In-class discussion of O'Reilly et al. (2004)

In class today we discussed O'Reilly et al. (2004) with topics of conversation ranging to include the pros and cons of different classes of genetic markers, including issues associated with allelic richness, as well as statistical issues including Bonferroni corrections for multiple comparisons, the power of a test, and effect sizes.

A conclusion from today's discussion of O'Reilly et al.

Can unusually high mutation rates at some microsatellite (SSR) loci cause problems for accurate estimation of F_{ST} and, consequently, inference of population subdivision? The issue is whether mutation rates at SSR loci are high enough to generate substantial homoplasy in the data. Homoplasy is the phenomenon where two alleles are identical in state but not identical by descent. Homoplasy is problematic because it causes populations to appear more closely related than they really are, leading to underestimates of divergence. This is potentially a greater issue for SSRs than other markers because to some degree they evolve according to a stepwise mutation model in which mutation in a particular repeat variant is likely to result in the formation of a new allele differing by only one or a few repeats from the original. As alleles are lost due to genetic drift among populations they can thus be replaced by non-homologous alleles arising by mutation from similarly sized alleles. If mutation rates are high enough they can counteract the effects of drift, resulting in a negative relationship between locus variability and the magnitude of estimated population subdivision. As observed in O'Reilly et al., estimates of F_{ST} did decline with locus polymorphism, resulting in diminished power to discriminate among samples, a loss they attributed to the effects of SSR size homoplasy.

Literature Cited

O'Reilly, P. T., M. F. Canino, K. M. Bailey, and P. Bentzen. 2004. Inverse relationship between F-ST and microsatellite polymorphism in the marine fish, walleye pollock (*Theragra chalcogramma*): implications for resolving weak population structure. Molecular Ecology 13:1799–1814.