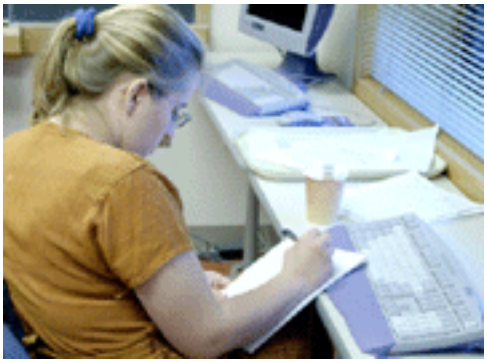
2003 Women in Mathematics Program

Monday, May 12, 2003 (All day) - Thursday, May 22, 2003 (All day)
(May 12-22, 2003)

Mathematical Biology

Course Descriptions:



Tandy Warnow - Undergraduate Course

1. Introduction to Mathematical Phylogenetics. We will cover basic questions, such as: What is a phylogeny? What kind of data is used to construct phylogenies? What are some simple Markov models of molecular sequence evolution? What are some simple methods for constructing phylogenies? The one issue we will explore in some depth is the mathematical aspects of distance-based methods for reconstructing phylogenies, and we will prove that distance-based methods are statistically consistent under simple Markov models of evolution.

2. Comparing trees -- distances, consensus, and agreement methods. Comparing two or more trees is a fundamental aspect of phylogenetic analysis, largely because such analyses often return more than one tree. In this talk we'll look at several approaches to these problems, discuss their relative weaknesses and strengths, and explore some open problems.

3. Stochastic models of evolution and the performance of simple tree reconstruction methods. In this talk we'll go into statistical performance criteria of phylogenetic reconstruction methods under Markov models of evolution, exploring in greater depth issues such as the convergence rate and robustness to model violations. We will specifically look at "fast converging methods".

4. Perfect phylogenies, triangulating colored graphs, and evolutionary trees. In this talk we will look at the inference of evolutionary trees for certain kinds of data (primarily morphological in biology, but more generally available in historical linguistics). For these data, "perfect phylogenies" can sometimes be obtained. We will look at algorithms for constructing perfect phylogenies, especially at the graph-theoretic versions which are based upon the equivalent problem of triangulating vertex-colored graphs.

Dorothy Buck - Undergraduate Course

Teaching Assistant: Jean Griffin

Our paradigm for this mini-course is modeling interesting phenomena in molecular biology or chemistry using topological tools. We will examine several topics in detail, focusing on stereochemical topology -- how topology, knot theory, and the topology of embedded graphs can be used to understand molecular structures. We'll consider the hierarchy of chirality of molecules, and what topological tools can be used to place a given molecule within that hierarchy. We'll also examine the topology of DNA more closely, and how it relates to geometric notions (in particular writhe).

Lisa Fauci - Graduate Course
Teaching Assistant: Katarzyna Anna Rejniak

The primary goal of these lectures will be to make students aware of how different areas of mathematics are directly applicable to problems in biology and physiology, and to introduce them to open problems that could be the subject of graduate research projects. In particular, topics covered will include aspects of cell motility, bacterial chemotaxis and biofilm processes, as well as developmental biology and blood clotting. Mathematical models may employ deterministic methods based on differential equations, probabilistic methods, elasticity models, fluid dynamics, or a combination of these. Scientific computing will be emphasized as a fundamental tool in model development and analysis.

Naomi Leonard - Graduate Course

A school of fish exhibits remarkable emergent behaviors: it maneuvers swiftly, it evades predators and it forages successfully. Biologists are developing models that can reproduce school behaviors with simple traffic rules for individual fish. In the robotic setting, the aim is similar but the problem is different: to design coordinated dynamics for a network of autonomous vehicles for use in search and discovery. Because the prescribed traffic rules will be implemented on real vehicles, it is important to prove stability, scalability and robustness of the schooling dynamics. In this course, I will present a collection of results from nonlinear control theory: stability and robustness analysis, controllability and control design, geometric approaches, and illustrate their application to understanding and emulating the behavior of individual animals and animal groups. I will try to emphasize the range of mathematics used in control theory and the ubiquity of control in biology and biology-inspired robotics. The course will include a lab visit to observe a robotic vehicle group in a large freshwater tank.

Lecturers:

Dorothy Buck - Brown University (Applied Math)
Lisa Fauci - Tulane University (Mathematics)
Naomi Leonard - Princeton University (Mechanical & Aerospace Engineering)
Tandy Warnow - University of Texas at Austin (Computer Science)

Overall Program Schedule

May 12-22, 2003

Monday, May 12

Registration (Fuld Hall Common Room)

12:00 p.m.

3:00-4:30 p.m. Afternoon Tea (Fuld Hall Common Room)

4:45 p.m. Tour of Institute campus (meet in Fuld Hall Common Room)

5:30 p.m. Informal supper and orientation, poster construction (Coffee Lounge, Institute Dining Hall)

Tuesday, May 13 - Friday, May 16 & Monday, May 19 - Wednesday, May 21

8:00-10:30 a.m.	Breakfast (Dining Hall)
9:30 a.m.	Undergraduate Lecture Series (Simonyi Hall Seminar Room)

10:30 a.m.	Break
10:45 a.m.	Graduate Lecture Series (Simonyi Hall Seminar Room)
12:00 noon	Lunch (Institute Dining Hall)
1:15 p.m.	West Building Lecture Hall
2:30 p.m.	Afternoon Tea (Fuld Hall Common Room)
3:45 p.m.	
4:00 p.m.	Research Seminar (Simonyi Hall Seminar Room)
5:00 p.m.	Women in Science Seminar (Dilworth Room)
6:30 p.m.	

Thursday, May 22

10th Anniversary Reunion Celebration

Reunion begins Friday, May 16 at 5:00 p.m. and ends after lunch

Day at Princeton University

May 19	Participants will spend the afternoon and evening at Princeton University.

Sunday, May 18. See Reunion Schedule for details. Morning schedule as usual; program ends at 12:00 noon

Daily Schedule