

**ANEQ575 – Computational Biology in Animal Breeding  
Fall, 2016**

**1. Instructor**

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**3. Course Description Statement**

Numerical analysis and use of computers to solve problems related to livestock improvement.  
*Prerequisites: ANEQ330, ANEQ334 or equivalent and graduate standing or written consent of instructor. Students must register for both lecture and lab sections.*

**4. Course Times and Office Hours**

Lecture: MW, 11:00 – 11:50, Animal Science Rm. 131  
Lab: T, 13:00 – 14:40, Animal Science Rm. 135  
Office Hours: TBA

**5. Academic Integrity:**

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 the Student Responsibilities and Academic Integrity policies at <http://www.catalog.colostate.edu/Content/files/2014/FrontPDF/1.6POLICIES.pdf>

**6. Learning Objectives**

Upon successful completion of this course, students should:

- 6.1 Extend their knowledge of material covered in ANEQ330, ANEQ334 (or equivalent) to include computationally intensive approaches,
- 6.2 Gain understanding of the mathematical basis and statistical concepts applicable to quantitative genetics,
- 6.3 Learn basic and applied concepts in linear models as applied to population and quantitative genetics,
- 6.4 Become familiar with software tools useful in animal breeding and improvement, and computing strategies for data preparation and analysis in quantitative genetics, and
- 6.5 Use modern computing approaches to organize and edit large data sets, and to set up and solve linear systems of equations.

## 7. Course Grading

The final course grade will be assigned on the basis of points accumulated throughout the semester. Homework and laboratory assignments will be given approximately every other week that will be based on both lecture material and laboratory work. The mid-term and final exams will be made available and their due date will be no less than five days later. Points earned on homework, lab work and the exams will be weighted equally in computing the final letter grade. For graduate students, 75% or higher is generally considered passing although a downward grading curve may be applied at the discretion of the instructor. On the basis of percentage of total available points earned, the following letter grades are guaranteed: A  $\geq$  90%, B  $\geq$  80%, C  $\geq$  70%, D  $\geq$  60%, and F < 60%.

## 8. Course Materials

There is no formal textbook requirement, but supplemental reading and reference to published papers in scientific journals will be used. Two useful reference textbooks are 1) *M. Kaps and W. Lamberson, Biostatistics for Animal Science, 2<sup>nd</sup> edition*, and 2) *R. A. Mrode, Linear Models for the Prediction of Animal Breeding Values, 3<sup>rd</sup> edition*; both can be found at <http://cabi.org> and/or a title search at <http://amazon.com>. This course is computationally intensive, and an emphasis will be placed on developing skills to use computers and develop computing algorithms applied to large data sets. Therefore, *students must have their own laptop* (Mac/iOS preferable) for use in the laboratory section, and in some cases lecture as well. A limited-access account on the CSU Livestock Genetics group computing network will be provided so that students will be able to run software within the Linux OS environment. Students using Windows-based laptops have the option of using the freeware terminal window PUTTY ([found here](#)) and file transfer program WinSCP (<http://winscp.net>). Downloads for octave, R, Python, etc., are also free for most platforms using freeware searches. Direct connections to network and specific tools for the course can be accessed directly using Mac/iOS computers via X11 with ssh or equivalent remote login protocols (e.g., gFTP may be useful).

## 9. General Outline of Topics

### *Quantitative Results from Population Genetics*

- The simple Mendelian model
- Equilibrium conditions
- Selection with single loci
- Single gene breeding value

### *A Functional Review of Matrix Algebra Applied to Linear Models*

- Matrix and vector notation
- Simple matrix math
- Common matrix and vector forms
- Direct and generalized inverses
- The matrix representation of solving linear systems of equations

### *Computing with Linux and Shell Scripts*

- Text editors in Linux and shell scripting
- Common shell commands and operations
- A primer on AWK with examples

### *Parameters, Statistics, Estimators and Models*

- Measures of central tendency, dispersion and association
- Rules of expectation
- Algebra of (co)variance
- Linear combinations of random variables
- Writing linear models
- Properties of estimators

### *Writing and Solving Equation Systems*

- Incidence matrices
- Writing systems of linear equations
- Regression and correlation coefficients
- Genetic interpretation of regression and correlation
- Using tools in the ABTK 4.x
- Solving linear equation systems
- Ordinary and Generalized Least Squares
- From OLS/GLS to MME

### *ANOVA and Regression in a Genetics Framework*

- Analysis of Variance and expected mean squares
- Linear regression
- Repeatability
- The simple sire model: estimation of direct heritability

### *Biotechnology and Genetic Improvement*

- The concept of major genes, SNP, QTL
- Genome Wide Association (GWAS)
- Genomic Selection
- Models for inclusion of markers
- Effects of genomic information on accuracy

### *Genetic Improvement and Mating Systems (If time allows)*

- Review of mating systems
- Expanded genetic model: gene combination value
- Additive and non-additive gene effects
- Data from crossbreeding experiments
- Estimation of breed effects
- Direct and maternal heterosis

### *Course Wrap Up & Final Exam*