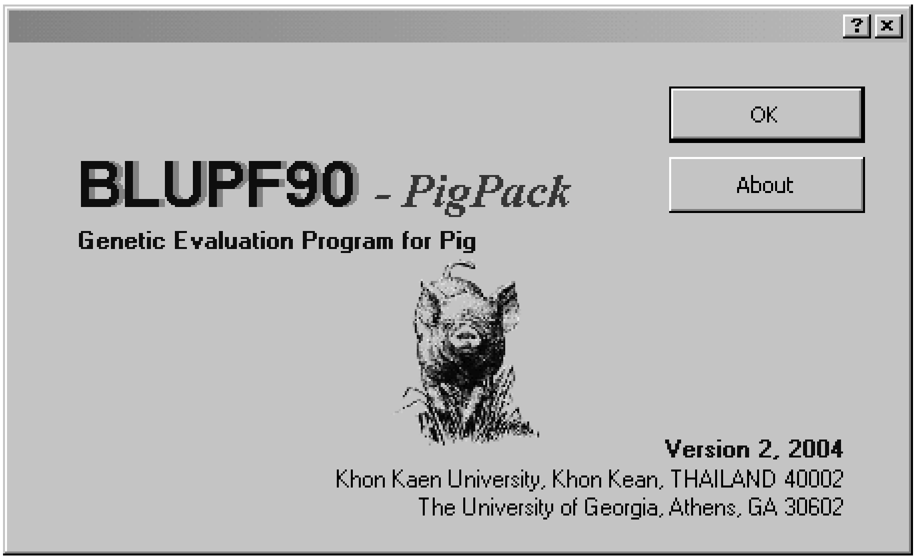
BLUPF90

PigPak

Version 2.5, 2005



BLUPF90 - *PigPack*

Genetic Evaluation Program for Pig

Version 2, 2004

Khon Kaen University, Khon Kean, THAILAND 40002

The University of Georgia, Athens, GA 30602

Monchai Duangjinda
Department of Animal Science
Khon Kaen University, Khon Kaen, Thailand 40002

Ignacy Misztal
Department of Animal and Dairy Science
The University of Georgia, Athens, GA30602

Shogo Tsuruta
Department of Animal and Dairy Science
The University of Georgia, Athens, GA30602

John Mabry
Department of Animal Science
Iowa State University, Ames, IA50011

Department of Animal Science
Khon Kaen University
&
Department of Animal and Dairy Science
The University of Georgia
&
Department of Animal Science
Iowa State University

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. "PigPAK" is a set of programs branched from "PCPak" with graphical user interface for simple use in Windows. PigPAK was developed for the specific purpose of pig genetic evaluation, and parts of programs in the BLUPF90 family are available, which are:

BLUPF90 : BLUP estimation using PCG.
REMLF90 : Variance component estimation using REML by EM algorithm.
AIREMLF90 : Variance component 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 of 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 PigPAK. This allows users to create all parameter files and BLUP reports with a point-and-click interface written in Visual BASIC for MS-EXCEL.

B. Overall Features

PigPAK is run using EXCEL. It manages genetic evaluation using a wizard interface which allows you to create a BLUP report in five steps. Only performance data and pedigrees are required. It will automatically renumber the animals and count the number of effects in the model. Mate (or service sire) effects for reproductive evaluations and litter effects for growth evaluation can be included in data file with alpha-numeric format. After variance component estimation or BLUP analysis is performed, PigPAK will create a BV report using the original animal ID. Users can keep data files and program files separately, however directories must be specified prior to analysis. BV reports with accuracy for up to four traits are available.

C. Specifications

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

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

With the PigPAK wizard interface, however, the single trait option will support only simple animal and animal with PE model. Multiple trait options will support up to four traits. Reports with accuracy are available only for single trait and multiple trait models. Variance component estimation by REML or AIREML is still available.

D. Conditions of Use

BLUPF90-*PigPAK* is distributed *free of charge* for academic and scientific use under the condition that it remains copyrighted. The use of any applications and compiled programs from PigPAK must be credited in any publications derived from their usage. For commercial or grant projects, personal communication of further agreements is required with any of the authors. There is no guarantee for correctness and there is no service for user purpose. However, specific questions, constructive criticism and debug reports are invited. Please email to monchai@kku.ac.th

E.How to Download Program

BLUPF90-PigPAK has been made available on 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.

F. OnlineRegistration

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

II. Installation

A. How to Install Program

BLUPF90-PigPAK is stored in one installation file named “PigPAK.Exe.” To install the programs, execute the following steps:

1. Run **PigPAK.EXE**.

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

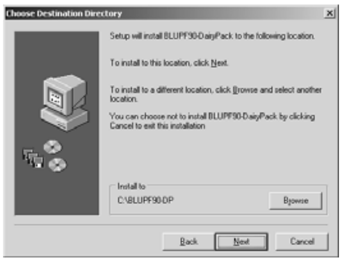
It is strongly recommended that you shut down all Windows applications before running this installation.

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 lead 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. PigPAK will install all F90 programs to the default directory “C:\BLUPF90-PP”. 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 Star Programt

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-DP\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

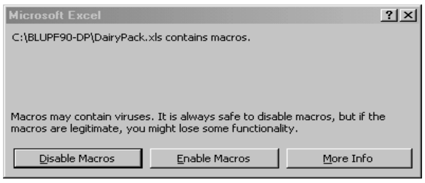
Note:

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 PigPAK**
2. Click **BlupF90 PigPAK** icon.

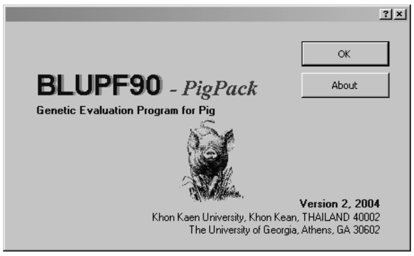
3. Excel program will run and PigPAK will ask for macro enables. Click **Enable Macros** button.
   (Note: BLUPF90-PigPAK cannot execute without macros for Visual Basic Applications. If there is a problem to enable macros, click menu **Tools > Macro > Security** in Excel. Then, set security level to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


Microsoft Excel

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.


BLUPF90 - *PigPack*

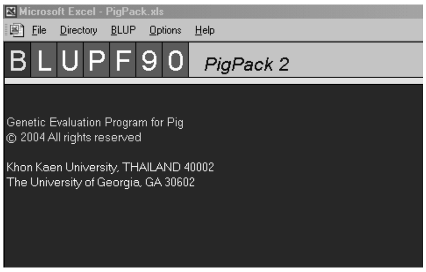
Genetic Evaluation Program for Pig

Version 2, 2004

Khon Kaen University, Khon Kean, THAILAND 40002

The University of Georgia, Athens, GA 30602

5. The main menu should look as below:


Microsoft Excel - PigPack.xls

BLUPF90 PigPack 2

Genetic Evaluation Program for Pig

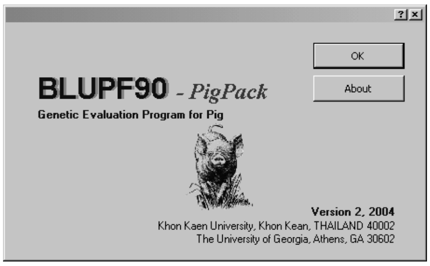
© 2004 All rights reserved

Khon Kaen University, THAILAND 40002

The University of Georgia, GA 30602

III. Genetic Evaluation At A Glance

A. General View



BLUPF90 - PigPack
Genetic Evaluation Program for Pig

Version 2, 2004
Khon Kaen University, Khon Kean, THAILAND 40002
The University of Georgia, Athens, GA 30602

1. *PigPAK* is a set of programs in BLUPF90 family with the specific purpose of pig genetic evaluation.

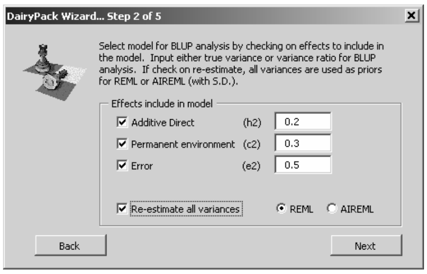
DairyPack Wizard... Start

DairyPack 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 calving, DIM, lactation, breed group, age at calving etc.)

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

2. *PigPAK* performs variance component estimation using REML and BLUP methodology with wizard interface.



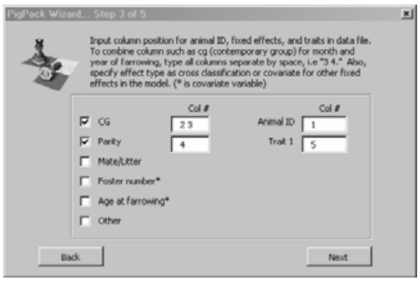
DairyPack Wizard... Step 2 of 5

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
☑ Additive Direct (h2) 0.2
☑ Permanent environment (c2) 0.3
☑ Error (e2) 0.5

☑ Re-estimate all variances ● REML ○ AIREML

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



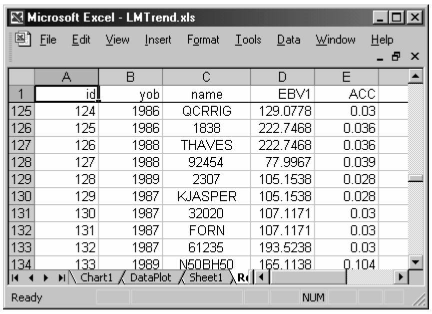
PigPack Wizard... Step 3 of 5

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 of farrowing, type all columns separate by space, i.e "3 4." Also, specify effect type as cross classification or covariate for other fixed effects in the model. (* is covariate variable)

	Col #		Col #
☑ CG	2 3	Animal ID	1
☑ Parity	4	Trait 1	5
☐ Mate/Litter			
☐ Foster number*			
☐ Age at farrowing*			
☐ Other			

4. Original performance data and pedigree files are used in the analysis. Therefore, all effects in the model are simply specified by column number in data file. Mate/Litter for sire/dam ID data file can be stored in alpha-numeric format and it will be automatically accounted for as a random effect if PE model in 3 is selected.

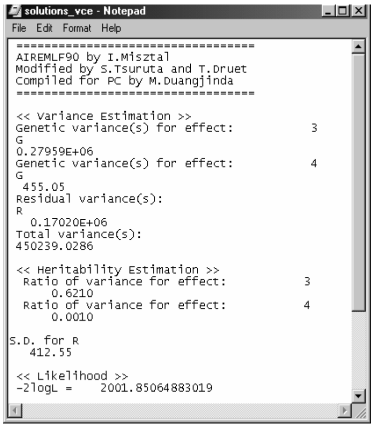
B. View of Reports



Microsoft Excel - LMTrend.xls

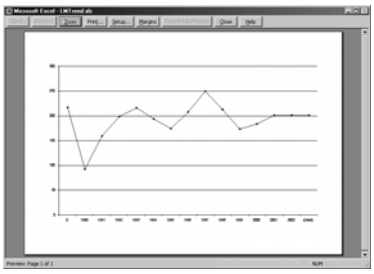
	A	B	C	D	E
1	id	yob	name	EBV1	ACC
125	124	1986	QCRRIG	129.0778	0.03
126	125	1986	1838	222.7468	0.036
127	126	1988	THAVES	222.7468	0.036
128	127	1988	92454	77.9967	0.039
129	128	1989	2307	105.1538	0.028
130	129	1987	KJASPER	105.1538	0.028
131	130	1987	32020	107.1171	0.03
132	131	1987	FORN	107.1171	0.03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

5. BLUP EBV report with accuracy is created using original ID in Excel format. Therefore sorting and filtering can be done simply using Excel functions.



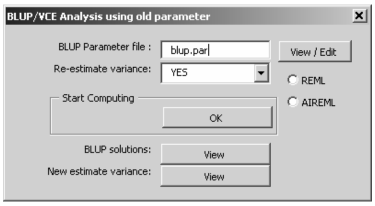
```
==================================
AIREMLF90 by I.Misztal
Modified by S.Tsuruta and T.Druet
Compiled for PC by M.Duangjinda
==================================

<< 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
```

6. If REML or AIREML variance component estimation is performed the new variance estimates are kept in a separate file.



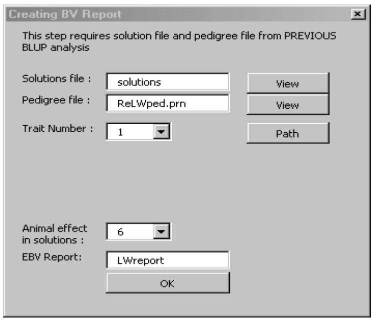
7. A genetic trend report is also created if desired. All graphic properties can be modified using general Excel features.

C. Advanced Options



BLUP Parameter file : blup.par
Re-estimate variance: YES
○ REML
○ AIREML
BLUP solutions:
New estimate variance:

8. Previous renumbered data and pedigree file with parameter file can be modified and reanalyzed.

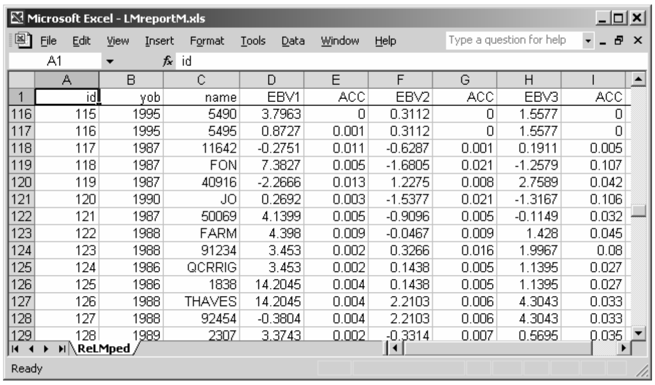


This step requires solution file and pedigree file from PREVIOUS BLUP analysis

Solutions file : solutions
Pedigree file : ReLWped.prn
Trait Number : 1
Animal effect in solutions : 6
EBV Report: LWreport

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

10. Multiple trait BV reports with accuracy can be created up to four traits.



	A	B	C	D	E	F	G	H	I
1	id	yob	name	EBV1	ACC	EBV2	ACC	EBV3	ACC
116	115	1995	5490	3.7963	0	0.3112	0	1.5577	0
117	116	1995	5495	0.8727	0.001	0.3112	0	1.5577	0
118	117	1987	11642	-0.2751	0.011	-0.6287	0.001	0.1911	0.005
119	118	1987	FON	7.3827	0.005	-1.6805	0.021	-1.2579	0.107
120	119	1987	40916	-2.2666	0.013	1.2275	0.008	2.7589	0.042
121	120	1990	JO	0.2692	0.003	-1.5377	0.021	-1.3167	0.106
122	121	1987	50069	4.1399	0.005	-0.9096	0.005	-0.1149	0.032
123	122	1988	FARM	4.398	0.009	-0.0467	0.009	1.428	0.045
124	123	1988	91234	3.453	0.002	0.3266	0.016	1.9967	0.08
125	124	1986	QCRRIG	3.453	0.002	0.1438	0.005	1.1395	0.027
126	125	1986	1838	14.2045	0.004	0.1438	0.005	1.1395	0.027
127	126	1988	THAVES	14.2045	0.004	2.2103	0.006	4.3043	0.033
128	127	1988	92454	-0.3804	0.004	2.2103	0.006	4.3043	0.033
129	128	1989	2307	3.3743	0.002	-0.3314	0.007	0.5695	0.035

IV. Model Descriptions

The main objective of BLUPF90-PigPAK is to utilize models generally used in swine genetic evaluation with a user friendly graphic interface for PC and Windows users. Using powerful features from BLUPF90, PigPAK can perform a wide range of genetic evaluation functions. PigPAK can estimate variance components using REML and perform BLUP breeding value analysis from linear mixed models including random animal effects as additive genetic and permanent environment effect. The following will provide more details of models that can be used in the analysis.

A. Basic Animal Model

PigPAK includes a 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 included for comprehensive use of mixed model technology. Fixed effects used in the model can be fitted as cross-classified variables and covariates. Combinations of fixed effects such as herd-year-season can be performed during the analysis, therefore, no additional data preparation is required. Normally, all traits analyzed with PigPAK should be continuous rather than ordinal scale for proper use in the linear mixed model analysis. Models with a single record per animal such as first lactation milk yield can be analyzed using the basic animal model as follows:

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

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. Repeatability Model

If multiple parity records are available, the permanent environment effect due to the animal needs to be taken into account. If mate effect from sire or litter effect for dam is available, it will be accounted as permanent environment effect instead. Fitting 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. Multi-trait Model

PigPAK 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 are available. To perform beyond this, parameter editing is required and do the analysis from menu **BLUP>Use old parameters**. Multi-trait analysis can perform model with the same single records or same repeated records, and different model with single and repeated records. The following is bivariate model with the same single record:

$$\begin{bmatrix} \boldsymbol{y}_1 \\ \boldsymbol{y}_2 \end{bmatrix} = \begin{bmatrix} \boldsymbol{X}_1 & \boldsymbol{0} \\ \boldsymbol{0} & \boldsymbol{X}_2 \end{bmatrix} \begin{bmatrix} \boldsymbol{\beta}_1 \\ \boldsymbol{\beta}_2 \end{bmatrix} + \begin{bmatrix} \boldsymbol{Z}_1 & \boldsymbol{0} \\ \boldsymbol{0} & \boldsymbol{Z}_2 \end{bmatrix} \begin{bmatrix} \boldsymbol{a}_1 \\ \boldsymbol{a}_2 \end{bmatrix} + \begin{bmatrix} \boldsymbol{\varepsilon}_1 \\ \boldsymbol{\varepsilon}_2 \end{bmatrix},\ V \begin{bmatrix} \boldsymbol{a}_i \\ \boldsymbol{e}_i \end{bmatrix} = \begin{bmatrix} \boldsymbol{G} \otimes \boldsymbol{A} & \boldsymbol{0} \\ \boldsymbol{0} & \boldsymbol{R} \otimes \boldsymbol{I} \end{bmatrix},$$

where $\boldsymbol{y}_1, \boldsymbol{y}_2$ is vector of response variable for trait 1 and 2, $\boldsymbol{\beta}_1, \boldsymbol{\beta}_2$ is vector of fixed effects, $\boldsymbol{a}_1, \boldsymbol{a}_2$ is vector of random additive genetic effects, $\boldsymbol{\varepsilon}_1, \boldsymbol{\varepsilon}_2$ 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, $\boldsymbol{G}$ is matrix of direct genetic variance-covariance for trait 1 and 2, $\boldsymbol{R}$ is matrix of residual variance-covariance for trait 1 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-PP. Two sub-directories of examples and helps are also created. Each directory will find the following programs and files.

Main directory:

Name	Type	Description
PigPAK.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
LWDAT.PRN	TXT	- Data file for model analysis with single trait and multi-trait with repeated records.
LWPED.PRN	TXT	- Pedigree file for analysis with LWDAT.
LWDAT.FMT	TXT	- Describe column number format for LWDAT.PRN

Helps directory:

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

B. The way program works

When performed the analysis with wizard interface in PigPAK. 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 PigPAK must be ASCII or TEXT file. Data must be in number, except for animal ID, Sire, Dam and Mate or Litter effect 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 for simpler operation. 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 LWDAT.PRN and LWPED.PRN, some additional files after analysis, which might be useful for later analysis, are:

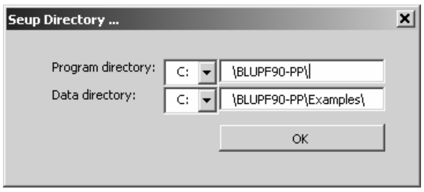
Name	Type	Description
RELWDAT.PRN	TXT	- Renumbered data file.
RELWPED.PRN	TXT	- Renumbered Pedigree file.
RENUM.PAR	TXT	- Parameter file for program RENUMMAT.
RENUM.MSG	TXT	- Log file from renumbering. Describe the levels of fixed and random effects after renum.
RENUM.PRN	TXT	- The details from renumbering. 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-10, however, users can choose their own by selecting menu **Options > Set Options**.

VI. Genetic Evaluation by Examples

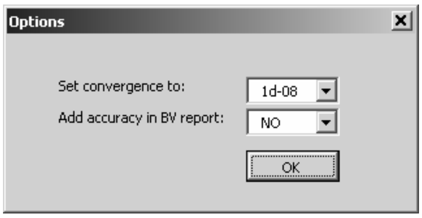
A. Setup Directory and Preferences



Program directory: C: \BLUPF90-PP\

Data directory: C: \BLUPF90-PP\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 number born alive. LWDAT.PRN is data file and LWPED.PRN is pedigree file.

Multi-trait analysis

The example will show how to estimate genetic correlation and predict multivariate breeding value for number born alive, number wean and litter wean weight. LWDAT.PRN is data file and LWPED.PRN is pedigree file.

File format

Format for LWDAT.PRN is stored in LWDAT.FMT. There are 9 columns of:

#1	ID
#2	Month of farrowing
#3	Year of farrowing
#4	Parity
#5	Number born alive (NBA)
#6	Number weaned (NW)
#7	Litter wean weight (LW)
#8	Sire Mate

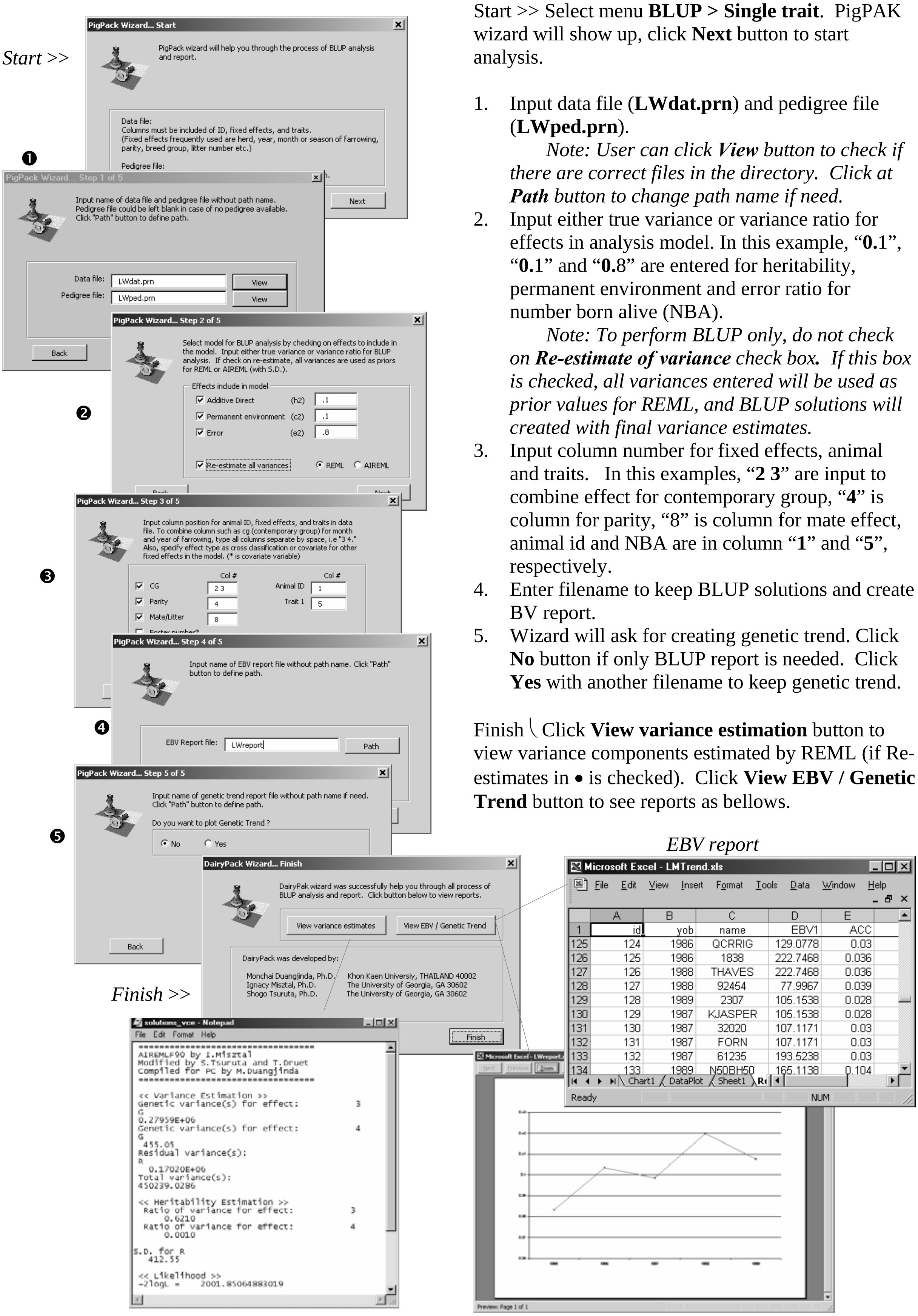
Format for pedigree has 4 columns of animal ID, sire ID, dam ID, and year of birth. Generally, year of birth can be omitted from pedigree file, but genetic trend will not to be created. Note: all files are stored in C:\BLUPF90-PP\EXAMPLES.

C. Single Trait Analysis Example

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

1. Input data file (**LWdat.prn**) and pedigree file (**LWped.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.**1", "**0.**1" and "**0.**8" are entered for heritability, permanent environment and error ratio for number born alive (NBA).
   *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, "**2 3**" are input to combine effect for contemporary group, "**4**" is column for parity, "8" is column for mate effect, animal id and NBA are in column "**1**" and "**5**", 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 • is checked). Click **View EBV / Genetic Trend** button to see reports as bellows.



Start >>

PigPack Wizard... Start

PigPack 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 farrowing, parity, breed group, litter number etc.)

Pedigree file:

❶ **PigPack 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: LWdat.prn
Pedigree file: LWped.prn

❷ **PigPack 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
☑ Additive Direct (h2) .1
☑ Permanent environment (c2) .1
☑ Error (e2) .8
☑ Re-estimate all variances ● REML ○ AIREML

❸ **PigPack 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 of farrowing, type all columns separate by space, i.e "3 4." Also, specify effect type as cross classification or covariate for other fixed effects in the model. (* is covariate variable)

	Col #		Col #
☑ CG	2 3	Animal ID	1
☑ Parity	4	Trait 1	5
☑ Mate/Litter	8		
☐ Foster number*			

❹ **PigPack Wizard... Step 4 of 5**

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

EBV Report file: LWreport

❺ **PigPack 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

Finish >>

DairyPack Wizard... Finish

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

DairyPack 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

EBV report

Microsoft Excel - LMTrend.xls

	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

solutions_vce - Notepad

```
====================================
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
```

VCE report

Genetic trend

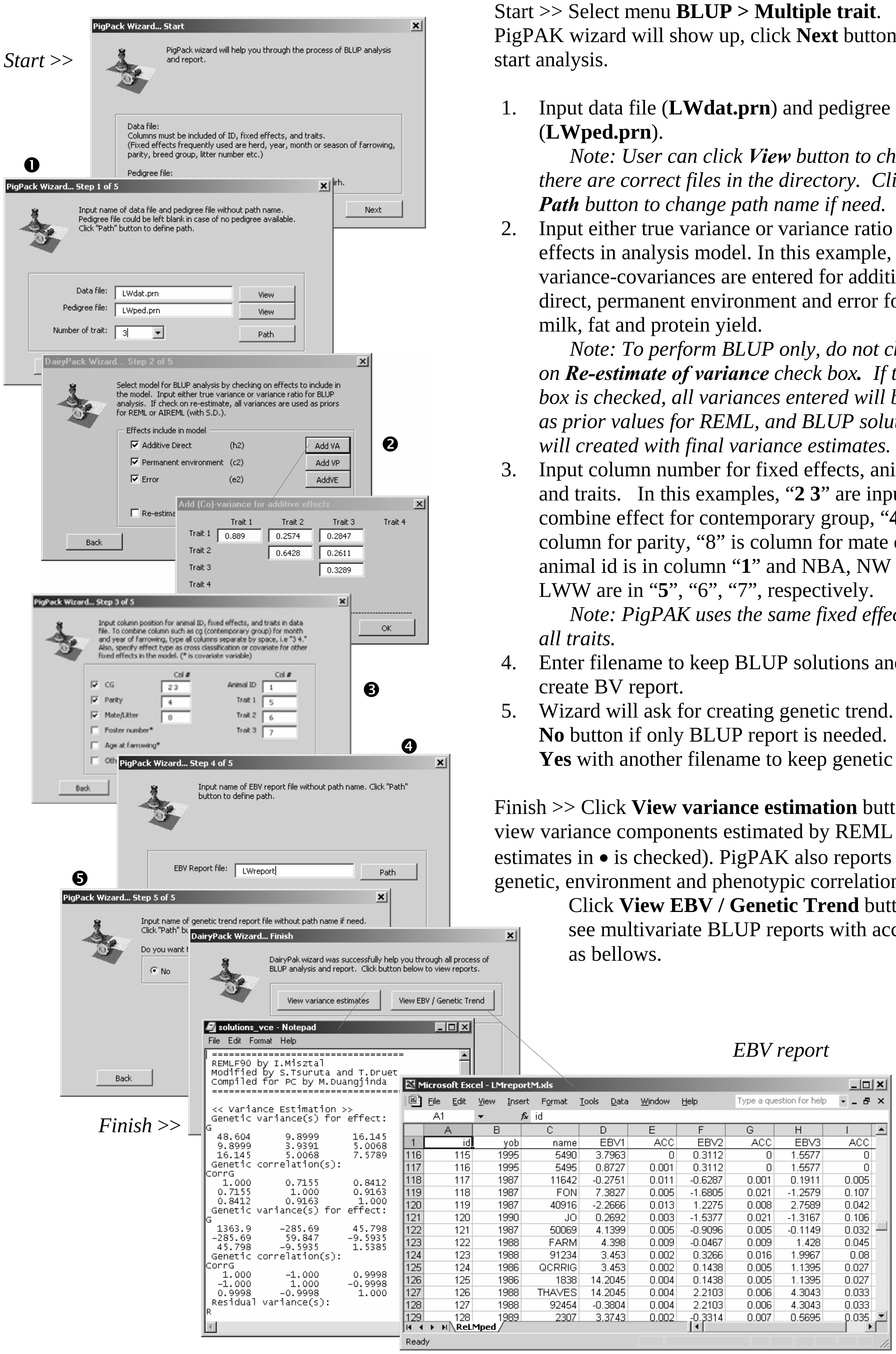
D. Multi-trait Analysis Example

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

1. Input data file (**LWdat.prn**) and pedigree file (**LWped.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, variance-covariances are entered for additive direct, permanent environment and error for trait milk, 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, “**2 3**” are input to combine effect for contemporary group, “**4**” is column for parity, “8” is column for mate effect, animal id is in column “**1**” and NBA, NW and LWW are in “**5**”, “6”, “7”, respectively.
   Note: PigPAK uses the same fixed effects for all traits.
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 • is checked). PigPAK also reports genetic, environment and phenotypic correlations.

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



PigPack Wizard... Start

PigPack 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 farrowing, parity, breed group, litter number etc.)

Pedigree file:

Next

PigPack 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: LWdat.prn
Pedigree file: LWped.prn
Number of trait: 3

DairyPack 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
☑ Additive Direct (h2) Add VA
☑ Permanent environment (c2) Add VP
☑ Error (e2) AddVE
☐ Re-estima

Add (Co)-variance for additive effects

	Trait 1	Trait 2	Trait 3	Trait 4
Trait 1	0.889	0.2574	0.2847	
Trait 2		0.6428	0.2611	
Trait 3			0.3289	
Trait 4				

PigPack 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 of farrowing, type all columns separate by space, i.e "3 4." Also, specify effect type as cross classification or covariate for other fixed effects in the model. (* is covariate variable)

	Col #		Col #
☑ CG	2 3	Animal ID	1
☑ Parity	4	Trait 1	5
☑ Mate/Litter	8	Trait 2	6
☐ Foster number*		Trait 3	7
☐ Age at farrowing*			
☐ Oth			

PigPack Wizard... Step 4 of 5

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

EBV Report file: LWreport

PigPack Wizard... Step 5 of 5

Input name of genetic trend report file without path name if need.
Click "Path" bu

Do you want t

● No

DairyPack Wizard... Finish

DairyPak 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
  48.604      9.8999      16.145
  9.8999      3.9391      5.0068
  16.145      5.0068      7.5789
 Genetic correlation(s):
CorrG
   1.000      0.7155      0.8412
  0.7155       1.000      0.9163
  0.8412      0.9163       1.000
 Genetic variance(s) for effect:
G
  1363.9     -285.69      45.798
 -285.69      59.847     -9.5935
  45.798     -9.5935      1.5385
 Genetic correlation(s):
CorrG
   1.000      -1.000      0.9998
  -1.000       1.000     -0.9998
  0.9998     -0.9998       1.000
 Residual variance(s):
R
```

Microsoft Excel - LMreportM.xls

A1 id

	A	B	C	D	E	F	G	H	I
1	id	yob	name	EBV1	ACC	EBV2	ACC	EBV3	ACC
116	115	1995	5490	3.7963	0	0.3112	0	1.5577	0
117	116	1995	5495	0.8727	0.001	0.3112	0	1.5577	0
118	117	1987	11642	-0.2751	0.011	-0.6287	0.001	0.1911	0.005
119	118	1987	FON	7.3827	0.005	-1.6805	0.021	-1.2579	0.107
120	119	1987	40916	-2.2666	0.013	1.2275	0.008	2.7589	0.042
121	120	1990	JO	0.2692	0.003	-1.5377	0.021	-1.3167	0.106
122	121	1987	50069	4.1399	0.005	-0.9096	0.005	-0.1149	0.032
123	122	1988	FARM	4.398	0.009	-0.0467	0.009	1.428	0.045
124	123	1988	91234	3.453	0.002	0.3266	0.016	1.9967	0.08
125	124	1986	QCRRIG	3.453	0.002	0.1438	0.005	1.1395	0.027
126	125	1986	1838	14.2045	0.004	0.1438	0.005	1.1395	0.027
127	126	1988	THAVES	14.2045	0.004	2.2103	0.006	4.3043	0.033
128	127	1988	92454	-0.3804	0.004	2.2103	0.006	4.3043	0.033
129	128	1989	2307	3.3743	0.002	-0.3314	0.007	0.5695	0.035

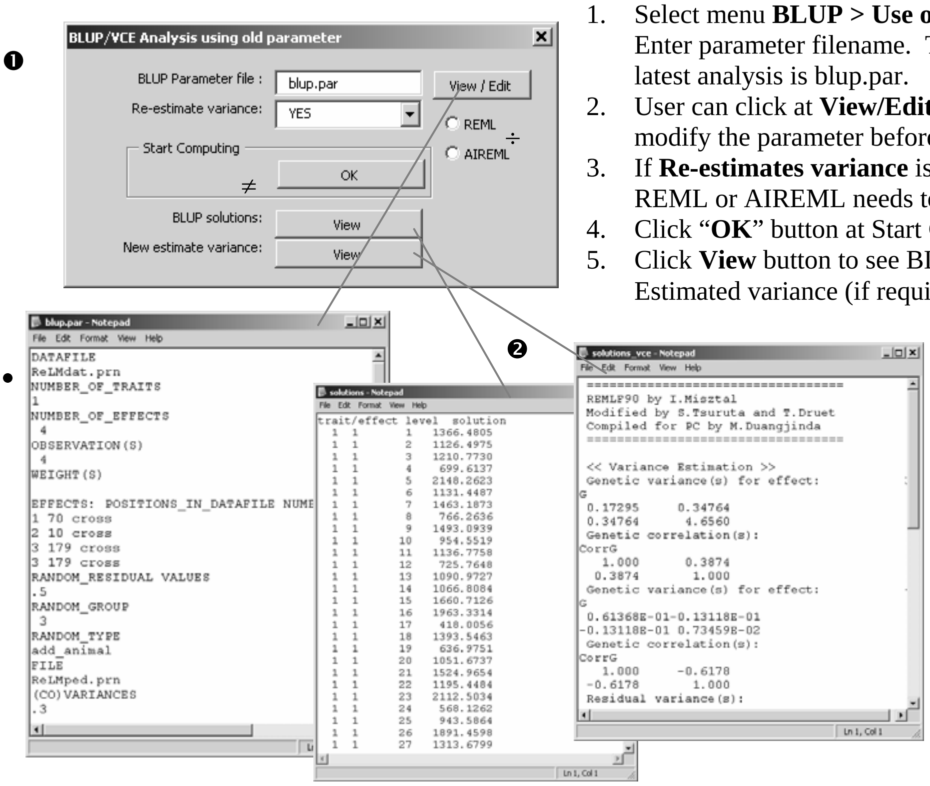
ReLMped

Ready

VII. Rapid Analysis from Previous Parameters

A. Re-analysis By Old Parameters

Without using wizards, which always start from the first step, PigPAK 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

○ REML
○ AIREML

BLUP solutions:

New estimate variance:

blup.par - Notepad

```
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
```

solutions - Notepad

```
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
```

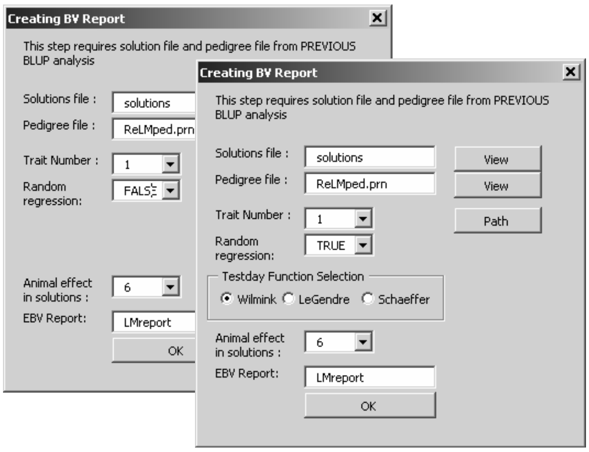
solutions_vce - Notepad

```
 ===================================
 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
 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 PigPAK 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 : ReLMped.prn

Trait Number : 1

Random regression: TRUE

Testday Function Selection: ● Wilmink ○ LeGendre ○ Schaeffer

Animal effect in solutions : 6

EBV Report: LMreport

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. If solutions are from random regression model, select "**TRUE**" for Random regression option with testday function.
5. Enter number of animal effect in solutions file.
6. Enter BV filename to save. Click "**OK**" button at Start Computing section.
7. Click **View** button to see BLUP report.

VIII. Parameter File Examples

A. Repeatability Model

Data File: LWdat.prn

```
 Id    month  year par nba nw lww     mate
15170009  5  1996  1  10   0  0      YIO3F030
15170010  4  1996  1  11   11 0      YIO3F030
15170011  1  1998  5  8    8  66.2   YIO3F030
15170011  3  1997  3  10   10 56.4   YIO3F030
15170011  3  1999  8  9    9  65.3   YIO3F030
15170011  5  1996  1  13   3  0      YIO3F030
15170011  6  1998  6  6    6  55.8   YIO3F030
15170011  8  1997  4  3    0  0      YIO3F030
15170011  10 1996  2  6    6  54.6   YIO3F030
15170011  10 1998  7  6    5  45.3   YIO3F030
15170012  1  1998  5  11   8  54.9   YIO3F030
```

Renum Data File: ReLWdat.prn

```
 Cg  parity  mate id   nba
 15     1      1   1    10
 11     1      1   2    11
 2      5      1   3    8
 8      3      1   3    10
 10     8      1   3    9
 15     1      1   3    13
 21     6      1   3    6
 28     4      1   3    3
 35     2      1   3    6
 37     7      1   3    6
```

Pedigree File: LWped.prn

```
Id        sire        dam        yob
15170010    YIO3F030    YIO4L016   1995
15170014    YIO3F030    YIO4L016   1995
15170009    YIO3F030    YIO4L016   1995
15170011    YIO3F030    YIO4L016   1995
15170012    YIO3F030    YIO4L016   1995
15170013    YIO3F030    YIO4L016   1995
15170014    YIO3F030    YIO4L016   1995
15170011    YIO3F030    YIO4L016   1995
15170012    YIO3F030    YIO4L016   1995
15170013    YIO3F030    YIO4L016   1995
```

Renum Pedigree File: ReLWped.prn

```
Id sire    dam    x  YOB   x x x x
 1  209     209    3 1986  2 1 0 1
 2  209     209    3 1986  2 1 0 2
 5  185     209    2 1987  2 1 0 10
 6  209     209    3 1987  2 1 0 11
 8  186      96    1 1991  2 1 1 14
 9  209     209    3 1986  2 1 0 17
10  185     209    2 1987  2 1 0 20
11  209     187    2 1988  2 1 0 21
15  185     209    2 1987  2 1 0 27
16  209     209    3 1986  2 1 0 28
```

*Note: *Cg is a combination of month-year of farrowing*

Parameter File: BLUP.PAR

```
DATAFILE
ReLWDat.prn
NUMBER_OF_TRAITS
 1 ❼
NUMBER_OF_EFFECTS
 4
OBSERVATION(S)
 5 ❽
WEIGHT(S)

EFFECTS: POSITIONS_IN_DATAFILE NUMBER_OF_LEVELS TYPE_OF_EFFECTS
1   46 cross ❶
2    9 cross ❷
3   50 cross ❸
4 1253 cross ❹
RANDOM_RESIDUAL VALUES
 0.8
RANDOM_GROUP ❺
 4
RANDOM_TYPE
add_animal
FILE
ReLWped.prn
(CO)VARIANCES
 0.1
RANDOM_GROUP ❻
 3
RANDOM_TYPE
diagonal
FILE

(CO)VARIANCES
 0.1
```

Note:
- ❶ Effect of contemporary groups in column #1 has 46 levels.
- ❷ Effect of parity in column #2 has 9 levels.
- ❸ Effect of PE from sire mate in column #3 has 50 levels.
- ❹ Effect of direct genetic from animal in column #4 has 1253 levels.
- ❺ Effect number 4 is random effect with add_animal type. This is genetic effects which require pedigree file.
- ❻ Effect number 3 is random effect with diagonal type for PE, which is uncorrelated.
- ❼ Analysis of single trait.
- ❽ Trait is in column #5 which is number born alive.

B. Multi-trait Model

Data File: LWdat.prn

```
 Id    month  year par nba nw lww    mate
15170009  5  1996  1  10   0  0      YIO3F030
15170010  4  1996  1  11   11 0      YIO3F030
15170011  1  1998  5  8    8  66.2   YIO3F030
15170011  3  1997  3  10   10 56.4   YIO3F030
15170011  3  1999  8  9    9  65.3   YIO3F030
15170011  5  1996  1  13   3  0      YIO3F030
15170011  6  1998  6  6    6  55.8   YIO3F030
15170011  8  1997  4  3    0  0      YIO3F030
15170011  10 1996  2  6    6  54.6   YIO3F030
15170011  10 1998  7  6    5  45.3   YIO3F030
15170012  1  1998  5  11   8  54.9   YIO3F030
```

Renum Data File: ReLWdat.prn

```
Cg  parity  mate id  nba    nw   lwt
 15     1     1   1   10     0    0
 11     1     1   2   11     11   0
 2      5     1   3   8      8    66
 8      3     1   3   10     10   56
 10     8     1   3   9      9    65
 15     1     1   3   13     3    0
 21     6     1   3   6      6    55
 28     4     1   3   3      5    45
 35     2     1   3   6      8    54
 37     7     1   3   6      6    43
```

Pedigree File: LWped.prn

```
Id       sire       dam       yob
15170010    YIO3F030    YIO4L016   1995
15170014    YIO3F030    YIO4L016   1995
15170009    YIO3F030    YIO4L016   1995
15170011    YIO3F030    YIO4L016   1995
15170012    YIO3F030    YIO4L016   1995
15170013    YIO3F030    YIO4L016   1995
15170014    YIO3F030    YIO4L016   1995
15170011    YIO3F030    YIO4L016   1995
15170012    YIO3F030    YIO4L016   1995
15170013    YIO3F030    YIO4L016   1995
```

Renum Pedigree File: ReLWped.prn

```
Id sire    dam    x  YOB   x x x x
 1  209     209    3 1986  2 1 0 1
 2  209     209    3 1986  2 1 0 2
 5  185     209    2 1987  2 1 0 10
 6  209     209    3 1987  2 1 0 11
 8  186      96    1 1991  2 1 1 14
 9  209     209    3 1986  2 1 0 17
10  185     209    2 1987  2 1 0 20
11  209     187    2 1988  2 1 0 21
15  185     209    2 1987  2 1 0 27
16  209     209    3 1986  2 1 0 28
```

*Note: *Cg is a combination of month-year of farrowing*

Parameter File: BLUP.PAR

```
DATAFILE
ReLWDat.prn
NUMBER_OF_TRAITS
 3 ❼
NUMBER_OF_EFFECTS
 4
OBSERVATION(S)
 5 6 7 ❽
WEIGHT(S)

EFFECTS: POSITIONS_IN_DATAFILE NUMBER_OF_LEVELS TYPE_OF_EFFECTS
1 1 1   46 cross ❶
2 2 2    9 cross ❷
3 3 3   50 cross ❸
4 4 4 1253 cross ❹
RANDOM_RESIDUAL VALUES
 60  5   1
 5   20  5
 1   5   10
RANDOM_GROUP ❺
 4
RANDOM_TYPE
add_animal
FILE
ReLMped.prn
(CO)VARIANCES
 10  5   1
 5   20  5
 1   5   10
RANDOM_GROUP ❻
 3
RANDOM_TYPE
diagonal
FILE

(CO)VARIANCES
 60  5   1
 5   20  5
 1   5   10
```

```
Note:
❶ Effect of contemporary groups in column #1 has
  46 levels.
❷ Effect of parity in column #2 has 9 levels.
❸ Effect of PE effect from mate in column #3 has
  50 levels.
❹ Effect of direct genetic from animal in column
  #4 has 1253 levels.
❺ Effect number 4 is random effect with
  add_animal type. This is genetic effects which
  require pedigree file.
❻ Effect number 3 is random effect with diagonal
  type for PE, which is uncorrelated.
❼ Analysis of 3 traits.
❽ Trait is in column #5 #6 #7 which is NBA, NW
  and LWT.
```

IX. Trouble Shooting

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

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

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: *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, PigPAK 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?.*

PigPAK 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

==========================

Who's who in BLUPF90-PCPAK

....

==========================

< 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*