1. (1 point) Sunflowers are fascinating plants. They can orient themselves to the sun over the course of the day, live in a wide-variety of habitats, and are incapable of self-fertilization. There are many species of sunflowers in North America, with the two most widespread being Helianthus annus and Helianthus petiolaris. If taken into a lab, less than 1% of crosses between these two sunflowers produce viable seeds, and the hybrids that result tend to have very low viability (around 5%). That is, 1% of the time you cross them you get viable seeds, then only 5% of those viable seeds are capable of growing into a plant that can also produce offspring. In the deserts of the southwest, among the dunes and in the salt flats, you may also find a few other strange sunflowers like Helianthus anomalus. The DNA of these desert sunflowers is about 50% identical to H. annuus and the other 50% of their DNA is identical to H. petiolaris. The genes in the desert sunflowers are found in long blocks (haplotypes) identical to similar chunks from the two widespread species, with many loci identical to one sunflower followed by a long stretch of loci identical to those from the other (think of long alternating bands). However, these desert sunflowers also often have large inversions and translocated genes. Cross-breeding the desert sunflowers to either of the two widespread species typically doesn’t work well, with fewer than 10% of the offspring being viable, although the desert sunflowers breed just fine (≥ 90% seed success, similar to the other species). (a) What is the probable origin of the desert sunflowers? (b) What is the likely explanation for the “large blocks” of widespread sunflower DNA in the desert sunflowers? (c & d) Please briefly (≤ 100 words) explain the importance of the inversions, translocations, and large blocks to understanding the origin of the desert sunflowers.

1. Helianthus anomalus is a hybridizied species resulting from cross pollination between Helianthus annus and Helianthus petiolaris which would explain the DNA of Helianthus anomalus. The speciation rate for these species is very fast because of the harsh environment that they are having to adapt to, and the large amount of offspring they can have. Since the speciation rate is high, it did not take long for a successful hybridization to be produced that is able to survive in desert like environments.
2. The large blocks are a result from rearrangements of chromosomes in the species that was then passed down to Helianthus anomalus. In class, we talked about that in order for the haploid to move between populations it has to go through each population. To do this, it would have to be a small DNA block rather than a large one. This would prove that Helianthus anomalus is a hybrid between the two species because the large blocks of DNA that is found in Helianthus anomalus would only have to travel through one population to another. These large blocks are responsible for the amazing adaption that the sunflower is capable of. They contain the perfect code for different adaptations that will help the desert sunflower survive, and they were passed throughout offspring. For instance, how the sunflower can move towards the light and/or the timing of flowering. Adaptations like these are very important for the Helianthis anomalus species because of the intense dryness that they are exposed to in the desert environment. If the flower flowers too soon in the peak of the hot summer, it could kill the plant.
3. The large blocks, translocation, and inversion of the sunflower is very important because you can track what parent DNA was passed down, where the change in DNA took place, and what adaptations did the species gain or lose due to the changes. These are also used to protect the parent DNA that are passed down together from recombination which would break apart the parental DNA segments. This can really help when trying to determine the origin of the flower because there will be a large amount of parental DNA left in the offspring.

2. (1 point) Above are data for 244 species of bird color-coded by clade from a 2013 paper by the Daniels Matute & Rabosky. The x-axis shows the estimated speed at which postzygotic barriers form in a specific species (based on rates of geneitc differences between populations, basically think Fst; lower numbers = more genetic differences). The y-axis shows the estimated speciation rates (based on the length of the branches that lead to each species; lower numbers = longer branches; n.b. speciation rate is defined the same way anywhere else you see it in this exam). In the same paper, they found essentially identical results across the many species of Drosophila fruit flies. Further, another study by Dr. Sonal Singhal and colleagues in 2018 found similar results when they compared Fst in Australian lizard populations to speciation rates. Please clearly explain to me how you interpret the meaning of these results in 500 words or fewer.

Based on lecture, we would expect to see a negative correlation because lower number the more genetic diff for longer time since divergence, but there is not in this graph.

Orange values should have higher speciation rate because of the low Fst values.

Lower postzygotic velocity higher speciation would be would you would expect.

Once the clades reach 0 it is more of what we would expect to see because speciation rate starts to decrease.

There are a few ways to interpret this graph I think, but all of them draw a conclusion that there is no relationship between the postzygotic RI velocity and speciation rate. First, I looked at the x-axis. I noticed that some clades have a wide range of genetic diversity (wide range on the x-axis), but the speciation rate is constant. For these species, the Fst value ranges from low to high, in other words, there are some species in the clade that are highly genetically different and some that are not. This proves that there is no relationship between postzygotic RI velocity and speciation because looking at these clades that have a very prominent genetic variation, but they have a constant speciation rate.

Secondly, I looked at the y-axis. The lowest species on the y-axis is the burnt yellow/orange color which is at around 0.06. This clade is shown to have longer branches which represents less speciation, and it is right under 0 on the x-axis. The highest on the y-axis is the dark purple which is around 1.18 and is still around 0 on the x-axis. This clade is shown to have short branches which represents high speciation rate. Looking at these two species, it also proves that there is no relationship between the speciation rate and postzygotic RI. These two species have the same amount of genetic diversity, but they have a drastically different speciation rate. The different speciation rate could be explained by environmental factors like geological isolations or reproductive isolation.

It is interesting to note that near 0 on the x-axis was where most of the clades saw the highest speciation rate. This could be linked to mutations like insertions and translocations preserving the DNA. The postzygotic barriers may influence some clades more than others when it comes to speciation rate, but for this graph overall, I think that is does not affect the speciation rate as a whole.

3. (2 points) Wolbachia is a profoundly strange bacterium. It infects insects, but it does so by actively invading their cells and living in their cytoplasm. When Wolbachia invades the germline cells, it can be passed on by the female to her eggs. That is, baby insects inherit this bacterium from their mother. Further, it has evolved the ability to manipulate gene expression in the insects it infects, which can make the cytoplasm of the sperm from male insects incompatible with the cytoplasm of female eggs if one or the other is uninfected or infected with a different strain. A study published early this year by Sicard et al. examined how different strains of Wolbachia present in mosquitoes of the species Culex pipiens impact the hatching rates of their eggs. They brought males with one of four different Wolbachia strains, and females with one of those same four strains into a lab, cross-bred them, and analyzed the hatching rate of their eggs. The data shown above reveal the success rate by cross. The x-axis shows the strain infecting the female mosquito, the y-axis shows the strain infecting the male, and the size and darkness of the points plotted are proportional to the hatching success (defined as the proportion of crosses with ≥ 78% hatching success). Wolbachia strains vary in frequency by region. How do you expect Wolbachia strain to impact (a) the linkage disequilibrium in Culex mosquitoes? (b) mutation rate in Culex ? (c) gene flow in Culex ? (d) local adaptation in Culex mosquito genes?

The bacteria acts as a genetic inheritable trait. Incompatibility which speeds up the speciation.

4. (2 points) Sticklebacks are fascinating little fish. They’re small and they live mostly in the oceans of the northern hemisphere. However, they breed in streams, and since the last Ice Age ended about 10,000 years ago, several populations invaded the large lakes that formed from the melting of the glaciers. Some also have taken up permanent residence in streams, giving up the return to the ocean. Once adapted to a freshwater setting, the fish rarely (if ever) return to the Ocean, and so cannot directly immigrate to other freshwater basins. Stickleback ecotypes refer to whether they live in marine or freshwater settings. In these freshwater systems, their primary predators are insect larvae such as dragonfly nymphs, which means that the spikes and bony armor that serve them well in the ocean (where fish eat them) do not work as well in freshwater. So freshwater sticklebacks tend to be smaller, with fewer bony plates and fewer spines than their oceanic relatives. The Ectodysplasin (Eda) gene has a major influence on the degree of armor. Above are data from one of many, many studies on sticklebacks showing their mating preferences in lab studies (left), a pattern of coalescent times for the Eda locus in different populations (multiple samples from some populations), and the pattern of population-level divergence times. (a - c) Provide three distinct but possible explanations for the discord between the population divergence and coalescent times brief (≤ 50 words for each explanation, so ≤ 150 total words). (d) Which of your answers from a-c is most likely? (e) Please describe a clear and specific dataset that could test your answer for part d.

4 information:

“Stickleback fishes, for example, can evolve reproductive isolation very quickly in postglacial lakes, but nascent species pairs typically fail to persist over geological timescales (46).”

1. Coalescent varies per loci and individual. So, the conflict could be due to the actual data set used since it varies depending on the individual.
2. Reproductive isolation.
3. Geography isolation
4. I think that reproduction isolation is the most relevant when it comes to the conflict between population level divergence and coalescent. These species in freshwater are more likely to reach reproduction isolation which would influence the divergence and coalescent of the populations.

5. (2 points) The rate at which reproductive incompatibilities accumulate between populations without gene flow has been a contentious topic for decades. As mutations accumulate within a lineage, some of them will be incompatible with alleles at other loci, resulting in epistatic incompatibilities. Yet the way this must work is that different alleles at different loci that interact epistatically have to go to fixation in the two populations. A recent study modeled this in a demographic framework, and the data shown above compare geographic range size to speciation rate for birds (left) and mammals (right). (a) What fitness effects do most mutations have? (b) Why might you expect the likelihood of a fitness effects for potentially-incompatible mutations to be different from the average mutation? (c) What force(s) have the strongest impact on the probability these incompatibilities go to fixation? (d) Please explain how the graphs reflects the relative importance of the force(s) described in part (c).

a) Mutations can increase the fitness if it adds or enhances the more fit alleles, but it can also decrease fitness if an allele is defective due to the mutations. It strongly depends on the type and placement of mutation. In general, sequences that are deleted through deletion or shifted through frame shift mutations are more detrimental to the fitness where insertions are not as detrimental.

b) The potentially-incompatible mutations will affect the fitness differently because you have to take into consideration the environment, the other loci’s in the organism, and phenotype of the organism. Fitness is based on multiple locus.

c) First, the adaptations that the species gains to survive in the environment will contribute to the reproduction of the species. The better the species is at surviving in their environment that more offspring they are going to be able to produce. The more offspring the more they pass down these genes which makes the genes reach fixation. Genetic drift may also lead to fixation. This can affect the population size.

d) There is a negative slope in both graphs. This shows that as range size decreases, speciation increases. As fixation occurs, speciation will decrease.

DONE:

6. (2 points) Shultz and Burns (2017) used spectrophotometry to measure the precise wavelengths of color coming from major feather patches from a 355 species of tanagers (Thraupidae). They used principal components analysis to reorient their data so they could analyze the axis of maximal color variation. More recently, Dr. Rosalyn Price-Waldman collaborated with them and used phylogenetic methods similar to what you did in your R assigment to calculate the speciation rates for the tanagers, and compared those rates to the plumage coloration (top row) and to the rate of change in plumage coloration (bottom row). Basically, for each species, they (1) measured the actual color of the bird, then used an evolutionary tree to estimate (2) the probability it would speciate soon, and (3) the probability it’s colors would change soon. The top set of figures shows speciation rate against color, while the bottom plot shows speciation rate against the rate of color evolution. Based on these data, please give a concise (≤ 100 words) explanation of how color effects speciation rate in tanagers.

The speciation rate increases as the evolution rate of plumage color increases and becomes more complex; and this is seen in both male and female according to the graphs. This could be due to the new colorations changing the mating signals which influences the groups of birds that reproduce with one another. For instance, a choosy female may not choose to mate with a male with a certain plumage color. This would cause reproduction isolation which increases the speciation rate. Also, the prezygotic barrier is going to decrease gene flow which in turn increases speciation rate.