What is the genetic signature of habitat fragmentation?

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The effects of fragmentation are of great concern for conservation and management of threatened taxa. A quantitative analysis of the population genetic effects of rapid, anthropogenic fragmentation and gradual, natural fragmentation are necessary to inform conservation and management strategies such as reintroduction or hybridization between populations. We simulated habitat fragmentation using the package data.tree in R, using a non-model group of threatened plants, *Chloropyron* (Orobanchaceae). These species are all diploid, annual herbs, with very low migration rates and historical records of population fragmentation. The package data.tree gave us a natural framework to deal with bifurcating populations and allowed us to track properties such as fragmentation timing, population size, and diversity. The simulation incorporates Wright-Fisher populations, each running for a randomly chosen geometric waiting time before one is picked at random to be bifurcated. The bifurcated population forms two subpopulations by randomly transmitting half of its individuals to one subpopulation and the half to the other.

The free parameters are:

a: number of alleles K: number of resulting fragment populations t: expected time between bifurcations c: smallest possible population size

The dependent parameters are:

 $E[Ttot] = (t-1)^{*}K$: expected total run time $N = c^{*}2^{A}(K-1)$: total individuals

We then used the Bayesian software package Structure to quantify the number of Hardy-Weinberg clusters, without admixture, among sampled individuals. Results are presented for a = 10 and 100, total time, Ttot = 200, 1000 (representing rapid and gradual fragmentation, respectively), when allowing for K = 2 and 5 fragmented populations. Estimates of population structure suggest that greater structure (i.e. population differentiation) is detected when expected time between bifurcations is greater, though the number of alleles can both counteract and augment this effect.