

## **Five-day course in genomic analyses with emphasis on single-step GBLUP**

Taught by Ignacy Misztal, University of Georgia, USA, and Ignacio Aguilar, INIA, Uruguay

The schedule below will be modified subject to background and interests of the participants.

### **1. Models, BLUPF90 suite, and parameter estimation**

- a. Parameter files in BLUPF90 suite
  - i. Animal model
    1. UPG
  - ii. Multiple trait model
  - iii. Maternal models
  - iv. Random regression model
  - v. Competition model
  - vi. Crossbred model
  - vii. Genomic model
- b. EM and AI REML
- c. Gibbs samplers

### **2. Threshold model, renumbering and introduction to genomic selection**

- a. Threshold models
- b. Renumbering program RENUMF90
- c. SNP chip
- d. SNP BLUP, Bayesian models, GBLUP
- e. What is SNP effect

### **3. Genomic relationship matrix and single-step**

- a. Genomic relationship matrix
  - i. Derivation from SNP BLUP
  - ii. Blending
  - iii. Effect of number of SNP
  - iv. Properties with different gene frequencies
  - v. Other types of G
  - vi. G and Imputation
- b. Single –step: H and  $H^{-1}$
- c. Rank of G and APY algorithm
  - i. Limited dimensionality of G due to effective population size
  - ii. Inverse of genomic relationship matrix

### **4. Single-step continued**

- a. Quality control for G
  - i. Calling rate
  - ii. Parental exclusions
  - iii. Distributions of diagonals of G
  - iv. Differences between matched G and A22
  - v. Heritability of gene content
  - vi. Elimination of sex and “0” chromosomes
  - vii. Eigenvalues/eigenvectors – population stratification
- b. G and A22
  - i. Properties of A22 as a function of base year
  - ii. A22 and incomplete pedigree recording

- iii. Matching G and A22
    1. Matching G by averages of A22
    2. Reduction of incomplete pedigrees by cutting old data
    3. Matching A (and A22) to G: metafounders
  - iv. Correlations between G and A22 elements
    1. Genomic and pedigree inbreeding
    2. Runs of homozygosity
  - v. Crossbreeding and G b
- 5. Meaning of GEBV, validation and GEBV/SNP conversions**
- a. Decomposition of GEBV into PA, DGV, CD, PC and PI
    - i. Weights, species and status of animals
  - b. Validation techniques for genomics
    - i.  $R^2$  for dairy bulls
    - ii. Predictability for animals with records
    - iii. Cross-validation when few genotyped animals with records (e.g., mortality or disease resistance)
    - iv. Selection bias in realized accuracies
  - c. Conversion of DGV to SNP effects
    - i. Indirect prediction
    - ii. GWAS
      1. Calculation of SNP weights
      2. LD blocks or SNP regions
      3. Options in postGSf90

Exercises in this course are based on the BLUPF90 family of programs. Genomics includes modules preGSf90 and postGSf90 by Ignacio Aguilar. See [nce.ads.uga.edu](http://nce.ads.uga.edu) for details.