTS keyword section
	Format of (co)variance matrix see: (Co)variance and residual matrices
RCOV	F: specifies the residual (co)variance matrix
	S: RCOV
	Followed by residual (co)variance matrix
	Format of residual matrix see: (Co)variance and residual matrices
COVFILE	F: specifies associated files storing or used to calculate (inverse) kinship matrix, for each random effect, except for residual. If not specified, an identity matrix will be used.
	S: COVFILE
	Followed by the corresponding information in a fixed format
	Format see: Description of COVFILE
MAXROUND	F: specifies the maximum round of iteration, default =

	10,000
	S: MAXROUND #n
	where: n = maximum round of iteration
CONV	F: specifies the convergence criterion, default = 1e-13
	S: CONV value
	where: v = convergence criterion
	Convergence indicator is the relative average difference between the right-hand and left-hand sides (Misztal, et al., 1987)

Description of effects

The effects for all the traits are specified in EFFECTS keyword section. One line for each trait containing the trait number (starts from 1) followed by information of effects in the model. Information of each effect, except for residual, is expressed as a string consisting of several parts, with delimiters of a comma (,), a slash (/), or a hyphen (-), e.g., 4/RR,1,1-3. Its syntax is as follows:

Type	Syntax				
	Part 1	Part 2	Part 3	Part 4	Part 5
Fixed effect	Column number of effect	F			
Fixed regression		FR	column number it nested in, if so, else, 0		
Random effect		R	CV* matrix number	number in CV matrix (default = 1)	
Random regression		RR	column number it	CV number	number in CV matrix

|			nested in		

*CV: (co)variance

Note: CV matrix number should be coded from 1 continuously.

(Co)variance and residual matrices

In parameter file, (co)variance and residual matrices should be listed as full square matrices.

(Co)variance matrix

In multivariate analysis, if the (co)variance matrix consists of n correlated effects and m traits, the order of effects and traits is as follows:
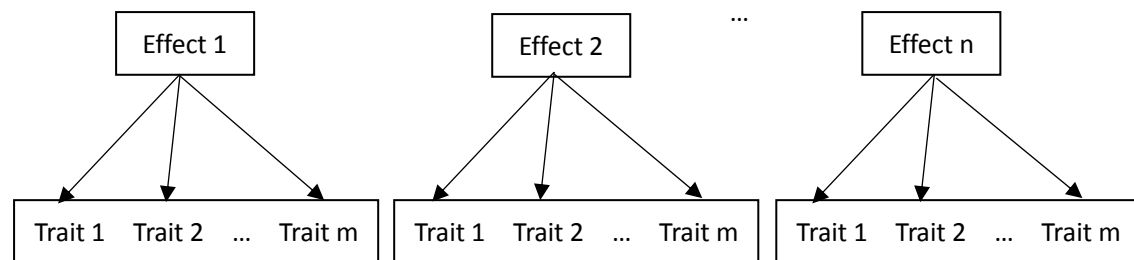
Residual matrix

The order of traits in residual matrix should be the same as those specified in TRAITS keyword section.

Description of COVFILE

In parameter file, the COVFILE consists of several columns. Associated files and information used to construct kinship matrices for random effects are specified in this section. The format of associated files see: Associated files. The syntax for different types of kinship matrices is as follows:

Type of kinship matrix	Syntax
Additive genetic relationship based on pedigree (**A**)	COVFILE #cv PED fped inbreed upg where: #cv = (co)variance matrix number it corresponds to

	fped = name of pedigree file Full path name if the file is not in the current directory inbreed = 0, if inbreed is not considered; else, 1 upg = 0, if unknown parent group is not considered; else, 1
Genomic relationship based on genotype file (**G**)	COVFILE #cv INVG fmarker ngid nmarker diag_g nearpd where: #cv = as in kinship matrix **A** fmarker = name of genotype file Full path name if the file is not in the current directory ngid = number of genotyped individuals nmarker = number of markers diag_g = a small number added to diagonal of **G**, e.g., 0.02 nearpd = 1 (compute the nearest positive definite matrix of **G**) or 0 (do not compute the nearest positive definite matrix of **G**) We have compared the estimated breeding values of genotyped individuals based on the two modified **G** matrices using several datasets, e.g., adding 0.01 on the diagonals of **G** and the nearest positive definite matrix of **G**. It turned out that the Pearson correlation coefficients were larger than 0.99 in all the cases. However, the nearest positive definite matrix of **G** matrix may has its advantage in particular situations.

| Hybrid relationship matrix (**H**) of **A** and **G** | COVFILE #cv HYBRID fped fmarker inbreed upg ngid nmarker diag_g nearpd adj t w_1 w_2

where: #cv, fped, inbreed, upg = as those in kinship matrix **A**

fmarker, ngid, nmarker, diag_g, nearpd = as those in kinship matrix **G**

adj = 1, adjust G according to (Christensen, et al., 2012); 0, do not adjust

t, w_1, w_2 = those in inverse of **H** matrix:

$$\mathbf{H}^{-1}=\mathbf{A}^{-1}+\begin{bmatrix} \mathbf{0} & \mathbf{0} \\ \mathbf{0} & t\left[\left(1-w_1\right)\mathbf{G}+w_1\mathbf{A}_{22}\right]^{-1}-w_2\mathbf{A}_{22}^{-1} \end{bmatrix}$$ |
| Kinship matrix built by the users | COVFILE #cv INV finv

where: #cv = as in kinship matrix **A**

finv = name of file containing the inverse of kinship matrix |

Associated files

Associated files include data file, pedigree file, genotype file and kinship file, if they are used. Files should be free-format ASCII files, with delimiters of one or several spaces/tabs. Classified variables can include alpha-numeric characters. Identifications of individuals should be consistent among different files.

Data file

Data file containing observations to be analyzed together with class variables and covariables for each model must be provided. One record in data file corresponds to an observation.

Integer inputs consist of all classified variables, followed by real inputs, which consist of the traits to be analyzed and all necessary covariables and weight variables. In

integer input, a zero (0) is treated as missing, whereas real inputs equaling to the value "miss" specified at the MISSING keyword section. Except for the requirement integer variables should be before real variables, there is no restriction on the order of variables within integer variables and real variables. The data file can contain variables that are not used.

Pedigree file

A pedigree file can be used to define an additive genetic relationship. If unknown parent group (UPG) is used, the file consists of four columns corresponding to four variables:

1: ID	Identification of the individual that enters into random effect (genetic effect) in the model
2: Sire ID	Identification of sire, or genetic group code for unknown sire
3: Dam ID	Identification of dam, or genetic group code for unknown dam
4: UPG	genetic group the ID belongs to, if UPG is used. Inbreeding coefficients are calculated according to Aguilar and Misztal (2008)

If UPG is not used, the file should consist of the first 3 columns.

Genotype file

A genotype file is used to construct a genomic relationship matrix. Genotypes of all markers for one individual is listed in a row. IDs should be listed in the first column, followed by genotype code for each marker. Genotypes are codes as 0 and 2 for the two homozygotes and 1 for the heterozygote. There are no missing values for genotypes, and genotypes cannot be left as missing. Markers with genotypes listed in genotype file will be used without filtering.

Kinship file

If a kinship matrix constructed by the user would be used, the kinship file containing the **inverse** of the kinship matrix should be specified. The full inverse matrix should be listed row by row in the following format: IdRow IdCol value, where IdRow and IdCol stand for identifications corresponding to row and column, respectively.

Weighted analysis

WEIGHT keyword is optional. A zero (0) indicates no weight is not applied. If weight is applied on at least one trait, WEIGHT must be specified.

The weight modifies the residual (co)variance to $\mathbf{V} = \dfrac{1}{w}\mathbf{V}_e$, where w is the weight, and $\mathbf{V}_e$ is residual (co)variance matrix specified in RCOV keyword section. In multivariate analysis, residual correlations are kept constant when applying weights.

References:

Aguilar, I. and Misztal, I. Technical note: Recursive algorithm for inbreeding coefficients assuming nonzero inbreeding of unknown parents. *J Dairy Sci* 2008;91(4):1669-1672.

Christensen, O.F*., et al.* Single-step methods for genomic evaluation in pigs. *Animal : an international journal of animal bioscience* 2012;6(10):1565-1571.

Misztal, I., Gianola, D. and Schaeffer, L.R. Extrapolation and Convergence Criteria with Jacobi and Gauss-Seidel Iteration in Animal-Models. *J Dairy Sci* 1987;70(12):2577-2584.

Running and Solution file

Running

Before running the program, please read **<u>dependencies</u>** first.

If you want to use nearpd to compute the nearest positive definite matrix of **G** matrix (nearpd == 1, see <u>Description of COVFILE</u>), which is added in PIBLUP v1.1, you must copy nearPD.R to the working directory.

Run the program with command:

PIBLUP m parfile

where:

PIBLUP = full path name if not in the current directory, or add its directory

into your PATH

m = number of processors to use (for MPI)

parfile = name of parameter file, full path name if not in the current directory

Solution file

File containing solution is named name_of_parameter_file.sol. Solution file contains

6 columns:

Column	Definition
1	Trait number
2	Effect number (useless for users)
3	Effect column in data file
4	Class code = 0, if it is fixed regression and not nested within fixed effects = class code where it nested, else

5	= Column number nests in, if it nests within an effect = 0, else
6	Solution

Examples for parameter file

Examples are those in example directory.

1. Animal model with pedigree

Model:

$$y_{ijk} = sex_i + birth\_mon_j + birth\_weight + a_k + e_{ijk},$$

where:

y_{ijkl}: weight

sex_i: sex

$birth\_mon_j$: birth month

birth_weight: birth weight

a_k: additive genetic effect

e_{ijkl}: residual

and

$$\text{var}(a) = 0.3, \text{var}(e) = 0.7.$$

Data file (data.txt):

(First 10 lines)

Format: ID/birth_mon/sex/birth_weight/weight

192243 2 2 27.50 147.35
192240 3 2 26.00 124.91
192242 3 2 29.50 142.78
192246 3 1 30.30 143.43
192241 3 1 36.20 147.95
192251 3 2 36.00 154.93
192245 3 2 32.00 142.20
192247 3 1 31.00 148.84
192250 3 1 29.00 123.64
192249 3 2 24.80 140.96

Pedigree (ped.txt):

(First 10 lines)

Format: ID/sire/dam

```
192243  181     4007
192240  3980    3762
192242  3980    4010
192246  3980    4899
192241  847     3525
192251  4597    4204
192245  3920    3588
192247  3980    4341
192250  4597    4464
192249  3980    184
```

Parameter file (1.par):

```
DATAFILE data.txt
NTRAITS 1
TRAITS 5
NEFFECTS 4
NVAR 5
MISSING -99
WEIGHT 0
EFFECTS
1 2/F 3/F 4/FR,0 1/R,1
COV 1
0.3
RCOV
0.7
COVFILE 1 PED ped.txt 0 0
```

Solution file (1.par.sol):

(First 10 lines)

```
1 1 2 2 0 43.9714
1 1 2 3 0 26.1468
1 1 2 4 0 15.3176
1 1 2 5 0 29.9166
1 1 2 6 0 29.0574
1 2 3 2 0 25.3442
1 2 3 1 0 22.4064
1 3 4 0 0 2.74704
1 4 1 192243 0 2.49802
1 4 1 192240 0 3.15123
```

2. Animal model with genotype file

Model:

$$y_i = \mu + a_i + e_i,$$

where:

y_{ij}: phenotype (pseudo-phenotype, EBV)

μ : mean

a_i: additive genetic effect

e_{ij}: residual

and

$$\mathrm{var}(a) = 200231, \mathrm{var}(e) = 1176064,$$

Residual variance is heterogeneous.

Data file (data.txt):

(First 10 lines)

Format: ID/ μ /observation/weight

4104	1	-1584.03502	1.94364
4123	1	-1220.60346	0.32261
4125	1	-4367.64766	0.31403
4129	1	-964.11084	0.30168
4130	1	-507.71934	1.90909
4143	1	-4299.13739	0.32762
4149	1	-273.90995	0.30886
4154	1	151.22413	1.92342
4158	1	-535.19628	1.93967
4168	1	-881.81554	1.92867

Genotype file (marker.txt):

(First 10 lines, first 10 columns)

```
4104 0 0 0 2 0 0 0 0 2
4123 0 0 0 2 0 0 0 0 1
4125 1 2 2 1 2 1 1 1 1
4129 0 1 1 1 1 1 1 1 2
4130 1 2 2 1 1 1 1 1 1
4143 0 0 1 2 1 0 0 0 2
4149 0 1 1 1 1 1 1 1 2
4154 0 0 0 2 0 0 1 0 1
```

4158 1 2 2 1 2 1 1 1 1
4168 0 0 0 2 0 0 1 0 1

Parameter file (2.par):

DATAFILE data.txt
NTRAITS 1
TRAITS 3
NEFFECTS 2
NVAR 4
MISSING -99
WEIGHT 4
EFFECTS
1 2/F 1/R,1,1
COV 1
200231
RCOV
1176064
COVFILE 1 INVG marker.txt 2000 20010 0.02

Solution file (2.par.sol):

(First 10 lines)

1 1 2 1 0 152.594
1 2 1 4104 0 -692.656
1 2 1 4123 0 -461.149
1 2 1 4125 0 -826.65
1 2 1 4129 0 -369.614
1 2 1 4130 0 -760.704
1 2 1 4143 0 -550.76
1 2 1 4149 0 -355.458
1 2 1 4154 0 -218.863
1 2 1 4158 0 -195.657

3. Random regression test-day model with pedigree and genotype file

Model:

$$y_{itk} = \sum_{k=1}^{3} \varphi_{itk} \beta_k + \sum_{k=1}^{3} \varphi_{itk} a_{ik} + \sum_{k=1}^{3} \varphi_{itk} pe_{ik} + e_{itk},$$

where:

    y_{tik}: test-day record of individual i made on time t

    φ_{itk}: the kth parameter of Wilmink function (W0, W1, W2)

β_k : fixed regression coefficients

a_{ik}: random regression coefficients for additive genetic effect

pe_{ik}: random regression coefficients for permanent environmental effect

e_{tik}: residual

and

$$\text{var}(a) = \begin{bmatrix} 5.8089184 & -9.75E-3 & -8.7098898 \\ -9.75E-3 & 9.81E-5 & 1.72E-2 \\ -8.7098898 & 1.72E-2 & 18.045758 \end{bmatrix},$$

$$\text{var}(pe) = \begin{bmatrix} 11.71613 & -3.29E-2 & -9.0165899 \\ -3.29E-2 & 1.9E-4 & 2.38E-2 \\ -9.0165899 & 2.38E-2 & 23.941236 \end{bmatrix},$$

$$\text{var}(e) = 3.984657$$

Data file (data.txt):

(First 10 lines)

Format: a/pe/W0/W1/W2/phe

```
4101    4101    1    25  2.865E-01    42.37
4101    4101    1    60  4.979E-02    41.88
4101    4101    1    86  1.357E-02    47.22
4101    4101    1    119 2.606E-03    43.05
4101    4101    1    150 5.531E-04    42.49
4101    4101    1    172 1.841E-04    40.27
4101    4101    1    196 5.545E-05    37.48
4101    4101    1    230 1.013E-05    38.65
4101    4101    1    264 1.851E-06    31.87
4101    4101    1    286 6.160E-07    31.94
```

Pedigree (ped.txt):

(First 10 lines)

Format: ID/sire/dam

```
4101 0 0
4102 0 0
4103 0 0
4104 0 0
4105 0 0
4106 0 0
4107 0 0
4108 0 0
```

4109 0 0
4110 0 0

Genotype file (marker.txt):

(First 10 lines, first 10 columns)

4104 0 0 0 2 0 0 0 0 2
4123 0 0 0 2 0 0 0 0 1
4125 1 2 2 1 2 1 1 1 1
4129 0 1 1 1 1 1 1 1 2
4130 1 2 2 1 1 1 1 1 1
4143 0 0 1 2 1 0 0 0 2
4149 0 1 1 1 1 1 1 1 2
4154 0 0 0 2 0 0 1 0 1
4158 1 2 2 1 2 1 1 1 1
4168 0 0 0 2 0 0 1 0 1

Parameter file (3.par):

DATAFILE data.txt
NTRAITS 1
TRAITS 6
NEFFECTS 9
NVAR 6
MISSING -99
EFFECTS
1 3/FR,0 4/FR,0 5/FR,0 1/R,1 2/R,2 4/RR,1,1-2 5/RR,1,1-3 4/RR,2,2-2 5/RR,2,2-3
COV 1
5.8089184   -9.75E-03   -8.7098898
-9.75E-03   9.81E-05   1.72E-02
-8.7098898   1.72E-02   18.045758
COV 2
11.71613   -3.29E-02   -9.0165899
-3.29E-02   1.90E-04   2.38E-02
-9.0165899   2.38E-02   23.941236
RCOV
3.984657
COVFILE 1 HYBRID ped.txt marker.txt 1 0 2000 20010 0.01 1 1 0.05 1

Solution file (3.par.sol):

(First 10 lines)

1 1 3 0 0 44.9568
1 2 4 0 0 -0.05023
1 3 5 0 0 -27.9127
1 4 1 4101 0 1.59294
1 5 4 4101 1 -0.00189875
1 6 5 4101 1 -1.79034

1 4 1 4102 0 -0.0292396
1 5 4 4102 1 0.00748955
1 6 5 4102 1 1.23103
1 4 1 4103 0 0.681633

4. Model with both additive genetic and epigenetic effects

Model:

$$y_i = a_i + epi_i + e_i ,$$

where:

y_i: observation

a_i: additive genetic effect

epi_i: epigenetic effect

e_i: residual

and

$$\mathrm{var}(a) = 1581628.4, \mathrm{var}(epi) = 1617241.9, \mathrm{var}(e) = 1536088.1$$

Data file (data.txt):

(First 10 lines)

Format: a/epi/observation

```
1    1    2.458E+04
2    2    2.680E+04
3    3    2.420E+04
4    4    2.264E+04
5    5    2.677E+04
6    6    2.836E+04
7    7    2.356E+04
8    8    2.310E+04
9    9    2.971E+04
10   10   2.464E+04
```

File containing inverse of kinship matrix for additive genetic effect (add.inv.txt):

(First 10 lines)

Format: ID1/ID2/value

1 1 11.9502
2 1 10.7577
2 2 12.5347

3 1 10.7502
3 2 10.6436
3 3 18.5077
4 1 10.7565
4 2 10.7163
4 3 3.66267
4 4 18.4615

File containing inverse of kinship matrix for epigenetic effect (epi.inv.txt):

(First 10 lines)

Format: ID1/ID2/value

1 1 1.13624
2 1 -0.00286483
2 2 1.1676
3 1 -0.000616532
3 2 -0.0366526
3 3 3.81434
4 1 -0.00147606
4 2 -0.0191144
4 3 -3.32862
4 4 3.80128

Parameter file (4.par):

DATAFILE data.txt
NTRAITS 1
TRAITS 3
NEFFECTS 2
NVAR 3
MISSING -99
WEIGHT 0
EFFECTS
1 1/R,1 2/R,2
COV 1
1581628.4
COV 2
1617241.9
RCOV
1536088.1
COVFILE 1 INV add.inv.txt
COVFILE 2 INV epi.inv.txt

Solution file (4.par.sol):

(First 10 lines)

1 1 1 1 0 1901.36

1 1 1 2 0 -6838.82
1 1 1 3 0 -10705.1
1 1 1 4 0 -10760.5
1 1 1 5 0 2104.78
1 1 1 6 0 2625.57
1 1 1 7 0 -9187.34
1 1 1 8 0 -9194.34
1 1 1 9 0 2458.65
1 1 1 10 0 2580.03

5. Multivariate random regression test-day model with pedigree

Model:

$$y_{mijkl} = s_i + c_j + \sum_{k=1}^{4} \varphi_{jtk}\beta_{jk} + \sum_{k=1}^{4} \varphi_{ltk}a_{lk} + \sum_{k=1}^{3} \varphi_{ltk}pe_{lk} + e_{mijkl},$$

where:

y_{tmijkl}: test-day record for trait m (tr1, tr2, tr3, tr4, tr5, tr6, tr7, tr8 and tr9) of individual j made on time t

s_i: herd test season

c_j: calving age and season

φ_{itk}: the kth Legendre polynomial (L1, L2, L3, L4)

β_{jk}: fixed regression coefficients nest within calving age and season

a_{lk}: random regression coefficients for additive genetic effect

pe_{lk}: random regression coefficients for permanent environmental effect

e_{tmijlk}: residual

and

$$\mathrm{var}(a) = mat1, \mathrm{var}(pe) = mat2, \mathrm{var}(e) = mat3,$$

Data file (data.txt):

(First 10 lines)

Format: a/pe/s/c/L1/L2/L3/L4/tr1/tr2/t3/tr4/tr5/tr6/tr7/tr8/tr9

7683 1 1 1 0.11   -0.77   -0.24   0.74   34 0.65   1.02   -99 -99 -99 -99 -99 -99
17677 2 2 2 0.32   -0.63   -0.65   0.30   21.4 0.62   0.61   -99 -99 -99 -99 -99 -99
10294 3 3 1 0.26   -0.68   -0.55   0.45   24.8 0.99   0.79   -99 -99 -99 -99 -99 -99

12542 4 4 2 0.56   -0.29   -0.84   -0.47   32.7 1.39   1.19   -99 -99 -99 -99 -99 -99

16282 5 5 3 0.47   -0.45   -0.81   -0.16   -99 -99 -99 20.90   0.83   0.81   -99 -99 -99

6531 6 6 2 0.56   -0.29   -0.84   -0.47   18 0.52   0.54   -99 -99 -99 -99 -99 -99

9384 7 7 1 0.51   -0.39   -0.83   -0.29   15.8 0.82   0.64   -99 -99 -99 -99 -99 -99

11849 8 8 2 -1.20   1.49   -1.65   1.72   13.7 0.68   0.51   -99 -99 -99 -99 -99 -99

10858 9 9 4 0.01   -0.79   -0.02   0.80   -99 -99 -99 14 0.602 0.49 -99 -99 -99

18722 10 10 2 -0.97   0.70   -0.11   -0.53   12.8 0.20   0.44   -99 -99 -99 -99 -99 -99

Pedigree (ped.txt):

(First 10 lines)

Format: ID/sire/dam

```
1    0    0
2    0    0
3    0    0
4    0    0
5    0    0
6    5    0
7    6    0
8    0    0
9    8    0
10   0    0
```

Parameter file (5.par):

DATAFILE data.txt
NTRAITS 9
TRAITS 9 10 11 12 13 14 15 16 17
NEFFECTS 15 15 15 15 15 15 15 15 15
NVAR 17
MISSING -99
WEIGHT 0 0 0 0 0 0 0 0 0
EFFECTS
1 3/F 4/F 1/R,1 2/R,2 5/FR,4 6/FR,4 7/FR,4 8/FR,4 5/RR,1,1-2 6/RR,1,1-3 7/RR,1,1-4 8/RR,1,1-5 5/RR,2,2-2 6/RR,2,2-3 7/RR,2,2-4
2 3/F 4/F 1/R,1 2/R,2 5/FR,4 6/FR,4 7/FR,4 8/FR,4 5/RR,1,1-2 6/RR,1,1-3 7/RR,1,1-4 8/RR,1,1-5 5/RR,2,2-2 6/RR,2,2-3 7/RR,2,2-4
3 3/F 4/F 1/R,1 2/R,2 5/FR,4 6/FR,4 7/FR,4 8/FR,4 5/RR,1,1-2 6/RR,1,1-3 7/RR,1,1-4 8/RR,1,1-5 5/RR,2,2-2 6/RR,2,2-3 7/RR,2,2-4
4 3/F 4/F 1/R,1 2/R,2 5/FR,4 6/FR,4 7/FR,4 8/FR,4 5/RR,1,1-2 6/RR,1,1-3 7/RR,1,1-4 8/RR,1,1-5 5/RR,2,2-2 6/RR,2,2-3 7/RR,2,2-4
5 3/F 4/F 1/R,1 2/R,2 5/FR,4 6/FR,4 7/FR,4 8/FR,4 5/RR,1,1-2 6/RR,1,1-3 7/RR,1,1-4 8/RR,1,1-5 5/RR,2,2-2 6/RR,2,2-3 7/RR,2,2-4
6 3/F 4/F 1/R,1 2/R,2 5/FR,4 6/FR,4 7/FR,4 8/FR,4 5/RR,1,1-2 6/RR,1,1-3 7/RR,1,1-4 8/RR,1,1-5 5/RR,2,2-2 6/RR,2,2-3 7/RR,2,2-4
7 3/F 4/F 1/R,1 2/R,2 5/FR,4 6/FR,4 7/FR,4 8/FR,4 5/RR,1,1-2 6/RR,1,1-3 7/RR,1,1-4

8/RR,1,1-5 5/RR,2,2-2 6/RR,2,2-3 7/RR,2,2-4

8 3/F 4/F 1/R,1 2/R,2 5/FR,4 6/FR,4 7/FR,4 8/FR,4 5/RR,1,1-2 6/RR,1,1-3 7/RR,1,1-4

8/RR,1,1-5 5/RR,2,2-2 6/RR,2,2-3 7/RR,2,2-4

9 3/F 4/F 1/R,1 2/R,2 5/FR,4 6/FR,4 7/FR,4 8/FR,4 5/RR,1,1-2 6/RR,1,1-3 7/RR,1,1-4

8/RR,1,1-5 5/RR,2,2-2 6/RR,2,2-3 7/RR,2,2-4

COV 1

mat1

COV 2

mat2

RCOV

mat3

COVFILE 1 PED ped.txt 0 0

Solution file (5.par.sol):

(First 10 lines)

1 1 3 1 0 17.4291

2 1 3 1 0 0.465003

3 1 3 1 0 0.582579

1 1 3 2 0 6.84124

2 1 3 2 0 0.157484

3 1 3 2 0 0.216496

1 1 3 3 0 12.0569

2 1 3 3 0 0.392848

3 1 3 3 0 0.381222

1 1 3 4 0 21.9266