

# 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)
<u>DATAFILE</u>	F: specifies name of the file with phenotypes S: <b>DATAFILE</b> fn where: fn = name of data file Full path name if the file is not in the current directory Format of data file see: <a href="#">Associated files</a>
<u>NVAR</u>	F: specifies the number of variables in data file

	<p>S: <a href="#">NVAR #var</a></p> <p>where: #var = number of variables, i.e., number of columns in data file</p>
<u>NTRAITS</u>	<p>F: specifies the number of traits to be analyzed</p> <p>S: <a href="#">NTRAITS #traits</a></p> <p>where: #traits = number of traits to be analyzed</p>
<u>TRAITS</u>	<p>F: specifies the position(s) of observations in data file, indicated by column number(s)</p> <p>S: <a href="#">TRAITS tr1 tr2 ...</a></p> <p>where: tr1 = the column number of observations for the 1<sup>st</sup> trait</p> <p style="padding-left: 40px;">tr2 = the column number of observations for the 2<sup>nd</sup> trait, if it exists</p>
<u>MISSING</u>	<p>F: specifies the value should be regarded as missing for real variables</p> <p>S: <a href="#">MISSING miss</a></p> <p>where: miss = reals equaling to this value are regarded as missing</p>
<u>NEFFECTS</u>	<p>F: specifies the number of effects, except for residual, in a model for each trait</p> <p>S: <a href="#">NEFFECTS #tr1 #tr2 ...</a></p> <p>where: #tr1 = number of effects for the 1<sup>st</sup> trait</p> <p style="padding-left: 40px;">#tr2 = number of effects for the 2<sup>nd</sup> trait</p>
<u>WEIGHT</u>	<p>F: specifies the position(s) of weight on observations for each trait, if used. More details see: <a href="#">Weighted analysis</a></p> <p>S: <a href="#">WEIGHT tr1 tr2 ...</a></p> <p>where: tr1 = the column number of weight for the 1<sup>st</sup> trait</p> <p style="padding-left: 40px;">tr2 = the column number of weight for the 2<sup>nd</sup> trait</p> <p>A zero (0) stands for weight is not applied for this trait</p>

<u>EFFECTS</u>	<p>F: specifies effects, except for residual, in the model for each trait</p> <p>S: <a href="#">EFFECTS</a></p> <p><a href="#">Followed by lines with effects specified in a fixed format for traits</a></p> <p>Format of effects see: <a href="#">Description of effects</a></p>
COV	<p>F: specifies (co)variance matrix for each random effect, except for residual. If the model includes random effects, COV must be specified.</p> <p>S: <a href="#">COV #ran</a></p> <p><a href="#">Followed by (co)variance matrix</a></p> <p>where: #ran = the unique CV number of the random effect, which is specified in EFFECTS keyword section</p> <p>Format of (co)variance matrix see: <a href="#">(Co)variance and residual matrices</a></p>
<u>RCOV</u>	<p>F: specifies the residual (co)variance matrix</p> <p>S: <a href="#">RCOV</a></p> <p><a href="#">Followed by residual (co)variance matrix</a></p> <p>Format of residual matrix see: <a href="#">(Co)variance and residual matrices</a></p>
COVFILE	<p>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.</p> <p>S: <a href="#">COVFILE</a></p> <p><a href="#">Followed by the corresponding information in a fixed format</a></p> <p>Format see: <a href="#">Description of COVFILE</a></p>
MAXROUND	<p>F: specifies the maximum round of iteration, default =</p>

	10,000 S: <b>MAXROUND #n</b> where: n = maximum round of iteration
CONV	F: specifies the convergence criterion, default = 1e-13 S: <b>CONV value</b> 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

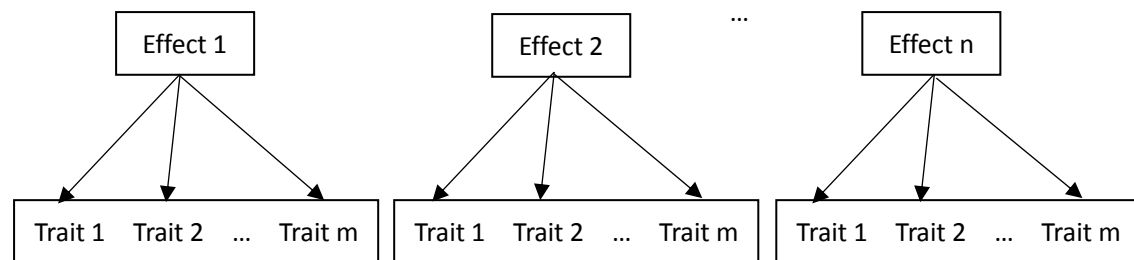
**Note: CV matrix number should be coded from 1 continuously.**

## (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 ( <b>A</b> )	<b>COVFILE #cv PED fped inbreed upg</b> where: #cv = (co)variance matrix number it corresponds to



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

	<p>using the nearest positive definite matrix of <b>G</b>.</p> <p>However, we do not deny that the nearest positive definite matrix of <b>G</b> matrix may has its advantage in particular situations.</p>
Hybrid relationship matrix ( <b>H</b> ) of <b>A</b> and <b>G</b>	<p><b>COVFILE #cv HYBRID fped fmarker inbreed upg ngid nmarker diag_g nearpd adj t w1 w2</b></p> <p>where: #cv, fped, inbreed, upg = as those in kinship matrix <b>A</b></p> <p>fmarker, ngid, nmarker, diag_g, nearpd = as those in kinship matrix <b>G</b></p> <p>adj = 1, adjust G according to (Christensen, et al., 2012); 0, do not adjust</p> <p>t, w1, w2 = those in inverse of <b>H</b> matrix:</p> $\mathbf{H}^{-1} = \mathbf{A}^{-1} + \begin{bmatrix} 0 & 0 \\ 0 & t[(1 - w_1)\mathbf{G} + w_1\mathbf{A}_{22}]^{-1} - w_2\mathbf{A}_{22}^{-1} \end{bmatrix}$
Kinship matrix built by the users	<p><b>COVFILE #cv INV finv</b></p> <p>where: #cv = as in kinship matrix <b>A</b></p> <p>finv = name of file containing the inverse of kinship matrix</p>

## 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  $\mathbf{V} = \frac{1}{w} \mathbf{V}_e$ , 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 [dependencies](#) first.

If you want to use nearpd to compute the nearest positive definite matrix of **G** matrix (nearpd == 1, see [Description of COVFILE](#)), 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:

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

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

$$Var(a) = 0.3, Var(e) = 0.7$$

[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)

$\mu$ : mean

$a_i$ : additive genetic effect

$e_{ij}$ : residual

and

$$\text{Var}(a) = 200231, \text{Var}(e) = 1176064$$

Residual variance is heterogeneous.

[Data file \(data.txt\):](#)

(First 10 lines)

Format: ID/  $\mu$ /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	2
4123	0	0	0	2	0	0	0	1
4125	1	2	2	1	2	1	1	1
4129	0	1	1	1	1	1	1	2
4130	1	2	2	1	1	1	1	1
4143	0	0	1	2	1	0	0	2
4149	0	1	1	1	1	1	1	2
4154	0	0	0	2	0	0	1	0

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:

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

where:

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

$\varphi_{itk}$ : the  $k$ th parameter of Wilmink function (W0, W1, W2)

$\beta_k$ : 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

$$Var(a) = \begin{bmatrix} 5.8089184 & -9.75E-03 & -8.7098898 \\ -9.75E-03 & 9.81E-05 & 1.72E-02 \\ -8.7098898 & 1.72E-02 & 18.045758 \end{bmatrix},$$

$$Var(pe) = \begin{bmatrix} 11.71613 & -3.29E-02 & -9.0165899 \\ -3.29E-02 & 1.90E-04 & 2.38E-02 \\ -9.0165899 & 2.38E-02 & 23.941236 \end{bmatrix},$$

$$Var(e) = 3.984657$$

[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

$$Var(a) = 1581628.4, Var(epi) = 1617241.9, Var(e) = 1536088.1$$

[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:

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

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

$\varphi_{itk}$ : the  $k$ th Legendre polynomial (L1, L2, L3, L4)

$\beta_{jk}$ : 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

$e_{tmijkl}$ : residual

and

$$Var(a) = mat1, Var(pe) = mat2, Var(e) = mat3$$

[Data file \(data.txt\):](#)

(First 10 lines)

Format: a/pe/s/c/L1/L2/L3/L4/tr1/tr2/tr3/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