

## Assignment 2 – THRGIBSSF90 and RENUMF90

### THRESHOLD MODELS

1. Download and extract the file **ex\_thr.zip**. This folder contains data from *exmr99s* example, it was converted so the first trait has 3 categories and second trait is a binary trait, while the rest were keep as linear. Estimate parameters, first with a linear model (*gibbs2f90*) and then with a threshold model (*thrgibbs1f90*). Use *postgibbsf90* to determine the number of needed samples. Are estimates of heritabilities and genetic correlations between data sets and programs similar?
2. Use the program *gen\_thr.exe* (included in *ex\_thr* folder) to generates linear and categorical data for a model with one fixed and one sire effect. Simulate the data using the following parameters:
  - 2 thresholds (3 categories)
  - 10 levels of fixed effect, 100 sires, 2000 records
  - $\text{var}(e)=100$ ,  $\text{var}(\text{sire})=10$
  - thresholds 1 = 0, threshold 2 = 8.
3. Prepare a parameter file and use *thrgibbs1f90* to analyze.
4. Use *postgibbsf90* for analysis.

### RENUMBERING DATA AND PEDIGREE FILES – RENUMF90

5. Download and extract **rrm\_renum.zip** from wiki.  
The folder *rrm\_renum* contains: *renumf90* parameter, data and pedigree files (*renrr.par*, *datrr.leg*, *pedrr*) 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.
  - a) Look the parameter file and identify components of *renumf90* parameter file
  - b) Run *renumf90* and then *blupf90* to obtain solutions
  - c) Look in output files from *renumf90* (*renf90.par*, *renaddxx.ped*, *renf90.dat*, *renf90.tables*)
6. Using the following example (from Mrode and Thompson, 2005 *Linear Models for Predicting Animal Breeding Value*)  
Create data, pedigree and parameter to run **renumf90** and then run **blupf90** to obtain solutions and reliabilities and compare with solutions and *pev* in the table

#### 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  $\sigma_e^2 = 20$  and  $\sigma_s^2 = 40$ ; 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  $j$ th calf of the  $i$ th sex,  $p_i$  = the fixed effect of the  $i$ th sex,  $a_j$  = random effect of the  $j$ th 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 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

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

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

- Download and extract **beef\_renum.zip** from wiki. The directory `beef_renum` includes data/pedigree files for a 3 trait maternal model in beef cattle. README.txt file contains header for datafile (`example10.dat`) and pedigree file (`example10.ped`)

- Create a `renumf90` parameter file for YW (yearling weight) that fits the following model:

$$y = CG + AOD + \text{animal} + \text{maternal} + \text{sire-herd} + e$$

Consider CG as fixed; AOD as covariable; animal, maternal, sire-herd as random. Starting values for variance components are:  $\text{var}(\text{animal})=438.90$   $\text{var}(\text{maternal})=73.24$ ;  $\text{cov}(\text{animal\_maternal})=-35.80$ ;  $\text{var}(\text{sire-herd})=242.12$ ;  $\text{var}(\text{residual})=751.13$

Use depth of pedigree equal 3

- Run `renumf90` and check the output files.
- Run `airemlf90` with an option to get SE for heritability and for genetic correlation between direct and maternal effects.
- Change the parameter file for `renumf90` for a 3-trait model (BW, WW, YW) and run `blupf90`. Variance components are in the README.txt file.