

Outline of the BLUPF90 course: Genomic analyses using BLUPF90

Daniela Lourenco and Yutaka Masuda, 7/30/19

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 Unix 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. Quality control of SNP data
2. Brief history and 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. Exercise: use of genomic programs with real data

Day 4:

1. Theory of Single-step GBLUP (ssGBLUP)
2. Forming Single-step equations
3. Validation techniques for testing genomic models
4. Quality control for genomic and pedigree relationships
 1. Calling rate
 2. Parental exclusions

3. Distributions of diagonals and off-diagonals of \mathbf{G}
 4. Differences between matched \mathbf{G} and \mathbf{A}_{22}
 5. Eigenvalues/eigenvectors – population stratification
5. Exercises: Application of quality control and use of single-step with simulated data set

Day 5:

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