

7.03 Problem Set 2

Due before 3 PM on Friday, February 25

Hand in answers in the box outside of 68-120

1. In the StarGenetics problem PS2-1 you are given two mutant flies with short aristae (antennae). Use appropriate genetic analysis to determine the mode of inheritance of each mutation and the relationship between them. Your analysis should lead to an assessment of whether or not the two mutations are in the same gene with an explanation of your reasoning. Describe the key crosses that you did, the outcomes, and the conclusions that you draw from these outcomes. Remember that in *Drosophila* meiotic crossing over occurs in females, but not in males.

Please place appropriate error estimates on the results of an experiment using the Poisson approximation to ascertain the standard deviation of your distance measurement. Note that for calculating the standard deviation as \sqrt{n} , n should be the number of actual individuals counted.

2. [NOTE: To do this problem you must download the “Beta” version of StarGenetics – available on the list on the right side of the StarGenetics web page.] In the StarGenetics problem PS2-2 you are given male and female flies from a true breeding wingless mutant strain. In addition this mutant carries 6 DNA based markers with alleles that differ from wild type. Three of these (Marker 1 – 3) are on chromosome 2 [in order : M1 – M2 – M3] and three (Marker 4 – 6) are on chromosome 3 [in order : M4 – M5 – M6]. Use these markers to first determine on which the wingless resides. A trick for doing this most easily is to set up a male as the heterozygous strain and since there is no meiotic crossing over in male *Drosophila* the wingless mutant will appear to be completely linked to every marker on the same chromosome. Once you have established the chromosome that the wingless mutation is on perform appropriate crosses to determine the relative map positions of the three DNA based markers and the wingless mutation (ie make a genetic map of the chromosome. As before, place appropriate error estimates on your map distances. [Hint: You will find that the “DNA Marker Summary” is the most useful way to look at the data. It will also make analysis easier if you only choose only one or two DNA markers at a time to analyze. Finally, when you are testing linkage of one DNA marker to another, you will need to combine winged and wingless phenotypic categories to obtain the proper counts of parental and crossover classes for the DNA markers under examination.]

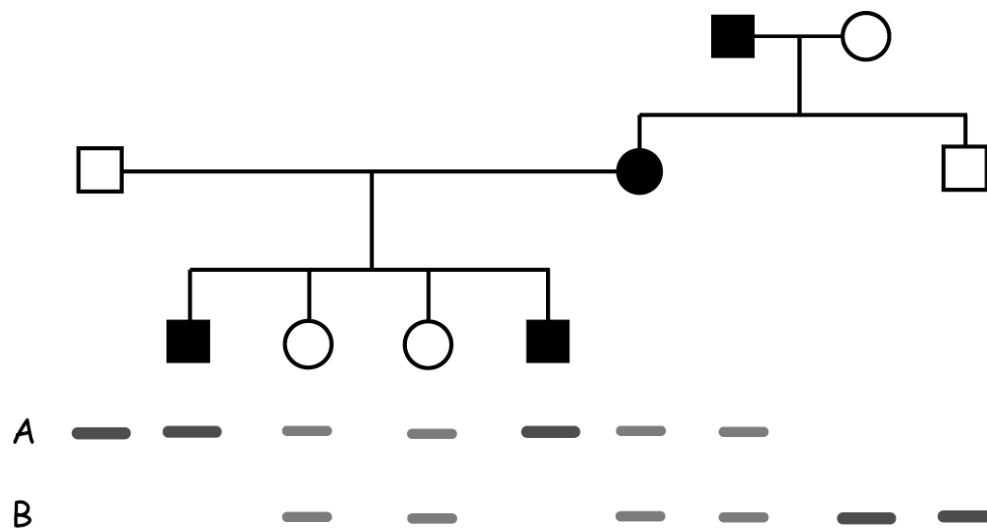
3. In the StarGenetics problem PS2-3 you are given four yeast strains that carry different temperature sensitive mutations. All of these strains also carry a *leu2⁻* mutation that was present in the strain background before the temperature sensitive mutations were isolated. You are also provided with wild type test strains of mating type **a** and alpha, each carrying a *lys9⁻* mutation. By performing the appropriate crosses analyze the relationship between the four mutations. Your answer should include an assessment of which mutations are in the same genes and give distances between any linked mutations in cM. (If any mutations appear to be completely linked, give an estimate based on the number of tetrads of the maximum distance separating the linked mutations.)

As usual, your analysis should begin by determining the mating type of each of the unknown strains. In addition you should perform appropriate tests on each temperature sensitive mutation to determine whether it is dominant or recessive. In some cases you will need to change the mating type of some of

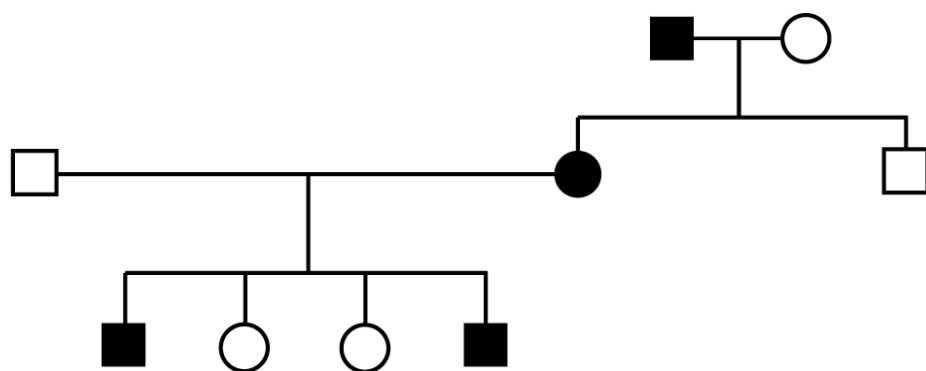
the temperature sensitive mutants. Mating type segregates as a single locus with two alleles: **a** and **alpha**. To switch mating type of a *ts* mutant, cross the mutant to wild type, sporulate the resulting diploid, then screen among the tetrads produced to find a recombinant that carries the *ts* mutation and is of the appropriate mating type.

4. In each of the pedigrees shown below an SSR marker with two alleles (A and B) appears to be completely linked to the dominant trait shown. Calculate the LOD score for complete linkage between the SSR marker and the trait. For these calculations it is important to consider all of the information you have available. It is also important to recognize when you don't have full information such as knowledge of phase information.

a)



b)



A — — — — — — — — —

B — — — — — — — —