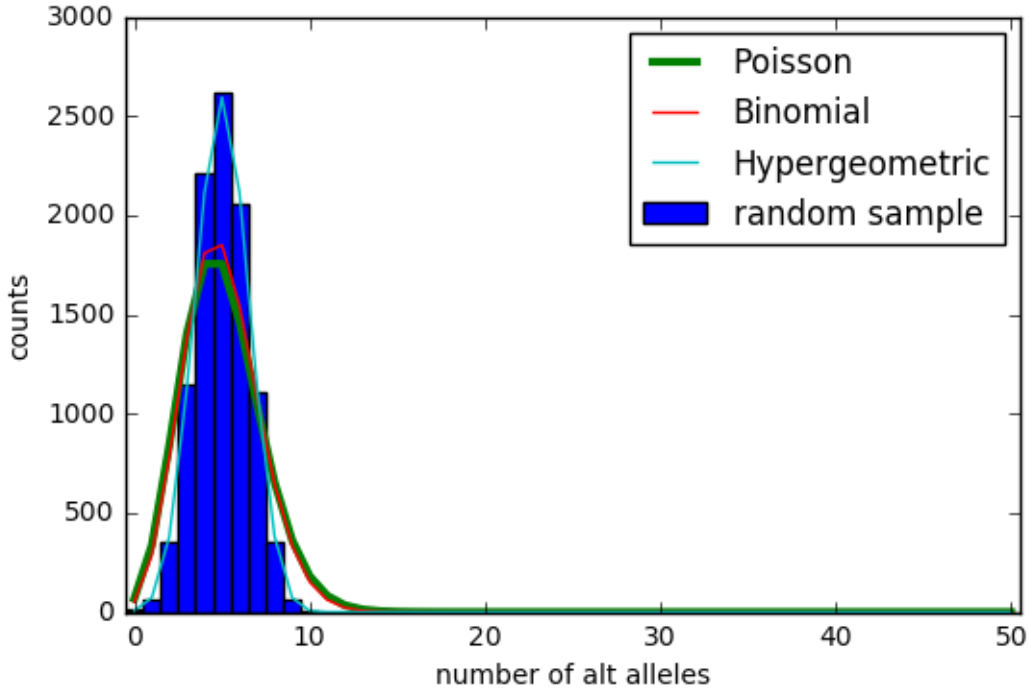
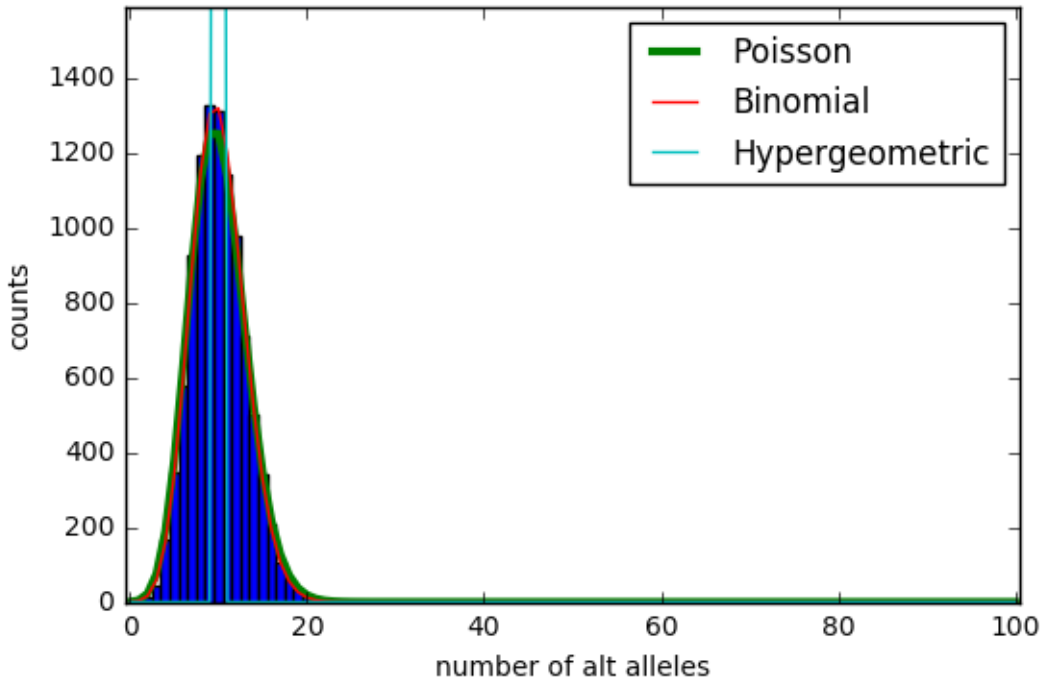
Wright-Fisher model

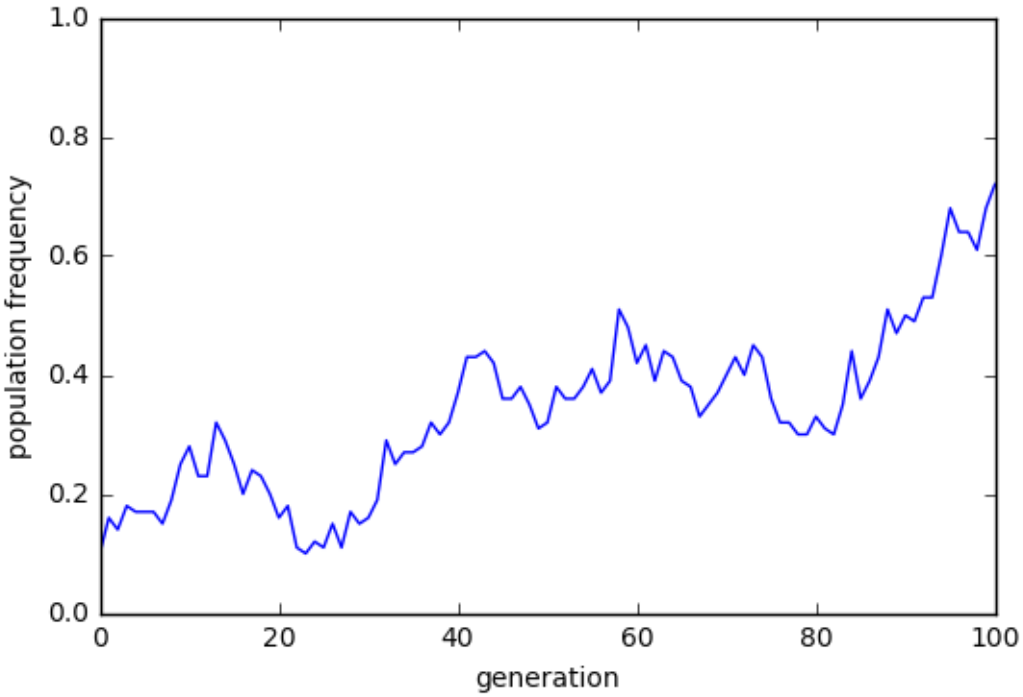
In our case the samples are not independent events because the samples are not replaced once they are drawn. Thus, after we select an allele with a value of 1, the probability of selecting an allele with a value of 1 in the second step will be 9/100 for the entire population. These arguments lead to the conclusion that this is hypergeometric distribution and it is confirmed by a graph.



Here we have independent events; two possible outcomes; the probability of each outcome remains the same across all trials. Binomial distribution describes the data better than other. This is confirmed by a graph.

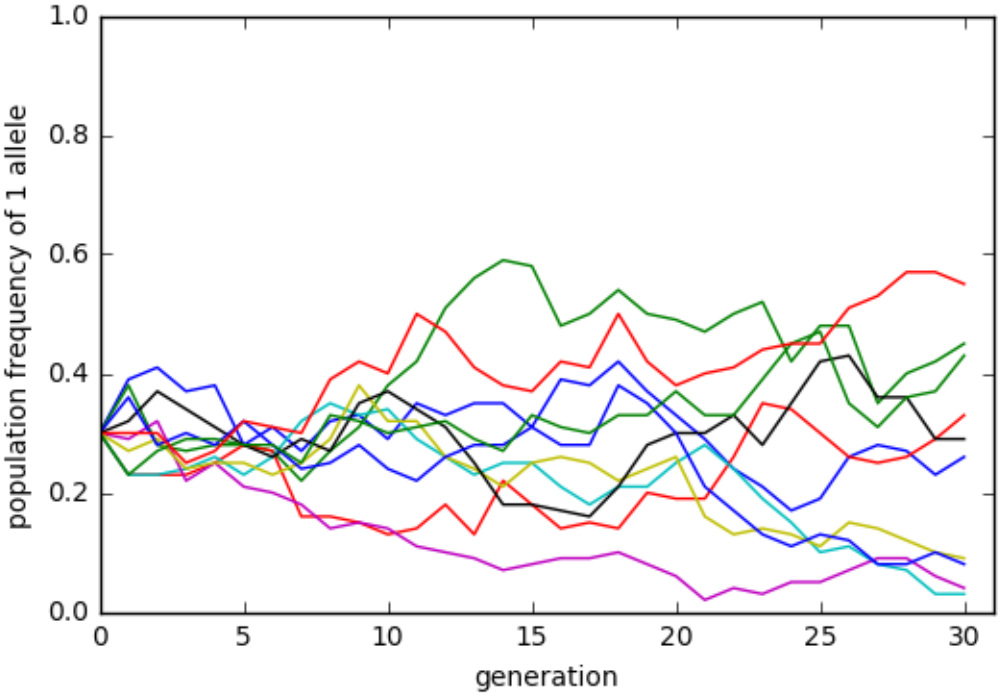


The allele frequency at each generation.

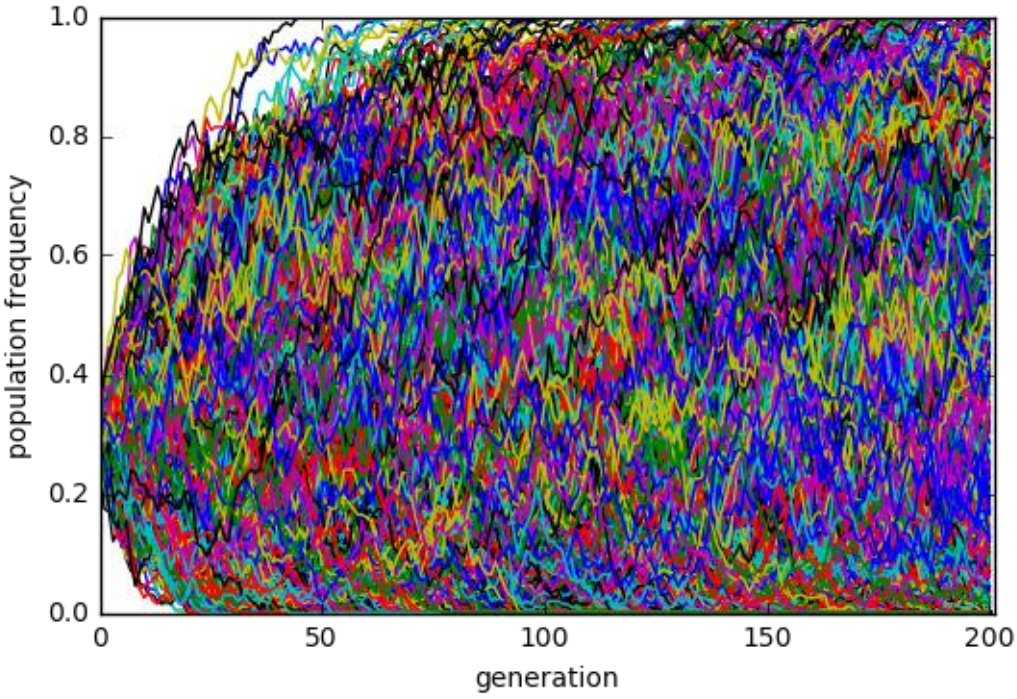


Exploration

Drift

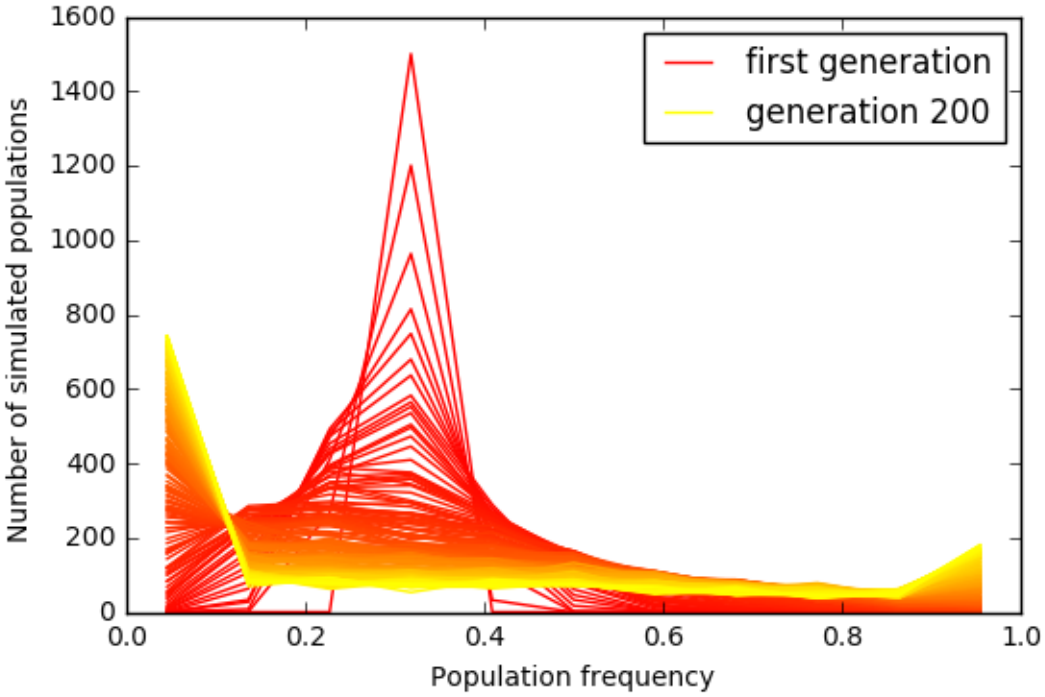


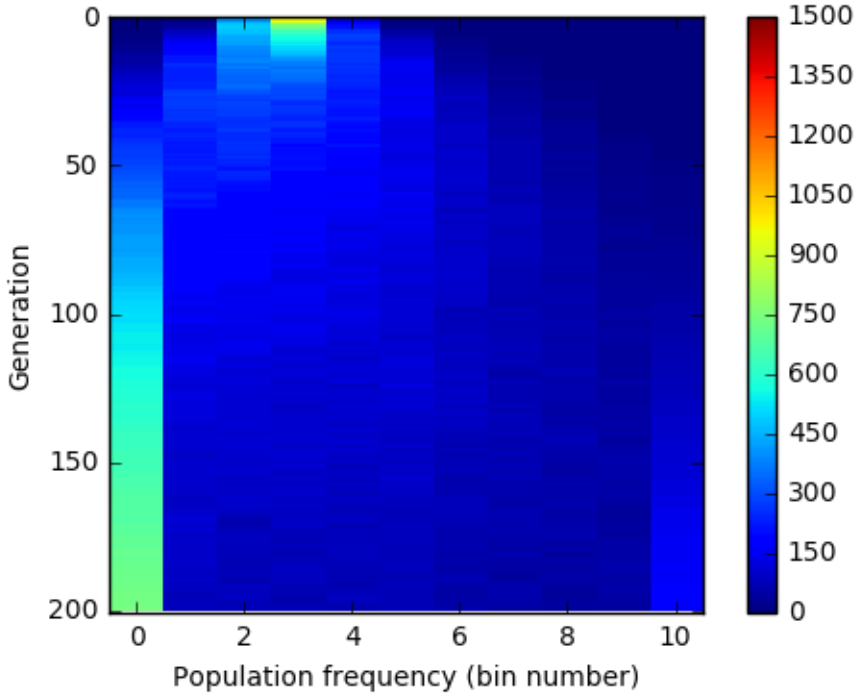
This graph was drawn for nRuns = 1500, nInd = 200, nGen = 200.

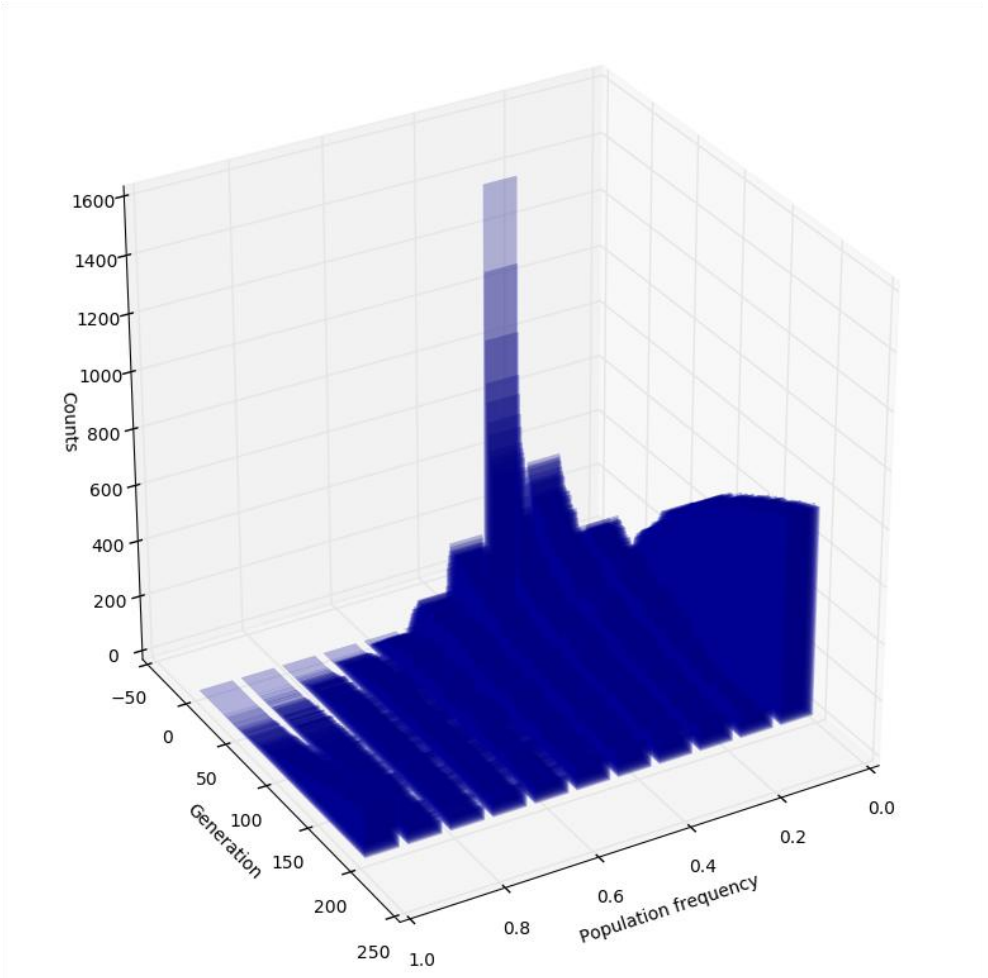


Over time, there are more and more populations at frequencies 0 and 1. (Why?)

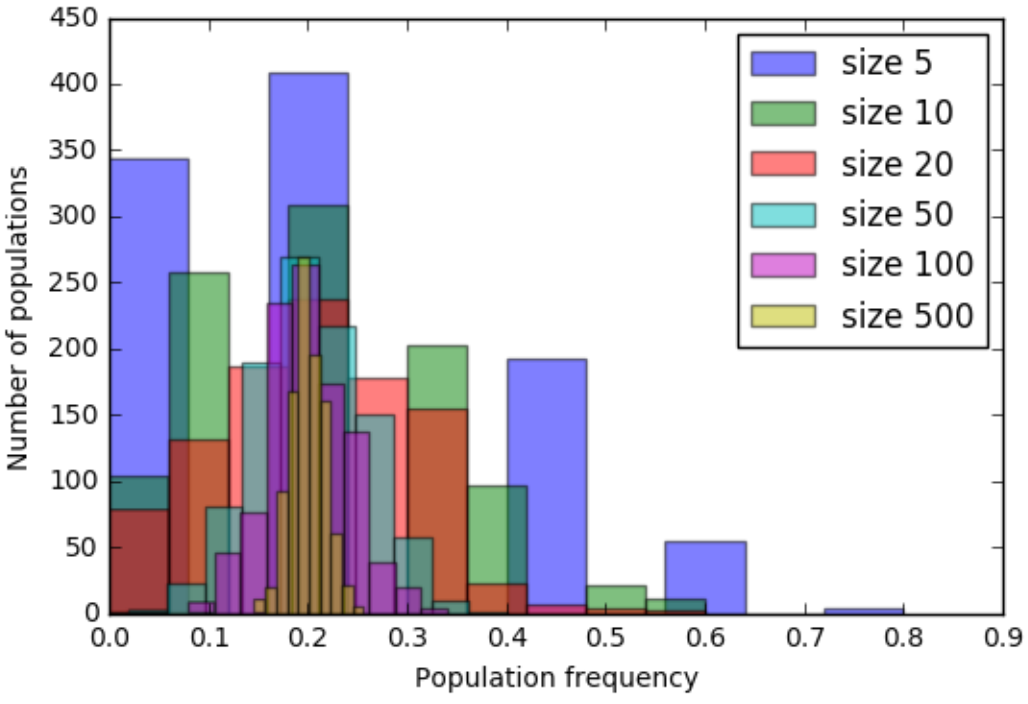
Because once all the values of allele in population becomes the same (either 0 or 1) next descendant population will take values for allele from that population and it could be only 0 or 1.



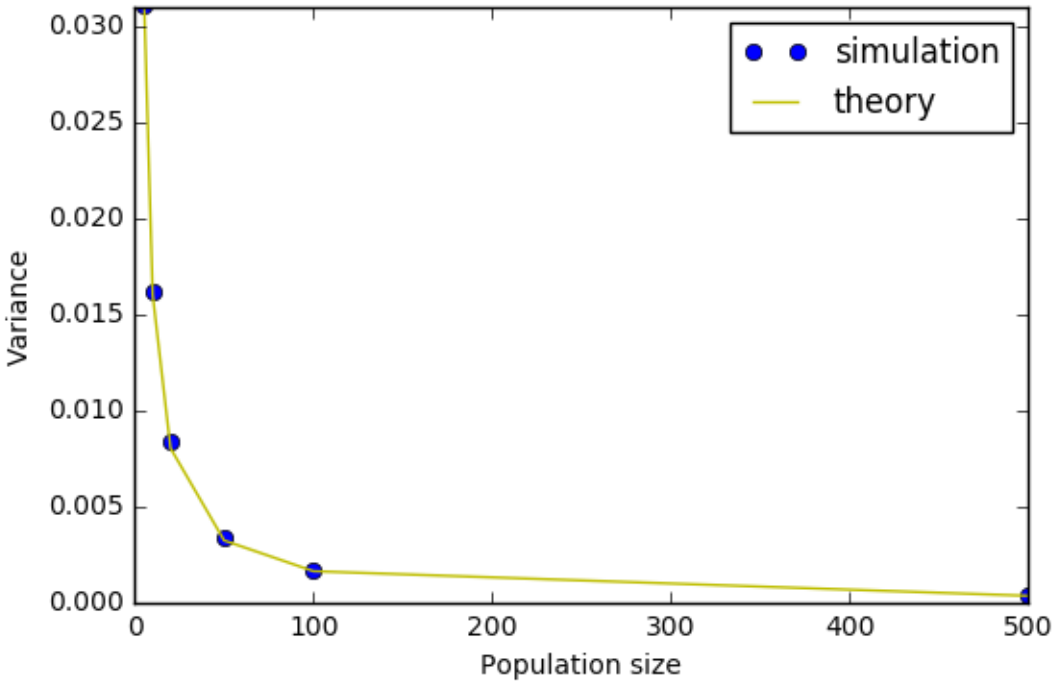


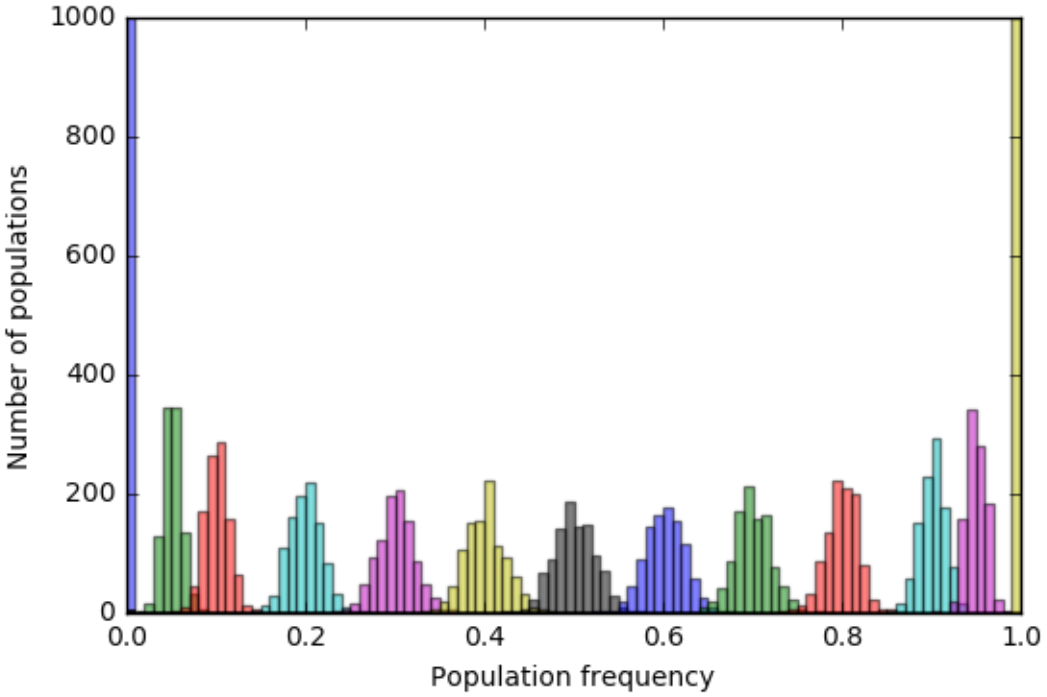


The expected distribution of allele frequencies after one generation is binomial.



theory = p0*(1-p0)/np.array(sizes)

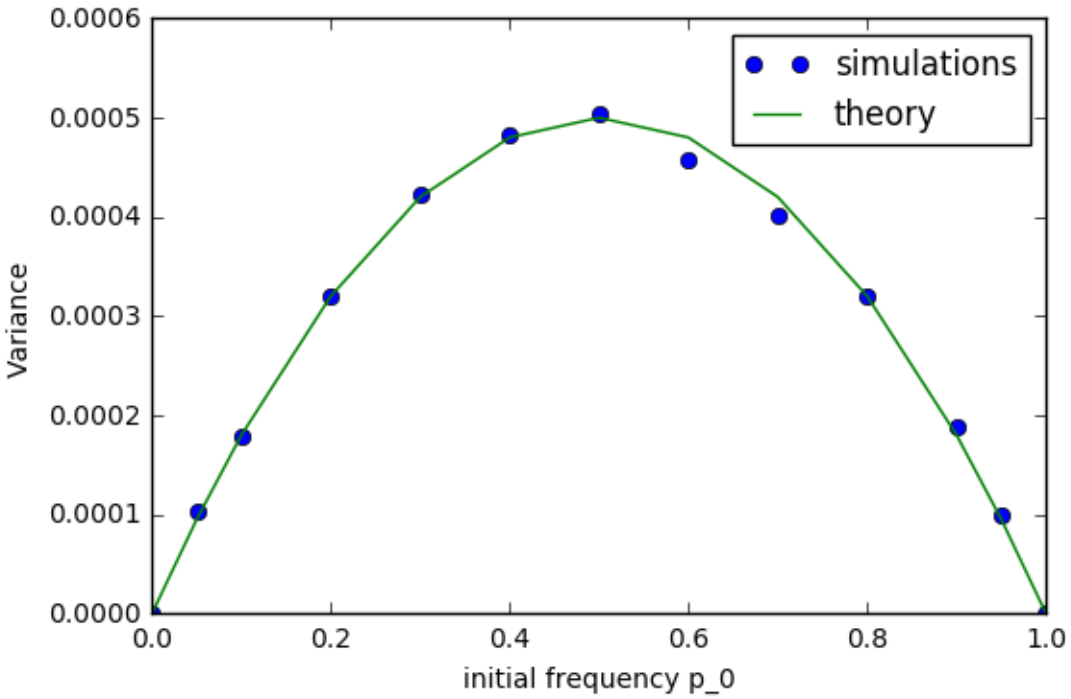




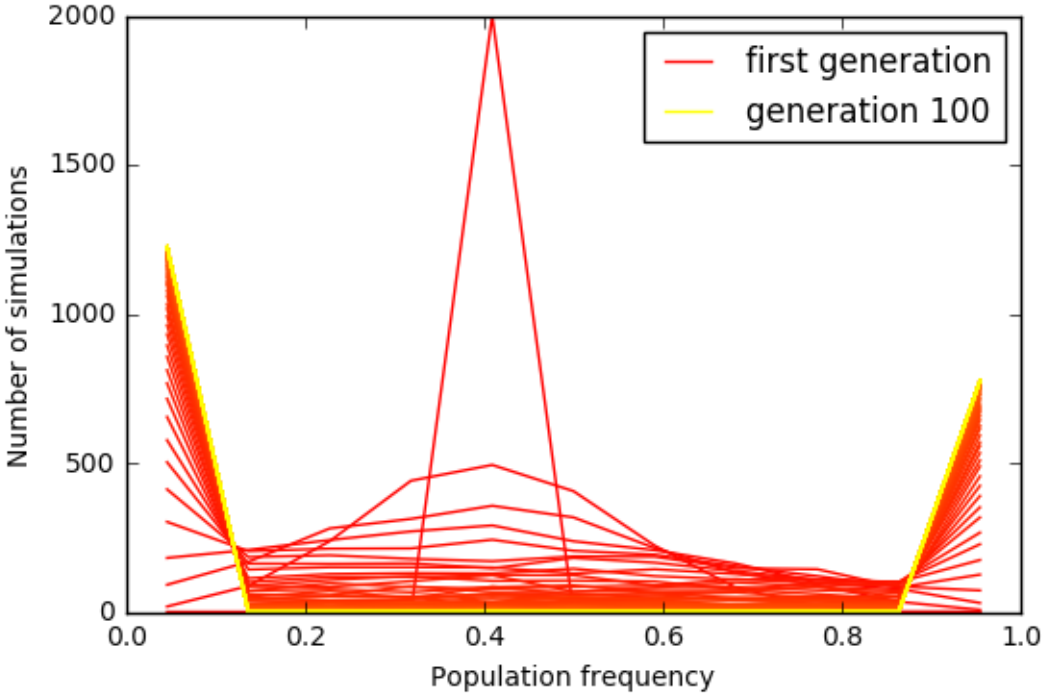
theory = (np.array(p0_list) - np.array(p0_list) ** 2) / nInd

Can you explain why this function is symmetrical around p0=0.5p0=0.5?

When p0=0.5 we have equal sizes of alleles with values 1 and 0. So the mean for the first generation is the highest when p0=0.5 for initial population. In our case the number of offspring that each from the initial populataion produces varies no more than expected by chance. For example, for initial populations with p0=0.3 and p0=0.7 we can see that quantity of 1 and 0 are equal to quantity of 0 and 1 respectively for these probabilities. Then these quantities will be changed no more than expected by chance. So the change for these two populations will be approximately the same and the variance are almost the same too.



Mutation



The probability that a new new mutation fixes in the population is equal to frequency for new mutation