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BIOL 595.01: Advanced Population Genetics

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ADVANCED POPULATION GENETICS

Instructor: Fred Allendorf, HS301, 243-5503, fred.allendorf@mso.umt.edu

Scheduled Class Meetings: Tuesday, 2:10 - 3:30, HS207
Thursday, 2:10 - 3:30, HS207

Description: Advanced Population Genetics (Biology 595, section 1, 3 credits) is a course for students who have already had a course in population genetics (Biol 480 or equivalent) and wish able to learn and discuss the important concepts in more detail and perhaps apply them in their own research.

All natural populations contain genetic differences among and within individuals. Population genetics is concerned with the distribution of genotypes among individuals and the evolutionary mechanisms that affect this variation.

Population genetics has a rich history that can be divided into three major periods. The *Classic Period* began with the rediscovery of Mendel's principles. Theory dominated this Period through the work of three intellectual giants: R.A. Fisher, J.B.S. Haldane, and Sewall Wright. All three of these scientists also made major contributions to many other areas of biology, especially statistics and mathematical biology. Theodosius Dobzhansky and his students did almost all of the empirical work during this period on *Drosophila*. The *Molecular Period* began in 1966 with the application of biochemical and molecular techniques to study genetic variation in all organisms. These techniques released empirical population genetics from working with organisms that could be bred quickly in the laboratory. For the first time, genetic variation could be detected and compared in all organisms, from elephants to blue whales to species that live in deep-sea hydrothermal vents. We have just entered the *Genomic Period*. Population genetics has taken the lead in interpreting the overwhelming amount of comparative sequence data that is being generated by genome projects on a variety of organisms.

We will try to strike a balance in this course between theory and empirical observations. I believe that those of us in this course, including myself, are more interested in organisms than mathematics. Nevertheless, we cannot understand the genetics of natural populations without a firm grasp of the theory. Population genetics is becoming increasingly valuable for conserving natural populations. In this course, we will emphasize those topics that are of special importance in conservation of natural populations.

Format: The class format will be largely interactive. I will present a structured lecture to introduce major topics. In addition, we will read the original literature where appropriate. Later in the course, I may ask students to present a brief lecture on specific topics.

Problems and data analysis will play a major role in the course. In my own experience, one really learns the complexities of population genetic theory only by applying the principles to real situations and solving specific questions of biological interest.

The course will not involve a great deal of advanced mathematics. Factorization of polynomial expressions, as we were taught in high school, is probably the most relevant mathematical technique for population genetics. Understanding the theory often requires a great deal of algebra and some elementary calculus. Elementary statistics and probability are also important. Matrix algebra is often used in population genetics, but it is not essential for understanding for the principles of population genetics.

We will use a variety of computer programs that are available to analyze data and to understand the theory of population genetics. We will use FSTAT (Goudet 2002), GENEPOP (Raymond and Rousset 1995), and other programs for analyzing and interpreting data. EASYPOP (Balloux 2001) will be used to generate simulated datasets under specified conditions to construct null hypothesis against which real data can be tested statistically and to explore of problems in population genetics that are too complex to be tracked analytically.

Texts: Readings will be primarily from the original literature. However, we will use several books as references.

The Origins of Theoretical Population Genetics with a New Afterword. (Provine 2001).

All students should read this book at the beginning of the course to gain an historical background of population genetics.

Genetics of Populations. (Hedrick 1999).

This book will serve as a reference and overview for the principles of population genetics.

Optional - *An Introduction to Population Genetic Theory* (Crow and Kimura 1970)

This book is out of date because it was written at the close of the Classic Period before molecular data from natural populations were available. Nevertheless, it remains the single best comprehensive source for basic (and not so basic) population genetics theory. This book is out of print, but I will order copies for interested students from a publisher that has permission to print copies.

Theoretical Evolutionary Genetics. (Felsenstein 2001).

This unpublished reference book will be available as a pdf file.

Other appropriate reference books and papers will be available outside my office in HS301 and on the course web page:

<http://biology.dbs.umt.edu/biol480/>.

Grades: This course can be taken pass/fail or for a letter grade. Grades will be based on a series of problems that you will work on outside of class. There will be no exams. Karma will play an important role in this course. That is, the more effort that you put into this class, the more you will get out of it.