1. Suppose that humans develop the technology to clone themselves, making offspring who are genetic duplicates of their parent. Planet Normal is settled using a starting population of 10,000 people and conventional sexual reproduction. Planet Clone is settled using a starting population of 10,000 people and cloning only. In both populations, reproduction is at random. That is, every individual has a chance to reproduce, but some have no children or clones, some have one, some have several–all **at random**. The two populations grow at the same rate. Also, cloning is of adults in the population: there is no gene bank to allow cloning of individuals from previous generations. Note that every time a cell divides, there is some chance of mutation.

   In general, you should be aware of the difference between cloning (offspring is a duplicate of its parent) and self-fertilization (offspring results from union of parent's egg and sperm and is NOT a duplicate of its parent.

   (a) (1 pt) After a few generations, do you expect Normal to have more, less, or the same amount of genetic variation **at a randomly chosen gene** as Clone? (Note that this asks about a single gene, not about combinations of alleles along a chromosome.) *Approximately the same. In general cloning does not change diversity AT A SINGLE LOCUS, even though it hugely reduces the number of combinations of alleles at DIFFERENT loci.*

   (b) (2 pts) What are two advantages of Planet Normal? Be sure to specify if these are short-term or long-term advantages. *It produces more different allele combinations, which may help people adapt to the new environment in the short term. It has less linkage disequilibrium in the long term, which may make it more nimble evolutionarily (good alleles won't be shackled to bad ones). In the very long term it will remain diploid and Planet Clone will probably not, which gives better prospects for repairing genome damage. In the long run it avoids Muller's Ratchet (really this is a restatement of "less linkage disequilibrium"). In the long run it maintains both sexes, which leads to a more diverse society. In the long run it retains evolutionary pressure for two-parent care, which may improve offspring survival.*

   (c) (2 pts) What are two advantages of Planet Clone? Be sure to specify if these are short-term or long-term advantages. *In the short term, it will not break up good allele combinations via recombination, so a good overall genome will be reproduced instead of reshuffled. In the longer term, it can fix heterozygote genotypes, which will help with overdominant loci. (If Planet Clone has malaria, the population could fix genotype AS.) If males are better than females on the new planet, or vice versa, Clone can improve fitness by varying the sex ratio, whereas Normal can't easily do so. Finally, less energy may be put into finding a mate, sexually transmitted diseases will not be a problem, and sexual selection will not have the chance to select for bad survival traits (like peacock tails).*

   (d) (1 pt) Based on what you know about humans, do you expect a 50/50 sex ratio on Planet Clone after a very long time? Explain briefly. *No. There's no force keeping it there, and males have a higher mortality rate. I'd expect more females eventually. Even if mortality was the same, eventually one sex will be lost due to drift.*

   (e) (1 pt) A technological breakthrough enables human females to self-fertilize, and Planet Amazon is colonized by 10,000 self-fertilizing females. How will Planet Amazon differ genetically from the other two after a few generations? (Hint: what happens to blood group AB?) *Everyone would end up homozygous for almost every locus. Blood group AB would vanish. Overdominant alleles would be lost. This population would be very different from the other two. Note that diploidy is NOT lost in self-fertilizers as if one copy deteriorates, self-fertilization can produce a lethal homozygote.*

   (f) (1 pt) Some writers suppose that cloning would "stop human evolution." Assuming that we clone current adult individuals (as opposed to making a gene bank and cloning our first colonists over and over), do you think this is true? Why or why not? *No. The major forces still function: mutation introduces new alleles, selection kills off unfit alleles, genetic drift makes random changes in the gene pool. If a new disease appears on Clone and 10% of the population is genetically resistant, the resistant alleles will spread. In order to stop evolution you would need to remove all fitness differences between individuals.*

   One student answered this succinctly with "Bacteria clone themselves, and they manage to evolve."

2. The ABO blood group system consists of one gene with three alleles: I^A and I^B alleles produce different cell-surface antigens (and are codominant to each other) and I^O allele produces nothing (and is recessive). Thus, a person with genotype I^AI^A or I^AI^O has blood group A, one with genotype I^BI^B or I^BI^O has blood group B, one with genotype I^AI^B has blood group AB, and one with genotype I^OI^O has blood group O.

   (a) (1 pt) For allele frequencies of $p(I^A) = 0.3$, $p(I^B) = 0.4$, $p(I^O) = 0.3$, calculate expected Hardy-Weinberg frequencies of blood groups A, B, AB, and O.

Type A: $p(AA) + p(AO) = 0.3^2 + 2 * 0.3 * 0.3 = 0.27$
Type B: $p(BB) + p(BO) = 0.4^2 + 2 * 0.4 * 0.3 = 0.40$
Type AB: $p(AB) = 2 * 0.3 * 0.4 = 0.24$
Type O: $p(OO) = 0.3^2 = 0.09$

Check to make sure they add to 1.0!

(b) (1 pt) Suppose that a new plague developed which affected all blood types except for AB, so that AB blood group individuals had fitness 1.0 and all other types had fitness 0.9. After a very long time, what frequencies of the three alleles would you expect? You can ignore mutation and drift. *This is symmetrical overdominance (with no role for the O allele). I would expect O to be lost and p(A)=p(B)=0.5. Be careful to answer the given question: many students calculated the one-generation answer instead. Unfortunately the one-generation answer can't be extrapolated out to the long-term answer very easily.*

(c) (2 pts) Consider a population with the fitnesses from (b). Suddenly a new chromosome appears which has a gene duplication, so that both A and B are on the same chromosome (in other words, it creates a new "allele" which has both A and B; call it I^{AB}). If the starting frequencies are $p(I^A) = 0.3$, $p(I^B) = 0.4$, $p(I^O) = 0.2$, and $p(I^{AB}) = 0.1$, what will the new frequencies be after ONE GENERATION? (Assume that genotypes such as $I^A I^{AB}$ are blood type AB.)

genotype	*AA*	*AO*	*BB*	*BO*	*AB*	*OO*	*AB/A*	*AB/B*	*AB/O*	*AB/AB*	*Total*
frequency	*0.09*	*0.12*	*0.16*	*0.16*	*0.24*	*0.04*	*0.06*	*0.08*	*0.04*	*0.01*	*1.0*
fitness	*0.9*	*0.9*	*0.9*	*0.9*	*1.0*	*0.9*	*1.0*	*1.0*	*1.0*	*1.0*	*1.0*
after select	*0.081*	*0.108*	*0.144*	*0.144*	*0.240*	*0.036*	*0.060*	*0.080*	*0.040*	*0.010*	*0.943*
normalized	*0.086*	*0.115*	*0.153*	*0.153*	*0.255*	*0.038*	*0.064*	*0.085*	*0.042*	*0.011*	*1.002*

New allele frequencies:

$p(A) = p(AA) + 0.5p(AO) + 0.5p(AB) + 0.5p(AB/A) = 0.086 + 0.5 * 0.115 + 0.5 * 0.255 + 0.5 * 0.064 = 0.303$
$p(B) = p(BB) + 0.5p(BO) + 0.5p(AB) + 0.5p(AB/B) = 0.153 + 0.5 * 0.153 + 0.5 * 0.255 + 0.5 * 0.085 = 0.399$
$P(O) = p(OO) + 0.5p(AO) + 0.5p(BO) + 0.5p(AB/O) = 0.038 + 0.5 * 0.115 + 0.5 * 0.153 + 0.5 * 0.042 = 0.193$
$P(AB) = p(AB/AB) + 0.5p(AB/A) + 0.5p(AB/B) + 0.5p(AB/O) = 0.011 + 0.5 * 0.064 + 0.5 * 0.085 + 0.5 * 0.042 = 0.107$

Some students went wrong here because of confusing blood group frequencies (i.e. frequency of type A blood) and allele frequencies (i.e. frequency of I^A). It is best to do all the math with allele frequencies.

(d) (2 pts) What long-term fate do you predict for this new chromosome (fixed, lost, polymorphic)? *Fixed or nearly fixed (other alleles may hide in the heterozygote at very low frequency). It is as good or better than any other allele in any combination. I did not accept "polymorphic" as that term implies a reasonable frequency of more than one allele–most papers use 5%–and that's not likely here since I^{AB} has a clear fitness advantage.*

3. In corn, each female meiosis produces 1 egg and several "polar bodies" which cannot be fertilized. A chromosomal variant called "knob" can guide the chromosome copy containing it into the egg rather than the polar body. This results in a knob+/knob- female producing 70% knob+ eggs.

(a) (2 pts) Assuming that knob+ and knob- are otherwise equally fit, male meiosis ignores knob, and the starting frequency is 10% knob+ in both sexes, what will be the allele frequencies in ONE GENERATION? (Hint: figure out the gene pool contributed by males and the gene pool contributed by females. The new allele frequencies will be the average of these.) *Male gametes will be 0.1 knob+ and 0.9 knob-.*

Female gametes will be as follows:

female type	*gametes*
-/- 0.81	*1.00 -*
+/- 0.18	*0.7 + 0.3 -*
+/+ 0.01	*1.00 +*

So the total female egg pool will be 0.136 knob+ and 0.864 knob-. Mating the males and females will average their allele frequencies, for 0.118 knob+ and 0.882 knob-. knob+ is increasing due to its meoitic drive.

Several students went wrong here by assuming that knob+ has an advantage all the time; but it has none in knob+/+ homozygotes.

(b) (1 pt) What would you expect to happen after a long time?

knob+ will fix. It has an advantage (meiotic drive) and no disadvantage. knob- will not be able to hide in the heterozygote as it has a disadvantage there!

(c) (1 pt) Suppose that when knob+ arises by mutation, it happens to be linked to a recessive lethal allele at a different gene. Suppose further that they are extremely close together so that they are not separated by recombination. In general terms, how would you expect this chromosome to behave? Would it be lost, fixed, or maintained as a polymorphism? (Assume it starts out common enough that drift is not important.) *I would expect it to be maintained as a polymorphism. When knob+ is very rare, the recessive lethal doesn't matter much, and the meiotic drive will make knob+ increase. If knob+ got very common, the recessive allele would also get very common, and many knob+ alleles would be lost due to selection on the linked recessive. So it will stabilize somewhere in the middle. (I would use computer simulation to find out exactly where; I don't know a formula.)*

(d) (2 pts) Based on your answers so far, do you think that knob-like genes are likely to be beneficial or harmful to species that have them? Explain briefly. *Harmful. They spread not because they are good for the organism, but because they are good for themselves. If they happen to link up with something bad, they will drag it to high frequency. (If they linked up with something good they would promote its spread, but bad mutations are more frequent than good ones, so the overall effect is bad.) Some students speculated that they will help a population cast out bad alleles by pairing them up and exposing them to selection, but this is outweighed by the fact that they are making linked bad alleles increase in frequency (due to hitchhiking). Another problem is that knob+ without an associated lethal will fix very fast, and this will remove genetic variation from nearby parts of the chromosome (like DuffyO in Africans). Reducing genetic variation is generally bad.*