**Abstract**

Populations of clonal or partially clonal organisms typically violate assumptions of Hardy-Weinberg equilibrium and random mating, which are required assumptions in models from which population genetic analyses are based. Hardy-Weinberg equilibrium gives an estimate of how genotypes are arranged within a locus and random mating necessitates that all loci are assorting independently within the population. One method used for testing for clonal reproduction in populations is to test for associations between unlinked loci. This can be achieved using the index of association, which is a ratio of observed variance of allelic state across all loci to sum of the variances at each locus. At equilibrium, these values are expected to be equivalent. Previous studies have shown the sensitivity of this index given different levels of clonal reproduction, but not addressed were evolutionary factors that might potentially confound the signal such as admixture or migration. Variable factors in sampling such as number of individuals and loci sampled along with the type of loci also have an unclear effect on this index.

This study aims to quantify the sensitivity of the index of association to the above factors in populations. We expect that 1) sensitivity to biological factors will increase non-linearly with respect to sample size of either loci or individuals, and 2) sensitivity to clonal reproduction will increase in combination with the above biological factors. To test these hypotheses, we will utilize time-forward simulations of populations with varying effective sizes, migration, admixture, clonal reproduction, and marker systems. The sensitivity of the index of association to these factors will be analyzed using Receiver Operating Characteristic curves. This analysis will help us understand the deeper impact of using the index of association to analyze clonality in populations.