

Math 186, Winter 2009, Prof. Tesler
Homework #2, Due Tuesday January 20, 2009 (since Monday's a school holiday)

Larsen & Marx **Fourth Edition:**

2.5# 1, 2, 4, 6, 7, 9, 14, 15, 19, 20, 22, 23, 29

2.6# 4, 19, 29

and the problems below: H-3, H-4

Problem H-3.

In *diploid* organisms, each cell has two copies of each chromosome, one copy inherited from each parent.

Each gene may come in two or more versions, called *alleles*. A diploid organism will have an allele inherited from one parent on one chromosome, and an allele inherited from the other parent on the other copy of that chromosome.

In pea plants, the gene for height comes in two alleles, T=tall, t=short, and the gene for seed shape comes in two alleles, R=round, r=wrinkled.

The possibilities (*genotypes*) of the two copies of the height gene that a particular pea plant has are TT, Tt, tt, and the possibilities for shape are RR, Rr, rr.

If the genotype for height is TT or Tt, the plant will be tall, while if it's tt, the plant will be short. This is called the *phenotype*. The interesting case is Tt — both alleles are present, and the plant turns out to be tall. We say that “T” is the *dominant* trait and “t” is the *recessive* trait. When both are present in the genotype, the dominant one prevails. When there are just two alleles for a trait, it is common to use a capital letter to denote the dominant allele and a lowercase letter to denote the recessive allele.

For shape, “R” is dominant and “r” is recessive, so if the genotype is RR or Rr, the phenotype is round, and if the genotype is rr, the phenotype is wrinkled.

If a plant is *homozygous* for a trait, meaning that the alleles on both chromosomes are the same (TT or tt), then it will donate one copy of that allele to each of its offspring. If it is *heterozygous* (Tt), then each allele has a 50% chance of being the one that is donated. The two parents donate their alleles independently.

- (a) The height gene and the shape gene are on different chromosomes, so the genes for these traits are inherited independently. If a pea plant with genotype Ttrr is crossed with a pea plant with genotype TtRr, compute the proportion of offspring that would be expected to have each genotype, and the proportion expected to have each phenotype. (Hint: there will be 6 different genotypes whose proportions are not 0.)
- (b) Flower color in pea plants can be purple (dominant) or white (recessive). Two plants with purple flowers are crossed. These original plants form the *P generation* (parental). Their offspring form the *F1 generation* (first filial generation). Some of the plants in the F1 generation have purple flowers and others have white flowers.
 - (i) What are the genotypes of the plants in the P generation?
 - (ii) If a plant in the F1 generation has purple flowers, what is the probability that it is heterozygous for the flower color trait?

Problem H-4. One of the coordinate systems for chromosomes is *centimorgans* (cM). A portion of mouse chromosome 1 is shown on the last page of this assignment, using coordinates in cM.

To compute the positions of genes (and other features) along a chromosome, biologists did breeding experiments and monitored many genes to determine the recombination rates between each pair of genes. Then they converted these recombination rates into distances in cM by the following method.

If gene *B* is in-between genes *A* and *C*, and r_{AB} is the recombination rate between *A* and *B*, and if crossovers between *A* and *B* are independent of those between *B* and *C*, we have Haldane's mapping function $r_{AC} = r_{AB} + r_{BC} - 2r_{AB}r_{BC}$ (see class notes for derivation). (There are also other formulas that allow for interference between crossovers, but we're not using them now.)

To convert this into a linear map of genes, we define the distance between two genes, in *Morgans* (M), to be $d = -\frac{1}{2} \ln(1 - 2r)$ (where r is expressed as a number between 0 and 1, not as a percentage between 0% and 100%). Multiply Morgans by 100 to convert to centimorgans (cM).

To convert a distance back to a recombination rate, change the distance from centimorgans back to Morgans by dividing by 100, and then plug into the formula $r = \frac{1}{2}(1 - \exp(-2d))$. Note that this is just the inverse function of the one above.

Distance is easier to work with than recombination rate since distance is additive; if gene B is in-between genes A and C , and d_{AB} is the distance between A and B , then $d_{AC} = d_{AB} + d_{BC}$.

On the map on the next page, the distance between *Cops5* and *Mybl1* is $|3.6 - 3.0| = 0.6$ cM. This is 0.006 M, so the recombination rate is $r = \frac{1}{2}(1 - \exp(-2(0.006))) = 0.0059641436 \approx 0.596\%$. Numerically, this percentage (0.596) is close to the distance (0.6) expressed in cM; this is true in general when both are small numbers.

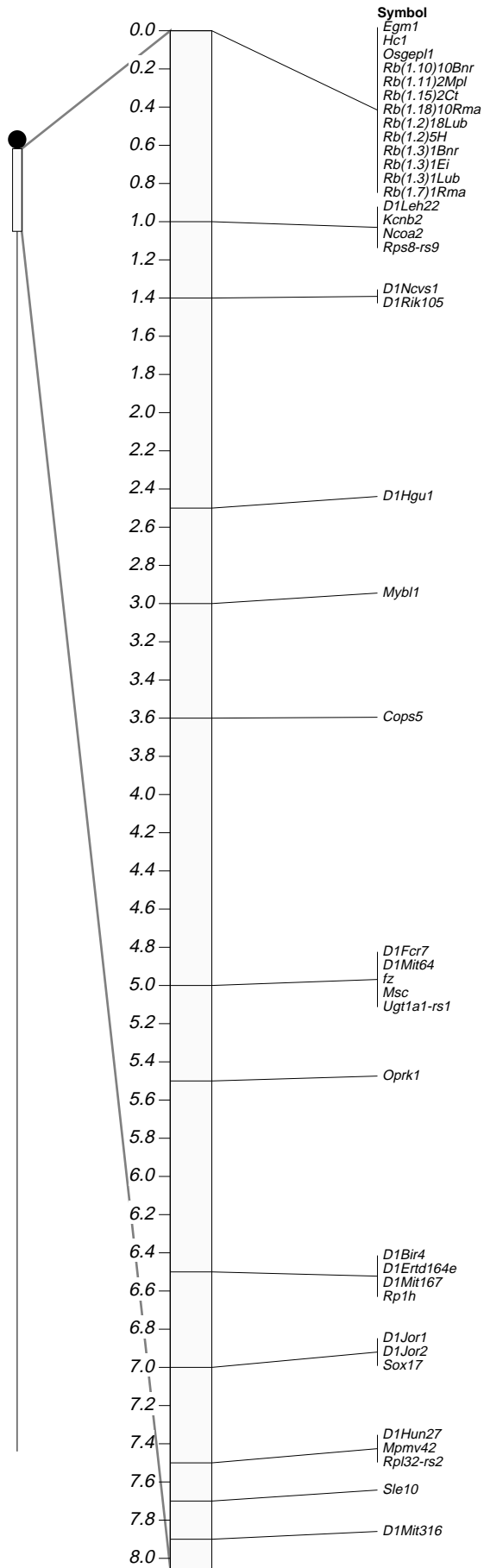
- (a) What is the maximum possible recombination rate for genes on the same chromosome? How does this compare to the constant recombination rate of $1/2$ for genes on separate chromosomes?
- (b) What is the distance and the recombination rate (to at least 3 significant figures) between *Msc* and *Sle10* on the map shown on the next page?
- (c) Now we will show where the formulas $r(d) = \frac{1}{2}(1 - \exp(-2d))$ and $d(r) = -\frac{1}{2} \ln(1 - 2r)$ for converting between distance and recombination rates arise.
 - (i) Show that these are inverse functions.
 - (ii) We derived Haldane's formula for recombination in class based on certain independence assumptions. Unfortunately, recombination rates are not additive. The formula for $d(r)$ was developed to make distances be additive in a way consistent with Haldane's formula.

Assume genes A , B , and C are in that order. Let $a = d_{AB}$, $b = d_{BC}$, $a + b = d_{AC}$.

Prove that $r(a + b) = r(a) + r(b) - 2r(a)r(b)$, where $r(d)$ is the function given above.

Hint: start by expanding the right side of the equation, and simplify until you get the left side.

MGD: Chromosome 1: 0.0 - 7.9 cM



This map was obtained from the Mouse Genome Database (MGD), Mouse Genome Informatics, The Jackson Laboratory, Bar Harbor, Maine. Jan. 19, 2004.

<http://www.informatics.jax.org/searches/linkmap.cgi>