

EART101: EVOLUTION – PATTERN AND PROCESS

Name: _____

This assignment involves two simple “toy” models to illustrate evolutionary pattern and processes. Although the models are simple, they provide a reasonable simulation of factors affecting speciation and morphological evolution, so will help you understand the principles of allopatric speciation, evolutionary modes (phyletic gradualism vs. punctuated equilibrium), and potential causes for stasis and rapid evolution in punctuated equilibrium.

Open the file `speciation.R` in RStudio. This model runs a very simplistic simulation of genetic evolution in two populations.

The model creates two populations, each with 100 individual organisms. Each organism has ten “genes” that can either be in state 0 or state 1. During each generation, the organisms are randomly paired to “mate” and the genetic composition of the offspring is randomly chosen from the two parent states (it’s a simple model so ignores dominant or recessive traits). You can set the “gene flow,” which in this model is the probability that individuals from population 1 will be paired with individuals from population 2 during the mating step. A gene flow value of 1 means that an individual from population 1 is just as likely to be paired with an individual of population 2 as it is with another individual from population 1. A gene flow of 0 means that individuals from a population can only mate with other individuals from that population. At each step, the average values for the 10 genes in each population are calculated and the “genetic distance” between the two populations (calculated as Euclidean distance, like calculating the distance between points on a graph) is output.

Run step 1. This won’t produce any output, but will store the simulation to be used later.

Run step 2. This sets the gene flow value and population size. Keep them at 1 and 100 for now, but you will change them later.

Run step 3. This will run the simulation for 20 generations with full gene flow between the two populations, and then for an additional 50 generations with the specified gene flow from step 2.

Run step 4A to plot the results. The vertical red line marks the shift from complete gene flow to the value you specified in step 2.

Question 1. Run step 3 and then 4B for the gene flow of 1, and then steps 3/4B one more time. Make sure to run step 4B and not 4A when you want to add data to an existing plot! Set gene flow in step 2 to 0.1 and re-run step 2. Run the step 3/4B sequence three times to add points to the graph, noting how genetic distance changes from the gene flow=1 example. Set gene flow in step 2 to 0.01 and re-run step 2. Run the step 3/4B sequence three more times to add points to the graph, noting how genetic distance changes from previous examples. **Why does the observed relationship between gene flow and genetic distance occur? If speciation is more likely to occur when genetic differences are larger, summarize how and why the amount of gene flow influences speciation.**

Question 2. Given your findings in question 1, how should speciation rates differ on average between species with planktotrophic larvae and those with lecithotrophic larvae? Why? (Remember that many marine invertebrate adults are completely or effectively sessile, so all redistribution occurs during the drifting larval phase).

Question 3. In step 2, set gene flow to 0 (complete isolation) but leave the population size at 100. Run steps 3 and 4A, and then run steps 3 and 4B three more times. Next, set population size in step 2 to 10, run step 2 again, and then run the step 3-4B sequence four times to add more points to the graph. A

population size of 10 means that all individuals in population 2 descended from just 10 of those present in generation 20 (when the “barrier” to gene flow formed), rather than from the complete population of 100. **Based on these results, how and why do changes in population size influence the likelihood of speciation?**

The preceding model assumed that all individuals were equally likely to produce successful offspring (i.e., that they all had equal evolutionary “fitness”), an assumption that is clearly not true. To address that issue, load `morphEv.R` in RStudio.

This simulation uses a simple, one-dimensional “morphology” variable but allows different morphological states to have different evolutionary fitness. Fitness is the probability of passing genetic information to the next generation by successfully producing offspring. The fitness landscape can be modified so that the range between “high” and “low” fitness is larger or smaller. The model starts with three individuals, randomly placed in the “fitness landscape” (the space described by morphology and fitness). During each step, each individual produces five offspring with morphologies randomly distributed near the parent morphology. The amount of morphological change from parent to child can also be modified. Only one offspring survives, chosen semi-randomly with probability of survival proportional to fitness.

Run steps 1 and 2 to plot the fitness landscape. There are three peaks corresponding to morphologies that have high fitness, separated by troughs of low fitness. The colored circles show the morphology and corresponding fitness of the initial three individuals. **Run step 3** a few times and watch how the morphology changes over time. Note that points typically move a small distances; larger jumps are rare.

Run step 4 to simulate 10,000 generations of morphological change. The final positions of the three specimens are plotted as squares on the fitness landscape and the lower panel shows how morphology (using the same x-axis as the fitness landscape) changed through time, from older at the bottom to younger at the top. You may need to run steps 2 and 4 a few times to see the behavior.

Question 4. Is the pattern of morphological change more consistent with phyletic gradualism or punctuated equilibrium? Explain why you made that decision, with reference to the pattern of morphological change. You can treat the three fitness peaks as three different “species.”

Question 5. What kind of selective pressure (stabilizing, directional, or disruptive) is represented by the fitness landscape? Given that selective pressure, what is required for a lineage to shift from one fitness peak to another? Hint: think about the size and direction of morphological changes from parent to offspring.

Question 6. In step 1, set the selection strength to 2 and re-run step 1. Run steps 2 and 4 a few times, noting the within-lineage morphological variability and how frequently lineages shift from one fitness peak to another. Go back to step 1 and set the morph variability to 5. Re-run step 1 and then run steps 2 and 4 a few more times. **What relationship do you observe between morphological variability within a lineage and the frequency of lineages shifting between fitness peaks? Why does this relationship occur? Given that, what prediction would you make for the relationship between within-population shape variation and evolutionary rate in the fossil record?**

If you finish early, here’s something else to consider. The first model (simulating genetic evolution) actually has a lot of similarities to the model of diversity inflation during time-averaging. Think about how barriers to gene flow are like immigration probability in a metacommunity and how duration affects both diversity inflation and genetic divergence.