Lab 1 – BLUPF90 family of programs
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Estimation of breeding values and reliabilities

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

2. Browse through FAQ for blupf90 programs
   (http://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** and then run **blupf90** to obtain solutions and reliabilities.

   Reliability for animal i can be calculated as:
   $Rel_i = 1 − PEV_i/VarA$

   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].

The 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

4. Read documentation for REMLF90 program in the wiki:
   http://nce.ads.uga.edu/wiki/doku.php and also in remlf90.pdf

5. Parameter files for the following exercises are in the website. Use curl to download it to your Linux or Mac device:
```
curl http://nce.ads.uga.edu/wiki/lib/exe/fetch.php?media=lab1_UF.zip -o lab1.zip
```

6. 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 **remlf90** and **airemlf90** using the parameter file exmr99s1.
   Record the number of rounds and CPU time using the following command:
   time echo renf90.par | remlf90 | 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).
   Repeat the computations for both models using AIREMLF90. How much slower is REMLF90 and how longer are the computations in the two-trait case?

   With AIREMLF90 add the option to get SE for heritability and genetic correlations. Look at wiki to add OPTIONS.

7. Run gibbs2f90 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 Windows (e.g., as provided by X emulation packages: Xming).

8. Estimate breeding values using gibbs2f90. 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.

OPTIONAL

9. Random regression models using renumf90 and blupf90
   Parameter, data, and pedigree files (renrr.par, datrr.leg, pedrr) for this exercise are in the directory lab1

   This data is for a random regression model using Legendre polynomials from example 7.2 of Mrode and Thompson, 2005 - *Linear Models for Predicting Animal Breeding Value*, Example 7. Look at the parameter file and identify components in the renumf90 parameter file. Run blupf90 to obtain solutions.