Lab 1 – BLUPF90 family of programs

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Estimation of breeding values and reliabilities

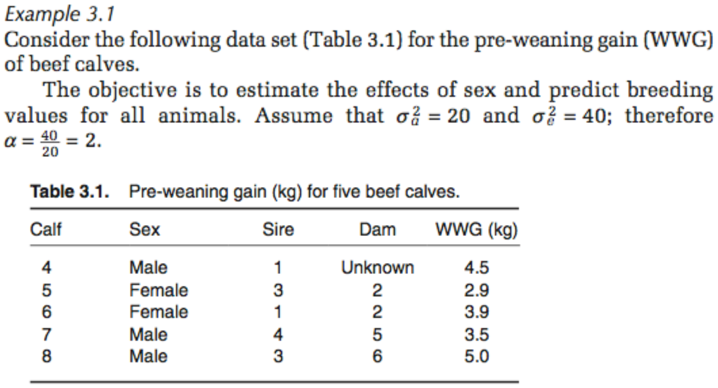
1. Documentation for BLUPF90 program in the wiki: https://nce.ads.uga.edu/wiki/doku.php?id=documentation#tutorial

2. Browse through FAQ for blupf90 programs (https://nce.ads.uga.edu/wiki/doku.php?id=faq). Read information on frequent mistakes in data, pedigree, and parameter files.

3. Using the following example (from Mrode and Thompson, 2005 *Linear Models for Predicting Animal Breeding Value*), create data, pedigree, and parameter file to run **renumf90**. Run **renumf90**, check the log (screen), and the output files created by the program.

4. Run **blupf90+** to obtain solutions and reliabilities based on SE using Unix tools, and then with OPTION store_accuracy.

   Reliability for animal i can also be calculated as: $\text{Rel}_i = 1 - \text{PEV}_i/\text{VarA}$
   Where:
   PEV is the prediction error variance (S.E. = sqrt(PEV))
   VarA is the additive genetic variance

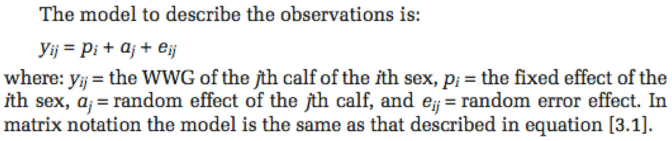


Example 3.1
Consider the following data set (Table 3.1) for the pre-weaning gain (WWG) of beef calves.

The objective is to estimate the effects of sex and predict breeding values for all animals. Assume that $\sigma_a^2 = 20$ and $\sigma_e^2 = 40$; therefore $\alpha = \frac{40}{20} = 2$.

Table 3.1. Pre-weaning gain (kg) for five beef calves.

Calf	Sex	Sire	Dam	WWG (kg)
4	Male	1	Unknown	4.5
5	Female	3	2	2.9
6	Female	1	2	3.9
7	Male	4	5	3.5
8	Male	3	6	5.0

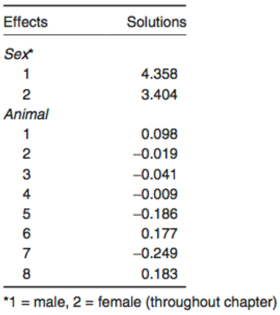


The model to describe the observations is:

$$y_{ij} = p_i + a_j + e_{ij}$$

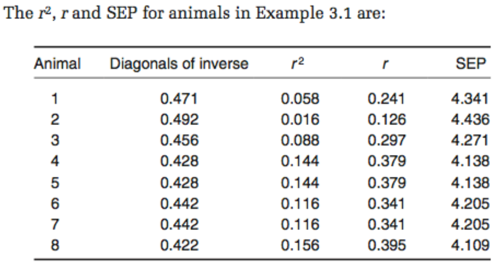
where: y_{ij} = the WWG of the jth calf of the ith sex, p_i = the fixed effect of the ith sex, a_j = random effect of the jth calf, and e_{ij} = random error effect. In matrix notation the model is the same as that described in equation [3.1].

Solutions from the example are:



Effects	Solutions
*Sex**	
1	4.358
2	3.404
Animal	
1	0.098
2	–0.019
3	–0.041
4	–0.009
5	–0.186
6	0.177
7	–0.249
8	0.183

*1 = male, 2 = female (throughout chapter)



The r^2, r and SEP for animals in Example 3.1 are:

Animal	Diagonals of inverse	r^2	r	SEP
1	0.471	0.058	0.241	4.341
2	0.492	0.016	0.126	4.436
3	0.456	0.088	0.297	4.271
4	0.428	0.144	0.379	4.138
5	0.428	0.144	0.379	4.138
6	0.442	0.116	0.341	4.205
7	0.442	0.116	0.341	4.205
8	0.422	0.156	0.395	4.109

Variance components estimation

5. Read documentation for **blupf90+** program in the wiki:
   https://nce.ads.uga.edu/wiki/doku.php

6. Parameter files for the following exercises are on the website. Download them to your laptop.

7. Files with *99 contain data for up to 14 traits. Parameter file exmr99s1 uses these files for a single-trait model, exmr99s2 uses for a two-trait model, and exmr99s for a three-trait model.

   Estimate variance components by EM-REML and AI-REML in **blupf90+** using the parameter file exmr99s1.
   Record the number of rounds and CPU time using the following command:
   time blupf90+ renf90.par | tee reml.log
   The CPU time will be printed on the screen after the program stops.

   Extend the model to 2 traits by adding the observations in column 4 (parameter file exmr99s2).
   Estimate variance components for the two-trait model using EM-REML and AI-REML in **blupf90+**. Add the option to get SE for heritability and genetic correlations when running AI-REML. Look at wiki to add the correct options.
   How much slower is REML and how longer are the computations in the two-trait case?

8. Run **gibbsf90+** for the single trait example; use the number of samples 1000 and burn-in 0. Run **postgibbsf90** with burn-in of 0; try burn-in of 200. For graphical output, **postgibbsf90** requires a plotting package GNUPLOT and X (e.g., as provided by X emulation packages: Xming in Windows or XQuartz in MacOS).

9. Estimate breeding values using **gibbsf90+**. Initial values should be replaced by posterior means. Check the manual to find the correct option to get EBV and SE. Use 1000 samples and burn-in of 200.