UNIVERSITY OF GEORGIA

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Animal Breeding and Genetics Group

Best practices in BLUPF90

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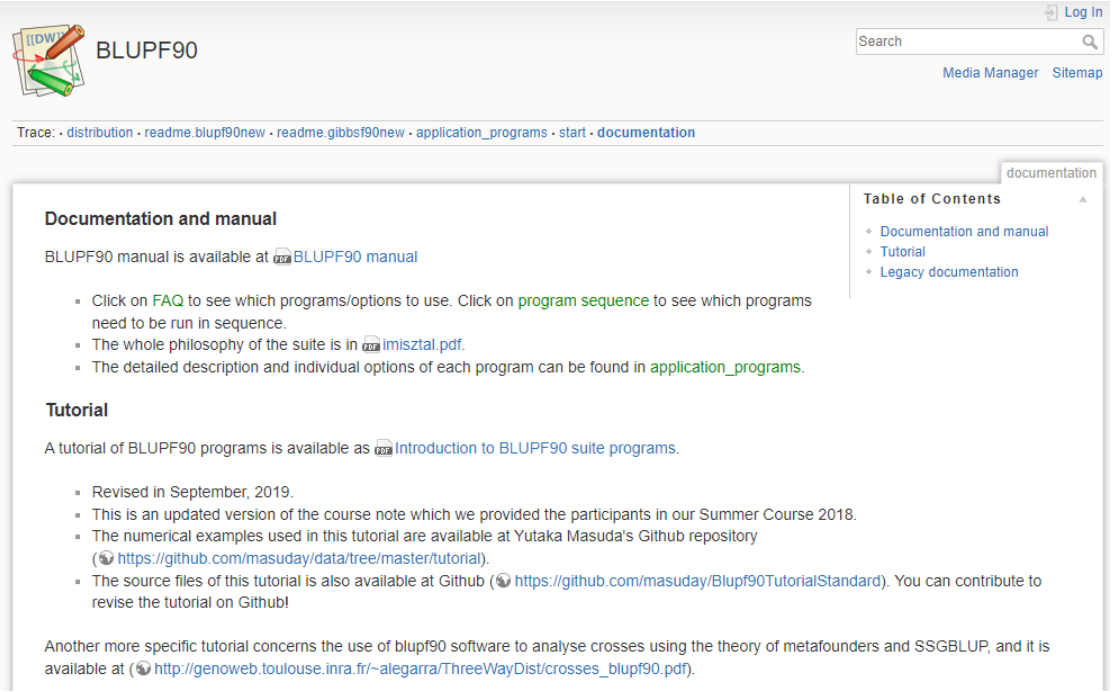
Best practices – BLUPF90

1. Read the manual
2. Understand what the programs can do for you
3. Understand the theory
4. Read the output of the programs

    blupf90+ renf90.par | tee blup.log

1. Understand the data

    How many genotypes?
    How many phenotypes?
    How many geno with pheno?
    Outliers?
    Population structure (PCA)



Best practices – BLUPF90

- Steps to estimate breeding values using BLUPF90 family of programs

1. renumf90 to renumber the data
2. Estimate variance components if they are not available
    1. If need to estimate: blupf90+ with OPTION method VCE

       The solutions file has EBV computed with the estimated VC
    1. If available: put the values into renf90.par and run blupf90+ to estimate (G)EBV

Best practices – BLUPF90

- Remove animals from the data file that have missing phenotypes
  - They are just increasing the number of equations
  - They will get predictions if they are in the pedigree or genotype file
  - In renumf90: `OPTION remove_all_missing`

- Dealing with genomic information
  - Run preGSf90 to perform quality control and save the clean files
  - `OPTION saveCleanSNP`
  - `OPTION createGInverse 0`
  - `OPTION createA22Inverse 0`
  - `OPTION createGimA22i 0`
  - The 3 last options avoid extensive computations

Best practices – BLUPF90

- Dealing with genomic information
  - Work with the clean file: snp.txt_clean
  - `OPTION SNP_file` snp.txt_clean
  - `OPTION no_quality_control`

- Investigate the output
  - What is the correlation between **G** and $\mathbf{A}_{22}$?
  - Diagonal = inbreeding correlation
  - All → ideal range [0.5 – 0.9]
    - Lower = incompatibility of genomic and ped information (at least one is wrong)
    - Lower = admixed population
    - Higher = limited advantage of genomic information

Best practices – BLUPF90

- Parent-progeny conflicts?
  - preGSf90: removes genotypes for progeny with conflict
  - Seekparentf90 can search for possible parents among genotyped animals
    - Corrects the pedigree
  - Which one is better?
    - Pedigree and genotypes may be wrong
    - Knowledge about the data

Best practices – BLUPF90

- Running any software that takes a parameter file besides renumf90?
  - Use `OPTION use_yams`
  - Speeds up several computations, especially with multi-trait models

- Estimating variance components with REML or AIREML in blupf90+?
  - Use `OPTION use_yams`
  - Do not use UPG or metafounders
    - Weird behavior if inverting the LHS of MME as in VCE
  - Need to know if convergence was reached?
    - Try blupf90+ and gibbsf90+

Best practices – BLUPF90

- blupf90+ and gibbsf90+ can compute SE for estimates
  - `OPTION se_covar_function <label> <function>`

```
 Sampling variances of covariances function of random effects (n=10000)

h2d  - Function: g_2_2_1_1/(g_2_2_1_1+r_1_1)
  Mean:   0.31113
  Sample Mean:   0.31103
  Sample SD:   0.82903E-02
 elapsed time  2.1800995E-03
```

- Is it SD or SE?
  - Sample SD = SE

Best practices – BLUPF90

- The output depends on the input

Plus
genomics

Adapted from Hartung (2016)