

April 25, 2008

Professor Lauren Ancel Meyers
University of Texas Austin
<http://www.biosci.utexas.edu/IB/faculty/meyers.htm>

Prior to colloquium, there was a discussion on bio-math programs. Brief notes follow.
Any errors are due to KMB.

- Possible programs to look at include: Paul Joyce at U Idaho; Florida State; Penn State; AZ State.
- Two components to bio math (not only ones)
 - Molecular
 - Computational molecular bio: huge data sets; interactive graphics; how genes interact
 - Currently hot
 - Ecology/Evolutionary
 - Analytical; decently funded
 - Hot area is disease modeling
 - NIH MIDAS:
<http://www.nigms.nih.gov/Initiatives/MIDAS/>
- Places to advertise
 - EVOLDIR: <http://evol.mcmaster.ca/evoldir.html>
 - ISBM: <http://www.ismb.org/>
 - Science: <http://sciencecareers.sciencemag.org/>
 - Nature: <http://www.nature.com/naturejobs/index.html>
 - PLOS Computational Biology: <http://www.ploscompbiol.org/home.action>
- Future Topic: Infectious Disease and Global Change
- U-Grad Program being developed
 - Calculus, Linear Algebra, Statistics starting math needs
- Scientific Computation Certificate
 - Currently being developed at UT by Professor Ancel Meyers
 - Student would obtain a major in one of natural sciences (Bio, Physics, Chem) and also get this certificate.
 - Good career opportunities
 - More info on Handout

Colloquium

Title: "Using Network Models to Forecast and Control Epidemics"

Abstract: In the early 20th century, two epidemiologists introduced a simple and powerful deterministic model for predicting infectious disease transmission which tracks the unidirectional movement of hosts among three states - susceptible (S), infected (I), and recovered (R). This SIR model provides important insight into the temporal progression of outbreaks and the efficacy of vaccination, and is the foundation for a recent proliferation in predictive methods. Contact network epidemiology is a

particularly promising development in which bond percolation on random graphs is applied to modeling disease transmission through heterogeneous populations. Her lecture will introduce the SIR model, explain its generalization to disease propagation on graphs in which vertices and edges represent individual hosts and disease-causing contacts, respectively, and link recent theoretical results to issues of public health and conservation.