

**Part 2: Mutation without selection**

- Use a starting allele A frequency of 0.5. Set genotype fitnesses to 1: AA = 1.0; Aa = 1.0; aa = 1.0. = no selection!!
- 250 generations
- Genetic drift turned OFF

A → a mutation rate	a → A mutation rate	Fate of population: • "A" Fixation • "A" Loss • Equilibrium • No equilibrium	If fixation/loss, which generation?	"Before" fitness	"After" fitness	"Before" het.	"After" het.	Affect on fitness? • Increase? • Decrease? • Stay same?	Affect on het? • Increase? • Decrease? • Stay same?
0.05	0								
0.1	0								
0	0.05								
0	0.1								
0.05	0.05								
0.1	0.1								

How does mutation affect variation and fitness in general?

Are the general effects of mutation influenced by its direction? (A → a, a → A, or both?) How?

Are the general effects of mutation influenced by its strength (0.05 vs 0.1)?

**Part 3: Mutation under directional selection** (*THINK: Compare to the very first directional selection simulation we did last week!!!*)

- Use a starting allele A frequency of 0.5. Set genotype fitnesses to *directional selection*: AA = 1.0; Aa = 0.9; aa = 0.8
- 250 generations
- Genetic drift turned OFF

A → a mutation rate	a → A mutation rate	Fate of population: • "A" Fixation • "A" Loss • Equilibrium • No equilibrium	If fixation/loss, which generation?	"Before" fitness	"After" fitness	"Before" het.	"After" het.	Affect on fitness? • Increase? • Decrease? • Stay same?	Affect on het? • Increase? • Decrease? • Stay same?
0.05	0								
0.1	0								
0	0.05								
0	0.1								
0.05	0.05								
0.1	0.1								

1. How does mutation *only towards* the most fit allele ( $a \rightarrow A$ ) influence:
  - a. Variation (heterozygosity)?
  - b. Fitness?
  - c. Time to fixation?
  - d. How does the mutation rate affect these answers?
  
2. How does mutation *only towards* the least fit allele ( $A \rightarrow a$ ) influence:
  - a. Variation (heterozygosity)?
  - b. Fitness?
  - c. Time to fixation?
  - d. How does the mutation rate affect these answers?
  
3. How does mutation *towards both alleles* influence:
  - a. Variation (heterozygosity)?
  - b. Fitness?
  - c. Time to fixation?
  - d. How does the mutation rate affect these answers?

**Part 4: Migration and selection (Use "MIGRATION" tab for this part only!)**

- **Continent** fixed allele A frequency = 1.0
  - This means 100% of alleles arriving to the island via migration (aka gene flow) will be "A".
  - *This further implies "A" is fixed on the continent!!!!*
- Starting **island** allele A frequency = 0.5. This means the starting heterozygosity on the island is always 50%.
- 250 generations

W(AA) on island	W(Aa) on island	W(aa) on island	Migration rate (% islanders who are migrants)	Fate of population: • "A" Fixation • "A" Loss • Equilibrium • No equilibrium	If fixation/loss, which generation?	"Before" ISLAND fitness	"After" ISLAND fitness	"Before" ISLAND heterozygosity	"After" ISLAND heterozygosity
1	1	1	0.05 (low)						
1	1	1	0.1 (medium)						
1	1	1	0.3 (high)						
1	0.9	0.8	0.1						
0.8	0.9	1	0.1						

- Considering migration alone (no selection), how is the island variation influenced by the migration rate?
- How does migration that mostly imports the FITTEST allele influence island fitness? variation? chance of fixation?
- How does migration that mostly imports the LEAST FIT allele influence fitness? variation? chance of fittest allele fixation?

**Part 5: Genetic drift (i.e., the effect of population size)**

- Use a starting allele A frequency of 0.5. This means starting heterozygosity is always 50%.
- Turn OFF natural selection by setting fitness: AA = 1.0; Aa = 1.0; aa = 1.0
- 250 generations
- Genetic drift turned ON! Specify 20 replicate populations.

N (population size). NO COMMAS!	# replicates where allele A fixed	RANGE of generations for replicates where "A" fixed (ie low - high, like 5-25)	# replicates where allele a fixed	RANGE of generations for replicates where "A" fixed	# replicates where <u>no</u> <u>fixation</u> occurred	Range of allele A FREQUENCIES for replicates where no fixation occurred	Range of "after" HETEROZYGOSITY for replicates where no fixation occurred
10							
25							
50							
100							
500							
1000							
10000							
100000							

**What is the effect of drift on POPULATION VARIATION? Is the answer what you thought it would be?**

*REMEMBER: Strong drift = SMALL populations. Weak drift = LARGE populations (opposite!):*

**Part 6: The combined effects of natural selection and genetic drift**

- Use a starting allele A frequency of 0.5. ***This means starting heterozygosity is always 50%.***
- 250 generations
- Genetic drift turned ON! Specify 20 replicate populations.
- Note: each simulation considers directional selection, at different strengths, similar to Part 1 of this activity. **Without drift, allele A fixes in:**
  - Moderate selection: 154 generations ; Strong selection: 32 generations ; Weak selection: >1000 generations

N	W(AA)	W(Aa)	W(aa)	Strength of selection	# reps where allele A fixed	Range of generations for "A" fixation	# reps where allele a fixed	Range of generations for "a" fixation	# reps where <i>no fixation</i> occurred	Final fitness range for ALL	Final het. range for ALL
10	1	0.9	0.8	Moderate							
25	1	0.9	0.8	Moderate							
100	1	0.9	0.8	Moderate							
1000	1	0.9	0.8	Moderate							
10	1	0.6	0.2	Strong							
25	1	0.6	0.2	Strong							
100	1	0.6	0.2	Strong							
1000	1	0.6	0.2	Strong							
10	1	0.99	0.98	Weak							
25	1	0.99	0.98	Weak							
100	1	0.99	0.98	Weak							
1000	1	0.99	0.98	Weak							

1. Under what **conditions** (selection and drift strength) did selection FAIL to fix "A", specifically when the outcome was:
  - a. No fixation?
  - b. Allele "a" fixation?
2. When is natural selection the MOST effective? I.e., when are results most similar to the corresponding simulation with drift turned OFF?
3. When is natural selection the LEAST effective? I.e., when are results most similar to the corresponding simulation with drift turned OFF?
4. Did genetic drift ever "aid" selection, i.e. by helping "A" fix faster than if there were no drift?
5. Is natural selection GUARANTEED to cause the most fit alleles to fix?