BIOL 502 Population Genetics
Spring 2017
Arun Sethuraman
Midterm 1 Review Problems

Hardy-Weinberg Equilibrium/Tests

1) Consider an X-linked gene in humans, with two alleles, X^A and X^a, present in a population at frequencies p and q respectively, such that p + q = 1 (biallelic). What are the expected genotype frequencies and allele frequencies after one generation of random mating if the population is in Hardy-Weinberg Equilibrium?

2) If a population is in Hardy-Weinberg Equilibrium at a biallelic genetic locus, A, with two alleles A and a at frequencies p and q, such that p = 0.99 and q = 0.01, what would be the expected heterozygote and homozygote frequencies after one generation of non-random mating (wherein only AA x AA, Aa x Aa, aa x aa matings occur)? What would be the expected allele frequencies?

3) Why can heterozygosity in a population in HWE never be more than ½? Show this mathematically.

4) Is this population in HWE or not? Use a chi-squared test, list your null and alternate hypotheses, test statistic, degrees of freedom, and interpret the results.

MM	MN	NN
10	10	10

5) Assume you have 5 individuals in a population, such that there are exactly 5 A and 5 a alleles, which genotype configurations would be accepted/rejected to be in HWE?

Linkage Equilibrium/Disequilbrium/Tests

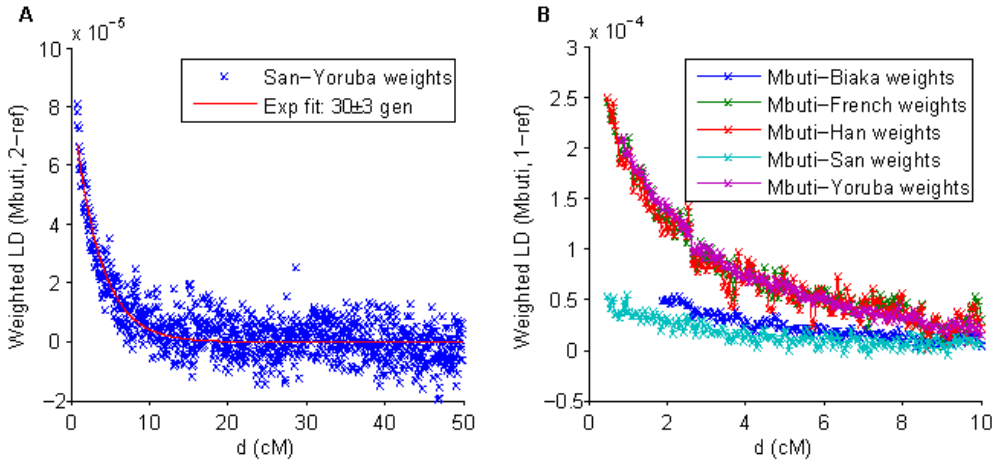
1) SNP locus A: A1=T, A2=C
SNP locus B: A1=1, A2=G

Observed haplotype data

Haplotype	Symbol	Frequency
A1B1	x_{11}	0.6
A1B2	x_{12}	0.1
A2B1	x_{21}	0.2
A2B2	x_{22}	0.1

Compute D. What does this mean for LE/LD between the A and B loci?

2) Why does LD decay with distance from centromere? (see figure on left). The figure on the right represents LD decay for Mbuti pygmies, in comparison with other African populations. Why is rate of LD decay different when compared with these different populations?



Drift, Effective Population Size

1) Humans when they evolved out of Africa underwent a series of bottlenecks, and range expansion. Assume that the African population that originally migrated out had an N_e of 7500 (Tenesa et al. 2007, DOI: 10.1101/gr.6023607). Assume that they went through a bottleneck such that N_e changed from 7500->1000->7500->1000->7500. Which one of these populations has the highest effective population size? What general statement can you make about the diversity of human populations based on this model?

2) Assume a population of size 2N is drifting randomly. Which one of these populations will have greater homozygosity after one generation? (a) 2N = 10, (b) 2N = 1000

3) If you sample any random individual at a single biallelic genomic locus, what is the probability that this individual's two alleles are identical by state (IBS)?

4) If a finite population of size 2N reaches an equilibrium in drift, what happens to the population's homozygosity? How about heterozygosity?

Coalescence

1) What happens to time to coalescence when a population undergoes a bottleneck? What happens with it undergoes an expansion?

2) Can two randomly sampled alleles at a locus never share a common ancestor? Why or why not?

Mutation and Neutral Theory

1) Observe the following sequences, and compute Θ_T and Θ_W, and what can you say about the history of this population based on the sign of Tajima's D?
Individual 1: AATAA Individual 3: AATAT
Individual 2: ATAAT Individual 4: ATTAA
2) What happens to homozygosity and heterozygosity in a population in mutation-drift equilibrium?

3) Why does per generation mutation rate increase with genome size in eukaryotes?