- 1. Figure 1 is a pedigree of miniature schnauzers (a dog breed). Female #2 has already had one litter, and male #3 has already sired two offspring with female #4. A breeder is interested in mating female #2 and male #3, but is worried about a recessive X-linked disorder called Von-Willibrands disease in their offspring. Answer the following:
 - (a) What are the genotypes of dogs #1, #3, and #4? (4pts)
 - (b) The breeder had female #2 tested for the disease, and the test result suggested she was a carrier. The test is imperfect, however, and 20% of the time returns an incorrect positive result. You are a geneticist brought in to advise the breeder. What is the most likely genotype of dog #2? Explain how you reach this conclusion. (4pts)
 - (c) Given the genotypes above, what is the probability that dogs #2 and #3 will have: (2 pts)
 - i. A male puppy with Von-Willibrands disease?
 - ii. A female puppy with Von-Willibrands disease?
 - iii. A normal female puppy?
 - iv. A normal male puppy?

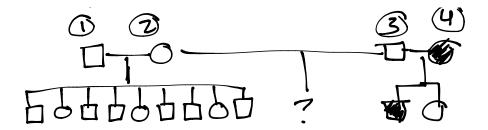


Figure 1: A pedigree of miniature schnauzers. Filled symbols (square=male, circle=female) represent dogs with Von-Willibrands disease. Empty symbols are dogs with wild-type phenotypes.

- 2. You are interested in understanding the genetics of furriness in rabbits. You recruit 18 rabbit owners to bring in their bunnies for measurement. Each bunny's fluffiness is measured on a scale of 1 (no hair) to 10 (maximum fluffy). Phenotypes for all 18 bunnies are shown in Table 1.
 - (a) Calculate the phenotypic variance for fluffiness (5 pts).
 - (b) In a separate study, you measure the fluffiness of a set of rabbit quadruplets that were sold by a breeder to 4 different families. The phenotypic variance among these four genetically identical rabbits is 3.2. If we can assume that these families are representative of the environments of the rabbits in Table 1, what is the broad sense heritability of fluffiness (5 pts).

Table 1: Rabbit phenotypes.

Rabbit Name	Fluffiness
Baby	2
Baggins	8
Bambi	9
Barbie	10
Basil	7
Bella	2
Benny	7
Big Boy	5
Big-Ears	2
Binky	10
Bluebell	8
Boo Boo	8
Buddy	4
Bugs	4
Bun Bun	4
Bunnicula	3
Bunzilla	6
Buttercup	4

3. Abscisic acid is an important regulator of seed maturation and germination in plants. You have two mutant maize plants that make insufficient levels of abscisic acid and thus their kernels germinate prematurely on the cob. When you self the first mutant it produces 345 mutant offspring. When you cross the second mutant to a wild-type plant all of the F1 are wild-type, and selfing the F1 results in 265 wild-type and 89 mutant offspring. When you cross both original mutants together they produce 563 wild-type offspring. Draw the genotypes of both mutant lines and the dominance of the alleles involved (10 pts).

- 4. The following two questions refer to the paper by Schempske and Bradshaw (1999).
 - (a) Briefly describe Schempske and Bradshaw's conclusions regarding the effect size of alleles important for speciation in *Mimulus* (5pts).
 - (b) Carotenoid content in *Mimulus* flowers is controlled by a single Mendelian locus called *yup*. At this locus the *M. cardinalis* allele is recessive to the *M. lewissii* allele. In a population of F2 plants generated from a cross between *M. lewissii* and *M. cardinalis*, provide an estimate and an explanation as to what you think the broad sense heritability for the orange/red color would be (*hint: no calculations are needed to answer this question*)(5 pts).

- 5. Figure 2 shows the karyotype of two individual plants of the genus Silene. The duplicated gene shown codes for an inorganic compound which causes plant tissue to appear significantly darker. The copy on chromosome 1 is expressed only in leaves, and the copy on chromosome 2 is expressed only in flower petals. Both loci are haplosufficient. (hint: reading Liu et al. 2012 may be helpful for figuring out this problem).
 - (a) Draw the karyotype and phenotype of the F1 and all possible F2 (6 pts).
 - (b) I make a mutant version of I207 in the lab which has pale flowers and breeds true. Sequencing shows this mutant is homozygous for a mutation in the gene on chromosome 2 shown in figure 2. If I cross this mutant line with the F1 between wild-type I207 and B97, what proportion of the offspring will have pale flowers (4 pts)?

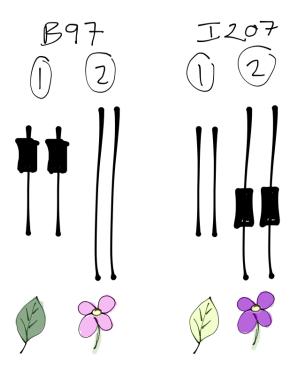


Figure 2: Karyotype for chromosomes 1 and 2 of *Silene* lines B97 and I207. Boxes on each chromosome represent the presence of a gene of interest (the absence of a box signifies that the gene is not present on that chromosome). The flower and leaf phenotype of each line is shown below the karyotype: B97 has dark leaves and pale flowers and I207 has pale leaves and dark flowers.

- 6. Use the phylogeny of the gene ahbp3 shown in figure 3 to answer the following questions.
 - (a) What term would you use to describe the relationship between the copies of *ahbp3* in rice and *Sorghum* marked in red in figure 3 (2 pts)?
 - (b) What evolutionary process would you ascribe to the gene copies in Zea marked in pink in figure 3 (2 pts)?
 - (c) Which of the gene copies in Zea marked in blue in figure 3 is more likely to be in a syntenic position relative to Sorghum (2 pts)?
 - (d) In what tissues do you think the gene copy ancestral to all the plants shown was expressed (2 pts)?
 - (e) If you compare the sequence of the Zea copy of ahbp3 expressed only in flowers to the ahbp3 locus in Agave, what do you predict would be the relationship between nonsynonymous substitutions and synonymous substitutions, and why (2pts)?

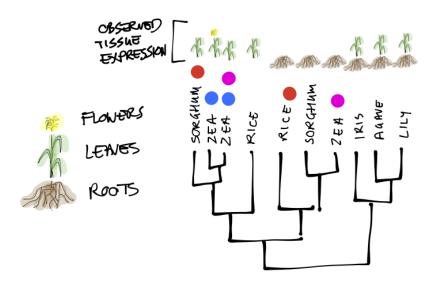


Figure 3: Shown is a phylogenetic tree of the sequences of the *ahbp3* locus in a groups of plants. The genus *Zea* has 3 copies of this gene, while *Sorghum* and rice each have two. Above the phylogeny is shown the tissues in which each copy is expressed.

7. Johnston

8. Genetic mapping

9. Ibarra-Laclette studied the genome of a carnivorous plant, *Utricularia gibba*. They found a small genome, with an average total number of genes. They use comparative genomics to answer questions about the genomic history of *U. gibba*. Using the following ancestral block of genes in Figure 4, answer these questions.

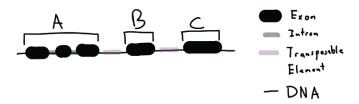


Figure 4: Small block of DNA from the ancestral chromosome of *U. gibba*, showing features according to the legend. Segment contains 3 genes, named A, B, and C.

(a) Ancestral gene block undergoes 2 whole genome duplications.

Total copy number of gene A:

Total copy number of gene B:

Is synteny retained?

Total amount of DNA goes (Circle one) up / down / stays the same

(b) Ancestral gene block experiences transposable element mediated movement of gene B to a new chromosome.

Total copy number of gene A:

Total copy number of gene B:

Is synteny retained?

Total amount of DNA goes (Circle one) up / down / stays the same

(c) DRAW the resulting gene block after the ancestral gene block experiences fractionation without impacting genes

10. Chromosomal evolution