

## **ANEQ731 – Advanced Genetic Prediction**

**Instructor:** Dr. Scott Speidel  
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**Catalog Statement:** Models and methods for the prediction of genetic merit in livestock populations.

**Prerequisites:** Graduate standing and ANEQ575 or written consent of instructor.

**Lecture:** MWF, 9:00 – 9:50 AM, Animal Science Room 33

**Objectives:** Upon successful completion of the course, students should be able to:

1. Apply linear models to livestock data from experimental and field populations,
2. Estimate breeding values using a wide range of models and methods,
3. Use genetic prediction tools to design optimal genetic improvement programs,
4. Use current or develop software for estimation of genetic parameters,
5. Assemble and solve large systems of linear mixed model equations,
6. Incorporate marker and phenotypic data into genetic prediction models
7. Understand the application of threshold models to categorical data, and
8. Use models and genetic parameters to predict improvement in net genetic merit.

**Integrity statement:** Colorado State University expects students to maintain standards of personal integrity that are in harmony with the educational goals of the institution; to observe national, state, and local laws, and University regulations; and to respect the rights, privileges, and property of other people (see Policies and Guiding Principles, <http://www.catalog.colostate.edu/>). Students will adhere to the Colorado State University General Catalog Academic Integrity Policy and Student Conduct Code.

We take academic integrity seriously. At a minimum, to achieve academic integrity no one will use another's work as their own. The CSU writing center defines plagiarism in this manner:

Plagiarism is the unauthorized or unacknowledged use of another person's academic or scholarly work. Done on purpose, it is cheating. Done accidentally, it is no less serious. Regardless of how it occurs, plagiarism is a theft of intellectual property and a violation of an ironclad rule demanding "credit be given where credit is due."

Source: (Writing Guides: Understanding Plagiarism. <http://writing.colostate.edu/guides/researchsources/understandingplagiarism/plagiarismoverview.cfm>. Accessed, January 21, 2015)

Plagiarism will result in lost credit for the assignment.

As put by Dr. Dickinson, Director of Graduate Studies, "Academic integrity lies at the core of our common goal: to create an intellectually honest and rigorous community."

**Grading:** The final course grade will be assigned on the basis of points accumulated on reading assignments, a mid-term exam, homework problems, and a project assigned throughout the semester. The minimum fraction of total points earned and corresponding letter grades are: 0.85 (A), 0.75 (B), 0.65 (C), and < 0.60 (F), respectively. A downward grading curve may be applied if necessary at the discretion of the instructor. The assignments are as follows:

Item	Item Points	Cumulative Point Total
Reading Assignments	100	100
Homework	350	450
Project	150	600

**Text:** Mrode, R. A. 2014. Linear Models for the Prediction of Animal Breeding Values. CABI, Cambridge, MA. ISBN 978.1.84593.981.6

**Course outline** (Course content is tentative, and subject to change throughout the semester)

- Review of moment statistics, measures of association
  - o Fixed and random effects
  - o Bias and Error
  - o Equations: OLS, GLS, mixed models
- Estimation of fixed effects
  - o Models, matrices, incidence and rank
  - o Constraints
  - o Class variables
  - o Estimation methods
    - Minimum error versus Maximum Likelihood
- Basic genetic prediction
  - o Animals with single data records
  - o Breeding value prediction from progeny and extended pedigree
  - o Prediction with correlated traits
  - o Correlated response

- Genetic antagonisms
- Classical genetic prediction models
  - Repeated Records
  - Sire model
  - Animal model
  - Reduced animal model
  - Maternal animal model
- Models and breeding values for unmeasured traits
- Multiple trait models
  - Multivariate models
  - MT models with no covariance
- Contemporary models
  - Analysis of longitudinal data
  - Fixed regression
  - Random regression
- Solving systems of equations
- Variance Estimates
  - Estimation using variance component estimation software
  - Genetic parameters
  - Genetic and non-genetic correlations
- Non-continuous and categorical data
  - Threshold models
- Accuracy
  - Prediction error variance and standard error of prediction
  - Inverse coefficient matrix
  - Reliability and accuracy
- Cross-bred models
  - Direct and maternal heterosis
  - Breed effects
- Genomic data
  - Detection of genes with large effect
  - Genetic variance attributable to SNP and SNP haplotypes
  - Marker assisted genetic evaluation