Population Genetics
Problem Set 9 (Note: for Final exam, not for Exam3)

1. What is the biological significance of a gamete being a "coupling" or "repulsion" gamete?

"Coupling" gametes have a haploid allele with the same designated subscript in two loci (e.g., A_1 with B_1; or A_2 with B_2) while "repulsion" gametes have a haploid allele with different subscripts given to the two loci (e.g., A_1 with B_2; or A_2 with B_1). Since the subscripts are just a means of nomenclature, there is no biological significance to them. (However, if the alleles do not follow random sorting, the two gamete "types" are used to measure deviation from random sorting and thereby used to calculate linkage disequilibrium.)

2. What is one way of estimating the rate of recombination, c, between two loci?

Estimated as the proportion of recombinant gametes produced by a parent.

3. In humans, what is the relationship between map units (centimorgans, cM) and the number of base pairs of DNA along a chromosome.

As a rule of thumb, 1 map unit or centimorgan (the name given to a 1% rate of recombination per generation) occurs along approximately 1 million base pairs.

4. What are two proposed disadvantages and two proposed advantages for the evolution of sexual reproduction (and recombination).

Disadvantages: 1. Parent only passes half of alleles to offspring; 2. Recombination can break up favorable allele combinations between two loci
Advantages: 1. Potential for allele combinations with higher fitness states; 2. Avoidance of Muller's ratchet.

5. Give the best definition for the following terms:

a. Epistasis: the interaction of fitness values at different loci

b. Linkage (or gametic) disequilibrium: the nonrandom association of alleles at different loci into haplotypes (or gametes)

c. Recombination: the process by which a strand of DNA is broken and joined to a different DNA molecule. Occurs during meiosis as chromosomal crossover between paired chromosomes.

d. Map unit or centimorgan, cM: a 1% chance that a marker at one locus on a chromosome will be separated from a marker at a second locus due to crossing over

in a single generation.

e. Genetic hitchhiking: when a neutral allele associated (in linkage disequilibrium) with an allele at a different locus is "carried along" and increases in frequency because of the selective advantage of the associated allele.

f. Selective sweep: reduction of heterozygosity and molecular variation in the region around a positively selected allele, due to genetic hitchhiking; e.g., selective sweeps with a selection coefficient of s = 0.01 can reduce variation 10 kb away from selected locus.

g. Background selection: The accidental purging of non-deleterious alleles due to their being linked to deleterious alleles that are purged.

h. Muller's ratchet: without sexual reproduction (recombination), detrimental mutations can accumulate and fitness will decline over time in asexual organisms.

6. Consider two loci (A and B) with two alleles each (A_1, A_2, B_1, and B_2). The population currently has the following gametic frequencies:

.3 A_1B_1, .15 A_1B_2, .1 A_2B_1, and .45 A_2B_2.

a) Estimate the current linkage (or gametic) disequilibrium.

Answer: $D = (.3)(.45) - (.15)(.1) = .135 - .015 = .12$

b) If the A and B loci are linked with recombination equal to .1, how much gametic disequilibrium is expected following 3 more generations of random matings?

Answer: $D_3 = (1 - c)^t \times D_0 = (1 - .1)^3 (.12) = .08748$

7. Consider the following genotypic numbers for an arbitrary population of two loci.

	Locus B			
Locus A	**BB**	**Bb**	**bb**	**Total**
AA	880	460	160	1500
Aa	76	300	24	400
aa	44	40	16	100
Total	1000	800	200	2000

a. What are the allele frequencies (please do not round) at each locus?

Answer: $Pr(A) = [1500 + .5(400)]/ 2{,}000 = .85$ $Pr(a) = .15$

Pr(B) = [1000 + .5(800)]/ 2,000 = .7 Pr(b) = .3

b. What are the expected genotypic frequencies at equilibrium for the A locus?

Pr(AA) = $(.85)^2$ = .7225 ; Pr(Aa) = 2(.85)(.15) = .255; Pr(aa) = $(.15)^2$ = .0225

Hint: draw a unit square just for the A locus

c. What is the equilibrium frequency of the bb genotype?

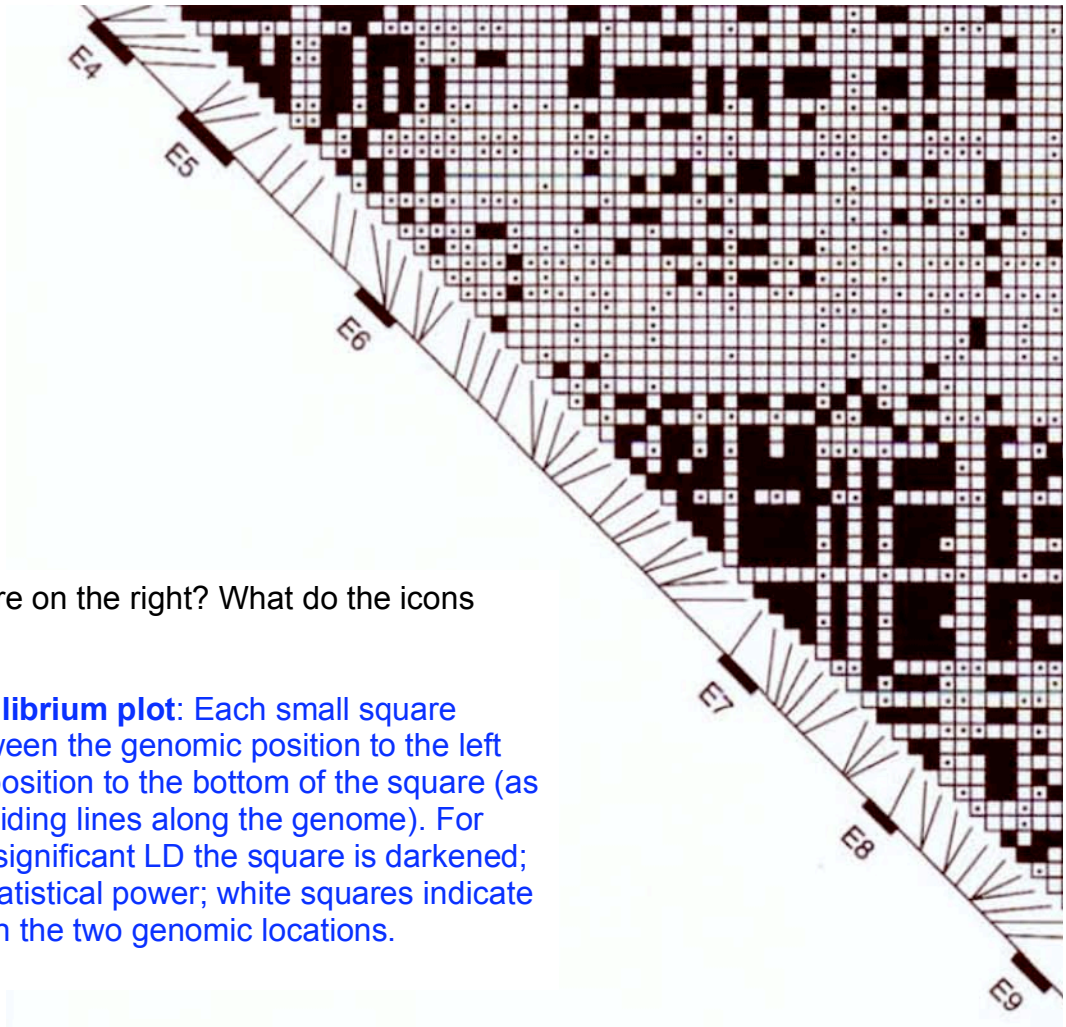
Pr(bb) = (.3)(.3) = .09 Hint: draw a unit square just for the B locus

d. What is the equilibrium frequency for the Aabb genotype? What is the current frequency of the Aabb genotype? What may explain the difference?

Pr_{eq}(Aabb) = Pr_{eq}(Aa) X Pr_{eq}(bb) = (.255)(.09) = .02295

Current genotypic frequency for Aabb is 24/2000 = 0.012

The A and B locus may be in linkage disequilibrium (i.e., in close proximity on the same chromosome); or the population is not in HWE due to some other factor (epistasis, population substructure, etc).



8. What is the figure on the right? What do the icons represent?

A linkage disequilibrium plot: Each small square measures LD between the genomic position to the left and the genomic position to the bottom of the square (as adjusted by the guiding lines along the genome). For pairs of sites with significant LD the square is darkened; dots indicate no statistical power; white squares indicate lack of LD between the two genomic locations.