Name \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

Molecular Ecology 13 September 2019

Due: 16 September 2019

**Genetic drift.** Run the simulations for scenarios 1-3 in the table. These only differ by population size.

1. What is the general trend from these three simulations?
2. Are the changes in allele frequencies similar to what you would have expected?

**Natural selection with drift.** Run the simulations for scenarios 4-6 in the table. These have a negative additive effect for individuals having the allele A, where homozygotes have a worse negative effect.

1. Does the allele frequency of A (as plotted with p) always get lost in these populations?
2. Why might a deleterious allele (i.e., under natural selection) become fixed in a population?
3. Run simulation 7, adding low migration. What is the effect of adding migration between small subpopulations relative to the results of simulation 6?
4. Run simulations 8 and 9, which reduces the strength of selection by making fitness differences between genotypes smaller. How do these results differ from simulations 5 and 6 and what is the lesson in these different results?

**Genetic drift with migration.** Rerun simulations 2 and 3 to refresh your memory of what the pure genetic drift simulation results look like. Then run simulations 10 and 11. Each have a low level of migration added to the models for simulations 2 and 3.

1. How does adding a little gene flow impact the allele frequencies in the populations relative to the simulations with drift alone?
2. Run simulation 12, with stronger gene flow. What is the overall effect of the stronger gene flow on allele frequencies within populations and overall across all populations?

**Heterozygote disadvantage.** Occasionally, two alleles will not go well with each other, creating a phenomenon known as heterozygote disadvantage. Here, both homozygous genotypes will have a higher fitness than the heterozygous genotype.

1. What happens in most or all populations? What if you changed the starting allele frequency to 0.4? Would you expect a similar result?
2. Across all populations in total (as if all populations were summed), what general trend did we observe for allele frequencies and genotype frequencies?
3. If you add low migration (simulation 14), what changes relative to a no gene flow situation? What implications does this have for the populations in the future?
4. Now add higher migration (simulation 15). How does this change the patterns in simulations 13 and 14?
5. What is one major takeaway from these simulations that you hadn’t considered or fully appreciated before today?

Run all simulations with 200 generations, no mutation rate (= 0), and 50 populations.

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| Sim. | Starting AF (A) | Fitness AA | Fitness  AB | Fitness BB | Migration Rate | Pop. Size | Fixed | Lost | General Trend(s)? |
| 1 | 0.5 | 1 | 1 | 1 | 0 | 1000 |  |  |  |
| 2 | 0.5 | 1 | 1 | 1 | 0 | 100 |  |  |  |
| 3 | 0.5 | 1 | 1 | 1 | 0 | 10 |  |  |  |
| 4 | 0.5 | 0.82 | 0.91 | 1 | 0 | 1000 |  |  |  |
| 5 | 0.5 | 0.82 | 0.91 | 1 | 0 | 100 |  |  |  |
| 6 | 0.5 | 0.82 | 0.91 | 1 | 0 | 10 |  |  |  |
| 7 | 0.5 | 0.82 | 0.91 | 1 | 0.02 | 10 |  |  |  |
| 8 | 0.5 | 0.9 | 0.95 | 1 | 0 | 100 |  |  |  |
| 9 | 0.5 | 0.9 | 0.95 | 1 | 0 | 10 |  |  |  |
| 10 | 0.5 | 1 | 1 | 1 | 0.02 | 100 |  |  |  |
| 11 | 0.5 | 1 | 1 | 1 | 0.02 | 10 |  |  |  |
| 12 | 0.5 | 1 | 1 | 1 | 0.2 | 100 |  |  |  |
| 13 | 0.5 | 1 | 0.8 | 1 | 0 | 1000 |  |  |  |
| 14 | 0.5 | 1 | 0.8 | 1 | 0.02 | 1000 |  |  |  |
| 15 | 0.5 | 1 | 0.8 | 1 | 0.1 | 1000 |  |  |  |