

Lab5mf – SNP effects, Indirect Predictions, GWAS, and Metafounders in single-step using the BLUPF90 family

Prepared by D. Lourenco, I. Aguilar, A. Legarra, and Z. Vitezica

1. Using metafounders to set the base populations. Files are available in the folder day5_metafounders: The data for this lab was simulated by D. Lourenco (Lourenco et al., 2016) using QMSim (Sargolzaei & Schenkel, 2009). A single trait animal model was simulated assuming heritability of 0.30. All the genetic variance was explained by 400 QTL. Two lines (1 and 2) under 9 generations of selection were simulated. Pure and F1 (12) progeny were generated in generation 10. Animals were genotyped for 40,000 SNP. The simulated additive genetic variance was 0.3 and the residual variance was 0.70. The phenotype was generated using the following model:

$$\text{Phenotype} = \text{general_mean} + \text{true_breeding_value} + \text{residual}$$

Files are available 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=lab5mf_une.zip -o
lab5mf.zip
```

Description of files:

newdata.txt:

- 1: animal ID
- 2: sire ID
- 3: dam ID
- 4: generation
- 5: phenotype
- 6: true breeding value (TBV)
- 7: line code
- 8: mean incidence

newped.txt:

- 1: animal ID
- 2: sire ID
- 3: dam ID

snp_file.txt:

- 1: animal ID
- 2: SNP genotype

- a) No metafounders: Run `renumf90` and `ssGBLUP` using **blupf90+**.
- b) With metafounders: In a separate folder, replace missing parents with -1 in line 1 and -2 in line 2 (MF coding). Run **renumf90** with the modified pedigree that contains metafounders, estimate Gamma using **gammaf90**, and run `ssGBLUP` using **blupf90+**. Do not forget to replace to rename `gamma.txt` and change the random type in the parameter file (check the slides).
- c) Compare solutions from a) and b). One way to compare the methods is to perform a validation for young individuals (e.g., accuracy, level bias – b_0 , and dispersion bias – b_1). For that, remove phenotypes for individuals in generation 10. Run `ssGBLUP` with and without metafounders. Correlate solutions with TBV (column 6 in `newdata.txt`). Do not forget that solutions are with renumbered IDs (different in `ssGBLUP` and `ssGBLUP` with MF) and TBV are with original IDs. Use `OPTION origID` to get solutions with original IDs