Empirical Population Genetics  -  EEOB/Gen 567, Fall 2004

Instructor:  John Nason, 341 Bessey Hall, 294-2268, jnason@iastate.edu.

Prerequisites:  Biol 303 and Stat 401 (or equivalents) are strongly recommended. Some knowledge of calculus (i.e., derivatives) will be helpful.

Subject:  The focus on this 3 credit course will be the use of genetic markers and population genetic theory to address pattern and process in ecology, ecological genetics, evolutionary biology, and systematics. The course will involve lectures, reading and discussion of papers, and problem solving exercises. Writing assignments will include a scientific paper summarizing analyses of a large data set and, in the final third of the semester, a NSF Doctoral Dissertation Improvement Grant (DDIG) proposal following official NSF guidelines.

Topics:
1. The four modes of evolutionary change: natural selection, mutation, gene flow, and random genetic drift.
2. Using the Hardy-Weinberg principle as a robust null model to test for evolutionary change and to identify its underlying causal processes.
3. The relative frequencies of deleterious, neutral and advantageous mutations.
4. Why use selectively neutral genetic markers for the study of evolutionary processes?
5. A brief introduction to effects of natural selection, mutation, gene flow, and random genetic drift on the organization of neutral genetic variation within and among populations.
   • Codominant markers: allozymes; microsatellites; RFLPs.
   • Dominant markers: AFLPs; RAPDs.
   • DNA sequence data.
   • Genetic variation as a function of rarity, range, growth form, and dispersal biology.
   • Variability of different genetic marker systems in different organismal groups.
8. A more detailed investigation of the effects of selection, mutation, gene flow, and drift on population genetic structure.
9. The fixation index and its relationship to the inbreeding coefficient.
10. Inbreeding effects per se.
    • Pedigree analysis - calculation of relatedness and inbreeding coefficients from pedigrees.
    • Effects of inbreeding on genotypic frequencies and individual and population fitness.
11. The concept of effective population size ($N_e$) and the Wahlund effect.
12. Models of demographic and genetic structure.
    • Island, stepping-stone, isolation-by-distance, metapopulation, and landscape context models.
13. Quantifying spatial patterns of genetic diversity within and among populations.
    • Single-locus estimators: Wright's $F$-statistics and their derivatives.
    • Multiple-locus estimators: AMOVA and $\Phi_{ST}$.
    • Single- and multiple-locus spatial autocorrelation analysis.
   • The analysis of biogeographic patterns of common ancestry among populations resulting from the effects of vicariance versus dispersal. Will discuss using genetic marker and sequence data from nuclear and organellar genomes.
   • Estimation of population phylogenies from gene trees.
   • Methods for testing concordance of observed phylogenetic topologies across codistributed taxa.

15. Statistical methods in population genetics – selected topics.
   • Monte Carlo simulation.
   • Bootstrapping to obtain variance estimates.
   • The Delta Method of variance estimation.
   • Bayesian methods.
   • Likelihood ratio tests.

   • Mating system analysis and the estimation of selfing and outcrossing rates.
   • Paternity analysis and the estimation of male fertilities.
   • Methods for estimating immigration.
   • Estimation of Wright’s neighborhood.
   • “TwoGener” analysis.
   • Hybridization and backcrossing.

17. The indirect estimation of historical gene movement via the analysis of genetic structure.
   • Equilibrium estimates of selfing and outcrossing from measures of genetic structure.
   • Geographical-level estimates of gene flow and isolation by distance.
   • Inferring introgression.

18. Genetic evidence and tests of historical population bottlenecks and admixture.

   • The reproductive and genetics characteristics of small and fragmented populations.

20. Issues in landscape genetics.
   • The “scaling-up” of available population genetic models.


22. Issues of interest to students.
   • Discussion of additional topics as indicated by student interest.