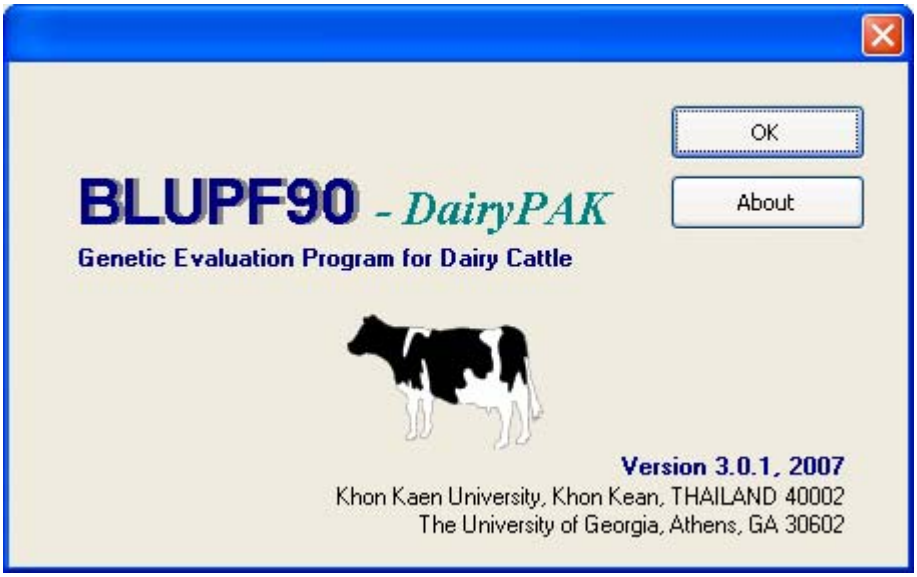
BLUPF90

DairyPAK

Version 3, 2007



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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. "DairyPAK" is a set of programs branched from "PC-PAK" with graphical user interface for simple use in Windows platform. DairyPAK was developed for the specific purpose of dairy genetic evaluation, and 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.
RENDOMN	: Renumber program for creating dominance pedigree file.
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 DairyPAK. 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

DairyPAK 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. After variance component estimation or BLUP analysis is performed, DairyPAK will create 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 report with accuracy up to four traits and Random regression for ten test days from 5 to 305 BV are available.

B. Specification

BLUPF90-DiaryPAK 3.0 requires windows 95/98/ME/XP/2000/2006 environment to install and Excel 98/2000/XP/2003/2006 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 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 structure of data. ACCF90 is an approximation that works with repeatability and maternal models.

With DairyPAK wizard interface, however, the single trait will support simple animal model, animal with PE model, and dominance model. Multiple traits will support up to four traits. Reports with accuracy are available only for single trait and multiple traits. Random regression will support for three DIM functions, which are Shaeffer and Dekkers, Wilmink and LeGendre. BV will be reported in ten testday from specified interval for all animals. Also, heritability against day in milk will be created if variance estimation option is selected.

C. Conditions of Use

BLUPF90-*DiaryPAK* is distributed *free of charge* for academic and scientific use under the conditions that it remains copyrighted. The use of any applications and compiled programs from DairyPAK must be credited in any publications derived from their usage. For commercial or grant project, personal communication of 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, constructive criticism and debug reports are invited. Please email to monchai@kku.ac.th

D. Program Download

BLUPF90-DairyPAK 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.

E. OnlineRegistration

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

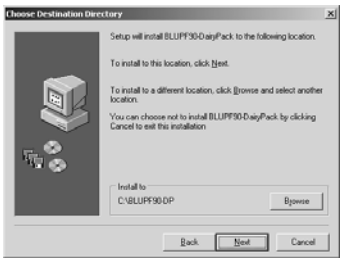
II. Installation

A. Installation

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

1. Run **DairyPAK.EXE**.

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



3. DairyPAK will install all F90 programs to the default directory "C:\Blup90DP". To modify the directory name, click **BROWSE** button.

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

B. How to Start Program

DOS environment

Each program can be run directly from directory \BLUPF90DP. 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:\BLUPF90DP**BLUPF90**

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

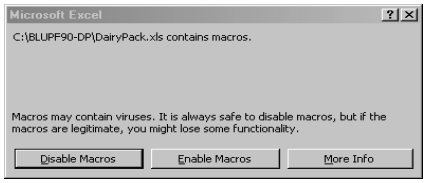
BLUPF90	: BLUP estimation using PCG.
REMLF90	: Variance estimation using REML by EM algorithm.
AIREMLF90	: Variance estimation using REML by AI Algorithm.
RENUMMAT	: Renumber program for creating data file and additive pedigree with animal ID in order number.
RENDOMN	: Renumber program for creating dominance pedigree.
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.

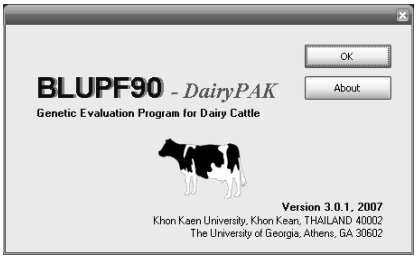
Windows environment

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

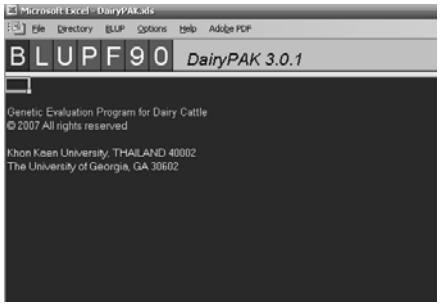
3. Excel program will run and DairyPAK will ask for macro enables. Click **Enable Macros** button.
(Note: BLUPF90-DairyPAK cannot execute without macros for Visual Basic Applications. If there is a problem to enable macros, click menu **Tools > Macro > Security** in Excel. Then, set security level to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



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

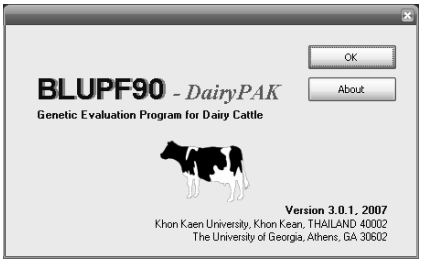


5. The main menu should look as below:

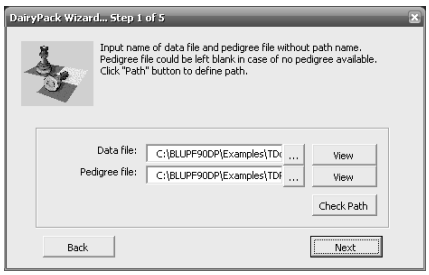


III. Genetic Evaluation At A Glance

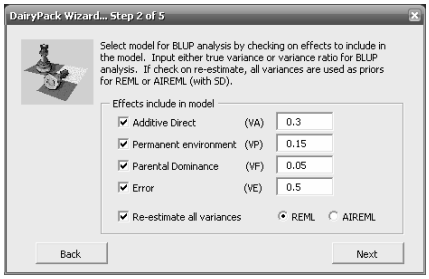
A. General View



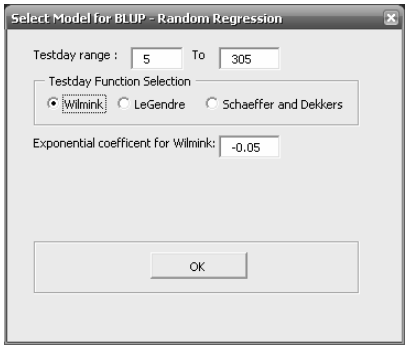
1. *DairyPAK* is a set of programs in BLUPF90 family with the specific purpose for dairy cattle evaluation.



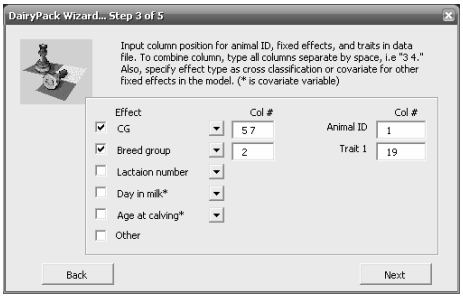
2. *DairyPAK* performs variance component estimation using REML and BLUP methodology with wizard interface. Data file and pedigree files can be browsed directly from computer.



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.

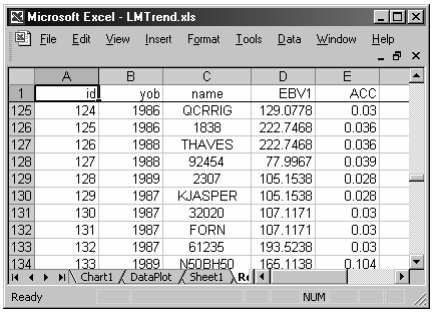


4. If random regression model is interested, three day in milk function of Wilmink, LeGendre, and Schaeffer and Dekkers can be selected. Range of DIM interval and exponential coefficient for Wilmink's function can be specified.



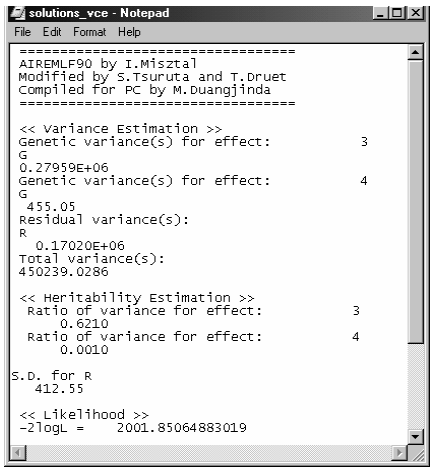
5. All effects in the model are simply specified by column number in original data file.

B. View of Reports

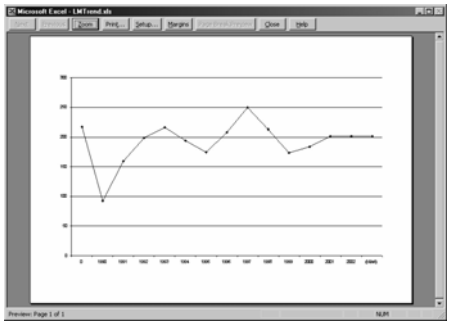


	A	B	C	D	E
1	id	yob	name	EBV1	ACC
125	124	1986	QCRRIG	129.0778	0.03
126	125	1986	1838	222.7468	0.036
127	126	1988	THAVES	222.7468	0.036
128	127	1988	92454	77.9967	0.039
129	128	1989	2307	105.1538	0.028
130	129	1987	KJASPER	105.1538	0.028
131	130	1987	32020	107.1171	0.03
132	131	1987	FORN	107.1171	0.03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

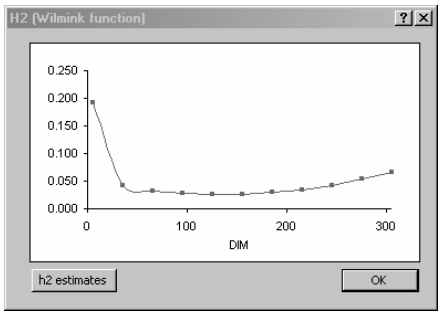
6. BLUP EBV report with accuracy is created using original ID in Excel format. Therefore, sorting, filtering can be done simply using Excel functions.



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

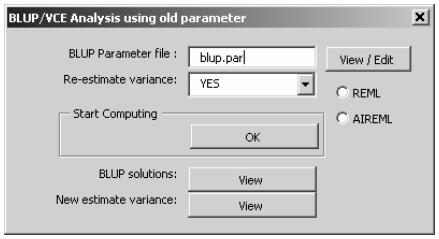


8. A genetic trend report is also created if desired. All graphic properties can be modified using general Excel features.

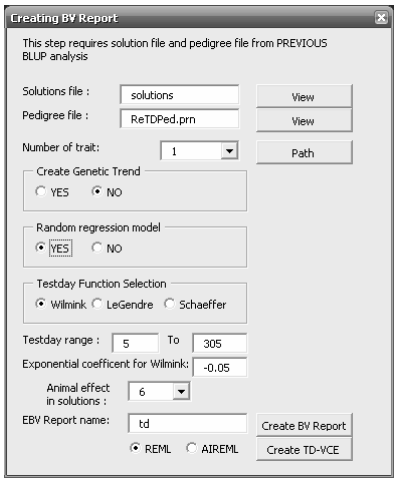


9. Estimates variance under random regression model provides test-day heritability plot.

C. Advanced Options

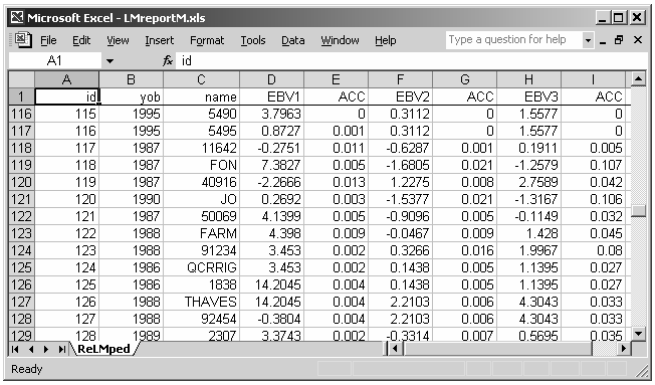


10. Previous renumbered data and pedigree file with parameter file can be modified and reanalyzed.



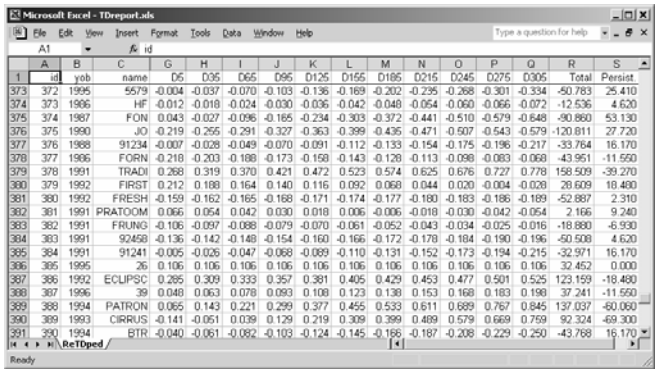
11. BV reports for single trait, multi-trait or random regression from previous solutions from DairyPAK or another BLUP family can be recreated with specified options.

12. 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

13. For random regression model, BV report for 10 test days from specified interval of day in milk was easily calculated. Therefore, BV for each sire can be plot against DIM later with Excel chart.



	A	B	C	G	H	I	J	K	L	M	N	O	P	Q	R	S
1	id	yob	name	D5	D35	D65	D95	D125	D155	D185	D215	D245	D275	D305	Total	Persist
373	372	1995	5579	-0.004	-0.037	-0.070	-0.103	-0.136	-0.169	-0.202	-0.235	-0.268	-0.301	-0.334	-50.783	25.410
374	373	1986	HF	-0.012	-0.018	-0.024	-0.030	-0.036	-0.042	-0.048	-0.054	-0.060	-0.066	-0.072	-12.536	4.620
375	374	1987	FON	0.043	-0.027	-0.096	-0.165	-0.234	-0.303	-0.372	-0.441	-0.510	-0.579	-0.648	-90.860	53.130
376	375	1990	JO	-0.219	-0.255	-0.291	-0.327	-0.363	-0.399	-0.435	-0.471	-0.507	-0.543	-0.579	-120.811	27.720
377	376	1988	91234	-0.007	-0.028	-0.049	-0.070	-0.091	-0.112	-0.133	-0.154	-0.175	-0.196	-0.217	-33.764	16.170
378	377	1986	FORN	-0.218	-0.203	-0.188	-0.173	-0.158	-0.143	-0.128	-0.113	-0.098	-0.083	-0.068	-43.951	-11.550
379	378	1991	TRADI	0.268	0.319	0.370	0.421	0.472	0.523	0.574	0.625	0.676	0.727	0.778	158.509	-39.270
380	379	1992	FIRST	0.212	0.188	0.164	0.140	0.116	0.092	0.068	0.044	0.020	-0.004	-0.028	28.609	18.480
381	380	1992	FRESH	-0.159	-0.162	-0.165	-0.168	-0.171	-0.174	-0.177	-0.180	-0.183	-0.186	-0.189	-52.887	2.310
382	381	1991	PRATOOM	0.066	0.054	0.042	0.030	0.018	0.006	-0.006	-0.018	-0.030	-0.042	-0.054	2.166	9.240
383	382	1991	FRUNG	-0.106	-0.097	-0.088	-0.079	-0.070	-0.061	-0.052	-0.043	-0.034	-0.025	-0.016	-18.880	-6.930
384	383	1991	92458	-0.136	-0.142	-0.148	-0.154	-0.160	-0.166	-0.172	-0.178	-0.184	-0.190	-0.196	-50.508	4.620
385	384	1991	91241	-0.005	-0.026	-0.047	-0.068	-0.089	-0.110	-0.131	-0.152	-0.173	-0.194	-0.215	-32.971	16.170
386	385	1995	26	0.106	0.106	0.106	0.106	0.106	0.106	0.106	0.106	0.106	0.106	0.106	32.452	0.000
387	386	1992	ECLIPSC	0.285	0.309	0.333	0.357	0.381	0.405	0.429	0.453	0.477	0.501	0.525	123.159	-18.480
388	387	1996	39	0.048	0.063	0.078	0.093	0.108	0.123	0.138	0.153	0.168	0.183	0.198	37.241	-11.550
389	388	1994	PATRON	0.065	0.143	0.221	0.299	0.377	0.455	0.533	0.611	0.689	0.767	0.845	137.037	-60.060
390	389	1993	CIRRUS	-0.141	-0.051	0.039	0.129	0.219	0.309	0.399	0.489	0.579	0.669	0.759	92.324	-69.300
391	390	1994	BTR	-0.040	-0.061	-0.082	-0.103	-0.124	-0.145	-0.166	-0.187	-0.208	-0.229	-0.250	-43.768	16.170

IV. Model Descriptions

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

A. Basic Animal Model

DairyPAK 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. Combination of fixed effects such as herd-year-season can be performed during the analysis, no additional data preparation is required. Normally, all traits analyzed with DairyPAK 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 lactation records are available, the permanent environment effect due to the animal need to be taken into account. Fitting permanent environment effect as uncorrelated random effects is generally used in genetic evaluation. The model for analysis is:

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

where $\boldsymbol{y}$ is vector of response variable, $\boldsymbol{\beta}$ is vector of fixed effects, $\boldsymbol{a}$ is vector of random additive genetic effects, $\boldsymbol{p}$ 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_p^2 is permanent environment variance, and σ_e^2 is residual variance.

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

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

C. Multi-trait Model

DairyPAK 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 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:

$$\begin{bmatrix} y_1 \\ y_2 \end{bmatrix}=\begin{bmatrix} X_1 & 0 \\ 0 & X_2 \end{bmatrix}\begin{bmatrix} \beta_1 \\ \beta_2 \end{bmatrix}+\begin{bmatrix} Z_1 & 0 \\ 0 & Z_2 \end{bmatrix}\begin{bmatrix} a_1 \\ a_2 \end{bmatrix}+\begin{bmatrix} \varepsilon_1 \\ \varepsilon_2 \end{bmatrix},\ V\begin{bmatrix} a_i \\ e_i \end{bmatrix}=\begin{bmatrix} G\otimes A & 0 \\ 0 & R\otimes I \end{bmatrix},$$

where y_1, y_2 is vector of response variable for trait 1 and 2, β_1, β_2 is vector of fixed effects, a_1, a_2 is vector of random additive genetic effects, $\varepsilon_1, \varepsilon_2$ is vector of random residual, X_1, X_2 and Z_1, Z_2 are incident matrices related to fixed and random effects, A is numerator relationship matrix, G is matrix of direct genetic variance-covariance for trait 1 and 2, R is matrix of residual variance-covariance for trait 1 and 2.

D. Random Regression Model

Random regression analysis in DairyPAK is a powerful feature. However, only three DIM functions from Schaeffer and Dekkers, Wilmink and LeGendre can be selected. All models keep error variance as constant. The analysis will include DIM function in both additive genetic and permanent environment effects. To perform more complicate model, parameter file can be edited and re-analyzed from menu **BLUP>Use old parameters** or use BLUPF90-PCPAK. Data file preparation in a random regression analysis is different from lactation model. Test day milk record from single lactation and day in milk after calving at each test date is required in the data file. The model for analysis is:

$$Y_{ijk} = HTD_i + \sum_{m=1}^{n} b_m X_{im} + \sum_{m=1}^{n} a_{jm} Z_{ijm} + \sum_{m=1}^{n} p_{jm} Z_{ijm} + e_{ijk}\ ,$$

where Y_{ijkl} is test day milk production, HTD_i is fixed effect of herd test date, b_m = fixed regression coefficient, a_{jm} and p_{jm} are random additive genetic and random permanent environment effect related to day in milk function, X_{im} and Z_{ijm} are incident matrix related fixed and random effect, and e_{ijk} = random residual. Day in milk function in the analysis can be described as:

$$f(t) = L_1 + L_2 + L_3 \qquad [1]$$

$$f(t) = a_0 + a_1 t^* + a_2 e^{-0.05t^*} \qquad [2]$$

$$f(t) = a_0 + a_1 t + a_2 ln(305/t) \qquad [3]$$

Where [1] is Legendre polynomials function (Gengler et al., 1999), [2] is Wilmink function (Wilmink, 1987) and [3] is Schaeffer and Dekkers function (Schaeffer and Dekkers, 1994); and $L1 = 1$, $L2 = \sqrt{3}L$, $L3 = \sqrt{5/4}(3L^2 - 1)$, $L = (-1) + 2*(t-1)/(305-1)$, $a_0 = 1$, a_1, a_2 = regression coefficients , $t = DIM$, and $t^* = DIM / 305$.

E. Dominance Model

In this version, the parental dominance effect or full-sib subclass effects can be taken into account in the model. DairyPAK will create dominance pedigree based on Hoeschele and Van Raden (1998). Dominance analysis is limit for single trait analysis only. To include parental dominance effect in multi-trait or random regression, parameter file can be edited and re-analyzed from menu **BLUP>Use old parameters**. The model for analysis is:

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

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, $\boldsymbol{X}$, $\boldsymbol{F}$ 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_f^2 is parental dominance genetic variance where $\sigma_f^2 = \frac{1}{4}\sigma_d^2$, and σ_e^2 is residual variance.

V. How Does The Program Functions?

A. Program and file components

After installation, programs are stored in main or user-specified directory, ie. C:\BlupF90DP. Two sub-directories of \examples and \helps are also created. Each directory will find the following programs and files.

Main directory:

Filename	Type	Description
DairyPAK.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.
RENDOMN.EXE	PROG	- Renumbering full-subclass for parental dominance pedigree file.

Examples directory:

Name	Type	Description
LMDAT.PRN	TXT	- Data file for lactation model analysis with single trait and multi-trait with repeated records.
LMPED.PRN	TXT	- Pedigree file for analysis with LMDAT.
TDDAT.PRN	TXT	- Data file for test day model analysis with random regression.
TDPED.PRN	TXT	- Pedigree file for analysis with TDDAT.
LMDAT.FMT	TXT	- Describe column number format for LMDAT.PRN
TDDAT.FMT	TXT	- Describe column number format for TDDAT.PRN

Helps directory:

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

B. The way program works

When performed the analysis with wizard interface in DairyPAK. All parameter entered in the form will be kept in particular Excel sheets. Parameter file will be written with corrected format for RENUMMAT, BLUPF90 and REMLF90 programs using visual basic. VB in Excel has specific function to operate EXE file without closing the Excel program.

Pedigree and solutions from the analysis are read back to Excel with original animal ID. Genetic trend can be created using excel function if required.

Data and Pedigree files used in DairyPAK must be ASCII or TEXT file. 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) or CSV file (Comma delimited) is preferable than Tab delimited.

Analysis files and reports will be 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 renamed to new name if need.

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

Name	Type	Description
RELMDAT.PRN	TXT	- Renumbered data file.
RELMPED.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.

If test day data is used, most additional files after analysis are the same except for data files. Suppose the original files for the analysis are TDDAT.PRN and TDPED.PRN, more additional are:

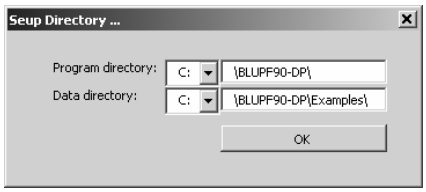
Name	Type	Description
RETDDAT.PRN	TXT	- Renumbered data file without columns for covariate function.
RELMPED.PRN	TXT	- Renumbered Pedigree file.
NewRETDDAT.PRN	TXT	- Renumbered data file with 3 additional columns for covariate functions of Wilmink, Schaeffer and Dekkers or LeGendre.

B. Solutions at Convergence

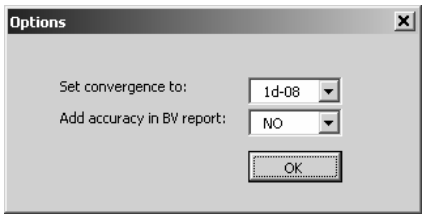
The default for convergence is 1d-08, however, users can choose their own by selecting menu **Options > Set Options**.

VI. Genetic Evaluation by Examples

A. Setup Directory and Preferences



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



2. Other options such as 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 adjusted 305 day milk yield. LMDAT.PRN is data file and LMPED.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. LMDAT.PRN is data file and LMPED.PRN is pedigree file.

Random regression analysis

The example will show how to predict breeding value for random regression testday model. TDDAT.PRN is data file and TDPED.PRN is pedigree file.

File format

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

#1	ID
#2	Month of calving
#3	Year of calving
#4	Breed Group
#5	Lactation
#6	Age of dam (month)
#7	Milk 305 (kg.)
#8	Fat 305 (kg.)
#9	Prot 305 (kg.)

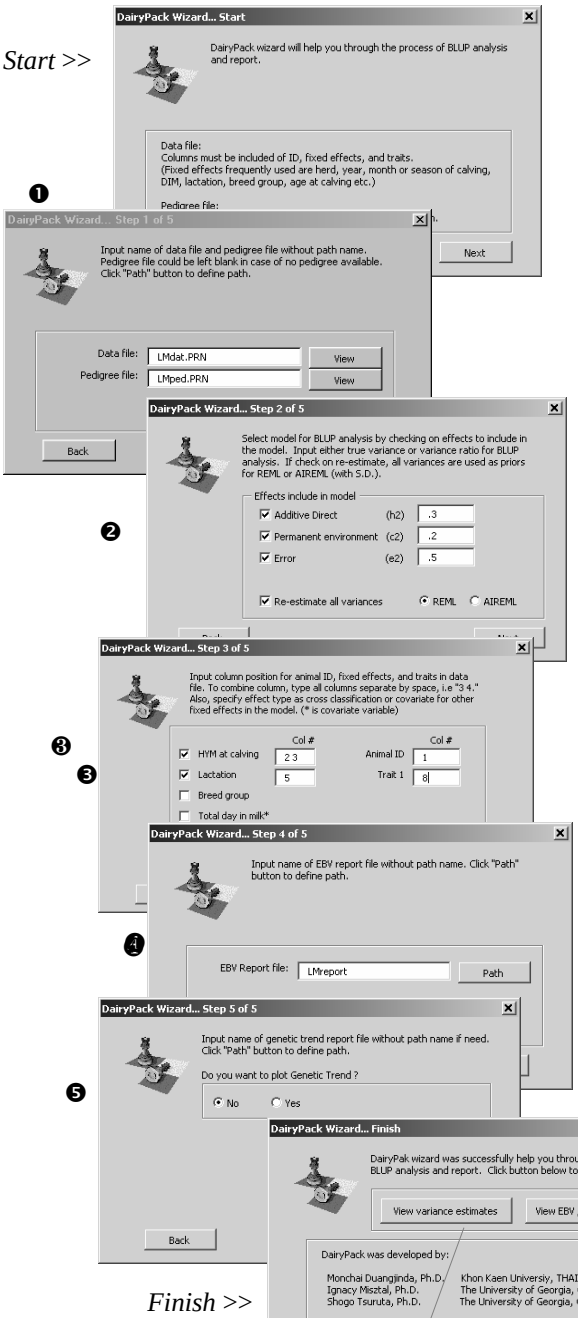
Format for TDDAT.PRN is stored in TDDAT.FMT. There are 8 columns of:

#1	ID
#2	Test Month
#3	Test Year
#4	Breed Group
#5	Lactation
#6	Age of dam (month)
#7	Day in milk
#8	Test day milk production (kg.)

Format for pedigree is the same. There are four columns of animal ID, sire ID, dam ID, and year of birth. Generally, year of birth can be omit from pedigree file, but genetic trend will not to be created. Note: all files are stored in C:\BlupF90DP\EXAMPLES.

C. Single Trait Analysis Example

Start >>



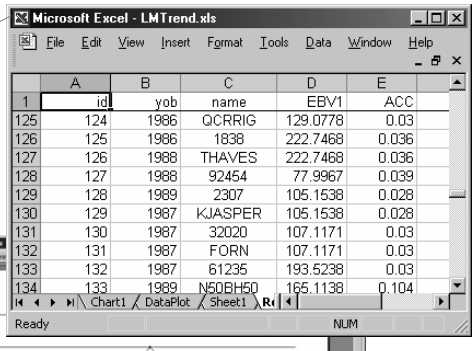
Finish >>

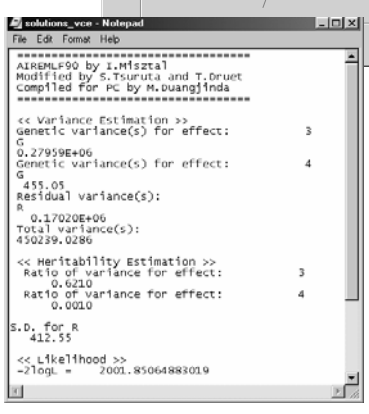
Start >> Select menu **BLUP > Single trait**. DairyPAK wizard will show up, click **Next** button to start analysis.

1. Input data file (**LMdat.prn**) and pedigree file (**LMped.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, "**0.3**", "**0.2**" and "**0.5**" are entered for heritability, permanent environment and error ratio for milk305 trait.
   *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, "**5**" is column for lactation, animal id and milk yield are in column "**1**" and "**7**", 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.

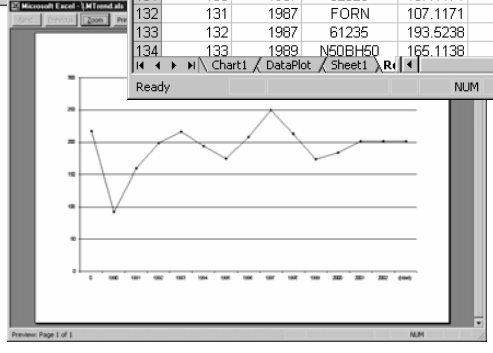
Finish >> Click **View variance estimation** button to view variance components estimated by REML (if Re-estimates in ❷ is checked. Variance components and ratio will report in order from additive genetic, permanent environment and error). Click **View EBV / Genetic Trend** button to see reports as bellows.

EBV report





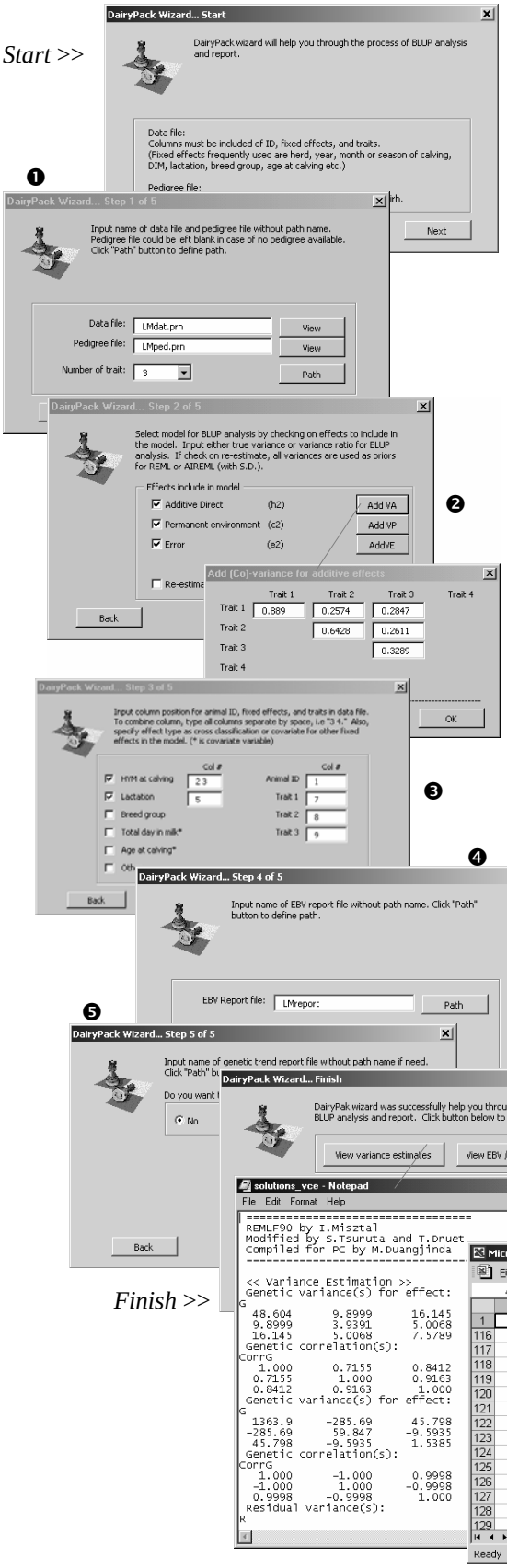
VCE report



Genetic trend

D. Multi-trait Analysis Example

Start >>



Finish >>

VCE report

EBV report

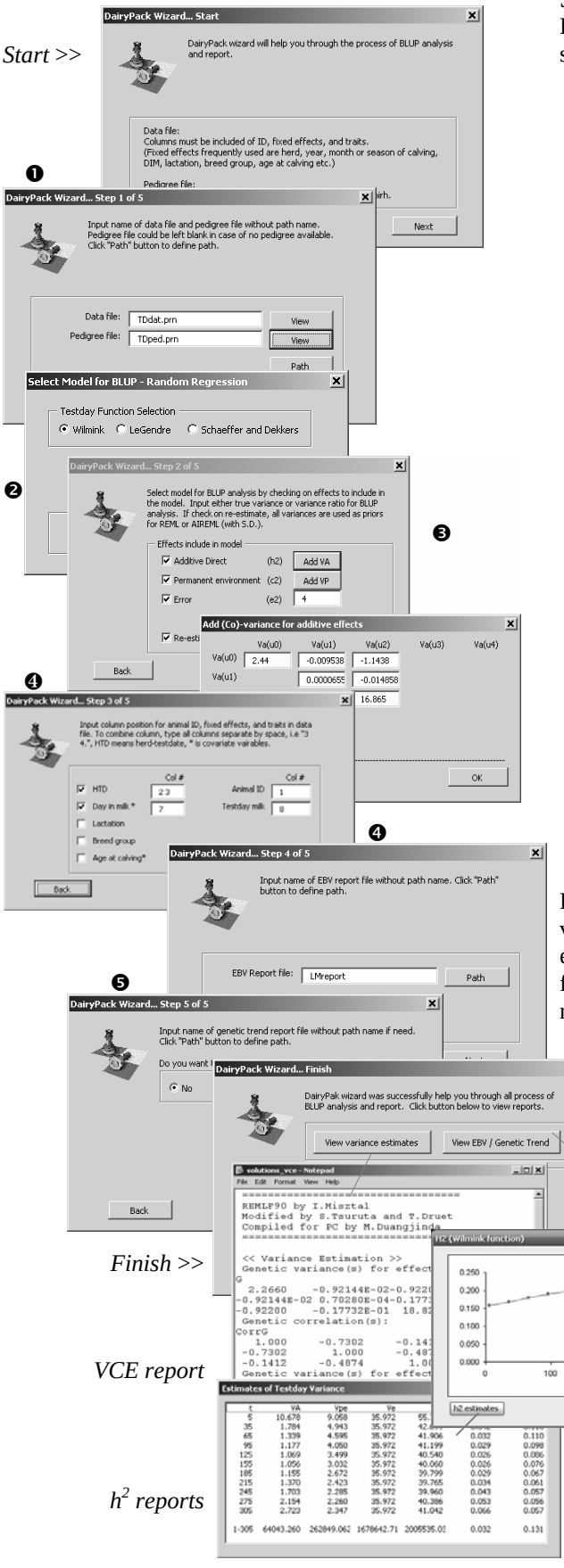
Start >> Select menu **BLUP > Multiple trait**. Dairypack wizard will show up, click **Next** button to start analysis.

1. Input data file (**LMdat.prn**) and pedigree file (**LMped.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, "**5**" is column for lactation, animal id is in column "**1**" and milk, fat and protein yield are in column "**7**", "**8**", "**9**", respectively.
   Note: DariyPack 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 ❷ is checked). DairyPack also reports genetic, environment and phenotypic correlations.

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

E. Random Regression Test day Analysis Example



Start >> Select menu **BLUP > Random regression**. Dairypack wizard will show up, click **Next** button to start analysis.

1. Input data file (**TDdat.prn**) and pedigree file (**TDped.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. Select milk function used in the model. In this example, Wilmink function is selected.
3. 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.*
4. Input column number for fixed effects, animal and traits. In this examples, "**2 3**" are input to combine effect for contemporary group, "**7**" is column for day in milk, animal id is in column "**1**" and test day milk is in column "**8**".
5. Enter filename to keep BLUP solutions and create BV report.
6. 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.

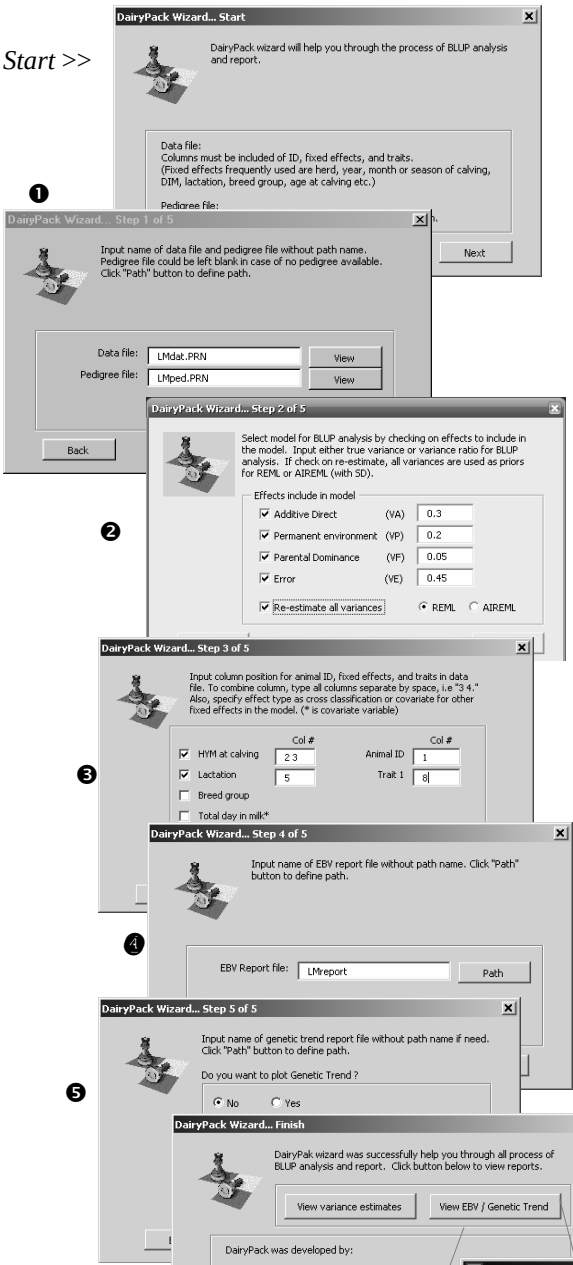
Finish ➡ Click **View variance estimation** button to view variance components estimated by REML (if Re-estimates in ❷ is checked. The correct variance ratio for testday will show in the chart). DairyPack also reports heritability plot along 305 day in milk.

Click **View EBV / Genetic Trend** button to see BLUP reports for 10 test day from 5 to 305 day in milk, and total EBV for 305 day as bellows.

Click this button to Print/Save h2 estimate for each testday, plot, and genetic covariance between tesdays in Excel format (H2.xls, CORR.xls).

F. Single Trait Analysis (Dominance model) Example

Start >>



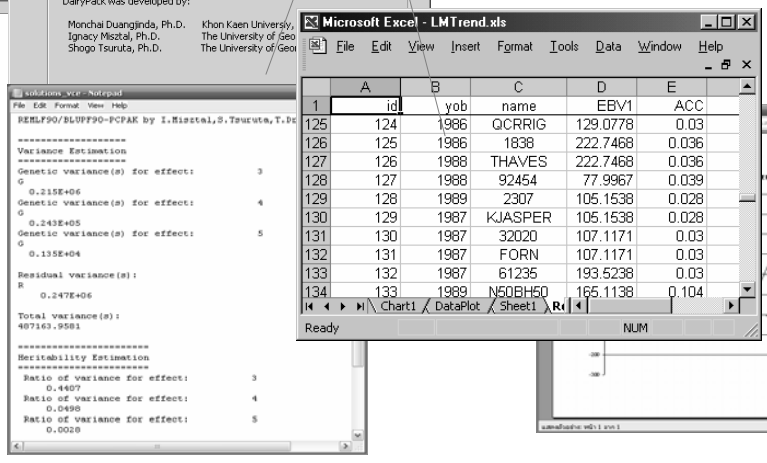
Start >> Select menu **BLUP > Single trait**. DairyPAK wizard will show up, click **Next** button to start analysis.

1. Input data file (**LMdat.prn**) and pedigree file (**LMped.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, "**0.3**", "**0.2**", "**0.05**", "**0.45**" and are entered for heritability, permanent environment, parental dominance and error ratio for milk305 trait.
   *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, "**5**" is column for lactation, animal id and milk yield are in column "**1**" and "**7**", 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.Variance components and ratio will report in order from additive genetic, permanent environment, parental domiance and error). **Parental domiance variance and ratio must multiply by four** to get individul dominance for population and error must deduct by three times of parental dominance. Click **View EBV / Genetic Trend** button to see reports (EBV adj for dominance) as bellows.

Finish >>

EBV report



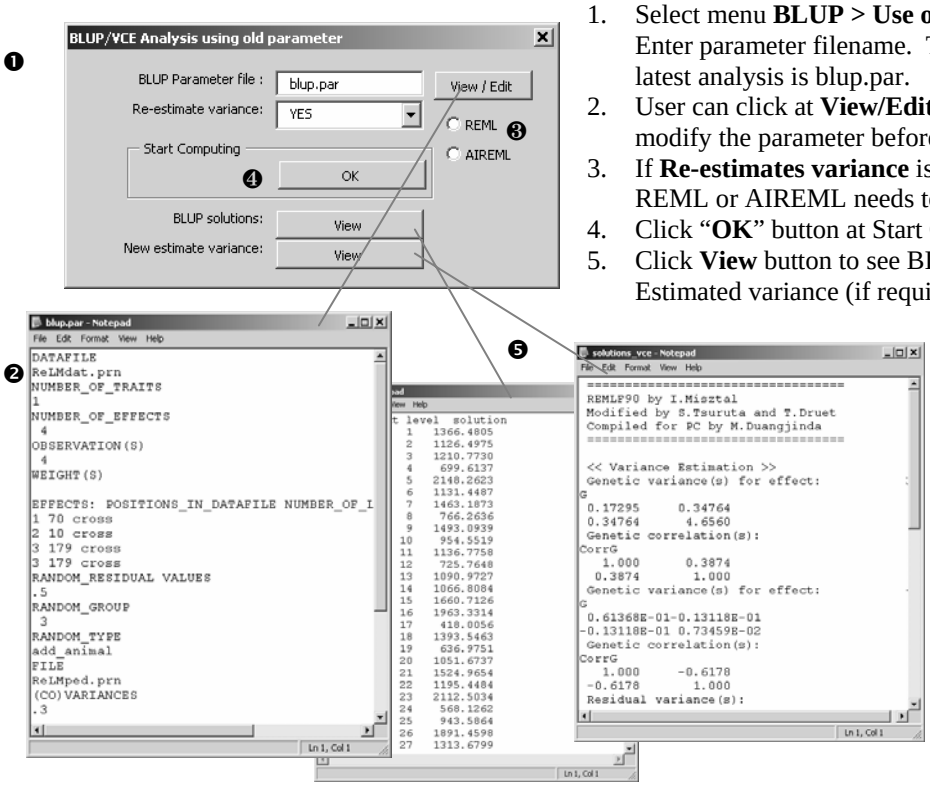
VCE report

Genetic trend

VII. Special Analysis and Report

A. Re-analysis from old parameter

Once the analysis has been done, the "blup.par" parameter and renumbering data and pedigree can be saved and reanalysis later if desired. (Note: renumbering data and pedigree will start with 'RE', it. RE+*Datafile* and RE+*Pedfie*). DairyPAK has a useful feature to achieve BLUP analysis from previous parameter files without using Wizard. The parameters can be modified for complicated model or other models not available in wizards (see next section).



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. Setting different fixed effects for multi-trait analysis

The analysis of multi-trait BLUP using Wizard in DairyPAK has limited with similar fixed effects. However, the different fixed effects for each trait can be applied by doing some modification in wizard steps and blup.par parameter file as follows:

1. When perform wizard steps, keep all the fixed effects.
2. After finish the wizard analysis, select menu **BLUP > Use old parameters**.
3. Click button **View/Edit** to view blup.par file and make some modification.

Example of parameter file editing:

This example is three trait analyses with three fixed effects plus animal effect. After wizard steps, blup.par parameter file will automatically created. The modification of blup.par will be as follow:

1) Find section "EFFECTS: POSITIONS_IN_DATAFILE".

```
EFFECTS: POSITIONS_IN_DATAFILE NUMBER_OF_LEVELS TYPE_OF_EFFECTS
1 1 1        28 cross             <- Col#1 in datafile is 1st effect with 28 levels
2 2 2        3  cross             <- Col#2 in datafile is 2nd effect with 3 levels
3 3 3        15 cross             <- Col#3 in datafile is 3rd effect with 15 levels
4 4 4        16851 cross          <- Col#4 in datafile is 4th effect with 16851 levels
```

2) Suppose column 1 in redat.prn is fixed effects for all traits, column 2 is for trait 1 and 2 and column 3 is for triat 3 only. This section must be modified. The new blup.par will be as follows:

```
EFFECTS: POSITIONS_IN_DATAFILE NUMBER_OF_LEVELS TYPE_OF_EFFECTS
1 1 1        28 cross         <-Fixed effect from Col#1 will adjust for trait 1,2,3
2 2 0        3  cross         <-Fixed effect from Col#1 will adjust for trait 1,2
0 0 3        15 cross         <-Fixed effect from Col#1 will adjust for trait 3
4 4 4        16851 cross      <-Column 4th is still animal ID with 16851 levels
```

C. Multi-trati analysis more than 4 traits

The analysis of multi-trait BLUP Wizard in DairyPAK has limited to four traits. However, the number of traits greater than 4 can be accomplished. Consequently, Excel report will not be available for this situation. Only solutions and VCE in text files are avaiable. You have to open the file "solutions" and "solutions_vce" with Notepad or word in the data directory to check the results. The modification of blup.par parameter file has to be done as follows:

1. Perform wizard steps with four traits as usual.
2. Open Excel program, then open renumbering data file (RE+*Datafile*) in the data directory. Add trait 5, 6, 7, … as desired continually from last column. Note: Please check carefully that added traits are related to the correct animal ID. Since animal ID in this file is renumbering from 1,…, n, therefore, the original Id can bechecked in renumbering pedigree file (RE+Pedfile).
3. Save As the file in 2 in .xls format for backing up data.
4. Save As the file in 2 again in .prn for using in BLUP analysis. (Rename to original RE+*Datfile* is required)
5. Select menu **BLUP > Use old parameters**.
6. Click button **View/Edit** to view blup.par file and make some modification.

Example of parameter file editing:

This example is start with four trait analyses with three fixed effects plus animal effect. After wizard steps, blup.par parameter file will automatically created. The modification of blup.par will be as follow:

1) Find section "OBSERVATION" and "EFFECTS: POSITIONS IN DATA FILE".

```
DATAFILE
Redat.prn
NUMBER_OF_TRAITS
 4
NUMBER_OF_EFFECTS
 4
OBSERVATION(S)
 5 6 7 8                     <- Four analysis traits are in column 5,6,7,8
WEIGHT(S)

EFFECTS: POSITIONS_IN_DATAFILE NUMBER_OF_LEVELS TYPE_OF_EFFECTS
1 1 1 1      28 cross         <-Fixed effect from Col#1 will adjust trait 1,2,3,4,
2 2 2 2      3  cross
3 3 3 3      15 cross
4 4 4 4      16851 cross
```

2) Suppose trait 5 and 6 are added in redat.prn at column 9 and 10. These two sections must be modified as follows:

```
DATAFILE
Redat.prn
NUMBER_OF_TRAITS
 4
NUMBER_OF_EFFECTS
 4
OBSERVATION(S)
 5 6 7 8 9 10                <- Four analysis traits are in column 5,6,7,8
WEIGHT(S)

EFFECTS: POSITIONS_IN_DATAFILE NUMBER_OF_LEVELS TYPE_OF_EFFECTS
1 1 1 1 1 1     28 cross      <-Fixed effect from Col#1 will adjust trait 1,2,3,4, 5,6
2 2 2 2 2 2     3  cross
3 3 3 3 3 3     15 cross
4 4 4 4 4 4     16851 cross
```

D. Setting random regression with covaraince function greater than 3x3

The analysis of random regression BLUP Wizard in DairyPAK has limited to 3x3 covariance function, such as Schaefer and Dekkers, Wilmink, and 2nd order LeGendre polynomials. However, other functions can be used. Consequently, Excel report will not be available for this situation. Only solutions and VCE in text files are avaiable. You have to open the file "solutions" and "solutions_vce" with Notepad or word in the data directory to check the results. The modification of blup.par parameter file has to be done as follows:

1. Perform wizard steps from random regression menu as usual.
2. Open Excel program, then open renumbering data file (NEWRE+*Datafile*) in the data directory. Insert the new calculated column or recalculated column for testday function that will be used in the analysis as desired. For example, if LeGendre polynomial is first used, DairyPAK will have column for L2 and L3 (L1 will be absorbed in animal effects) in the "NEWRE+*Datafile*". For new analysis with 5x5 covariance function, the L2, L3 must be recalculated and L4 and L5 must be calculated and add next to L2 and L3.
3. Save As the file in 2 in .xls format for backing up data.
4. Save As the file in 2 again in .prn for using in BLUP analysis. (Rename to original RE+*Datfile* is required)
5. Select menu **BLUP > Use old parameters**.
6. Click button **View/Edit** to view blup.par file and make some modification.

Example of parameter file editing:

This example is start with 3x3 covariance function. After wizard steps, blup.par parameter file will automatically created. The modification of blup.par will be as follow:

3) Find section "Number of effects" and "EFFECTS: POSITIONS IN DATA FILE".

```
DATAFILE
NewRelac1.prn
NUMBER_OF_TRAITS
1
NUMBER_OF_EFFECTS
 8              <- The effects are 8 (2 are for fixed + 3 for genetic + 3 for PE)
OBSERVATION(S)
 4
WEIGHT(S)

EFFECTS: POSITIONS_IN_DATAFILE NUMBER_OF_LEVELS TYPE_OF_EFFECTS
1 180 cross            <- First fixed effect (HTD) are in col 1
2 50 cross             <- Second fixed effect are in col 2
3 7068 cross           <- Animal effect are in col 3 for G
8 7068 cov 3           <- L2 function are in col 8 and nested with animal for G
9 7068 cov 3           <- L3 function are in col 9 and nested with animal for G
3 7068 cross           <- Animal effect are in col 3 for PE
8 7068 cov 3           <- L2 function are in col 8 and nested with animal for PE
9 7068 cov 3           <- L3 function are in col 8 and nested with animal for PE
```

4) Suppose 5x5 covariance will be used instead. These two sections must be modified as follows:

```
DATAFILE
NewRelac1.prn
NUMBER_OF_TRAITS
1
NUMBER_OF_EFFECTS
 11                    <- the effects are changed to 12 (add 2 for G and 2 for PE)
OBSERVATION(S)
 4
WEIGHT(S)

EFFECTS: POSITIONS_IN_DATAFILE NUMBER_OF_LEVELS TYPE_OF_EFFECTS
 1  180 cross
 2   50 cross
 3 7068 cross
 8 7068 cov 3
 9 7068 cov 3
10 7068 cov 3          <- Add L4 function are in col 10 and nested with animal for G
11 7068 cov 3          <- Add L5 function are in col 11 and nested with animal for G
 3 7068 cross
 8 7068 cov 3
 9 7068 cov 3
10 7068 cov 3          <- Add L4 function are in col 10 and nested with animal for PE
11 7068 cov 3          <- Add L5 function are in col 11 and nested with animal for PE
```

1) Find section "RANDOM_GROUP".

```
RANDOM_GROUP
 3   4   5             <- Add.genetic variance are estimated from effects 3,4,5
RANDOM_TYPE
add_an_upg
FILE
Reped.prn              <- name of pedigree used
(CO)VARIANCES
4.6 -1 -0.02           <- starting of 3x3 variance structure for Add Genetic
-1 1 -0.02
-0.02 -0.02 0.1
RANDOM_GROUP
 6   7   8             <- PE variance are estimated from effects 6,7,8
RANDOM_TYPE
diagonal
FILE
                       <- No pedigree need in estimating PE
(CO)VARIANCES
10 -2 -0.1             <- starting of 3x3 variance structure for PE
-2 4.1 -0.2
-0.1 -0.2 0.1
```

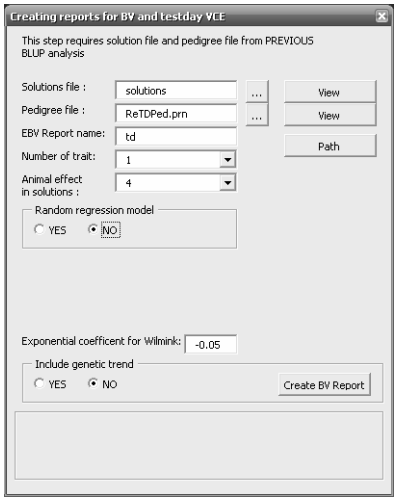
5) To change to 5x5 covariance structure. This section must be modified as follows:

```
RANDOM_GROUP
 3 4 5 6 7             <- Add.genetic effects are changed to 3,4,5,6,7
RANDOM_TYPE
add_an_upg
FILE
Reped.prn
(CO)VARIANCES
 4.6  -1   -0.02 -0.01   -0.002      <- G covariance structure will be changed to 5x5
-1.0   1   -0.02 -0.01   -0.002
-0.02 -0.02 0.1  -0.005  -0.001
-0.01 -0.01 -0.005 0.001 -0.001
-0.002 -0.002 -0.001 -0.001 0.0008
RANDOM_GROUP
 8 9 10 11 12          <- PE variance are estimated from effects 8,9,10,11,12
RANDOM_TYPE
diagonal
FILE

(CO)VARIANCES
  10   -2 -0.1 -0.05 -0.05           <- PE covariance structure will be changed to 5x5
  -2  4.1 -0.2 -0.02 -0.02
-0.1 -0.2  0.1 -0.01 -0.01
-0.05 -0.02 -0.01 0.05 -0.005
-0.05 -0.02 -0.01 -0.005 0.008
```

E. Creating BLUP report from previous solutions

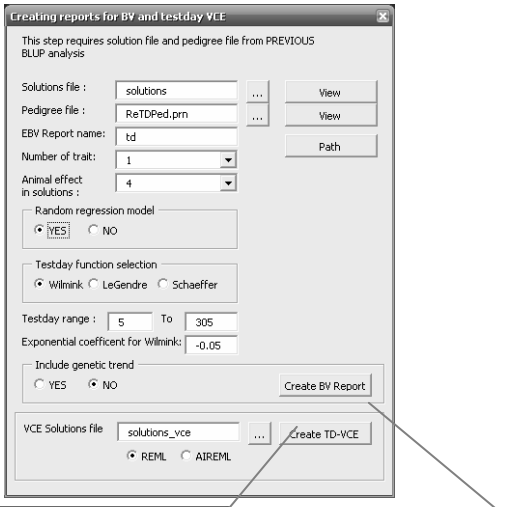
All solutions from the analysis of BLUPF90 family programs. Such as BLUPF90, REMLF90/AIREMLF90, BLUPF90-PCPAK, can be brought into DairyPAK to create BV reports. This step requires solutions file and renumbering pedigree file from previous analysis.



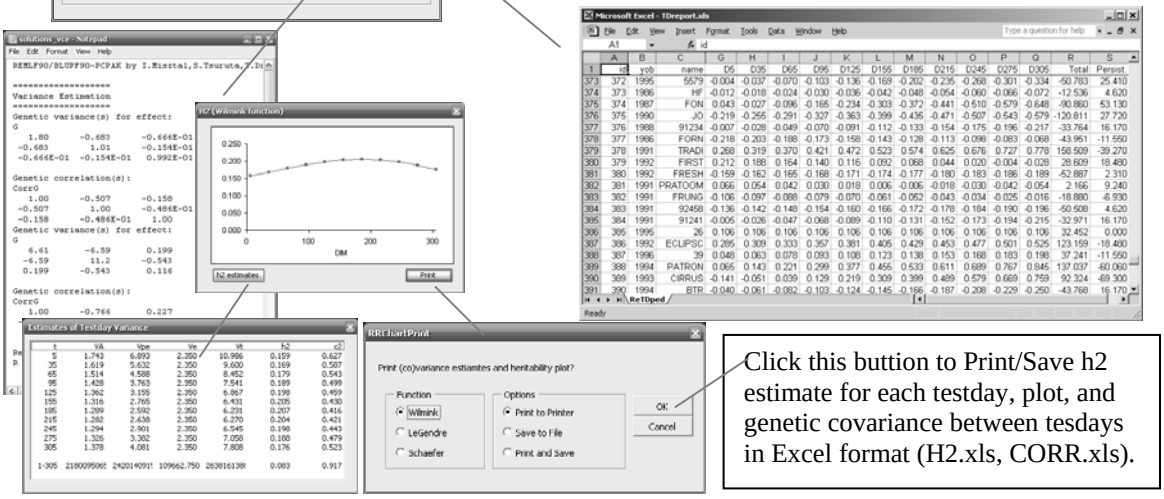
1. Select menu **BLUP > Create BV /TD-VCE reports**. Enter solution and renum-pedigree filenames.
2. User can click at **View** button to check the correct file name. Click **Path** to change path.
3. Select option Random regression model to "**NO**".
4. If solutions are from multi-trait BLUP analysis, specify number of trait.
5. Enter number of animal effect in solutions file.
6. Select "**YES**" for creating genetic trend if desired.
7. Enter BV filename to save. Click "**OK**" button at Start Computing section.
8. Click **View** button to see BLUP report.

F. Creating testday variance components /EBV from previous solutions

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



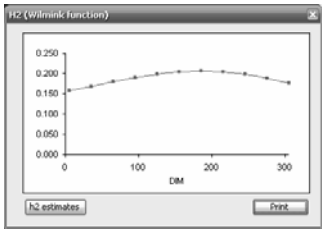
1. Select menu **BLUP > Create BV /TD-VCE reports**. Enter solution and renum-pedigree filenames.
2. User can click at **View** button to check the correct file name. Click **Path** to change path.
3. Enter number of trait to 1.
4. Select option Random regression model to "**YES**".
5. Choose particular testday function related to solutions.
6. Enter number of animal effect in solutions file.
7. Select "**YES**" for creating genetic trend if desired.
8. Enter BV filename to save. Click "**OK**" button at Start Computing section.
9. Click **View** button to see BLUP report.

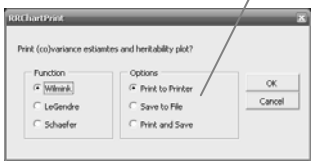


Click this button to Print/Save h2 estimate for each testday, plot, and genetic covariance between tesdays in Excel format (H2.xls, CORR.xls).

G. Creating genetic correlations between testday

DairyPAK cannot create the genetic correlation between testday directly. However, all genetic (co) variances and correlations between testday are calculated and saved in Excel format. Further 3D plotting software, such as SAS, GNU plot, etc., can be further applied.





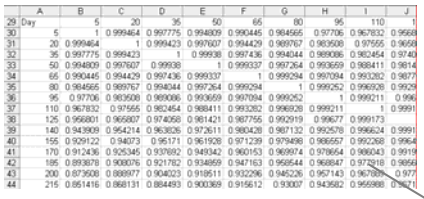
To keep testday (co) variances and correlations, do the followings:

1. From H2 plot windows, click button “PRINT”
2. Select option “Save to File”
3. The h2 for each testday and h2 plot will be saved in “H2.xls” and genetic (co) variances and correlations will be saved in “CORR.xls” in the data directory.

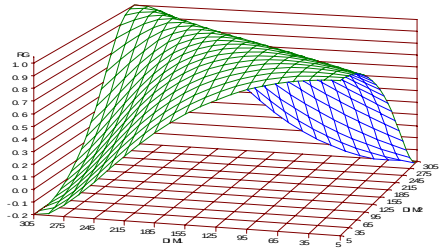
To plot 3D genetic corrleation between testday using SAS:

1. Open file name “CORR.xls” with Excel
2. Copy area of genetic correlation, then paste into SAS.
3. Type SAS statement as follows

Genetic correlations in CORR.xls >>



Genetic correlations plot from SAS G3D >>




```
DATA rg;
  INPUT dim r1-r21;
  ARRAY temp[21] r1-r21;
  t1+1;
  DO t2 = 1 TO 21;
    rg = temp[t2];
    OUTPUT;
  END;
  KEEP t1 t2 rg;
CARDS;
 5       1.000      0.997      . . .      0.974
 20      0.997      1.000      . . .      0.988
 35      0.989      0.997      . . .      0.997
 50      0.974      0.988      . . .      1.000
 65      0.952      0.972      . . .      0.997
. .      . . .      . . .      . . .      . . .
. .      . . .      . . .      . . .      . . .
. .      . . .      . . .      . . .      . . .
. .      . . .      . . .      . . .      . . .
275     -0.109     -0.084      . . .     -0.019
290     -0.182     -0.167      . . .     -0.121
305     -0.236     -0.230      . . .      1.000
;
DATA plot;
  SET rg;
  dim1 = (t1-1)*15+5;
  dim2 = (t2-1)*15+5;

PROC G3D;
  PLOT dim1*dim2 = rg /GRID XTICKNUM=11 YTICKNUM=11
                       ZTICKNUM=13 ROTATE = 75
                       ZMIN = -0.20 ZMAX = 1.00;
RUN;
```

VIII. Parameter File Examples

A. Repeatability Model

Data File: LMdat.prn

Id	month	year	bg	lact	age	milk	fat	prot
1	6	1995	1	6	114	2479	62	72
1	10	1996	1	7	130	1220	0	0
2	2	1999	1	10	156	3896	215	152
2	4	1997	1	8	135	3335	151	123
2	2	1996	1	7	120	2745	102	69
8	7	1996	1	7	112	2448	191	183
9	11	1997	1	8	129	3508	334	231
9	2	1995	1	6	96	2877	260	207
9	1	1999	1	9	143	2410	222	172
10	9	1996	1	7	114	3407	185	111

Renum Data File: ReLMdat.prn

❶	❷	❸	❽		
Cg	lact	id	milk	fat	prot
21	6	1	2479	62	72
39	7	1	1220	0	0
9	10	2	3896	215	152
16	8	2	3335	151	123
6	7	2	2745	102	69
24	7	3	2448	191	183
45	8	4	3508	334	231
5	6	4	2877	260	207
4	9	4	2410	222	172
34	7	5	3407	185	111

Pedigree File: LMped.prn

Id	sire	dam	yob
1	EMAPLE	67940	1986
2	HF	60602	1986
10	FON	40916	1987
11	SMAJIE	60042	1987
14	JO	137	1991
17	RPAUL	68472	1986
20	FON	50069	1987
21	FARM	91234	1988
27	FON	60901	1987
28	QCRRIG	1838	1986

Renum Pedigree File: ReLMped.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 calving*

Parameter File: BLUP.PAR

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

EFFECTS: POSITIONS_IN_DATAFILE NUMBER_OF_LEVELS TYPE_OF_EFFECTS
1  50 cross ❶
2  10 cross ❷
3 209 cross ❸
3 209 cross ❹
RANDOM_RESIDUAL VALUES
550000
RANDOM_GROUP ❺
 3
RANDOM_TYPE
add_animal
FILE
ReLMped.prn
(CO)VARIANCES
250000
RANDOM_GROUP ❻
 4
RANDOM_TYPE
diagonal
FILE

(CO)VARIANCES
250000
```

Note:
❶ Effect of contemporary groups in column #1 has 50 levels.
❷ Effect of lactation in column #2 has 10 levels.
❸ Effect of direct genetic from animal in column #3 has 209 levels.
❹ Effect of PE from animal in column #3 has 209 levels.
❺ Effect number 3 is random effect with add_animal type. This is genetic effects which require pedigree file.
❻ Effect number 4 is random effect with diagonal type for PE, which is uncorrelated.
❼ Analysis of single trait.
❽ Trait is in column #4 which is milk production.

B. Multi-trait Model

Data File: LMdat.prn

```
Id month year bg lact age   milk   fat  prot
 1  6  1995   1    6  114   2479   62    72
 1  10 1996   1    7  130   1220   0     0
 2  2  1999   1    10 156   3896   215   152
 2  4  1997   1    8  135   3335   151   123
 2  2  1996   1    7  120   2745   102   69
 8  7  1996   1    7  112   2448   191   183
 9  11 1997   1    8  129   3508   334   231
 9  2  1995   1    6  96    2877   260   207
 9  1  1999   1    9  143   2410   222   172
 10 9  1996   1    7  114   3407   185   111
```

Renum Data File: ReLMdat.prn

```
   ❶    ❷     ❸     ❽    ❽    ❽
Cg   lact   id   milk   fat   prot
21    6     1   2479   62    72
39    7     1   1220   0     0
9     10    2   3896   215   152
16    8     2   3335   151   123
6     7     2   2745   102   69
24    7     3   2448   191   183
45    8     4   3508   334   231
5     6     4   2877   260   207
4     9     4   2410   222   172
34    7     5   3407   185   111
```

Pedigree File: LMped.prn

```
1       EMAPLE  67940   1986
2       HF      60602   1986
10      FON     40916   1987
11      SMAJIE  60042   1987
14      JO      137     1991
17      RPAUL   68472   1986
20      FON     50069   1987
21      FARM    91234   1988
27      FON     60901   1987
28      QCRRIG  1838    1986
```

Renum Pedigree File: ReLMped.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 calving*

Parameter File: BLUP.PAR

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

EFFECTS: POSITIONS_IN_DATAFILE NUMBER_OF_LEVELS TYPE_OF_EFFECTS
1 1 1  50 cross ❶
2 2 2  10 cross ❷
3 3 3 209 cross ❸
3 3 3 209 cross ❹
RANDOM_RESIDUAL VALUES
250000   40000   27000
 40000    5000    3000
 27000    3000    2000
RANDOM_GROUP ❺
 3
RANDOM_TYPE
add_animal
FILE
ReLMped.prn
(CO)VARIANCES
 200000 -10000  -15000
  -10000   1000    1000
  -15000   1000    1500
RANDOM_GROUP ❻
 4
RANDOM_TYPE
diagonal
FILE

(CO)VARIANCES
 200000 -10000  -15000
  -10000   1000    1000
  -15000   1000    1500
```

Note:
❶ Effect of contemporary groups in column #1 has 50 levels.
❷ Effect of lactation in column #2 has 10 levels.
❸ Effect of direct genetic from animal in column #3 has 209 levels.
❹ Effect of PE from animal in column #3 has 209 levels.
❺ Effect number 3 is random effect with add_animal type. This is genetic effects which require pedigree file.
❻ Effect number 4 is random effect with diagonal type for PE, which is uncorrelated.
❼ Analysis of 3 traits.
❽ Trait is in column #4 #5 #6 which is milk, fat and protein production.

C. Random Regression Model

Data File: TDdat.prn

```
Id month year bg lact age  dim  td-milk
 1  7    1995  1  6    114   24    12.5
 1  8    1995  1  6    114   55    10.5
 1  9    1995  1  6    114   86    8
 1  10   1995  1  6    114   116   5.5
 1  11   1995  1  6    114   147   9
 1  12   1995  1  6    114   177   6
 1  1    1996  1  6    114   208   5.4
 2  2    1996  1  7    120   14    14.2
 2  3    1996  1  7    120   43    8.8
```

Renum Data File: NewReTDdat.prn

```
 ❶          ③      ❷       ❸
 Cg  id td-milk   L1      L2     dim
 49  1   12    0.2621   -1.0412  24
 57  1   10    0.6153   -0.6947  55
 65  1   8     0.9686   -0.0692  86
 73  1   5     1.3104    0.8019  116
 81  1   9     1.6637    1.9765  147
 89  1   6     2.0055    3.3789  177
 1   1   5     2.3588    5.1025  208
 9   2   14    0.1481   -1.0935  14
 18  2   8     0.4786   -0.8620  43
```

Pedigree File: TDped.prn

```
Id      sire       dam       yob
1       EMAPLE  67940   1986
2       HF      60602   1986
10      FON     40916   1987
11      SMAJIE  60042   1987
14      JO      137     1991
17      RPAUL   68472   1986
20      FON     50069   1987
21      FARM    91234   1988
27      FON     60901   1987
28      QCRRIG  1838    1986
```

Renum Pedigree File: ReTDped.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 testdate (milk sampling date)*; `L1,L2,L3 are LeGendre function.`

Parameter File: BLUP.PAR

```
DATAFILE
NewReTDdat.prn
NUMBER_OF_TRAITS
 1  ②
NUMBER_OF_EFFECTS
 9
OBSERVATION(S)
 3   ③
WEIGHT(S)

EFFECTS: POSITIONS_IN_DATAFILE NUMBER_OF_LEVELS TYPE_OF_EFFECTS
1  96 cross  ❶
4   1 cov    ❷
5   1 cov    ❸
2 258 cross  ❹
4 258 cov 2  ❺
5 258 cov 2  ❻
2 258 cross  ❼
4 258 cov 2  ❽
5 258 cov 2  ❾
RANDOM_RESIDUAL VALUES
 4
RANDOM_GROUP  ❿
 4   5   6
RANDOM_TYPE
add_animal   ❿
FILE
ReTDped.prn
(CO)VARIANCES
  4.6  -1     0.01
 -1     3    -0.01
  0.01 -0.01  0.1
RANDOM_GROUP ①
 7   8   9
RANDOM_TYPE
diagonal
FILE

(CO)VARIANCES
10   -2     0.1
-2    4.1  -0.2
0.1  -0.2   0.1
```

Note:
❶ Effect of contemporary groups in column #1 has 96 levels.
❷ Effect of covariate function for L1 in column #4.
❸ Effect of covariate function for L2 in column #5.
❹ Effect of direct genetic from animal in column #2 has 258 levels.
❺ Effect of covariate function for L1 in column #4 nested in direct genetic from animal in column #2.
❻ Effect of covariate function for L2 in column #4 nested in direct genetic from animal in column #2.
❼ Effect of PE from animal in column #2 has 258 levels.
❽ Effect of covariate function for L1 in column #4 nested in PE from animal in column #2.
❾ Effect of covariate function for L2 in column #4 nested in PE from animal in column #2.
❿ Effect number 4 5 6 is correlated random effect with add_animal type. This is genetic effects which require pedigree file.
① Effect number 7 8 9 is correlated random effect for PE with diagonal type.
② Analysis of single trait.
③ Trait is in #3 which is testday milk production.

D. Diminance with PE Model

Data File: LMdat.prn

Id	month	year	bg	lact	age	milk	fat	prot
1	6	1995	1	6	114	2479	62	72
1	10	1996	1	7	130	1220	0	0
2	2	1999	1	10	156	3896	215	152
2	4	1997	1	8	135	3335	151	123
2	2	1996	1	7	120	2745	102	69
8	7	1996	1	7	112	2448	191	183
9	11	1997	1	8	129	3508	334	231
9	2	1995	1	6	96	2877	260	207
9	1	1999	1	9	143	2410	222	172
10	9	1996	1	7	114	3407	185	111

Renum Data File: DomrecReLMdat.prn

❶	❷	❸	❽				❺
Cg	lact	id	milk	fat	prot	inb	subcl
21	6	1	2479	62	72	0	17
39	7	1	1220	0	0	0	17
9	10	2	3896	215	152	0	18
16	8	2	3335	151	123	0	18
6	7	2	2745	102	69	0	18
24	7	3	2448	191	183	0	19
45	8	4	3508	334	231	0	20
5	6	4	2877	260	207	0	20
4	9	4	2410	222	172	0	20
34	7	5	3407	185	111	0	21

Pedigree File: LMped.prn

Id	sire	dam	yob
1	EMAPLE	67940	1986
2	HF	60602	1986
10	FON	40916	1987
11	SMAJIE	60042	1987
14	JO	137	1991
17	RPAUL	68472	1986
20	FON	50069	1987
21	FARM	91234	1988
27	FON	60901	1987
28	QCRRIG	1838	1986

Renum Pedigree File: ReLMped.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 calving*

Parameter File: BLUP.PAR

```
DATAFILE
domrecReLMDat.prn
NUMBER_OF_TRAITS
 1 ❾
NUMBER_OF_EFFECTS
 5
OBSERVATION(S)
 4 ❿
WEIGHT(S)

EFFECTS: POSITIONS_IN_DATAFILE NUMBER_OF_LEVELS TYPE_OF_EFFECTS
1  50 cross ❶
2  10 cross ❷
3 209 cross ❸
3 209 cross ❹
8 183 cross ❺
RANDOM_RESIDUAL VALUES
550000
RANDOM_GROUP ❻
 3
RANDOM_TYPE
add_animal
FILE
ReLMped.prn
(CO)VARIANCES
250000
RANDOM_GROUP ❼
 4
RANDOM_TYPE
diagonal
FILE

(CO)VARIANCES
250000
RANDOM_GROUP ❽
 5
RANDOM_TYPE
par_domin
FILE

(CO)VARIANCES
250000
```

Note:
❶ Effect of contemporary groups in column #1 has 50 levels.
❷ Effect of lactation in column #2 has 10 levels.
❸ Effect of direct genetic from animal in column #3 has 209 levels.
❹ Effect of PE from animal in column #3 has 209 levels.
❺ Effect of parental subclass in column #8 has 183 levels.
❻ Effect number 3 is random effect with add_animal type. This is genetic effects which require pedigree file.
❼ Effect number 4 is random effect with diagonal type for PE, which is uncorrelated.
❽ Effect number 5 is random effect with par_domin type. This parental dominance genetic effects required pedigree.
❾ Analysis of single trait.
❿ Trait is in column #4 which is milk production.

IX. Trouble Shooting

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

DairyPAK might be opened with disable macro. DairyPAK interface will work only when macro enable. You have to set security in macro menu 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: *All menus disappear and all buttons do not work properly.*

DairyPAK might be opened in disable macro. To use the interfaces in DairyPAK, 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, DairyPAK 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?.*

DairyPAK does not support all models. For very complicated model, BLUPF90-PCPAK is more flexible. However, PCPAK is not easy-clicked handle, background in animal model and BLUP is important. The user modified blup parameter can be accomplished this problem. Please note the details on page 21.

Q: *Cannot find the BV report.*

BV report and genetic trend reports (in Excel format) are kept in DATA directory, not in Program directory. If directory or filename contains spaces, this problem might be occurred.

X. Who's who

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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*
ACCF90	: *Thomas Strabel, Ignacy Misztal*

< Graphic Interface Design and Compilation for PC>----------

Graphic Interface design	: *Monchai Duangjinda*
PC-Compilation	: *Monchai Duangjinda*
SE of heritability	: *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*
LAPAK90	: *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*