Genomic Selection in Livestock

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USE AND ACKNOWLEDGEMENT OF SHORT COURSE MATERIALS

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OUTLINE / TOPICS

- Introduction and motivation (Jack)
- Conventional prediction using pedigree relationships (Dorian)
- Models to predict single SNP effects (Dorian)
 - Fixed effect models
 - Fitting SNPs as random effects
- Bayesian methods (Rohan)
 - Bayes theorem
 - o Gibbs sampler vs Metropolis Hastings
- Genomic prediction (Dorian)
 - An equivalent (animal) model for genomic prediction
 - Some alternative computing strategies that are not equivalent models
- Bayesian methods applied to genomic prediction (Rohan)
 - Bayes A and B
 - Bayes C and G-BLUP
 - o Bayes N
- Contributions to genomic predictions (Jack)
 - o Linkage Disequilibrium
 - Genetic relationships
 - o Linkage
- Application of genomic prediction models to real data (Dorian and Jack)
 - Training and validation
 - Within and across breed prediction
- GWAS and finding QTL regions (Rohan and Dorian)
- Other genomic prediction methods (Rohan)
 - Bayes $C\pi$ and estimation of π
 - o Estimating the scale factor
 - Alternative distributions Heavy-tailed vs. Normal distributions
- Imputation and using low-density panels (Jack)