Outline of the BLUPF90 course: Genomic analyses using BLUPF90
Daniela Lourenco and Yutaka Masuda, 7/26/19

Day 1:

1. Introduction to BLUPF90 family of programs
   a) Mixed models
   b) Multiple trait model
   c) Repeatability models
2. BLUPF90 family of programs for variance components estimation
   a) REML and AIREML
   b) Gibbs Sampling for linear and categorical traits
3. Introduction to Linux environment
4. Exercise: use of programs for datasets with single and multiple traits

Day 2:

1. Basis of SNP data
2. Data simulation using QMSim (Sargolzaei and Schenkel, 2009)
3. Data manipulation and scripts with Unix tools
4. Exercise: Simulating and editing genomic data

Day 3:

1. Brief history of genomic selection
2. Theory of genomic selection
3. Genomic relationship matrix (**G**)
4. Creation and handling of genomic relationship matrices with preGSf90
5. GBLUP, GREML and GGIBBBS using BLUPF90
6. Validation techniques for testing genomic models
7. Exercise: use of genomic programs with simulated data

Day 4:

1. Theory of Single-step GBLUP (ssGBLUP)
2. Forming Single-step equations
3. Quality control for genomic data
   1. Calling rate
   2. Parental exclusions

3. Distributions of diagonals of $\mathbf{G}$
4. Differences between matched $\mathbf{G}$ and $\mathbf{A}_{22}$
5. Heritability of gene content
6. Eigenvalues/eigenvectors – population stratification

4. Exercises: Application of quality control and use of single-step with simulated data set

Day 5:

1. Estimating SNP effects for GBLUP-based models
2. Weighted GBLUP and ssGBLUP
3. Genome-wide association (GWA)
4. Exercises: Application of weighted ssGBLUP and GWA