

Homework Questions due Sept. 23, 2008.

The exam will cover material from **lectures 1-6**.

Homework is 20 points altogether. Review questions begin after the homework (pg. 3).

Please put your answers on another piece of paper.

If you use more than one piece of paper **please** use a stapler.

1. (1 point) Here is the sequence of the template strand of a DNA fragment:

5' CAAGTTGTA ACTCTAGGTTAGTCGCTACCTGTAGTCATTTA 3'

Which of the following would be the complementary, nontemplate, strand?

- a) 5' TAAATGACTACAGGTAGCGACTAACCTAGAGTTACA ACTTG 3'
- b) 5' ATTTACTGATGTCCATCGCTGATTGGATCTCAATGTTGAAC 3'
- c) 5' CAAGTTGTA ACTCTAGGTTAGTCGCTACCTGTAGTCATTTA 3'
- d) 5' GTTCAACATTGAGATCCAATCAGCGATGGACATCAGTAAAT 3'

2. Consider two genes: *ABC1* and *DEF1*.

When a wild-type (*ABC1* and *DEF1*) strain is crossed to a doubly mutant strain (*abc1* and *def1*), the following tetrads are observed:

170 tetrads with two *ABC1 DEF1* spores and two *abc1 def1* spores.

2 tetrads with two *ABC1 def1* spores and two *abc1 DEF1* spores.

28 tetrads with:

one *ABC1 DEF1* spore, one *abc1 def1* spore, one *ABC1 def1* spore and one *abc1 DEF1* spores

- a) (1 point) What is the observed recombination fraction?
- b) (1 point) What is your best estimate of the distance between *ABC1* and *DEF1* in cM.? Explain

3. (2 points) Consider two genes: *GHI1* and *GHI2*. *GHI1* is almost precisely at the centromere of a chromosome while *GHI2* is 60 cM. away from the centromere on one arm of the same chromosome. When a wild-type (*GHI1* and *GHI2*) strain is crossed to a doubly mutant strain (*ghi1* and *ghi2*) and sporulated, what is the expected number of tetrads of each type if 1,000 tetrads are examined? Neglect interference. In other words, per 1,000 tetrads, how many of each of the following types do you expect?

tetrads with two *GHI1 GHI2* spores and two *ghi1 ghi2* spores;

tetrads with two *GHI1 ghi2* spores and two *ghi1 GHI2* spores; and

tetrads with one *GHI1 GHI2* spore, one *ghi1 ghi2* spore, one *GHI1 ghi2* spore and one *ghi1 GHI2* spore

4. Consider a family with three children in which both parents are carriers for cystic fibrosis.

- a) (1 pt.). What is the probability that they will have no affected children?
- b) (1 pt.). What is the probability that they will have exactly one affected child?
- c) (1 pt.). What is the probability that they will have exactly two affected children?
- d) (1 pt.). What is the probability that all three children will be affected?

5. You carry out a study of families with cystic fibrosis children. Your study group consists of families with exactly three children that are full siblings, at least one of which has cystic fibrosis. You even verify that each child in the study is actually the genetic descendent of the two parents. The fraction of children in the study that are affected is greater than 1/4. Why is that? (the answer is known as "ascertainment bias").

(2 pts.) What fraction of children in the study population do you expect to be affected?

6. You are new to a laboratory that studies yeast. Your lab mate initiated a project with two closely linked genes, *ABC1* and *ABC2*, that are involved in the same metabolic pathway. She previously measured the recombination rate between these two genes very precisely and deduced that when *abc1 ABC2 / ABC1 abc2* heterozygous diploids are sporulated, almost exactly 1/1,000 of the resulting haploid cells are wild type (*ABC1 ABC2*). You repeat her experiment, sporulating 500 cells to yield 2,000 haploid spores, and find four recombinant *ABC1 ABC2* spores. How likely is that (given the 1/1,000 expected rate)? In other words

a) (1 pt.). What is the probability that you would obtain exactly four wild-type (*ABC1 ABC2*) spores? Calculate this answer exactly using the binomial distribution.

b) (1 pt.). What is the probability that you would obtain four or more wild-type (*ABC1 ABC2*) spores? Calculate this answer exactly using the binomial distribution.

c) (1 pt.) Once again, use the Poisson approximation to calculate your answer to a. What answer would you get?

d) (1 pt.) Again assuming that the 1/1,000 number is precisely correct (for the expected number of recombinant *ABC1 ABC2* haploids), how far apart are *ABC1* and *ABC2* (in cM.)?

7. A white-eyed beetle was crossed to a beetle with wild-type (dark red) eyes. The F1 progeny all had wild-type (dark red) eye color. When F1 males and females were crossed to each other, 47 beetles with dark red eyes and 13 beetles with white eyes were observed.

a) (1 point) What pattern of dominance is likely based on this observation?

b) (1 points) If you mate a pair of dark red-eyed F2 beetles what is the probability that **some** white-eyed progeny will be observed among the several dozen progeny for that specific mating?

8. (1 point) Two wild-type alleles, 1 and 2, are present in a population in Hardy-Weinberg equilibrium and together make up 96% of the allele frequency at that locus.

Homozygotes for allele 1 represent 9% of the population.

What fraction of the population is homozygous for allele 2?

9. (1 point) A single X-linked gene in a male cell during the G1 phase is present as part of a single (double-stranded) molecule. You are studying a protein that binds to a single site on the X chromosome only in males. The *Drosophila* genome is approximately 150 Mb., which means that a single haploid genome (one allele of each gene) would be 150,000,000 base pairs. Recalling that Avogadro's number is 6×10^{23} (no units; this is a "pure" number), how many diploid G1 male *Drosophila* cells would be needed to have 1 picomole of protein-DNA complex?

Study material:

The first exam will be held on **Thursday, October 2, 2008**.

The exam will cover material from **lectures 1-6**.

The readings are specified on the web site (</syllabus.html>). We have not covered everything in all of the chapters, and you are not generally responsible for topics that were completely skipped in class.

This review is designed to help you focus on what's important.

You may also want to consult exams from earlier years, which are available online.

Terms and concepts. I may simply ask for a definition of a given term, or I may devise a question that tests whether you understand the meaning of the term or concept.

tRNA	diploid	parental ditype
mRNA	microfilaments	nonparental ditype
rRNA	microtubules	tetratype
primer	centriole	twin spot
template	centromere	informative meiosis
transcription	sister chromatid	BLAST
translation	kinetochore	BLOSUM62
exon	synapsis	E value
intron	homolog	BLink
mitosis	semidominant	RefSeq
meiosis	codominant	GenBank
prophase	mutually exclusive events	Entrez
metaphase	haplotype	sample space
anaphase	centiMorgan	
haploid	progeny test	

Review:

Be able to look at a human pedigree showing an inherited trait and indicate whether it shows autosomal dominant, autosomal recessive, X-linked recessive, X-linked dominant, maternal (mitochondrial), or Y-linked inheritance.

Be able to use the Hardy-Weinberg equation to 1) calculate the frequency of carriers from the frequency of affected individuals. 2) calculate the frequency of affected individuals from the frequency of carriers or from the allele frequency 3) determine from the frequency of various genotypes whether or not alleles at a locus are in Hardy-Weinberg equilibrium.

Be able to predict the outcome of a monohybrid cross and a dihybrid cross. Be able to calculate recombination frequency from the results of a two-factor or three-factor cross and obtain the gene order from a three-factor cross. Be able to predict the results of unordered tetrad analyses (see problems in Hartwell, especially 5-31 through 5-35, for practice).

Two yeast genes are unlinked and very far from the centromere: what do you expect the ratio of PD, NPD and T tetrads to be? What if they were both precisely at the centromere?

Be able to **recognize** the chemical structure for each of the four bases and each of the 20 amino acid side chains. Know which amino acids are basic, acidic, hydrophobic and hydrophilic. Be familiar with the single-letter amino acid code.
Be familiar with the prefixes atto- through penta-

You must be aware of basic concepts in probability, including intersection, union, and sample space. You should be able to know when to apply the binomial or Poisson distributions, the formula for the binomial and the formula for the zero term of the Poisson. You should know how to adjust the probability of an outcome to account for a change in the sample space.

Problems: Be able to answer questions like the following.

1. Label **each** of the following six statements as true or false.

- Sister chromatids (products of the replication of a single chromosome) separate at mitosis.
- Sister chromatids separate at the first meiotic division.
- Sister chromatids separate at the second meiotic division.
- Homologs separate at mitosis.
- Homologs separate at the first meiotic division.
- Homologs separate at the second meiotic division.

2. In shorthorn cattle, the genotype RR causes a red coat, the genotype rr causes a white coat, and the genotype Rr causes a roan coat. A breeder has red, white and roan cows and bulls. What phenotypes might be expected from the following matings, and in what proportions.

- red X red
- red X roan
- red X white
- roan X roan

3. Chickens that carry both the alleles for rose comb (R) and pea comb (P) have walnut combs, while chickens that lack both of those alleles (that is, they are genotypically *rr pp*) have single combs. Rose-combed chickens mated with pea-comb chickens produced 21 walnut chicks and 23 rose chicks. What is the genotype of the parents?

4. DNA polymerase can be used to label which **end** of a DNA strand with ^{32}P ?

5. In the following molecule, which end (left or right) has a 5' overhang?

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5'      AAGGGTGGCAATGCATGGCGGTTAGTGCCTCTAGCACTAATGG      3'
3'      CCCACCGTTACGTACCGCCAATCACGGAGATCGTGATTA      5'
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6. If you were to use DNA polymerase to label the DNA shown in question 5 with ^{32}P , which nucleotide (A, C, G or T) would you want to use?

7. Did you use the size of the *Drosophila* genome in your answer to homework problem 9?
If so, how would your answer be different if the genome size were 300 Mb. rather than 150 Mb.?

8. A woman finds a particular trait of her father's to be extremely annoying. She (of course) marries a man who does not have this trait. She learns by reading an article in the newspaper

about genetic research that this common trait is monogenic and is controlled by autosomal recessive alleles at a single locus. The overall allele frequency of the causative alleles in the population is 1 in 3, so about 1 person in 9 shows the trait. What is probability that her child will have this trait?