

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 $\sigma_a^2 = 40$; 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.