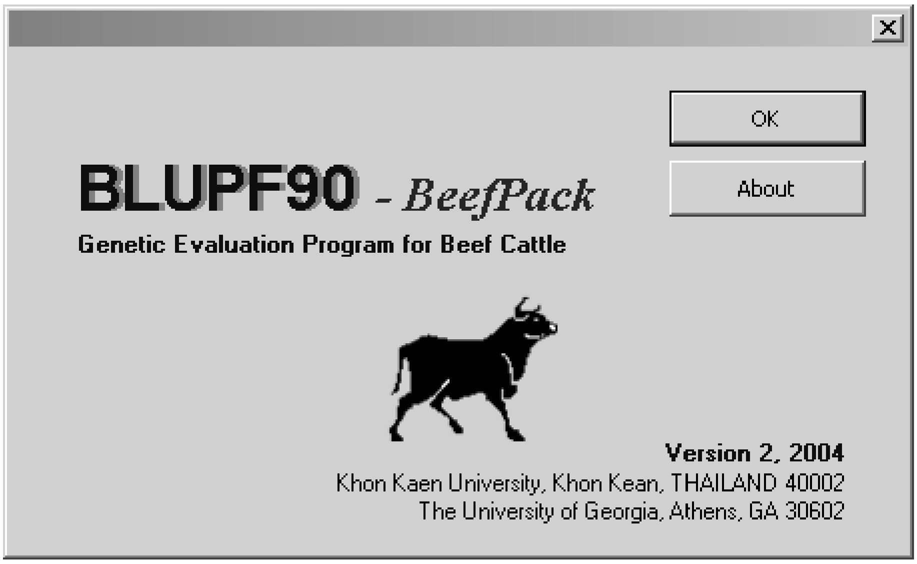
BLUPF90

BeefPack

Version 2.5, 2006



BLUPF90 - *BeefPack*

Genetic Evaluation Program for Beef Cattle

Version 2, 2004
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Contents

I. Introduction

A. Background

"BLUPF90" and related programs were developed in the lab of Ignacy Misztal with the purpose of providing comprehensive computing capabilities to problems related to mixed models in animal breeding. See http://nce.ads.uga.edu/~ignacy for details and documentation. These programs are mostly written in Fortran 90 and have a line-mode interface. "BeefPack" is a set of programs branched from "PCPack" with graphical user interface for simply used in Windows. BeefPack was developed with specific purpose for beef genetic evaluation, therefore parts of programs in the BLUPF90 family are available, which are:

BLUPF90	: BLUP estimation using PCG.
REMLF90	: Variance estimation using REML by EM algorithm.
AIREMLF90	: Variance estimation using REML by AI Algorithm.
RENUMMAT	: Renumber program for creating data file and additive pedigree with animal ID in order number.
ACCF90	: Approximate accuracy for BLUP solutions for direct and maternal models

All programs were compiled separately under Microsoft Windows using Visual Fortran version 5.1. Users can run all programs separately using MS-DOS prompt or from the menu in BeefPack. It allows users to create all parameter files and creating BLUP reports with a point-and-click interface written in Visual BASIC application for MS-EXCEL.

B. Overall Features

BeefPack performs under EXCEL. It manages genetic evaluation using wizard interface which allows you to create BLUP report within 5 steps. Only original data and pedigree are requires. It will automatically renumber the animals and count the number of effects in the model. After variance estimation or BLUP analysis were performed, it will create BV report with the original animal ID. Users can keep data files and program files separately, however specified directories are required before the analysis. BV with accuracy and genetic trend report for direct genetics up to 4 traits and for maternal genetics up to 2 traits are available.

B. Specification

BLUPF90-*BeefPack 2* requires windows 95/98/ME/XP/2000 environment to install and Excel 98/2000/XP/2002/2003 for running applications. It also requires at least 32 MB for memory and 5 MB of disk space for storing programs.

For BLUP and variance estimation, BLUPF90 and REMLF90 support general single and multiple trait models, i.e. sire-maternal grandsire, animal model, maternal model, repeatability model, and dominance model, with missing values and different models for each trait. Random regression models are also supported. AIREMLF90 may not support some models and some particular structure of data. ACCF90 is an approximation that works with repeatability and maternal models.

With BeefPack wizard interface, however, the single trait will support only simple animal, animal with PE model and direct-maternal with PE model. Multiple traits will support up to 4 traits for direct genetics and up to 2 traits with maternal genetics. Variance estimation and BV report with accuracy are available for both single and multiple traits.

C. Conditions of Use

BLUPF90-*BeefPack* is distributed *free of charge* for academic and scientific use under the conditions that it remains copyright. The use of any applications and compiled programs from BeefPack needs to be credited in any publications. For commercial or grant project, personal communication for further agreements is required with any of the authors. There is no guarantee for its correctness and there is no-service for user purpose. However, specific questions, criticism and bug reports are invited. Please email to monchai@kku.ac.th

D. Program Download

BLUPF90-*BeefPack* has been made available on the CD. However, the updated version is available at BLUPF90 homepage, http://agserver.kku.ac.th/monchai/BlupF90. The complete package provides program files, manuals and examples.

E. Online Registration

Online registration is requested for further breeding and genetic group connection and update version information. The registration page for BLUPF90-*BeefPack* is also available at BLUPF90 homepage, http://agserver.kku.ac.th/monchai/BlupF90.

II. Installation

A. Installation

BLUPF90-BeefPack is stored in one installation file named "BeefPack.Exe." To install the programs, do the following steps:

1. Run **BeefPack.EXE**.

Welcome to the BLUPF90-DairyPack Setup program. This program will install BLUPF90-DairyPack on your computer.

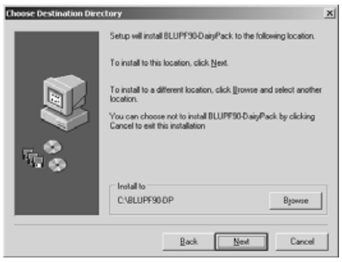
It is strongly recommended that you shut down all Windows applications before running this installation.

Click Cancel to exit Setup and close any applications you have running. Click Next to continue the installation.

WARNING: This program is protected by copyright law and international treaties.

Unauthorized reproduction or distribution of this program, or any portion of it, may result in severe civil and criminal penalties, and will be prosecuted to the maximum extent possible under law.

2. Setup Wizards will tell you through the installation steps.



Setup will install BLUPF90-DairyPack to the following location.

To install to this location, click Next.

To install to a different location, click Browse and select another location.

You can choose not to install BLUPF90-DairyPack by clicking Cancel to exit this installation

Install to
C:\BLUPF90-DP

3. BeefPack will install all F90 programs to the default directory "C:\BLUPF90-BP". To modify the directory name, click **BROWSE** button.

Setup has successfully installed and configured BLUPF90-DairyPack on your computer.

Please click the Finish button to complete the installation of BLUPF90-DairyPack.

4. Click **FINISH** button to complete the installation.

B. How to Start

DOS environment

Each program can be run directly from directory \BLUPF90. The following are executable programs that can be called at DOS prompt. For example, to run BLUPF90 program, type the following at the command prompt:

```
C:\BLUPF90-BP\BLUPF90
```

The programs that can be called from the dos prompt are:

BLUPF90	: BLUP estimation using PCG.
REMLF90	: Variance estimation using REML by EM algorithm.
AIREMLF90	: Variance estimation using REML by AI Algorithm.
RENUMMAT	: Renumber program for creating data file and additive pedigree with animal ID in order number.
ACCF90	: Approximate accuracy for BLUP solutions for direct and maternal models

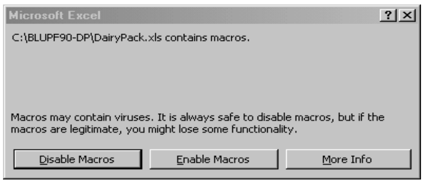
Note:

All programs require specific parameter files, which need to be created before calling the programs. For parameter file examples, see section 6.

Windows environment

1. At the windows task bar, click on **Start Menu > Programs > BLUPF90 > BeefPack**
2. Click **BlupF90 BeefPack** icon.

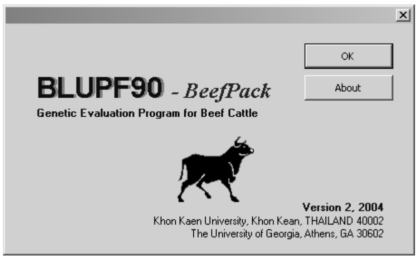
3. Excel program will and BeefPack will ask for macro enables. Click **Enable Macros** button.
(Note: BLUPF90-BeefPack cannot execute without macros for Visual Basic Applications. If there is a problem, enable macros by clicking menu **Tools > Macro > Security** in Excel. Then, set security level to Medium)



C:\BLUPF90-DP\DairyPack.xls contains macros.

Macros may contain viruses. It is always safe to disable macros, but if the macros are legitimate, you might lose some functionality.

4. Click **OK** button at splash dialog to start the program.



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The University of Georgia, Athens, GA 30602

5. The main menu should look as below:

Genetic Evaluation Program for Beef Cattle

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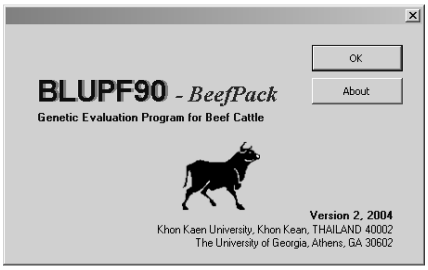
Khon Kaen University, THAILAND 40002

The University of Georgia, GA 30602

III. Genetic Evaluation At A Glance

A. General View



BLUPF90 - *BeefPack*
Genetic Evaluation Program for Beef Cattle

Version 2, 2004
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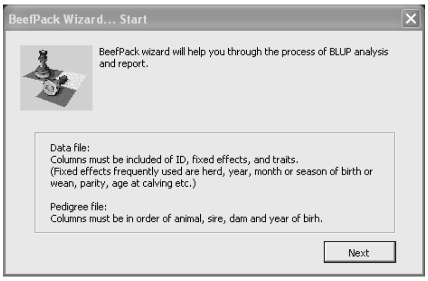
1. *BeefPack* is a set of programs in BLUPF90 family with a specific purpose for dairy cattle evaluation.



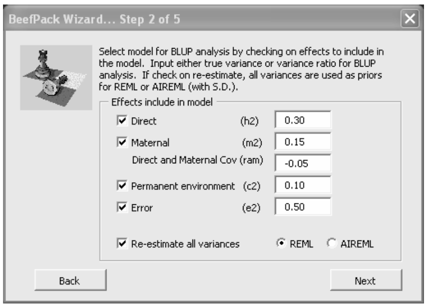
BeefPack Wizard... Start

BeefPack wizard will help you through the process of BLUP analysis and report.

Data file:
Columns must be included of ID, fixed effects, and traits.
(Fixed effects frequently used are herd, year, month or season of birth or wean, parity, age at calving etc.)

Pedigree file:
Columns must be in order of animal, sire, dam and year of birh.

2. *BeefPack* performs variance estimation using REML and BLUP analysis with wizard interface.



BeefPack Wizard... Step 2 of 5

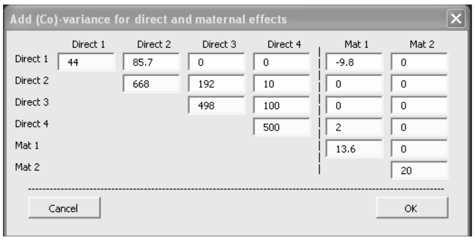
Select model for BLUP analysis by checking on effects to include in the model. Input either true variance or variance ratio for BLUP analysis. If check on re-estimate, all variances are used as priors for REML or AIREML (with S.D.).

Effects include in model

☑ Direct (h2) 0.30
☑ Maternal (m2) 0.15
Direct and Maternal Cov (ram) -0.05
☑ Permanent environment (c2) 0.10
☑ Error (e2) 0.50

☑ Re-estimate all variances ● REML ○ AIREML

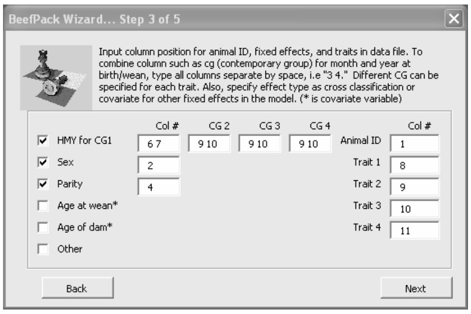
3. BLUP analysis can be done directly with true variance or variance ratio. In addition, re-estimate variance components with REML or AIREML can also apply.



Add (Co)-variance for direct and maternal effects

	Direct 1	Direct 2	Direct 3	Direct 4	Mat 1	Mat 2
Direct 1	44	85.7	0	0	-9.8	0
Direct 2		668	192	10	0	0
Direct 3			498	100	0	0
Direct 4				500	2	0
Mat 1					13.6	0
Mat 2						20

4. If multiple trait model is interested, Direct and maternal genetic effects can be evaluated.



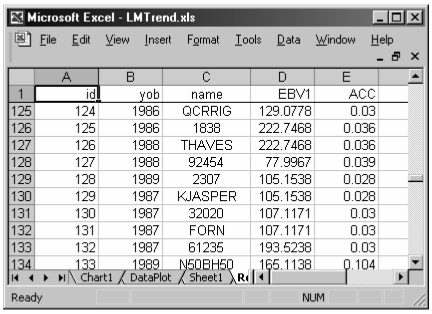
BeefPack Wizard... Step 3 of 5

Input column position for animal ID, fixed effects, and traits in data file. To combine column such as cg (contemporary group) for month and year at birth/wean, type all columns separate by space, i.e "3 4." Different CG can be specified for each trait. Also, specify effect type as cross classification or covariate for other fixed effects in the model. (* is covariate variable)

	Col #	CG 2	CG 3	CG 4		Col #
☑ HMY for CG1	6 7	9 10	9 10	9 10	Animal ID	1
☑ Sex	2				Trait 1	8
☑ Parity	4				Trait 2	9
☐ Age at wean*					Trait 3	10
☐ Age of dam*					Trait 4	11
☐ Other						

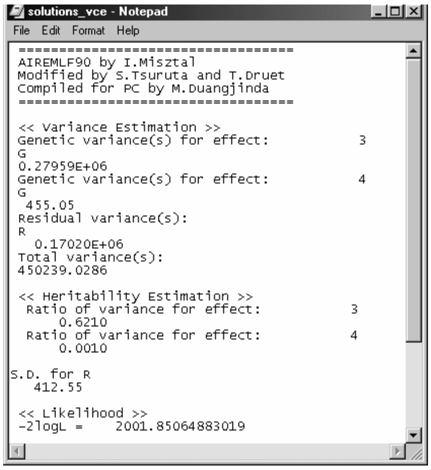
5. Original data and pedigree files are used in the analysis. Therefore, all effects in the model are simply specified by column number in data file. For multi-trait model, different contemporary groups for each trait can be specified. For maternal direct or PE model, dam column is not required in data file (program will automatically creat from pedigreed).

B. Report View



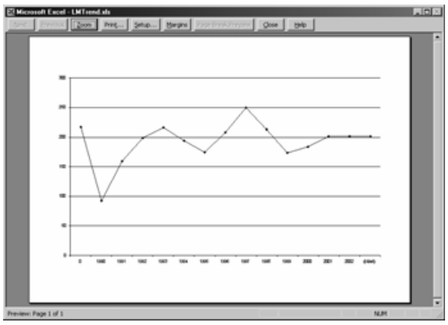
	A	B	C	D	E
1	id	yob	name	EBV1	ACC
125	124	1986	QCRRIG	129.0778	0.03
126	125	1986	1838	222.7468	0.036
127	126	1988	THAVES	222.7468	0.036
128	127	1988	92454	77.9967	0.039
129	128	1989	2307	105.1538	0.028
130	129	1987	KJASPER	105.1538	0.028
131	130	1987	32020	107.1171	0.03
132	131	1987	FORN	107.1171	0.03
133	132	1987	61235	193.5238	0.03
134	133	1989	N50BH50	165.1138	0.104

6. BLUP report with accuracy is created with original ID in Excel format. Therefore, sorting, filtering can simply perform using Excel functions.



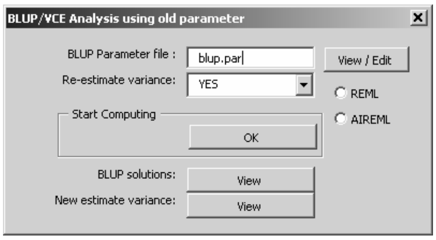
```
==================================
AIREMLF90 by I.Misztal
Modified by S.Tsuruta and T.Druet
Compiled for PC by M.Duangjinda
==================================

<< Variance Estimation >>
Genetic variance(s) for effect:           3
G
0.27959E+06
Genetic variance(s) for effect:           4
G
 455.05
Residual variance(s):
R
  0.17020E+06
Total variance(s):
450239.0286

<< Heritability Estimation >>
 Ratio of variance for effect:           3
     0.6210
 Ratio of variance for effect:           4
     0.0010

S.D. for R
   412.55

<< Likelihood >>
-2logL =    2001.85064883019
```

7. If REML or AIREML is performed. New variance estimates are kept in separate file.



8. Genetic trend report is also created if require. All graphic properties can be modified using general Excel features.

C. Advanced Options

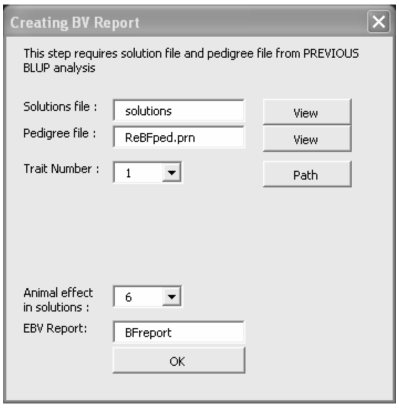


BLUP/VCE Analysis using old parameter

BLUP Parameter file : blup.par

Re-estimate variance: YES

9. Previous renumbered data and pedigree file with parameter file can be modified and reanalysis.



Creating BV Report

This step requires solution file and pedigree file from PREVIOUS BLUP analysis

Solutions file : solutions

Pedigree file : ReBFped.prn

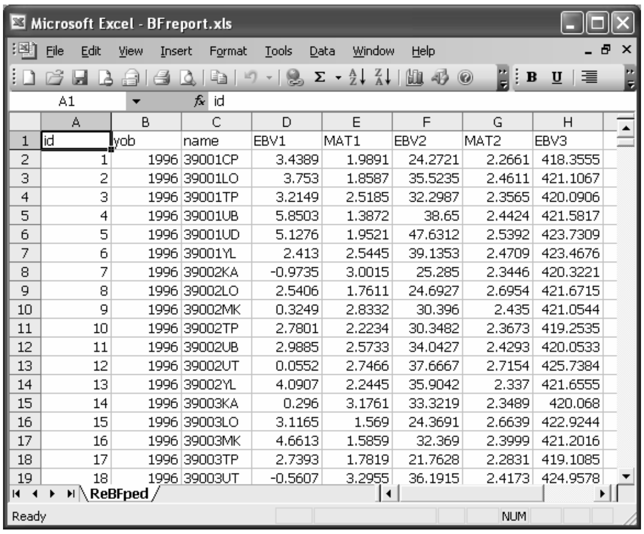
Trait Number : 1

Animal effect in solutions : 6

EBV Report: BFreport

10. BV reports for single trait and multiple trait from previous solutions from BeefPack or another BLUP family can be recreated with specified options.

11. Multiple trait BV reports for direct and maternal can be created up to 4 traits.

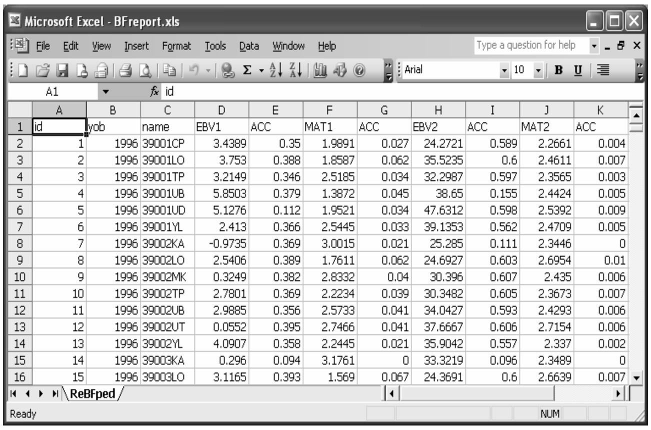


Microsoft Excel - BFreport.xls

A1 id

	A	B	C	D	E	F	G	H
1	id	yob	name	EBV1	MAT1	EBV2	MAT2	EBV3
2	1	1996	39001CP	3.4389	1.9891	24.2721	2.2661	418.3555
3	2	1996	39001LO	3.753	1.8587	35.5235	2.4611	421.1067
4	3	1996	39001TP	3.2149	2.5185	32.2987	2.3565	420.0906
5	4	1996	39001UB	5.8503	1.3872	38.65	2.4424	421.5817
6	5	1996	39001UD	5.1276	1.9521	47.6312	2.5392	423.7309
7	6	1996	39001YL	2.413	2.5445	39.1353	2.4709	423.4676
8	7	1996	39002KA	-0.9735	3.0015	25.285	2.3446	420.3221
9	8	1996	39002LO	2.5406	1.7611	24.6927	2.6954	421.6715
10	9	1996	39002MK	0.3249	2.8332	30.396	2.435	421.0544
11	10	1996	39002TP	2.7801	2.2234	30.3482	2.3673	419.2535
12	11	1996	39002UB	2.9885	2.5733	34.0427	2.4293	420.0533
13	12	1996	39002UT	0.0552	2.7466	37.6667	2.7154	425.7384
14	13	1996	39002YL	4.0907	2.2445	35.9042	2.337	421.6555
15	14	1996	39003KA	0.296	3.1761	33.3219	2.3489	420.068
16	15	1996	39003LO	3.1165	1.569	24.3691	2.6639	422.9244
17	16	1996	39003MK	4.6613	1.5859	32.369	2.3999	421.2016
18	17	1996	39003TP	2.7393	1.7819	21.7628	2.2831	419.1085
19	18	1996	39003UT	-0.5607	3.2955	36.1915	2.4173	424.9578

12. Report with accuracy can also be created.



Microsoft Excel - BFreport.xls

A1 id

	A	B	C	D	E	F	G	H	I	J	K
1	id	yob	name	EBV1	ACC	MAT1	ACC	EBV2	ACC	MAT2	ACC
2	1	1996	39001CP	3.4389	0.35	1.9891	0.027	24.2721	0.589	2.2661	0.004
3	2	1996	39001LO	3.753	0.388	1.8587	0.062	35.5235	0.6	2.4611	0.007
4	3	1996	39001TP	3.2149	0.346	2.5185	0.034	32.2987	0.597	2.3565	0.003
5	4	1996	39001UB	5.8503	0.379	1.3872	0.045	38.65	0.155	2.4424	0.005
6	5	1996	39001UD	5.1276	0.112	1.9521	0.034	47.6312	0.598	2.5392	0.009
7	6	1996	39001YL	2.413	0.366	2.5445	0.033	39.1353	0.562	2.4709	0.005
8	7	1996	39002KA	-0.9735	0.369	3.0015	0.021	25.285	0.111	2.3446	0
9	8	1996	39002LO	2.5406	0.389	1.7611	0.062	24.6927	0.603	2.6954	0.01
10	9	1996	39002MK	0.3249	0.382	2.8332	0.04	30.396	0.607	2.435	0.006
11	10	1996	39002TP	2.7801	0.369	2.2234	0.039	30.3482	0.605	2.3673	0.007
12	11	1996	39002UB	2.9885	0.356	2.5733	0.041	34.0427	0.593	2.4293	0.006
13	12	1996	39002UT	0.0552	0.395	2.7466	0.041	37.6667	0.606	2.7154	0.006
14	13	1996	39002YL	4.0907	0.358	2.2445	0.021	35.9042	0.557	2.337	0.002
15	14	1996	39003KA	0.296	0.094	3.1761	0	33.3219	0.096	2.3489	0
16	15	1996	39003LO	3.1165	0.393	1.569	0.067	24.3691	0.6	2.6639	0.007

IV. Model Descriptions

The main objective of BLUPF90-BeefPack is to accomplish various model generally used in beef cattle evaluation with friendly graphic interface for PC and Windows users. Using powerful features from programs of BLUPF90, BeefPack can accomplish a wide range of genetic evaluation. BeefPack can estimate variance components with REML and perform BLUP analysis from linear mixed model which includes random effect of animal as additive genetic or permanent environment effect. The following will describe more details of model that can be used in the analysis.

A. Basic Animal Model

BeefPack provide basic animal model which allows animals in the data and animals in the pedigree to be included in the analysis so that all known relationships can be taken into account. Other effects, fixed and random, can be including for comprehensive use of mixed model. Fixed effects used in the model can be fitted as cross-classified variable and covariate. Combination of fixed effects such as herd-year-season can be performed during the analysis, therefore, no adding step of data preparation is required. Normally, all traits used in BeefPack should be continuous rather than ordinal scale for proper use in the analysis of linear mixed model. Model with single record per animal such as daily gain yield can be analyzed by basic animal model as follow:

$$\boldsymbol{y} = \boldsymbol{X\beta} + \boldsymbol{Za} + \boldsymbol{\varepsilon} \text{, and } V\begin{bmatrix} \boldsymbol{a} \\ \boldsymbol{\varepsilon} \end{bmatrix} = \begin{bmatrix} \boldsymbol{A}\sigma_a^2 & \boldsymbol{0} \\ \boldsymbol{0} & \boldsymbol{I}\sigma_e^2 \end{bmatrix},$$

where $\boldsymbol{y}$ is vector of response variable, $\boldsymbol{\beta}$ is vector of fixed effects, $\boldsymbol{a}$ is vector of random additive genetic effects, $\boldsymbol{\varepsilon}$ is vector of random residual, $\boldsymbol{X}$ and $\boldsymbol{Z}$ are incident matrices related to fixed and random effects, $\boldsymbol{A}$ is numerator relationship matrix, σ_a^2 is additive genetic variance, and σ_e^2 is residual variance.

To perform BLUP, Henderson's MME can be written as:

$$\begin{bmatrix} \boldsymbol{X'X} & \boldsymbol{X'Z} \\ \boldsymbol{Z'X} & \boldsymbol{Z'Z} + \alpha \boldsymbol{A}^{-1} \end{bmatrix} \begin{bmatrix} \boldsymbol{\beta} \\ \boldsymbol{a} \end{bmatrix} = \begin{bmatrix} \boldsymbol{X'y} \\ \boldsymbol{Z'y} \end{bmatrix} \text{, where } \alpha = \frac{\sigma_e^2}{\sigma_a^2}$$

B. Animal with PE Model

If multiple parity records are available, the maternal permanent environment effect due to dam need to be taken into account. Fitting maternal permanent environment effect as uncorrelated random effects is generally used in genetic evaluation. The model for analysis is:

$$\boldsymbol{y} = \boldsymbol{X\beta} + \boldsymbol{Za} + \boldsymbol{Wc} + \boldsymbol{\varepsilon} \text{, and } V\begin{bmatrix} \boldsymbol{a} \\ \boldsymbol{c} \\ \boldsymbol{\varepsilon} \end{bmatrix} = \begin{bmatrix} \boldsymbol{A}\sigma_a^2 & \boldsymbol{0} & \boldsymbol{0} \\ \boldsymbol{0} & \boldsymbol{I}\sigma_c^2 & \boldsymbol{0} \\ \boldsymbol{0} & \boldsymbol{0} & \boldsymbol{I}\sigma_e^2 \end{bmatrix},$$

where $\boldsymbol{y}$ is vector of response variable, $\boldsymbol{\beta}$ is vector of fixed effects, $\boldsymbol{a}$ is vector of random additive genetic effects, $\boldsymbol{c}$ is vector of random permanent environment effects, $\boldsymbol{\varepsilon}$ is vector of random residual, $\boldsymbol{X}$, $\boldsymbol{W}$ and $\boldsymbol{Z}$ are incident matrices related to fixed and random effects, $\boldsymbol{A}$ is numerator relationship matrix, σ_a^2 is additive genetic variance, σ_c^2 is additive genetic variance, and σ_e^2 is residual variance.

To perform BLUP, Henderson's MME can be written as:

$$\begin{bmatrix} \boldsymbol{X'X} & \boldsymbol{X'Z} & \boldsymbol{X'W} \\ \boldsymbol{Z'X} & \boldsymbol{Z'Z}+\alpha \boldsymbol{A}^{-1} & \boldsymbol{Z'W} \\ \boldsymbol{W'X} & \boldsymbol{W'Z} & \boldsymbol{W'W}+\gamma \boldsymbol{I} \end{bmatrix} \begin{bmatrix} \boldsymbol{\beta} \\ \boldsymbol{a} \\ \boldsymbol{c} \end{bmatrix} = \begin{bmatrix} \boldsymbol{X'y} \\ \boldsymbol{Z'y} \\ \boldsymbol{W'y} \end{bmatrix}, \text{ where } \alpha = \frac{\sigma_e^2}{\sigma_a^2},\ \gamma = \frac{\sigma_e^2}{\sigma_c^2}$$

C. Maternal Model

If multiple parity records are available, also such trait could be effected by maternal genetic, therefore the maternal permanent environment effect and maternal genetic due to dam need to be taken into account. Fitting maternal permanent environment effect as uncorrelated random effects and maternal genetic effect as correlated random effects are generally used in genetic evaluation. The model for analysis is:

$$\boldsymbol{y} = \boldsymbol{X\beta} + \boldsymbol{Z_1 a} + \boldsymbol{Z_2 m} + \boldsymbol{Wc} + \boldsymbol{\varepsilon}, \text{ and } V\begin{bmatrix} \boldsymbol{a} \\ \boldsymbol{m} \\ \boldsymbol{c} \\ \boldsymbol{\varepsilon} \end{bmatrix} = \begin{bmatrix} \boldsymbol{A}\sigma_a^2 & \boldsymbol{A}\sigma_{am} & \boldsymbol{0} & \boldsymbol{0} \\ \boldsymbol{A}\sigma_{am} & \boldsymbol{A}\sigma_m^2 & \boldsymbol{0} & \boldsymbol{0} \\ \boldsymbol{0} & \boldsymbol{0} & \boldsymbol{I}\sigma_c^2 & \boldsymbol{0} \\ \boldsymbol{0} & \boldsymbol{0} & \boldsymbol{0} & \boldsymbol{I}\sigma_e^2 \end{bmatrix},$$

where $\boldsymbol{y}$ is vector of response variable, $\boldsymbol{\beta}$ is vector of fixed effects, $\boldsymbol{a}$ is vector of random additive direct genetic effects, $\boldsymbol{m}$ is vector of random additive maternal genetic effects, $\boldsymbol{c}$ is vector of random permanent environment effects, $\boldsymbol{\varepsilon}$ is vector of random residual, $\boldsymbol{X}$, $\boldsymbol{W}$, $\boldsymbol{Z_1}$ and $\boldsymbol{Z}_2$ are incident matrices related to fixed and random effects, $\boldsymbol{A}$ is numerator relationship matrix, σ_a^2 is additive direct genetic variance, σ_m^2 is additive maternal genetic variance, , σ_{am} is direct-maternal genetic covariance, σ_c^2 is maternal permanent environmental variance, and σ_e^2 is residual variance.

To perform BLUP, Henderson's MME can be written as:

$$\begin{bmatrix} \boldsymbol{X'X} & \boldsymbol{X'Z_1} & \boldsymbol{X'Z}_2 & \boldsymbol{X'W} \\ \boldsymbol{Z_1'X} & \boldsymbol{Z_1'Z_1}+\alpha^{11}\boldsymbol{A}^{-1} & \boldsymbol{Z_1'Z_2}+\alpha^{12}\boldsymbol{A}^{-1} & \boldsymbol{Z_1'W} \\ \boldsymbol{Z_2'X} & \boldsymbol{Z_2'Z_1}+\alpha^{21}\boldsymbol{A}^{-1} & \boldsymbol{Z_2'Z_2}+\alpha^{22}\boldsymbol{A}^{-1} & \boldsymbol{Z_2'W} \\ \boldsymbol{W'X} & \boldsymbol{W'Z_1} & \boldsymbol{W'Z}_2 & \boldsymbol{W'W}+\gamma\boldsymbol{I} \end{bmatrix} \begin{bmatrix} \boldsymbol{\beta} \\ \boldsymbol{a} \\ \boldsymbol{m} \\ \boldsymbol{c} \end{bmatrix} = \begin{bmatrix} \boldsymbol{X'y} \\ \boldsymbol{Z_1'y} \\ \boldsymbol{Z_2'y} \\ \boldsymbol{W'y} \end{bmatrix},$$

$$\text{where} \begin{bmatrix} \alpha^{11} & \alpha^{12} \\ \alpha^{21} & \alpha^{22} \end{bmatrix} = \sigma_e^2 \begin{bmatrix} \sigma_a^2 & \sigma_{am} \\ \sigma_{am} & \sigma_m^2 \end{bmatrix}^{-1},\ \gamma = \frac{\sigma_e^2}{\sigma_c^2}$$

D. Multi-trait Model

BeefPack can also perform multi-trait analysis. Estimation of genetic correlations among traits and multivariate BLUP analysis can be accomplished. However, for graphic user interface, not greater than 4 traits is available. To perform beyond this, parameter editing is required and do the analysis from menu **BLUP>Use old parameters**. Multi-trait analysis can perform similar model for all traits, missing records for some traits, different model for each trait, also different contemporary group for each trait. For example, the following traits for birth weight, weaning weight and yearling weight can be analyzed together.

$$\begin{bmatrix} \boldsymbol{y_1} \\ \boldsymbol{y_2} \\ \boldsymbol{y_3} \end{bmatrix} = \begin{bmatrix} \boldsymbol{X_1} & \boldsymbol{0} & \boldsymbol{0} \\ \boldsymbol{0} & \boldsymbol{X_2} & \boldsymbol{0} \\ \boldsymbol{0} & \boldsymbol{0} & \boldsymbol{X_3} \end{bmatrix} \begin{bmatrix} \boldsymbol{\beta_1} \\ \boldsymbol{\beta_2} \\ \boldsymbol{\beta_3} \end{bmatrix} + \begin{bmatrix} \boldsymbol{Z_1} & \boldsymbol{0} & \boldsymbol{0} \\ \boldsymbol{0} & \boldsymbol{Z_2} & \boldsymbol{0} \\ \boldsymbol{0} & \boldsymbol{0} & \boldsymbol{Z_3} \end{bmatrix} \begin{bmatrix} \boldsymbol{a_1} \\ \boldsymbol{a_2} \\ \boldsymbol{a_3} \end{bmatrix} + \begin{bmatrix} \boldsymbol{M_1} & \boldsymbol{0} & \boldsymbol{0} \\ \boldsymbol{0} & \boldsymbol{M_2} & \boldsymbol{0} \\ \boldsymbol{0} & \boldsymbol{0} & \boldsymbol{0} \end{bmatrix} \begin{bmatrix} \boldsymbol{m_1} \\ \boldsymbol{m_2} \\ \boldsymbol{0} \end{bmatrix} + \begin{bmatrix} \boldsymbol{W_1} & \boldsymbol{0} & \boldsymbol{0} \\ \boldsymbol{0} & \boldsymbol{W_2} & \boldsymbol{0} \\ \boldsymbol{0} & \boldsymbol{0} & \boldsymbol{0} \end{bmatrix} \begin{bmatrix} \boldsymbol{c_1} \\ \boldsymbol{c_2} \\ \boldsymbol{0} \end{bmatrix} + \begin{bmatrix} \boldsymbol{\varepsilon_1} \\ \boldsymbol{\varepsilon_2} \\ \boldsymbol{\varepsilon_3} \end{bmatrix}$$

Where $V\begin{bmatrix} \boldsymbol{a} \\ \boldsymbol{m} \end{bmatrix} = \boldsymbol{G} \otimes \boldsymbol{A}$, $V[\boldsymbol{c}] = \boldsymbol{W} \otimes \boldsymbol{I}$, $V[\varepsilon] = \boldsymbol{R} \otimes \boldsymbol{I}$

where $\boldsymbol{y_1}, \boldsymbol{y_2}, \boldsymbol{y_3}$ is vector of response variable for trait 1, 2 and 3; $\boldsymbol{\beta_1}, \boldsymbol{\beta_2}, \boldsymbol{\beta_3}$ is vector of fixed effects; $\boldsymbol{a_1}, \boldsymbol{a_2}, \boldsymbol{a_3}$ is vector of random additive direct genetic effects; $\boldsymbol{m_1}, \boldsymbol{m_2}$ is vector of random additive maternal genetic effects; $\boldsymbol{c_1}, \boldsymbol{c_2}$ is vector of random maternal permanent environmental effects; $\boldsymbol{\varepsilon_1}, \boldsymbol{\varepsilon_2}, \boldsymbol{\varepsilon_3}$ is vector of random residual, $\boldsymbol{X}$, $\boldsymbol{M}$, $\boldsymbol{W}$ and $\boldsymbol{Z}$ are incident matrices related to fixed and random effects, $\boldsymbol{A}$ is numerator relationship matrix, $\boldsymbol{G}$ is matrix of direct-maternal genetic variance-covariance for trait 1, 2 and 3; $\boldsymbol{W}$ is matrix of maternal permanent environmental variance-covariance for trait 1 and 2; $\boldsymbol{R}$ is matrix of residual variance-covariance for trait 1,2 and 2.

V. How Program Functions?

A. Program and file components

After installation, programs are stored in main or user-specified directory, ie. C:\BLUPF90-BP. Two sub-directories of examples and helps are also created. Each directory will find the following programs and files.

Main directory:

Name	Type	Description
BeefPack.xls	XLS	- Main graphic user interface. - Creating BLUP and REML parameter files. - Creating BLUP and VCE report in excel format. - Creating genetic trend. - Computing BV and h^2 for test day model.
BLUPF90.EXE	PROG	- Computing BLUP solutions.
REMLF90.EXE	PROG	- Estimating variance components using REML with EM algorithm.
AIREMLF90.EXE	PROG	- Estimating variance components using REML with AI algorithm.
ACCF90.EXE	PROG	- Computing approximate accuracy for BLUP solutions.
RENUMMAT.EXE	PROG	- Renumbering animal in data and pedigree file in consecutive order number.

Examples directory:

Name	Type	Description
BFDAT.PRN	TXT	- Data file for analysis with single trait and multi-trait with maternal effects and repeated records.
BFPED.PRN	TXT	- Pedigree file for analysis with BFDAT.
BFDAT.FMT	TXT	- Describe column number format for BFDAT.PRN

Helps directory:

Name	Type	Description
WHOSWHO.TXT	TXT	- Accredit for key persons involved in BLUPF90 family.
Manual-BP.PDF	PDF	- Manual for BLUPF90 BeefPack

B. The way program works

When performed the analysis with wizard interface in BeefPack. All parameters entered in the form will be kept in particular Excel sheets. They will be written with corrected format as parameter file for RENUM and BLUPF90 using visual basic. Batch file to call the program with the parameter is also need to be created. VB in Excel has specific function to operate EXE file in this batch without closing the Excel program. Pedigree and solutions from the analysis are read to Excel sheets to join back the original animal ID, and also genetic trend will be created using chart function if user required.

Data and Pedigree files used in BeefPack must be ASCII or TEXT file. All data must be in number, except for animal ID, Sire, and Dam that can be alpha-numeric format. If create from Excel, Save as PRN file (Text file delimited with space) is preferable than Tab delimited or comma delimited.

If analyzing data is kept in different directory of programs. All execute programs will be copied to the data directory. After analysis, a few file will be created, which can be copied to new name if need.

Suppose the original files for the analysis are BFDAT.PRN and BFPED.PRN, some additional files after analysis, which might be useful for later analysis, are:

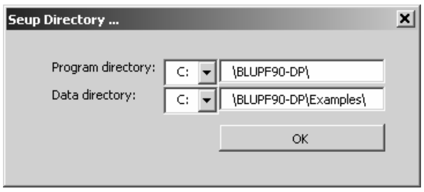
Name	Type	Description
REBFDAT.PRN	TXT	- Renumbered data file.
REBFPED.PRN	TXT	- Renumbered Pedigree file.
RENUM.PAR	TXT	- Parameter file for program RENUMMAT.
RENUM.MSG	TXT	- Log file from renumbering. Describe the levels of fixed and random effects after renum.
RENUM.PRN	TXT	- The details from renumbering. Describe how effects are combined and replications of each effects.
BLUP.PAR	TXT	- Parameter files for REML and BLUP analysis
SOLUTIONS	TXT	- BLUP solutions file.
SOLUTIONS_VCE	TXT	- This file keeps variance estimation if performed.

B. Solutions at Convergence

The default for convergence is 1d-08, however, users can choose their own by selecting menu **Options > Set Options**.

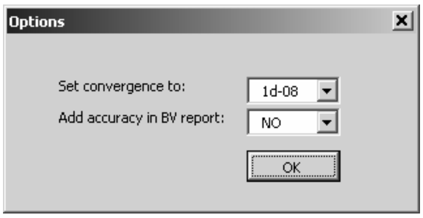
VI. Genetic Evaluation by Examples

A. Setup Directory and Preferences



Program directory: C: \BLUPF90-DP\
Data directory: C: \BLUPF90-DP\Examples\

1. The correct directory for program files and data files need to be checked or set up before starting the analysis. Select menu **Directory >Setup Directory**.



Set convergence to: 1d-08
Add accuracy in BV report: NO

2. Other options like convergence levels and accuracy in the reports can be chosen. Select menu **Options > Set Options**.

B. Data and Pedigree files

Single trait analysis

The example will show how to predict breeding value for milk production adjusted for 305 day. BFDAT.PRN is data file and BFPED.PRN is pedigree file.

Multi-trait analysis

The example will show how to estimate genetic correlation and predict multivariate breeding value for milk305, fat and protein yield. BFDAT.PRN is data file and BFPED.PRN is pedigree file.

File format

Format for BFDAT.PRN is stored in BFMDAT.FMT. There are 11 columns of:

#1	ID
#2	Sex
#3	Herd
#4	Parity
#5	Age of dam (month)
#6	Month at birth
#7	Year at birth
#8	Birth weight
#9	Month at weaning
#10	Year at weaning
#11	Weaning weight

Format for pedigree is the same. There are 4 columns of:

#1	Animal ID
#2	Sire ID
#3	Dam ID
#4	Year of birth.

Generally, year of birth can be omit from pedigree file, however genetic trend cannot to be created. For maternal direct or PE model, dam column is not required in data file (program will automatically creat from pedigreed).

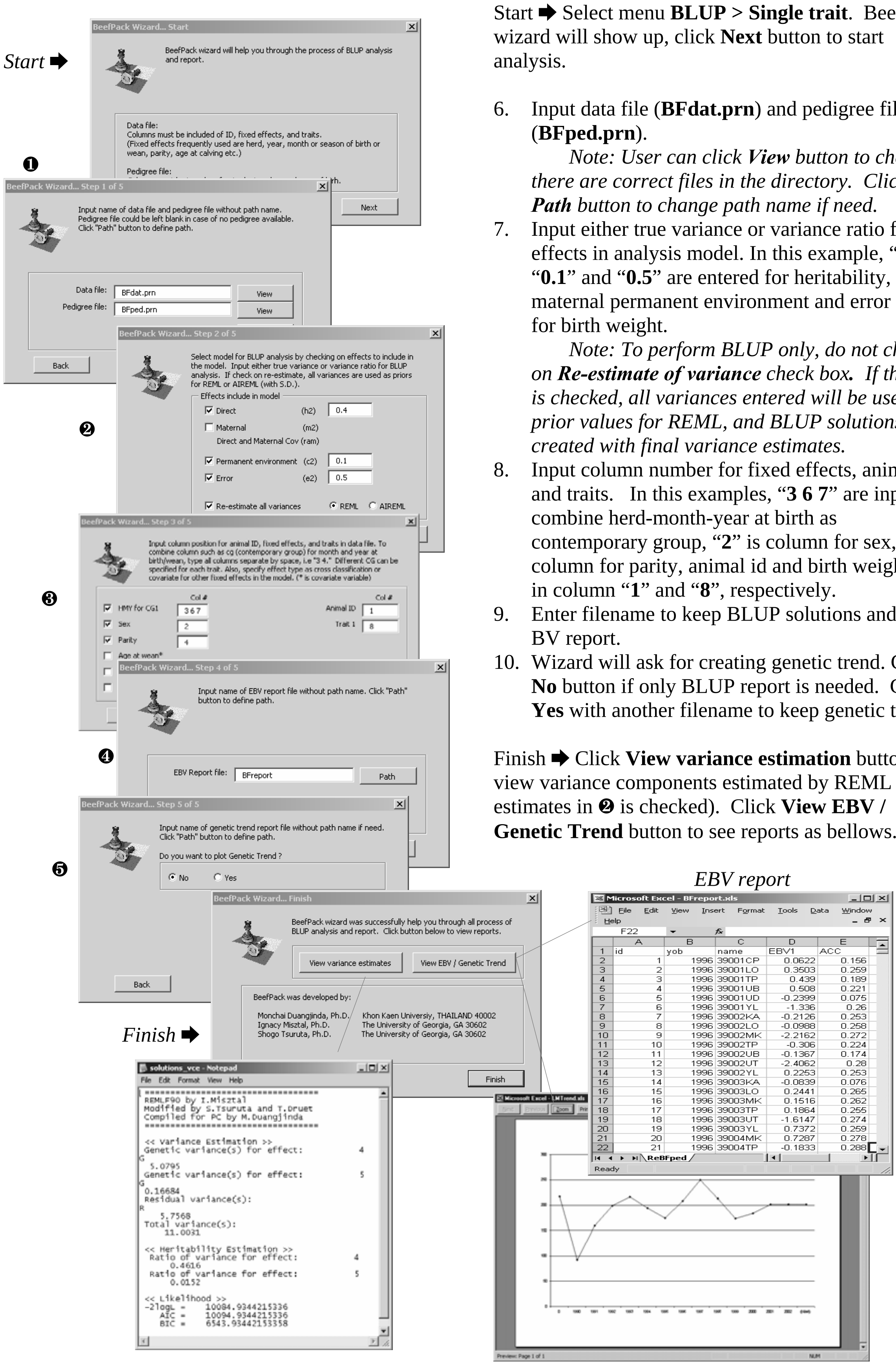
Note: all files are stored in C:\BLUPF90-BP\EXAMPLES.

C. Single Trait Analysis Example

Start ➡ Select menu **BLUP > Single trait**. BeefPack wizard will show up, click **Next** button to start analysis.

6. Input data file (**BFdat.prn**) and pedigree file (**BFped.prn**).
   *Note: User can click **View** button to check if there are correct files in the directory. Click at **Path** button to change path name if need.*
7. Input either true variance or variance ratio for effects in analysis model. In this example, "**0.4**", "**0.1**" and "**0.5**" are entered for heritability, maternal permanent environment and error ratio for birth weight.
   *Note: To perform BLUP only, do not check on **Re-estimate of variance** check box. If this box is checked, all variances entered will be used as prior values for REML, and BLUP solutions will created with final variance estimates.*
8. Input column number for fixed effects, animal and traits. In this examples, "**3 6 7**" are input to combine herd-month-year at birth as contemporary group, "**2**" is column for sex, "**4**" is column for parity, animal id and birth weight are in column "**1**" and "**8**", respectively.
9. Enter filename to keep BLUP solutions and create BV report.
10. Wizard will ask for creating genetic trend. Click **No** button if only BLUP report is needed. Click **Yes** with another filename to keep genetic trend.

Finish ➡ Click **View variance estimation** button to view variance components estimated by REML (if Re-estimates in ❷ is checked). Click **View EBV / Genetic Trend** button to see reports as bellows.



BeefPack wizard will help you through the process of BLUP analysis and report.

Data file:
Columns must be included of ID, fixed effects, and traits.
(Fixed effects frequently used are herd, year, month or season of birth or wean, parity, age at calving etc.)

Pedigree file:

Input name of data file and pedigree file without path name. Pedigree file could be left blank in case of no pedigree available. Click "Path" button to define path.

Data file: BFdat.prn
Pedigree file: BFped.prn

Select model for BLUP analysis by checking on effects to include in the model. Input either true variance or variance ratio for BLUP analysis. If check on re-estimate, all variances are used as priors for REML or AIREML (with S.D.).

Effects include in model
☑ Direct (h2) 0.4
☐ Maternal (m2)
Direct and Maternal Cov (ram)
☑ Permanent environment (c2) 0.1
☑ Error (e2) 0.5
☑ Re-estimate all variances ● REML ○ AIREML

Input column position for animal ID, fixed effects, and traits in data file. To combine column such as cg (contemporary group) for month and year at birth/wean, type all columns separate by space, i.e "3 4." Different CG can be specified for each trait. Also, specify effect type as cross classification or covariate for other fixed effects in the model. (* is covariate variable)

	Col #		Col #
☑ HMY for CG1	3 6 7	Animal ID	1
☑ Sex	2	Trait 1	8
☑ Parity	4		
☐ Age at wean*			
☐			
☐			

Input name of EBV report file without path name. Click "Path" button to define path.

EBV Report file: BFreport

Input name of genetic trend report file without path name if need. Click "Path" button to define path.

Do you want to plot Genetic Trend ?
● No ○ Yes

BeefPack wizard was successfully help you through all process of BLUP analysis and report. Click button below to view reports.

BeefPack was developed by:

Monchai Duangjinda, Ph.D. Khon Kaen Universiy, THAILAND 40002
Ignacy Misztal, Ph.D. The University of Georgia, GA 30602
Shogo Tsuruta, Ph.D. The University of Georgia, GA 30602

```
 ===================================
 REMLF90 by I.Misztal
 Modified by S.Tsuruta and T.Druet
 Compiled for PC by M.Duangjinda
 ===================================

 << Variance Estimation >>
 Genetic variance(s) for effect:          4
G
  5.0795
 Genetic variance(s) for effect:          5
G
 0.16684
 Residual variance(s):
R
    5.7568
 Total variance(s):
     11.0031

 << Heritability Estimation >>
  Ratio of variance for effect:          4
      0.4616
  Ratio of variance for effect:          5
      0.0152

 << Likelihood >>
 -2logL =    10084.9344215336
    AIC =    10094.9344215336
    BIC =    6543.93442153358
```

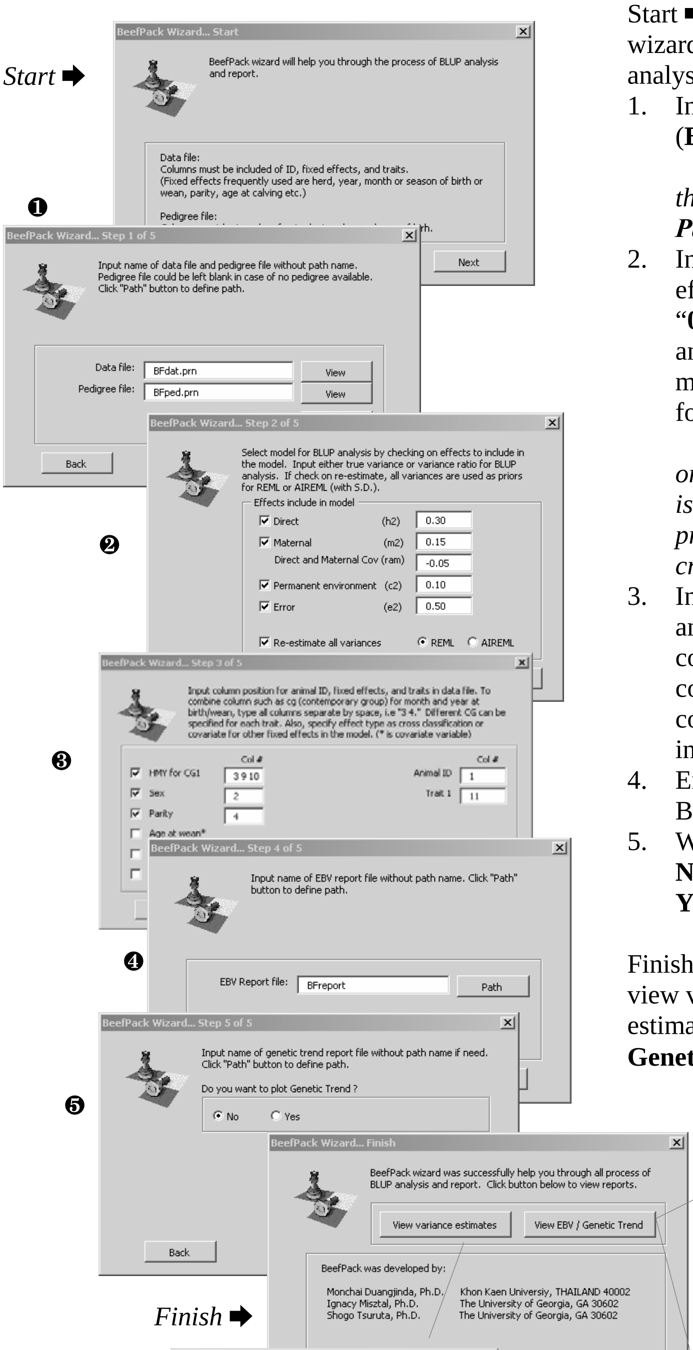
	A	B	C	D	E
1	id	yob	name	EBV1	ACC
2	1	1996	39001CP	0.0622	0.156
3	2	1996	39001LO	0.3503	0.259
4	3	1996	39001TP	0.439	0.189
5	4	1996	39001UB	0.508	0.221
6	5	1996	39001UD	-0.2399	0.075
7	6	1996	39001YL	-1.336	0.26
8	7	1996	39002KA	-0.2126	0.253
9	8	1996	39002LO	-0.0988	0.258
10	9	1996	39002MK	-2.2162	0.272
11	10	1996	39002TP	-0.306	0.224
12	11	1996	39002UB	-0.1367	0.174
13	12	1996	39002UT	-2.4062	0.28
14	13	1996	39002YL	0.2253	0.253
15	14	1996	39003KA	-0.0839	0.076
16	15	1996	39003LO	0.2441	0.265
17	16	1996	39003MK	0.1516	0.262
18	17	1996	39003TP	0.1864	0.255
19	18	1996	39003UT	-1.6147	0.274
20	19	1996	39003YL	0.7372	0.259
21	20	1996	39004MK	0.7287	0.278
22	21	1996	39004TP	-0.1833	0.288

EBV report

VCE report

Genetic trend

D. Maternal with PE Model Example



BeefPack Wizard... Start

BeefPack wizard will help you through the process of BLUP analysis and report.

Data file:
Columns must be included of ID, fixed effects, and traits.
(Fixed effects frequently used are herd, year, month or season of birth or wean, parity, age at calving etc.)

Pedigree file:

BeefPack Wizard... Step 1 of 5

Input name of data file and pedigree file without path name. Pedigree file could be left blank in case of no pedigree available. Click "Path" button to define path.

Data file: BFdat.prn
Pedigree file: BFped.prn

BeefPack Wizard... Step 2 of 5

Select model for BLUP analysis by checking on effects to include in the model. Input either true variance or variance ratio for BLUP analysis. If check on re-estimate, all variances are used as priors for REML or AIREML (with S.D.).

Effects include in model
☑ Direct (h2) 0.30
☑ Maternal (m2) 0.15
Direct and Maternal Cov (ram) -0.05
☑ Permanent environment (c2) 0.10
☑ Error (e2) 0.50
☑ Re-estimate all variances ● REML ○ AIREML

BeefPack Wizard... Step 3 of 5

Input column position for animal ID, fixed effects, and traits in data file. To combine column such as cg (contemporary group) for month and year at birth/wean, type all columns separate by space, i.e "3 4." Different CG can be specified for each trait. Also, specify effect type as cross classification or covariate for other fixed effects in the model. (* is covariate variable)

	Col #		Col #
☑ HMY for CG1	3 9 10	Animal ID	1
☑ Sex	2	Trait 1	11
☑ Parity	4		
☐ Age at wean*			

BeefPack Wizard... Step 4 of 5

Input name of EBV report file without path name. Click "Path" button to define path.

EBV Report file: BFreport

BeefPack Wizard... Step 5 of 5

Input name of genetic trend report file without path name if need. Click "Path" button to define path.

Do you want to plot Genetic Trend ?
● No ○ Yes

BeefPack Wizard... Finish

BeefPack wizard was successfully help you through all process of BLUP analysis and report. Click button below to view reports.

View variance estimates | View EBV / Genetic Trend

BeefPack was developed by:

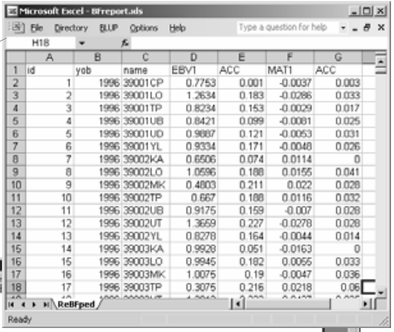
Monchai Duangjinda, Ph.D. Khon Kaen Universiy, THAILAND 40002
Ignacy Misztal, Ph.D. The University of Georgia, GA 30602
Shogo Tsuruta, Ph.D. The University of Georgia, GA 30602

Start ➡ Select menu **BLUP > Single trait**. BeefPack wizard will show up, click **Next** button to start analysis.

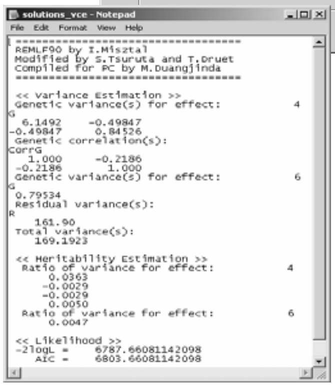
1. Input data file (**BFdat.prn**) and pedigree file (**BFped.prn**).
   *Note: User can click **View** button to check if there are correct files in the directory. Click at **Path** button to change path name if need.*
2. Input either true variance or variance ratio for effects in analysis model. In this example, "**0.30**", "**0.15**" and "-**0.05**" are entered for direct, maternal and covariance ratio; "**0.10**" and "**0.50**" for maternal permanent environment and error ratio for weaning weight.
   *Note: To perform BLUP only, do not check on **Re-estimate of variance** check box. If this box is checked, all variances entered will be used as prior values for REML, and BLUP solutions will created with final variance estimates.*
3. Input column number for fixed effects, animal and traits. In this examples, "**3 9 10**" are input to combine herd-month-year at birth as contemporary group, "**2**" is column for sex, "**4**" is column for parity, animal id and birth weight are in column "**1**" and "**11**", respectively.
4. Enter filename to keep BLUP solutions and create BV report.
5. Wizard will ask for creating genetic trend. Click **No** button if only BLUP report is needed. Click **Yes** with another filename to keep genetic trend.

Finish ➡ Click **View variance estimation** button to view variance components estimated by REML (if Re-estimates in ❷ is checked). Click **View EBV / Genetic Trend** button to see reports as bellows.

EBV report

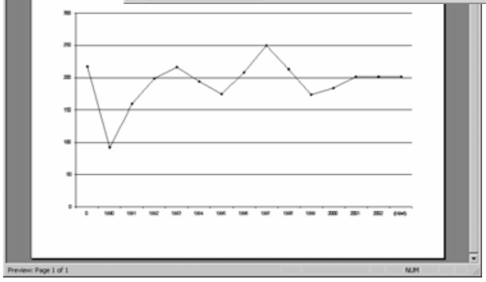


	A	B	C	D	E	F	G
1	id	yob	name	EBV1	ACC	MAT1	ACC
2	1	1996	39001CP	0.7753	0.001	-0.0037	0.003
3	2	1996	39001LO	1.2634	0.183	-0.0286	0.033
4	3	1996	39001TP	0.8234	0.153	-0.0029	0.017
5	4	1996	39001UB	0.8421	0.099	-0.0081	0.025
6	5	1996	39001UD	0.9887	0.121	-0.0053	0.031
7	6	1996	39001YL	0.9334	0.171	-0.0048	0.026
8	7	1996	39002KA	0.6506	0.074	0.0114	0
9	8	1996	39002LO	1.0596	0.188	0.0155	0.041
10	9	1996	39002MK	0.4803	0.211	0.022	0.028
11	10	1996	39002TP	0.667	0.188	0.0116	0.032
12	11	1996	39002UB	0.9175	0.159	-0.007	0.028
13	12	1996	39002UT	1.3659	0.227	-0.0278	0.028
14	13	1996	39002YL	0.8278	0.164	-0.0044	0.014
15	14	1996	39003KA	0.9928	0.051	-0.0163	0
16	15	1996	39003LO	0.9945	0.182	0.0055	0.033
17	16	1996	39003MK	1.0075	0.19	-0.0047	0.036
18	17	1996	39003TP	0.3075	0.216	0.0218	0.06



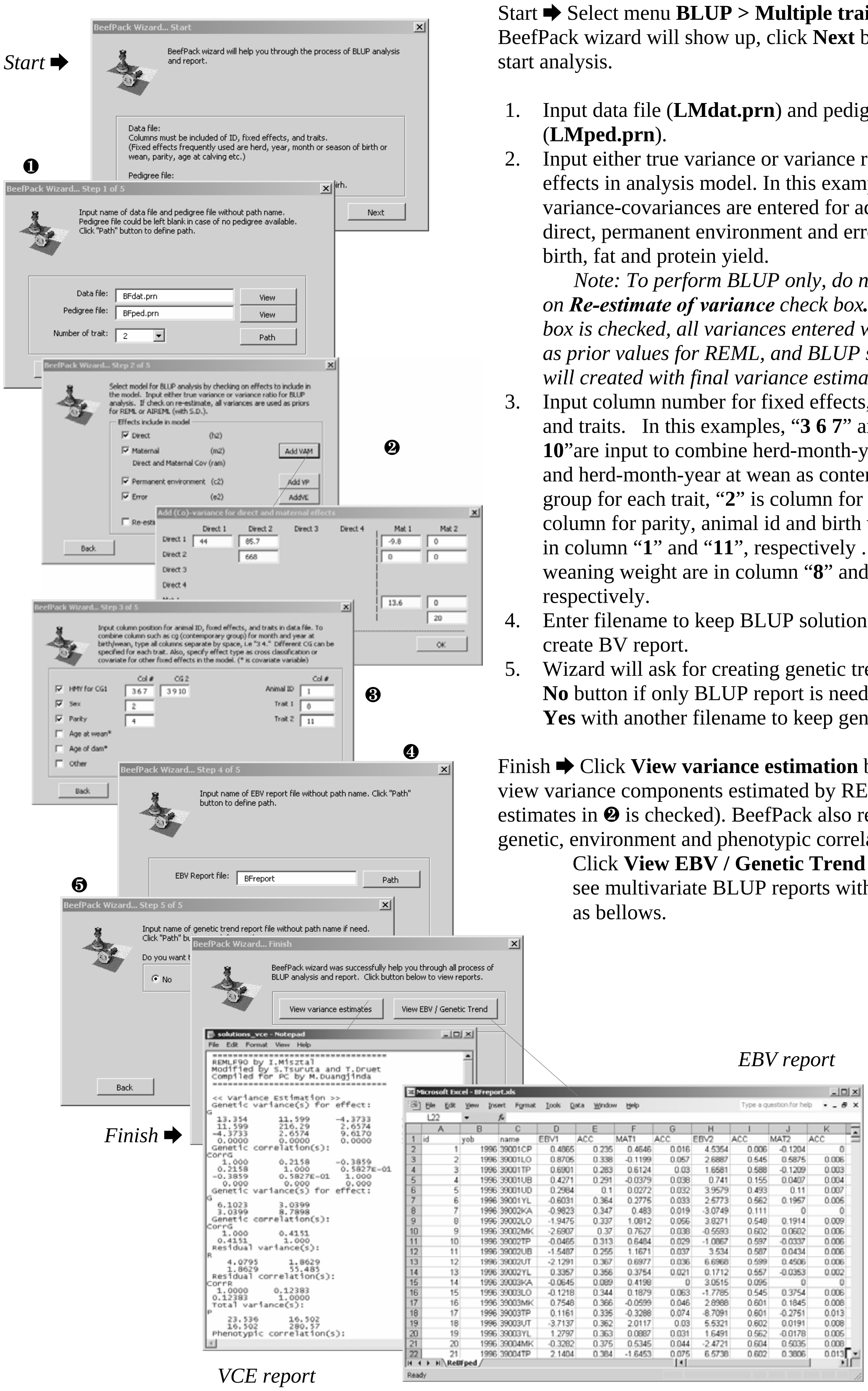
```
 ===================================
 REMLF90 by I.Misztal
 Modified by S.Tsuruta and T.Druet
 Compiled for PC by M.Duangjinda
 ===================================

 << Variance Estimation >>
 Genetic variance(s) for effect:        4
G
  6.1492     -0.49847
-0.49847      0.84526
 Genetic correlation(s):
CorrG
   1.000      -0.2186
 -0.2186        1.000
 Genetic variance(s) for effect:        6
G
 0.79534
 Residual variance(s):
R
    161.90
 Total variance(s):
    169.1923

 << Heritability Estimation >>
  Ratio of variance for effect:        4
      0.0363
     -0.0029
     -0.0029
      0.0050
  Ratio of variance for effect:        6
      0.0047

 << Likelihood >>
 -2logL =     6787.66081142098
    AIC =     6803.66081142098
```

VCE report



Genetic trend

E. Multi-trait Analysis Example



Start ➨ Select menu **BLUP > Multiple trait**. BeefPack wizard will show up, click **Next** button to start analysis.

1. Input data file (**LMdat.prn**) and pedigree file (**LMped.prn**).
2. Input either true variance or variance ratio for effects in analysis model. In this example, variance-covariances are entered for additive direct, permanent environment and error for trait birth, fat and protein yield.

   *Note: To perform BLUP only, do not check on **Re-estimate of variance** check box. If this box is checked, all variances entered will be used as prior values for REML, and BLUP solutions will created with final variance estimates.*
3. Input column number for fixed effects, animal and traits. In this examples, "**3 6 7**" and "**3 9 10**"are input to combine herd-month-year at birth and herd-month-year at wean as contemporary group for each trait, "**2**" is column for sex, "**4**" is column for parity, animal id and birth weight are in column "**1**" and "**11**", respectively . Birth and weaning weight are in column "**8**" and "**11**", respectively.
4. Enter filename to keep BLUP solutions and create BV report.
5. Wizard will ask for creating genetic trend. Click **No** button if only BLUP report is needed. Click **Yes** with another filename to keep genetic trend.

Finish ➨ Click **View variance estimation** button to view variance components estimated by REML (if Re-estimates in ❷ is checked). BeefPack also reports genetic, environment and phenotypic correlations.

Click **View EBV / Genetic Trend** button to see multivariate BLUP reports with accuracy as bellows.

BeefPack Wizard... Start

BeefPack wizard will help you through the process of BLUP analysis and report.

Data file:
Columns must be included of ID, fixed effects, and traits.
(Fixed effects frequently used are herd, year, month or season of birth or wean, parity, age at calving etc.)

Pedigree file:

BeefPack Wizard... Step 1 of 5

Input name of data file and pedigree file without path name. Pedigree file could be left blank in case of no pedigree available. Click "Path" button to define path.

Data file: BFdat.prn
Pedigree file: BFped.prn
Number of trait: 2

BeefPack Wizard... Step 2 of 5

Select model for BLUP analysis by checking on effects to include in the model. Input either true variance or variance ratio for BLUP analysis. If check on re-estimate, all variances are used as priors for REML or AIREML (with S.D.).

Effects include in model
☑ Direct (h2)
☑ Maternal (m2)
Direct and Maternal Cov (ram)
☑ Permanent environment (c2)
☑ Error (e2)
☐ Re-esti

Add (Co)-variance for direct and maternal effects

	Direct 1	Direct 2	Direct 3	Direct 4	Mat 1	Mat 2
Direct 1	44	85.7			-9.8	0
Direct 2		668			0	0
Direct 3						
Direct 4						
					13.6	0
						20

BeefPack Wizard... Step 3 of 5

Input column position for animal ID, fixed effects, and traits in data file. To combine column such as cg (contemporary group) for month and year at birth/wean, type all columns separate by space, i.e "3 4." Different CG can be specified for each trait. Also, specify effect type as cross classification or covariate for other fixed effects in the model. (* is covariate variable)

	Col #	CG 2
☑ HMY for CG1	3 6 7	3 9 10
☑ Sex	2	
☑ Parity	4	
☐ Age at wean*		
☐ Age of dam*		
☐ Other		

	Col #
Animal ID	1
Trait 1	8
Trait 2	11

BeefPack Wizard... Step 4 of 5

Input name of EBV report file without path name. Click "Path" button to define path.

EBV Report file: BFreport

BeefPack Wizard... Step 5 of 5

Input name of genetic trend report file without path name if need.

● No

BeefPack Wizard... Finish

BeefPack wizard was successfully help you through all process of BLUP analysis and report. Click button below to view reports.

solutions_vce - Notepad

```
 ==================================
 REMLF90 by I.Misztal
 Modified by S.Tsuruta and T.Druet
 Compiled for PC by M.Duangjinda
 ==================================

 << Variance Estimation >>
 Genetic variance(s) for effect:
G
  13.354       11.599      -4.3733
  11.599       216.29       2.6574
 -4.3733       2.6574       9.6170
  0.0000       0.0000       0.0000
 Genetic correlation(s):
CorrG
   1.000       0.2158      -0.3859
  0.2158        1.000       0.5827E-01
 -0.3859       0.5827E-01   1.000
   0.000        0.000       0.000
 Genetic variance(s) for effect:
G
  6.1023       3.0399
  3.0399       8.7898
 Genetic correlation(s):
CorrG
   1.000       0.4151
  0.4151        1.000
 Residual variance(s):
R
    4.0795       1.8629
    1.8629       55.485
 Residual correlation(s):
CorrR
  1.0000      0.12383
 0.12383       1.0000
 Total variance(s):
P
    23.536       16.502
    16.502       280.57
 Phenotypic correlation(s):
```

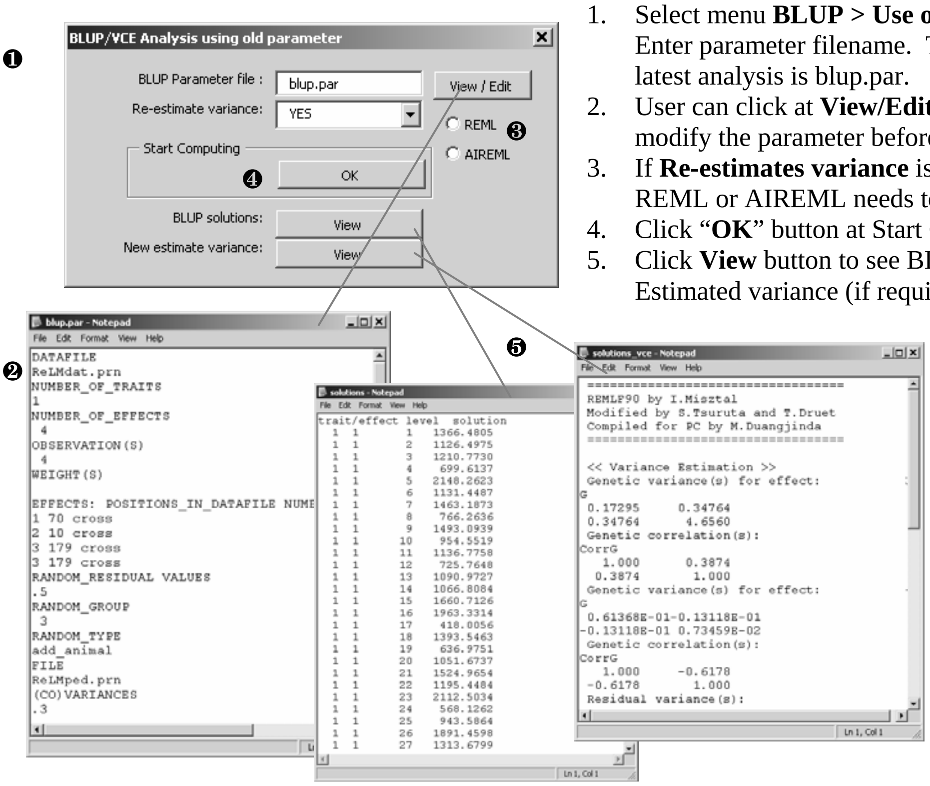
Microsoft Excel - BFreport.xls

	A	B	C	D	E	F	G	H	I	J	K
1	id	yob	name	EBV1	ACC	MAT1	ACC	EBV2	ACC	MAT2	ACC
2	1	1996	39001CP	0.4865	0.235	0.4646	0.016	4.5354	0.006	-0.1204	0
3	2	1996	39001LO	0.8705	0.338	-0.1199	0.057	2.6887	0.545	0.5875	0.006
4	3	1996	39001TP	0.6901	0.283	0.6124	0.03	1.6581	0.588	-0.1209	0.003
5	4	1996	39001UB	0.4271	0.291	-0.0379	0.038	0.741	0.155	0.0407	0.004
6	5	1996	39001UD	0.2984	0.1	0.0272	0.032	3.9579	0.493	0.11	0.007
7	6	1996	39001YL	-0.6031	0.364	0.2775	0.033	2.5773	0.562	0.1957	0.005
8	7	1996	39002KA	-0.9823	0.347	0.483	0.019	-3.0749	0.111	0	0
9	8	1996	39002LO	-1.9475	0.337	1.0812	0.056	3.8271	0.548	0.1914	0.009
10	9	1996	39002MK	-2.6907	0.37	0.7627	0.038	-0.5593	0.602	0.0602	0.006
11	10	1996	39002TP	-0.0465	0.313	0.6484	0.029	-1.0867	0.597	-0.0337	0.006
12	11	1996	39002UB	-1.5487	0.255	1.1671	0.037	3.534	0.587	0.0434	0.006
13	12	1996	39002UT	-2.1291	0.367	0.6977	0.036	6.6968	0.599	0.4506	0.006
14	13	1996	39002YL	0.3357	0.356	0.3754	0.021	0.1712	0.557	-0.0353	0.002
15	14	1996	39003KA	-0.0645	0.089	0.4198	0	3.0515	0.095	0	0
16	15	1996	39003LO	-0.1218	0.344	0.1879	0.063	-1.7785	0.545	0.3754	0.006
17	16	1996	39003MK	0.7548	0.366	-0.0599	0.046	2.8988	0.601	0.1845	0.008
18	17	1996	39003TP	0.1161	0.335	-0.3288	0.074	-8.7091	0.601	-0.2751	0.013
19	18	1996	39003UT	-3.7137	0.362	2.0117	0.03	5.5321	0.602	0.0191	0.008
20	19	1996	39003YL	1.2797	0.363	0.0887	0.031	1.6491	0.562	-0.0178	0.005
21	20	1996	39004MK	-0.3282	0.375	0.5345	0.044	-2.4721	0.604	0.5035	0.008
22	21	1996	39004TP	2.1404	0.384	-1.6453	0.075	6.5738	0.602	0.3806	0.013

VII. Rapid Analysis from Previous Parameters

A. Re-analysis By Old Parameters

Without using wizards, which always start from the first step, BeefPack has a useful feature to help user perform BLUP from previous parameter files. The parameters can be modified for complicated model or other models not available in wizards.



BLUP Parameter file : blup.par

Re-estimate variance: YES

BLUP solutions:

New estimate variance:

```
DATAFILE
ReLMdat.prn
NUMBER_OF_TRAITS
1
NUMBER_OF_EFFECTS
 4
OBSERVATION(S)
 4
WEIGHT(S)

EFFECTS: POSITIONS_IN_DATAFILE NUME
1 70 cross
2 10 cross
3 179 cross
3 179 cross
RANDOM_RESIDUAL VALUES
.5
RANDOM_GROUP
 3
RANDOM_TYPE
add_animal
FILE
ReLMped.prn
(CO)VARIANCES
.3
```

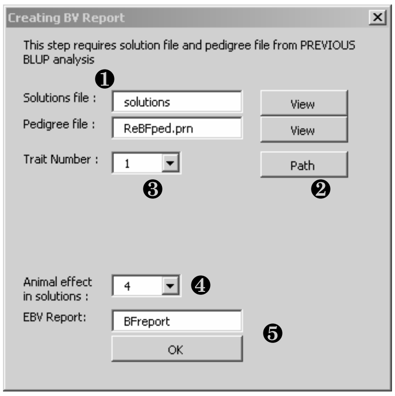
```
trait/effect level  solution
  1  1        1   1366.4805
  1  1        2   1126.4975
  1  1        3   1210.7730
  1  1        4    699.6137
  1  1        5   2148.2623
  1  1        6   1131.4487
  1  1        7   1463.1873
  1  1        8    766.2636
  1  1        9   1493.0939
  1  1       10    954.5519
  1  1       11   1136.7758
  1  1       12    725.7648
  1  1       13   1090.9727
  1  1       14   1066.8084
  1  1       15   1660.7126
  1  1       16   1963.3314
  1  1       17    418.0056
  1  1       18   1393.5463
  1  1       19    636.9751
  1  1       20   1051.6737
  1  1       21   1524.9654
  1  1       22   1195.4484
  1  1       23   2112.5034
  1  1       24    568.1262
  1  1       25    943.5864
  1  1       26   1891.4598
  1  1       27   1313.6799
```

```
 ==================================
 REMLF90 by I.Misztal
 Modified by S.Tsuruta and T.Druet
 Compiled for PC by M.Duangjinda
 ==================================


 << Variance Estimation >>
 Genetic variance(s) for effect:
G
 0.17295     0.34764
 0.34764      4.6560
 Genetic correlation(s):
CorrG
   1.000      0.3874
  0.3874       1.000
 Genetic variance(s) for effect:
G
 0.61368E-01-0.13118E-01
-0.13118E-01 0.73459E-02
 Genetic correlation(s):
CorrG
   1.000     -0.6178
 -0.6178       1.000
 Residual variance(s):
```

1. Select menu **BLUP > Use old parameters**. Enter parameter filename. The default from the latest analysis is blup.par.
2. User can click at **View/Edit** button to check or modify the parameter before the analysis.
3. If **Re-estimates variance** is “**YES**”, option for REML or AIREML needs to be selected.
4. Click “**OK**” button at Start Computing section.
5. Click **View** button to see BLUP solutions and Estimated variance (if required).

B. Creating BLUP Report From Previous Solutions

All solutions from the analysis of BLUPF90 family programs. Such as BLUPF90, REMLF90/AIREMLF90, BLUPF90-PCPACK, can be brought into BeefPack to create BV reports. This step requires solutions file and renum-pedigree file from previous analysis.



This step requires solution file and pedigree file from PREVIOUS BLUP analysis

Solutions file : solutions

Pedigree file : ReBFped.prn

Trait Number : 1

Animal effect in solutions : 4

EBV Report: BFreport

1. Select menu **BLUP > Create BV reports**. Enter solution and renum-pedigree filenames.
2. User can click at **View** button to check the correct file name. Click **Path** to change path.
3. If solutions are from multi-trait BLUP analysis, specify number of trait.
4. Enter number of animal effect or maternal effect in solutions file.
5. Enter BV filename to save. Click “**OK**” button at Start Computing section.
6. Click **View** button to see BLUP report.

VIII. Parameter File Examples

A. Animal with PE Model

Data File: BFdat.prn

```
Id      sex hd   par age mb yb   bwt  mw  yw   wwt
39001CP  2  89  2    59  2  1996  27  9   1996 200
39001LO  1  94  3    64  2  1996  28  9   1996 214
39001TP  1  141 4    95  2  1996  29  10  1996 209
39001UB  2  151 2    58  2  1996  29  9   1996 0
39001UD  2  178 2    65  2  1996  0   9   1996 228
39001YL  1  344 1    43  1  1996  26  7   1996 211
39002KA  2  90  2    59  2  1996  20  8   1996 0
39002LO  1  94  2    60  2  1996  27  9   1996 199
39002MK  2  96  2    78  3  1996  22  10  1996 209
39002TP  1  141 8    137 2  1996  27  10  1996 208
```

Renum Data File: ReBFdat.prn

```
 Cg  sex   par  id   bwt   dam
 5    2      2   1    27    2283
 5    1      3   2    28    2284
 5    1      4   3    29    2285
 5    2      2   4    29    2286
 5    2      2   5    0     2287
 1    1      1   6    26    2288
 5    2      2   7    20    2289
 5    1      2   8    27    2290
 9    2      2   9    22    2291
 5    1      8   10   27    2292
```

Pedigree File: BFped.prn

```
 Id          sire      dam       yob
 39001CP     31131MK   34075MK    1996
 39001KA     35003SS   32287AWD   1996
 39001LO     35010MK   33059LO    1996
 39001MK     28831AI   27134MK    1996
 39001TP     31397UDT  31542UTV   1996
 39001UB     35014TP   34162UMA   1996
 39001UD     29044MK   33053TP    1996
 39001UT     35007UB   34710ULO   1996
 39001YL     35006LO   35021USB   1996
```

Renum Pedigree File: ReBFped.prn

```
 Id sire  dam  x   YOB  x  x  x  orig ID
 1  3498  2283  1   1996  2  1  0  39001CP
 2  3499  2284  1   1996  2  1  0  39001LO
 3  3500  2285  1   1996  2  1  0  39001TP
 4  3501  2286  1   1996  2  1  0  39001UB
 5  3502  2287  1   1996  2  1  0  39001UD
 6  3503  2288  1   1996  2  1  0  39001YL
 7  3504  2289  1   1996  2  1  0  39002KA
 8  3499  2290  1   1996  2  1  0  39002LO
 9  3505  2291  1   1996  2  1  0  39002MK
 10 3506  2292  1   1996  2  1  0  39002TP
```

*Note: *Cg is a combination of herd-month-year at birth*

Parameter File: BLUP.PAR

```
DATAFILE
ReBFDat.prn
NUMBER_OF_TRAITS
 1 ❽
NUMBER_OF_EFFECTS
 5
OBSERVATION(S)
 5 ❾
WEIGHT(S)

EFFECTS: POSITIONS_IN_DATAFILE NUMBER_OF_LEVELS TYPE_OF_EFFECTS
1   48 cross ❶
2    2 cross ❷
3   11 cross ❸
4 3768 cross ❹
6 3768 cross ❺
RANDOM_RESIDUAL VALUES
0.5
RANDOM_GROUP ❻
 4
RANDOM_TYPE
add_animal
FILE
ReBFped.prn
(CO)VARIANCES
0.4
RANDOM_GROUP ❼
 5
RANDOM_TYPE
diagonal
FILE

(CO)VARIANCES
0.1
```

Note:
❶ Effect of contemporary groups in column #1 has 48 levels.
❷ Effect of sex in column #2 has 2 levels.
❸ Effect of parity in column #3 has 11 levels.
❹ Effect of direct genetic from animal in column #4 has 3768 levels.
❺ Effect of maternal PE from dam in column #6 has 3768 levels.
❻ Effect number 4 is random effect with add_animal type. This is genetic effects which require pedigree file.
❼ Effect number 5 is random effect with diagonal type for PE, which is uncorrelated.
❽ Analysis of single trait.
❾ Trait is in column #5 which is birth weight.

B. Matenal with PE Model

Data File: BFdat.prn

```
Id      sex hd  par age mb yb   bwt  mw  yw   wwt
39001CP 2  89  2   59  2  1996 27  9   1996 200
39001LO 1  94  3   64  2  1996 28  9   1996 214
39001TP 1  141 4   95  2  1996 29  10  1996 209
39001UB 2  151 2   58  2  1996 29  9   1996 0
39001UD 2  178 2   65  2  1996 0   9   1996 228
39001YL 1  344 1   43  1  1996 26  7   1996 211
39002KA 2  90  2   59  2  1996 20  8   1996 0
39002LO 1  94  2   60  2  1996 27  9   1996 199
39002MK 2  96  2   78  3  1996 22  10  1996 209
39002TP 1  141 8   137 2  1996 27  10  1996 208
```

Renum Data File: ReBFdat.prn

```
 Cg  sex  par   id    wwt    dam
 7    2    2    1      200    2283
 47   1    3    2      214    2284
 129  1    4    3      209    2285
 151  2    2    4     0       2286
 177  2    2    5      228    2287
 220  1    1    6      211    2288
 27   2    2    7     0       2289
 47   1    2    8      199    2290
 97   2    2    9      209    2291
 129  1    8    10     208    2292
```

Pedigree File: BFped.prn

```
 Id          sire       dam       yob
 39001CP     31131MK   34075MK    1996
 39001KA     35003SS   32287AWD   1996
 39001LO     35010MK   33059LO    1996
 39001MK     28831AI   27134MK    1996
 39001TP     31397UDT  31542UTV   1996
 39001UB     35014TP   34162UMA   1996
 39001UD     29044MK   33053TP    1996
 39001UT     35007UB   34710ULO   1996
 39001YL     35006LO   35021USB   1996
```

Renum Pedigree File: ReBFped.prn

```
 Id sire  dam  x   YOB  x  x  x  orig ID
  1  3498  2283  1   1996  2  1  0  39001CP
  2  3499  2284  1   1996  2  1  0  39001LO
  3  3500  2285  1   1996  2  1  0  39001TP
  4  3501  2286  1   1996  2  1  0  39001UB
  5  3502  2287  1   1996  2  1  0  39001UD
  6  3503  2288  1   1996  2  1  0  39001YL
  7  3504  2289  1   1996  2  1  0  39002KA
  8  3499  2290  1   1996  2  1  0  39002LO
  9  3505  2291  1   1996  2  1  0  39002MK
 10  3506  2292  1   1996  2  1  0  39002TP
```

*Note: *Cg is a combination of herd-month-year at wean*

Parameter File: BLUP.PAR

```
DATAFILE
ReBFDat.prn
NUMBER_OF_TRAITS
 1 ❾
NUMBER_OF_EFFECTS
 6
OBSERVATION(S)
 5 ❿
WEIGHT(S)

EFFECTS: POSITIONS_IN_DATAFILE NUMBER_OF_LEVELS TYPE_OF_EFFECTS
1  233 cross ❶
2    2 cross ❷
3   11 cross ❸
4 3768 cross ❹
6 3768 cross ❺
6 3768 cross ❻
RANDOM_RESIDUAL VALUES
0.50
RANDOM_GROUP ❼
 4   5
RANDOM_TYPE
add_animal
FILE
ReBFped.prn
(CO)VARIANCES
0.30   -0.05
-0.05   0.15
RANDOM_GROUP ❽
 6
RANDOM_TYPE
diagonal
FILE

(CO)VARIANCES
0.10
```

Note:
❶ Effect of contemporary groups in column #1 has 48 levels.
❷ Effect of sex in column #2 has 2 levels.
❸ Effect of parity in column #3 has 11 levels.
❹ Effect of direct genetic from animal in column #4 has 3768 levels.
❺ Effect of maternal genetic from dam in column #6 has 3768 levels.
❻ Effect of maternal PE from dam in column #6 has 3768 levels.
❼ Effect number 4 and 5 is random effect with add_animal type. This is genetic effects which require pedigree file. Note: covariance structure required direct, maternal and covariances.
❽ Effect number 5 is random effect with diagonal type for PE, which is uncorrelated.
❾ Analysis of single trait.
❿ Trait is in column #5 which is weaning weight.

C. Multi-trait Model

Data File: BFdat.prn

```
Id       sex hd  par age mb yb   bwt  mw  yw   wwt
39001CP  2  89  2   59  2  1996  27  9   1996  200
39001LO  1  94  3   64  2  1996  28  9   1996  214
39001TP  1  141 4   95  2  1996  29  10  1996  209
39001UB  2  151 2   58  2  1996  29  9   1996  0
39001UD  2  178 2   65  2  1996  0   9   1996  228
39001YL  1  344 1   43  1  1996  26  7   1996  211
39002KA  2  90  2   59  2  1996  20  8   1996  0
39002LO  1  94  2   60  2  1996  27  9   1996  199
39002MK  2  96  2   78  3  1996  22  10  1996  209
39002TP  1  141 8   137 2  1996  27  10  1996  208
```

Renum Data File: ReLMdat.prn

```
 Cg1   Cg2   sex par  id   bwt   wwt  dam
  4    7     2   2    1    27    200  2283
 44    47    1   3    2    28    214  2284
 160   129   1   4    3    29    209  2285
 199   151   2   2    4    29    0    2286
 237   177   2   2    5    0     228  2287
 303   220   1   1    6    26    211  2288
 14    27    2   2    7    20    0    2289
 44    47    1   2    8    27    199  2290
 112   97    2   2    9    22    209  2291
 160   129   1   8    10   27    208  2292
```

Pedigree File: BFped.prn

```
Id          sire      dam       yob
39001CP     31131MK   34075MK   1996
39001KA     35003SS   32287AWD  1996
39001LO     35010MK   33059LO   1996
39001MK     28831AI   27134MK   1996
39001TP     31397UDT  31542UTV  1996
39001UB     35014TP   34162UMA  1996
39001UD     29044MK   33053TP   1996
39001UT     35007UB   34710ULO  1996
39001YL     35006LO   35021USB  1996
```

Renum Pedigree File: ReBFped.prn

```
Id sire  dam  x   YOB  x  x  x  orig ID
 1  3498 2283 1   1996 2  1  0  39001CP
 2  3499 2284 1   1996 2  1  0  39001LO
 3  3500 2285 1   1996 2  1  0  39001TP
 4  3501 2286 1   1996 2  1  0  39001UB
 5  3502 2287 1   1996 2  1  0  39001UD
 6  3503 2288 1   1996 2  1  0  39001YL
 7  3504 2289 1   1996 2  1  0  39002KA
 8  3499 2290 1   1996 2  1  0  39002LO
 9  3505 2291 1   1996 2  1  0  39002MK
 10 3506 2292 1   1996 2  1  0  39002TP
```

*Note: *Cg1, Cg2 is a combination of herd-month-year at birth and wean, respectively.*

Parameter File: BLUP.PAR

```
DATAFILE
ReBFDat.prn
NUMBER_OF_TRAITS
 2 ❾
NUMBER_OF_EFFECTS
 6
OBSERVATION(S)
 6 7 ❿
WEIGHT(S)

EFFECTS: POSITIONS_IN_DATAFILE NUMBER_OF_LEVELS TYPE_OF_EFFECTS
1 2  233 cross ❶
3 3    2 cross ❷
4 4   11 cross ❸
5 5 3768 cross ❹
8 8 3768 cross ❺
8 8 3768 cross ❻
RANDOM_RESIDUAL VALUES
10   5
 5 100
RANDOM_GROUP ❼
 4   5
RANDOM_TYPE
add_animal
FILE
ReBFped.prn
(CO)VARIANCES
44.0 85.5  -9.8   0
85.5  668     0   0
-9.8   0   13.6   0
   0   0      0  20
RANDOM_GROUP ❽
 6
RANDOM_TYPE
diagonal
FILE

(CO)VARIANCES
10 5
5 10
```

Note:

❶ Effect of contemporary groups for trait 1 and 2 in column #1 and #2 has maximum at 233 levels.
❷ Effect of sex in column #3 has 2 levels.
❸ Effect of parity in column #4 has 11 levels.
❹ Effect of direct genetic from animal in column #5 has 3768 levels.
❺ Effect of maternal genetic from dam in column #8 has 3768 levels.
❻ Effect of maternal PE from dam in column #8 has 3768 levels.
❼ Effect number 4 and 5 is random effect with add_animal type. This is genetic effects which require pedigree file. Note on covariance structure required direct1, direct2, covariance between direct; maternal1, maternal2, covariance between maternal; and covariance between each direct and each maternal.
❽ Effect number 5 is random effect with diagonal type for PE. Note on covariance structure.
❾ Analysis of bivariate trait.
❿ Trait is in column #6 and #7 which are birth weight and weaning weight.

IX. Trouble Shooting

Q: *How to get accuracy in BV reports?*

This option has to modify from main menu. Click menu **Option > Set option**, then change the **Add accuracy in reports** option to “**YES**”.

Q: *All menus disappear and all buttons do not work properly.*

BeefPack might be opened in disable macro. To use the interfaces in BeefPack, macro always need to be set to “**ENABLE**”. If no dialog appears for setting the macro, read details on page 7.

Q: *How to decrease or increase convergence of program?.*

This option has to modify from main menu, like adding accuracy. Click menu **Option > Set option**, then change the **Set convergence to** option to “**1d-06**”, “**1d-08**”, “**1d-10**”, etc.

Q: *External programs of BLUPF90 seem not run?.*

Generally, BeefPack calls the external programs of BLUPF90 to do the analysis in windows environment. However, if nothing seems to happen, check the correct directory, data and pedigree file. Check variance structure in model (multi-trait or random regression analysis), i.e. non-symmetric, not-positive definite, missing element.

Q: *How to analyze multi-trait more than 4 triats, or random regression with other test day function?.*

BeefPack does not support all models. For very complicated model, BLUPF90-PCPACK is more flexible. However, PCPACK is not easy-clicked handle, background in animal model and BLUP is important.

Q: *Cannot find the BV report.*

BV report and genetic trend reports (in Excel format) are kept in DATA directory, not in Program directory.

X. Who's who

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Who's who in BLUPF90-PCPAK
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< Program >--------------------

BLUPF90 : *Ignacy Misztal*
REMLF90 : *Ignacy Misztal, Shogo Tsurata*
AIREML90 : *Shogo Tsurata, Ignacy Misztal, Tom Druet*
RENUMMAT : *Ignacy Misztal*
RENDOMN : *Nicholus Gengler, Ignacy Misztal*
Windows Interface : *Monchai Duangjinda*
PC-Compilation : *Monchai Duangjinda*

< Libraries >--------------------

DENSEOP : *Tomasz Strabel, Ignacy Misztal*
FSPAK : *Miguel Perez-Enciso, Ignacy Misztal, Mauricio Elzo*
FSPAK90 : *Ignacy Misztal*
Ginv : *Rohan Fernando*
IOUNF : *Ignacy Misztal*
LAPACK90 : *UNI-C, Denmark; Univ. of Tennessee, USA; NAG Ltd., UK*
Univ. of California Berkeley, Courant Institute,
Argonne National Lab, and Rice University,
Alan Miller, Jack Dongarra, Sven Hammarling
SPARSEM : *Ignacy Misztal*
PROB : *Luis Varona, Ignacy Misztal*