Lab 3 – BLUPF90 family of programs for complex models

Multivariate, random regression, and reaction norm models

1. Folder lab3_UF2024/data1 includes data and pedigree files for a three-trait maternal model in beef cattle. README file contains the header for example10.dat and example10.ped.
   a) Create a `renumf90` parameter file for YW (yearling weight) that fits the following model:

      Y = CG + β AOD + animal + maternal + sire-herd + e

      Consider CG as fixed; AOD as covariable; animal, maternal, sire-herd as random. Starting values for variance components are: $\sigma_a^2 = 438.90$; $\sigma_m^2 = 73.24$; $\sigma_{am} = -35.80$; $\sigma_{sh}^2 = 242.12$; $\sigma_e^2 = 751.13$
      Use depth of pedigree equal 3

   b) Run `renumf90` and check the output files.

   c) Run `blupf90+` with options for estimating variance components with AI-REML and options to get SE for heritability and genetic correlation between direct and maternal effects.

   d) Change the parameter file for `renumf90` for a 3-trait model (BW, WW, YW) and run `blupf90+`. Variance components are in the README file.

2. Random regression models using **renumf90** and **blupf90+**
   Parameter, data, and pedigree files (renrr.par, datrr.leg, pedrr) for this exercise are in the folder lab3_UF2024/data2. This data is for a random regression model using Legendre polynomials from example in Table 9.1 of Mrode and Thompson, 2013 - *Linear Models for Predicting Animal Breeding Value*, Example 9.2. Please check README.txt

   a) Look at the parameter file and identify components in the **renumf90** parameter file. Run **blupf90+** to obtain solutions. Use the Legendre coefficients present in the data (datarr.leg).

   b) Run **renumf90** again setting the program to compute the Legendre coefficients and rerun **blupf90+**.

   c) Run **rrmebvf90** to obtain breeding values for 305 days in milk.

   d) Run **rrmebvf90** again to obtain cumulative breeding values from 5 to 305 days in milk and reliabilities. To compute reliabilities, **rrmebvf90** will look for a file named pev_pec_bf90, which is created by **blupf90+** when using OPTION store_pev_pec x (x is the number of the animal effect).

3. Multi-trait genomic evaluation using **renumf90** and **blupf90+**
   The data for this lab is based on a public pig dataset from PIC (Cleveland et al. 2012 - G3 Journal). Originally, this dataset was filtered for MAF and missing SNP were imputed, however

some modifications were introduced to generate commons problems that are found in real datasets.

a) Modify renum.par to a five-trait model, run **renumf90** and **blupf90+** to estimate GEBV under ssGBLUP. Check the computing time when running **blupf90+**.

b) Add the option to construct a block-diagonal preconditioner accounting for the correct number of traits. Run **blupf90+** again. Compare the computing time and solutions with the run in the previous step.

c) Remove the option to read the SNP file and run regular BLUP using **blupf90+**. Record the computing time and compare with the previous run. Why are the computing times so different?