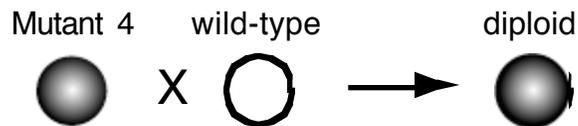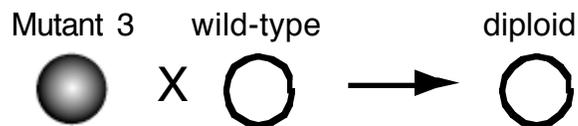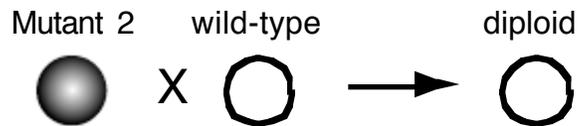# 7.03 Problem Set 1
Due before 5 PM on Thursday, September 18
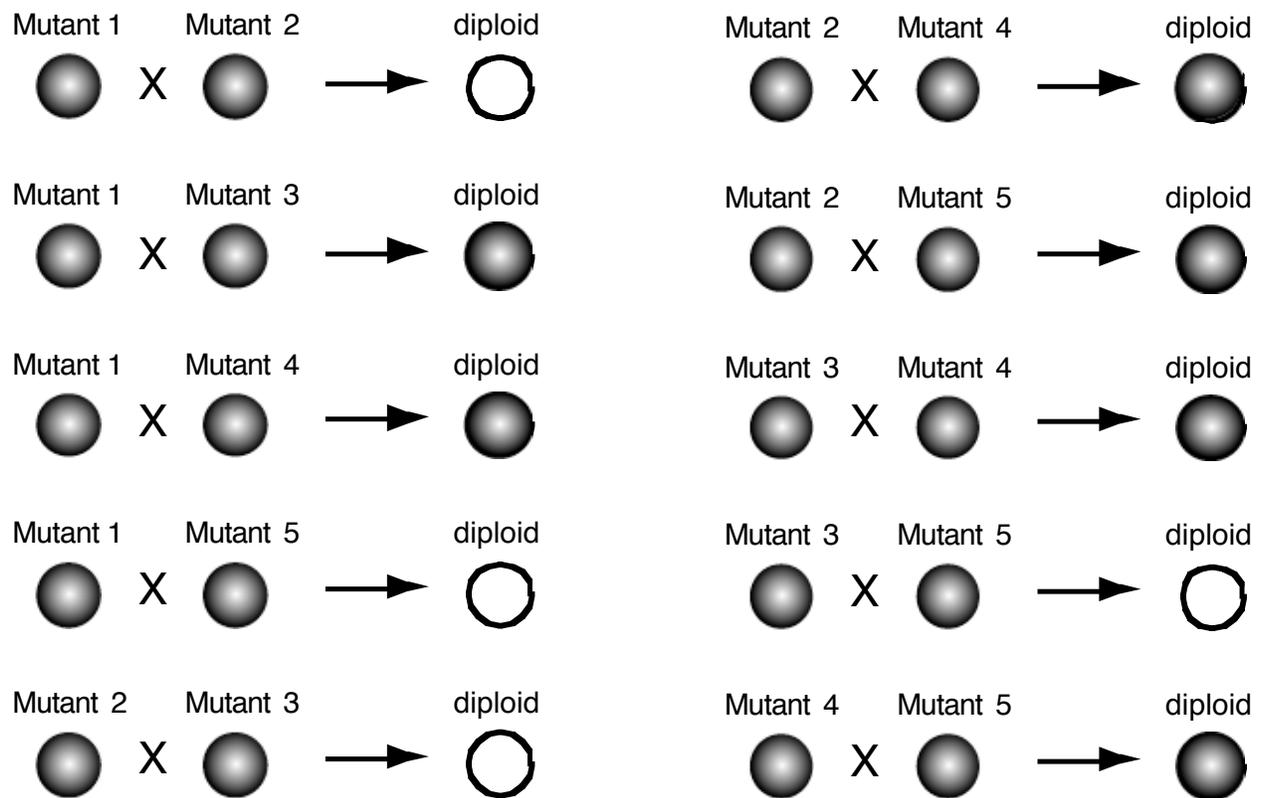Hand in answers in recitation section or in the box outside the class

1. You have isolated a set of five yeast mutants that form dark red colonies instead of the usual white colonies of wild-type yeast. You cross each of the mutants to a wild-type haploid strain and obtain the results shown below
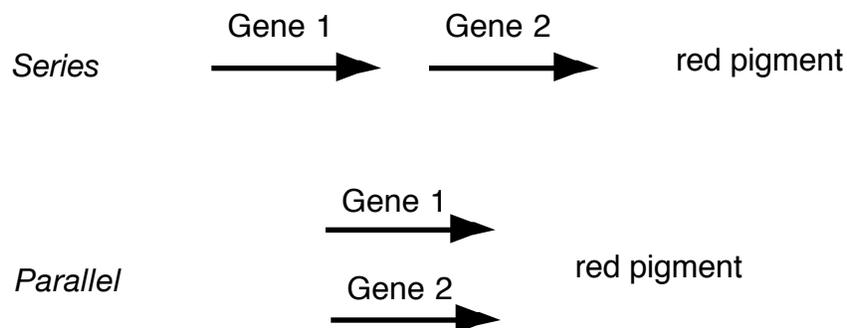

(a) What do these results tell you about each of the mutants?

(b) Next you cross each haploid mutant strain to a different haploid mutant of the opposite mating type. From the results shown below deduce as much as you can about which mutations lie in the same gene. Clearly state any remaining ambiguities and suggest some general ways that the ambiguities might be resolved.

Mutant 1   Mutant 2   diploid   Mutant 2   Mutant 4   diploid

X

Mutant 1   Mutant 3   diploid   Mutant 2   Mutant 5   diploid

X

Mutant 1   Mutant 4   diploid   Mutant 3   Mutant 4   diploid

X

Mutant 1   Mutant 5   diploid   Mutant 3   Mutant 5   diploid

X

Mutant 2   Mutant 3   diploid   Mutant 4   Mutant 5   diploid

X

2. In this problem we will explore some of the many ways that mutations in two different genes can interact to produce different Mendelian ratios. Consider a hypothetical insect species that has red eyes. Imagine mutations in two different unlinked genes that can, in certain combinations, block the formation of red eye pigment yielding mutants with white eyes. In principle, there are two different possible arrangements for two biochemical steps responsible for the formation of red eye pigment. The two genes might act in *series* such that a mutation in *either* gene would block the formation of red pigment. Alternatively, the two genes could act in *parallel* such that mutations in *both* genes would be required to block the formation of red pigment.

                Gene 1   Gene 2

Series   ⟶   ⟶   red pigment

                    Gene 1

Parallel   ⟶   red pigment

                    Gene 2   ⟶

Further complexity arises from the possibility that mutations in either gene that lead to a block in enzymatic activity could be either dominant or recessive.

a) Such considerations yield the following six possibilities:
1) Pathways in series with recessive mutations in both genes.
2) Pathways in series with a recessive mutation in one gene and a dominant mutation in the other.
3) Pathways in series with dominant mutations in both genes.
4) Pathways in parallel with recessive mutations in both genes.
5) Pathways in parallel with a recessive mutation in one gene and a dominant mutation in the other.
6) Pathways in parallel with dominant mutations in both genes.

First let's consider the possible outcomes from these possibilities in crosses between a wild type insect with red eyes and a true breeding white eyed strain with mutations in both genes. For each of the six possible cases outlined above, determine the phenotype of the F1 progeny (either red or white eyes) and the expected phenotypic ratio of red to white eyed insects in the F2.

b) You obtain a true-breeding white-eyed mutant, which you cross to wild type. All of the progeny have normal looking red eyes. Crosses among these F1 insects yield 24 progeny; 5 with white eyes and 19 with red eyes. Determine whether this data is consistent with each of the six possibilities outlined in part (a). For your answer also consider the additional possibilities that the true-breeding white eyed phenotype is due to: 7) a recessive mutation in a single gene, or 8) a dominant mutation in a single gene. Use the table below of chi-squared probabilities for any statistical tests.

p value:	.995	.975	0.9	0.5	0.1	0.05	0.025	0.01	0.005
df = 1	.000	.000	.016	.46	2.7	3.8	5.0	6.6	7.9
df = 2	.01	.05	.21	1.4	4.6	6.0	7.4	9.2	10.6
df = 3	.07	.22	.58	2.4	6.3	7.8	9.3	11.3	12.8

3. Genes that control coat color in mammals represent some of the best early examples of genes with multiple alleles exhibiting different phenotypes. A classic example is the C gene in hamsters. Three of the known alleles of this gene are C, c^k and c^a. Each supplies a different amount of black pigment to the coat hair. The phenotypes of three different homozygous strains are as follows.

Genotype	Phenotype
C C	Black fur
$c^k c^k$	Sepia colored fur
$c^a c^a$	Albino fur

(a) Based on the concepts of dominance, recessivity, and complementation, describe a set of crosses and the interpretation of their outcomes that would have allowed early mammalian geneticists to conclude that c^a and c^k are actually alleles of the same gene rather than recessive mutations in two different coat color genes. (To answer this question you will need to make some reasonable assumptions about the coat color of heterozygous strains)

(b) Now describe a different set of crosses and their interpretation that would have allowed geneticists to come to the conclusion that c^a and c^k were likely to be alleles of the same using the concept that alleles of the same gene will be tightly linked.

4. In the following pedigree shows the segregation of two different recessive traits.

= female showing trait 1 only

= male showing trait 2 only

= male showing both traits

?
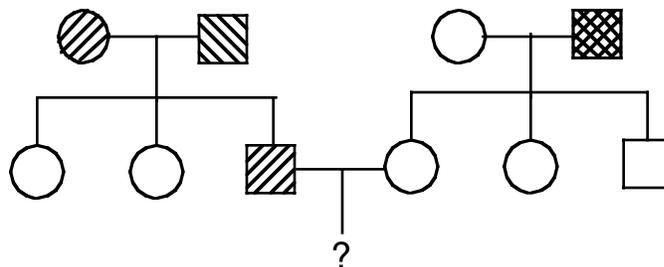
(a) Assuming that both traits are due to linked autosomal genes that are 10 cM apart, calculate the probability that the indicated child will have both recessive traits.

(b) Derive a general equation relating the probability that the child will have both traits expressed as a function of the distance between the markers in cM.

(c) Assuming that both traits are 10 cM apart on the X chromosome, what is the probability that a male child will have both recessive traits?

(d) Assuming that both traits are 10 cM apart on the X chromosome, what is the probability that a female child will have both recessive traits?