Lab2 Quality control of SNP data, GBLUP, and ssGBLUP

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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.

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=lab2_UF.zip –o lab2.zip
```

Description of files

phenotypes.txt:

1: Animal ID
2: Trait 1
3: Trait 2
4: Trait 3
5: Trait 4
6: Trait 5
7: Mean indicator

pedigree.txt :

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

genotypes.txt :

1: animal ID
2: marker information

1. Look into the files and identify if all individuals in the pedigree have genotypes.

2. Run renumf90 in the single-trait context.

3. Run preGSf90 to do quality control of genomic data and get statistics for the SNP data. Save the clean files.
   Check the initial number of SNPs, all statistics related to SNPs, and reasons why SNPs did not pass the quality control.

   Remember that preGSf90 does the quality control and sets up the genomic and pedigree relationship matrices for genotyped animals. To avoid matrix inversions and perform only quality control, use the following options:

   ```
   OPTION createGInverse 0
   OPTION createA22Inverse 0
   OPTION createGimA22i 0
   ```

4. Run ssGBLUP using the clean SNP file. The blupf90 is automatically set to run ssGBLUP if a pedigree and a SNP file is provided. Don't forget to turn QC off (`OPTION no_quality_control`). If you want to get SE of GEBV, include `OPTION sol se`. Check the output of blupf90 and the solution file `(solutions)`

5. Tricking BLUPF90 to run GBLUP: Copy phenotypes.txt, pedigree.txt, and genotypes.txt_clean to a separate folder. Using Unix commands, create a dummy pedigree file (i.e., animal 0 0) and a file with phenotypes only for genotyped animals.

6. Run renumf90 using PED_DEPTH 1

7. Run GBLUP in blupf90. Check the options you need to include in the parameter file for blupf90 (slides day2_3). Check the output of blupf90 and `solutions`

8. Let's assume you are working on a project and your objective is to test different models using the same data under GBLUP. You can run preGSf90 with clean data once and save **G**. Every time you change your model, you can just read **G** from a file avoiding the creation of this matrix every time. This can save some computing resources. Check the documentation for preGSf90 and explore the options to save **G**. http://nce.ads.uga.edu/wiki/doku.php?id=readme.pregsf90

   Run preGSf90 and save **G**. Run blupf90 with an option to read **G**. Compare the current solutions with solutions from exercise 6.

9. blupf90 has an interesting option where an external covariance matrix can be used. This is especially useful when different relationship matrices are needed (e.g., polyploid populations) or dominance effects are to be considered. Check how this can be done: http://nce.ads.uga.edu/wiki/doku.php?id=user_defined_files_for_covariances_of_random_effects

   Run preGSf90 with an option to save $\mathbf{G}^{-1}$ in text format
   `OPTION saveAscii` and `OPTION saveGInverse`

   Run blupf90 with the option to read an external covariance matrix.
   Be aware that the first two columns in $\mathbf{G}^{-1}$ are the position of genotyped animals in the genotype and genotype_XrefID files. When you use a user file in blupf90, IDs in the covariance matrix should match IDs in the phenotype file.

   Before running blupf90, you can change the IDs for the animals in the phenotype file using the following commands:

   ```
   awk '{print $1,NR}' genotypes.txt_clean_XrefID | sort
   +0 -1 > index.gen
   awk '{print $3,$0}' renf90.dat | sort +0 -1 >
   srenf90.temp
   join -1 +1 -2 +1 srenf90.temp index.gen | awk '{print
   $2,$3,$5,$4}' | sort -n +2 -3 > srenf90.dat
   ```

   Do not forget the IDs in solutions are now the position of genotyped animals in the genotype and genotype_XrefID files!