MATH 583 Section # 55872 - Spring 1995

# EVOLUTIONARY THEORY

Instructor: Lou Gross, Professor of Mathematics and Ecology
Time: 2:30 - 3:20 Monday, Wednesday and Friday
Place: Ayres Hall 309B

This course will cover the basic mathematical models utilized in population genetics and evolutionary ecology. Topics to be covered include: models of natural selection at one and many loci; effects of multiple alleles, mutation, and neutrality; recombination and linkage disequilibrium; assortative mating; density and frequency-dependent selection; evolutionarily stable strategies and life history theory; kin selection; sexual selection; evolution in spatially and temporally varying environments; and the effects of random environmental variation. Thoughout, the emphasis will be on analyzing models of importance to evolutionary ecology, and we will focus on microevolution rather than macroevolution. As time permits, discussion of molecular genetics and sequence analysis will be included.

The course is oriented towards students with mathematical maturity at the level of advanced calculus, with some prior exposure to basic probability or statistics. Biologically trained students without this background are welcome and will be accomodated in the course structure.

The text for the course is: *Theoretical Evolutionary Ecology* by Michael Bulmer, with supplementary material coming from several sources including: *Theory of Population Genetics and Evolutionary Ecology: an Introduction* by Jonathan Roughgarden, *Mathematical Evolutionary Theory,* Marcus W. Feldman (ed.) *Evolutionary Genetics* by John Maynard Smith and *Mathematical Population Genetics* by Warren Ewens.

## COURSE GOALS

1. To provide an introduction to the diversity of mathematical approaches used to address evolutionary questions.

2. To investigate in a mathematically rigorous framework historically-significant models in population genetics.

3. To provide an introduction to areas of current research in evolutionary ecology.

4. To provide participants the opportunity to work as a team to address an open question in evolutionary theory.

5. To introduce participants to computer packages useful in investigating several areas of modern evolutionary theory.

## COURSE OUTLINE

The text by Bulmer includes several chapters at the beginning (Chapters 1-7) which cover topics contained within the Math 581-2 course sequence. It will be assumed that course participants already have had some exposure to these topics, and they will not be elaborated upon in this course. Similarly, the Appendices include mathematical background that will be assumed as prerequisite for the course, though we will go over the mathematical details as necessary for course participants whose background is primarily biological. We will cover much of the rest of the text (Chapters 7-12) in the course, but will preceed this with detailed examination of a variety of topics in mathematical population genetics. An overview of topic coverage is:

Overview - Population genetics and optimization models
Basic population genetics - one locus, two alleles; natural selection, mutation, drift.
Fundamental theorem of natural selection.
Diffusion approximations.
Multiple alleles and multiple loci models.
Spatially varying environments.
Density-dependent selection.
Frequency-dependent selection.
Evolutionary game theory.
Kin and group selection.

Sexual selection.

COURSE GRADING

There will be a variety of problem assignments throughout the semester which will be graded. It is recommended that you work individually on these problems, though occasional consultations with other students would be alright. I will give hints to problem solutions if you get stuck. I expect to give either an oral or take-home final. Additionally, there will be a class project in which each course participant will be assigned a part.

TENTATIVE CLASS PROJECTS

1. **Individual-based population genetics in a spatially-heterogeneous habitat.**
This project will focus on the construction of a relatively simple population genetics model (e.g. few loci), with selection, some form of assortative mating (most likely based upon spatial movement of individuals), and spatially and temporally varying habitat characteristics which affect selection. Goals are to (a) understand the assumptions inherent in constructing an individually-based genetics model; (b) analyze the interactions between spatial variation in selection and population characteristics; (c) compare results to analytic approaches to spatially-varying selection - particularly in dealing with spatial correlation in habitat; and (d) investigate drift and gene flow in small populations with spatial movement. One possible form for constructing this model is to make use of the EcoBeaker code available on the MacIntosh - assuming some participants are sufficiently C++ literate to modify the code.

2. **Antibiotic resistance, selection and gene flow.** This project concerns some practical issues in the spread of antibiotic resistance for certain human pathogens, and alternative schemes to alleviate the spread (see Science 265:589 and Science 266:1462). It thus will include aspects of epidemiology of disease, population genetics, and spatial spread. In particular, we would deal with what occurs under selection to resistant strains if anti-biotic use is restricted, and what the effects would be of gene flow when new individuals carrying resistant strains move into a community which restricts antibiotic use to control resistant strains. The key questions here are (a) can we characterize on what time scale restriction of antibiotic use within a community will be effective in reducing health risks from resistant strains; (b) what would be the effect of "rotation strategies" in which several antibiotics were rotated in use in a local region to control bacterial pathogens; (c) how do the patterns of spatial movement of individuals between regions affect these results - e.g. how much gene flow will swamp out the benefits of restricting antibiotic use; and (d) is it possible to devise "spatially-varying rotation strategies" for antibiotic use that ameliorate the effects of gene flow. This project will involve digging into literature on antibiotic resistance, developing a local model for resistance spread and control by antibiotics (there may be a some models already constructed for this), developing methods to couple local models together due to gene flow, and possibly adding to this some control model that allows variation in control variables such as the periods for antibiotic use and/or rotation.

ASSIGNMENT #1 - REVIEW OF A COMPUTER PROGRAM DEALING WITH EVOLUTION

The purpose of this assignment is for each participant to evaluate a program or part of a program that analyzes some issue in evolutionary theory. The review should contain the following information: (a) name of the program or any subprogram being reviewed, along with author/pubisher; (b) brief description of objectives of the program; (c) description of key inputs/outputs, including parameters under users control, graphs produced, etc.; (d) summary of what you did in analyzing the program, such as varying particular parameters, changing he cases investigated, etc.; (e) comments on what you learned from the program; and (f) overall critique of the program, including suggestions for improvements. This review should be typed in whatever word processor you want, and both a hard copy and electronic version handed in (or e-mailed to gross@math.utk.edu) by Wednesday, January 18 during class. The overall length of the review should be 3-5 pages. As I do not want two participants reviewing the same program or subprogram, make a choice of what you want to review, and write down your name and the exact program/subprogram on the sheet of paper I will leave posted in the Ayres 207 anteroom.

Programs to look at:

**MS-DOS:**
Note that programs are all available on the 486 in Ayres 207.

**Populus** (Version 3.4) - this is shareware and is therefore freely available for you to take to any DOS machine. There are two versions: pop34p.exe will extract to a version appropriate for any 286 or higher and pop34r.exe for older machines. The main menu has the following choices:

Selection - 10 subprogram choices some of which have additional subchoices
Genetic Drift - 4 subprogram choices
Quantitative Genetics - 3 subprogram choices
Coevolution - 2 subprogram choices
Games - 2 subprogram choices

Choose only one of the many subprogram choices to review.

**SimLife** This is a game program that is quite complex, allowing you to construct worlds, organisms with different characteristics, genetic-type interactions for mating and survival, disasters, spatial variation in habitats, and lots of other good stuff. I suggest you take one of the preset scenarios and evaluate it. It is also available on the Macintosh. It cannot be copied.

**Nemesis** - this is only available on the 486 in A207 and may not be copied. It has a number of subprograms, but only a limited number under genetics. It is designed to analyze problems in conservation biology.

**Macintosh:**
Note that all Mac programs are on the Mac in A207 under the folder Biology Software.

**SimLife** See above under MS-DOS. It cannot be copied.

**Evolve** This is a BioQuest Collection Candidate, so it is in the BioQuest folder. It has a number of preset laboratory scenarios, and I suggest you evaluate only one of these. Manuals are in Word.

**EcoBeaker** (Version 0.85) This may be copied and taken to another Mac - copy the .sea file or BinHex it first. However, the copy must be destroyed at the end of the course. The manuals are in Word. This is an individual-based, spatially explicit modeling package. It has a number of preset labs included, and I request that you evaluate one of these dealing with evolutionary issues.