1. Find the genotypes of the parents:

    a. +/sp ; +/ap   x   sp/sp ; ap/ap

2. Cross the parents to find your predicted ratio:

|	+/+	+ / ap	sp / +	sp / ap
sp / ap	+/sp ; +/ ap	+ / sp ; ap/ap	sp/sp ; +/ap	sp/sp ; ap/ap
sp / ap	+/sp ; +/ ap	+ / sp ; ap/ap	sp/sp ; +/ap	sp/sp ; ap/ap
sp / ap	+/sp ; +/ ap	+ / sp ; ap/ap	sp/sp ; +/ap	sp/sp ; ap/ap
sp / ap	+/sp ; +/ ap	+ / sp ; ap/ap	sp/sp ; +/ap	sp/sp ; ap/ap

   Determine the phenotypes from the cross:

   4 wild/ wild   4 wild/ apterous   4 sepia/ wild   4 sepia/apterous

   or 1:1:1:1

3. Now, calculate your predicted numbers from your TOTAL offspring:

    a. 250 + 125 + 125 + 250 = 750

    b. 750/4 (not 16 simply b/c this is a 1:1:1:1 ratio – so you have 4 categories) = 187.5

    c. Therefore – each phenotype SHOULD have the same number – 187.5

4. Compare to your actual data – does this predicted number match your actual?

    a. If yes (it's close) = unlinked genes

    b. If no (it's WAY off – look at your homozygous recessive numbers) = linked genes

5. So – LINKED. To do map units – total your recombinants. These are the phenotypes that are MIXED and NOT like your original parents (original parents were: wild and totally recessive). So, your recombinants are:

    a. wild / apterous &   sepia / wild

    b. Add your ACTUAL numbers: 125 + 125 = 250

    c. Now, divide that by the TOTAL flies overall: 250/750 = .33 recombination frequency

    d. Map units = .33 x 100 = 33 map units

Problem 2: Linkage Map

       This is a really a case of logic. Draw out a straight line first to represent your chromosome. Find your two genes that are farthest apart first (b, d) and place them on opposite ends of the line. Then, gradually fill in the middle parts (or maybe the outside of the first genes) based on the percentages given. Each percentage is the same as a map unit without a percent sign.
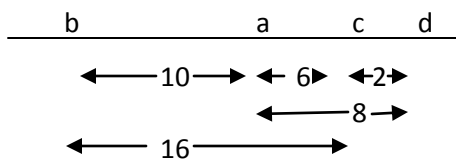
Problem 3 – Recombination Part I

1. If it is assumed that you know the map units – convert this back to a decimal.
    a. 12 = 0.12
    b. Multiply 0.12 x 1000 (total # of offspring) to determine how many offspring SHOULD be recombinants
    c. 0.12 x 1000 = 120 recombinants
    d. HOWEVER – this number includes BOTH categories of organisms that have done recombination – so, divide by 2 to find the number for each category
    e. 120 / 2 = 60
2. Now: subtract the number of recombinants from your total number of offspring: 1000-120 = 880
    a. Again, divide by TWO to get the two parent categories (your homozygous dominant and homozygous recessive parents) – 880/2 = 440
    b. So, here are you categories
        • Parent (homozygous dominant for both traits):   440
        • Recessive / Dominant: 60
        • Dominant / Recessive: 60
        • Parent (homozygous recessive for both traits): 440

Problem 3 – Recombination Part II
Compare the numbers that you just did to the actual data collected.
If it does not support linked genes – show WHY using predicted numbers.
What SHOULD those be – if they are unlinked, then you only have one choice: 9:3:3:1 WHY?
    Look back at the problem – it is NOT a test cross! It says "2 heterozygous parents" – if both parents are heterozygous for BOTH traits, then you are back to Mendel's magic numbers.
Find your offspring for the 9:3:3:1 by:

1. 1000 / 16 (you divide by 16 here since you are looking for the 1/16 number of offspring first): 62.5
2. Now, multiply to find your other categories:
    a. Homozygous dominant for both: 9 x 62.5 = 562.5
    b. Recessive / Dominant: 3 x 62.5 = 187.5
    c. Dominant / Recessive: 3 x 62.5 = 187.5
    d. Homozygous recessive for both: 1 x 62.5 = 62.5
3. Compare your predicted data to the actual data to make your conclusion/explanation.