NIMBioS Interdisciplinary Seminar

Dr. Michael DeGiorgio
Dept. of Integrative Biology
University of California, Berkeley

3:30 p.m.*, March 29, 2012
NIMBioS, Blount Hall, 1534 White Ave, 4th floor

"Genetic variation and modern human origins"

This talk will focus on using mathematical models to understand the demographic processes that have shaped the current distribution of genetic variation among human populations. Typical human population-genetic datasets contain genotypes from closely related individuals. Because relatives share recent common ancestors, their presence in such datasets biases estimates of genetic diversity. Thus, using pedigree analysis techniques, I derive an estimator that corrects this bias, enabling me to accurately measure genetic diversity in a study of human origins. Further, I extend the estimator to accommodate samples of arbitrary ploidy, solving the most general case and enabling investigators to apply my estimator to any species. Next, I apply my estimator as well as other measures of variation to worldwide human genetic data to investigate the extent to which models of human origins are consistent with observed patterns. I develop models of human demographic history to represent two main hypotheses, "the out-of-Africa" and "multiregional" hypotheses, for modern human origins. Using both simulations and analytical formulas, I compare measures of genetic variation observed from human data with those predicted by my models. I find that the model representing the out-of-Africa hypothesis produces patterns that mimic those observed from human data, whereas the model representing the multiregional hypothesis produces opposite patterns. These results lend support to the out-of-Africa hypothesis.

☙

Join us for refreshments in the NIMBioS Lobby on the 4th floor at 3 p.m.

For more information about this and other NIMBioS Seminars, visit http://www.nimbios.org/seminars