

BIO 345 Evolution: Genetic drift

Dylan Padilla
Fall, 2022

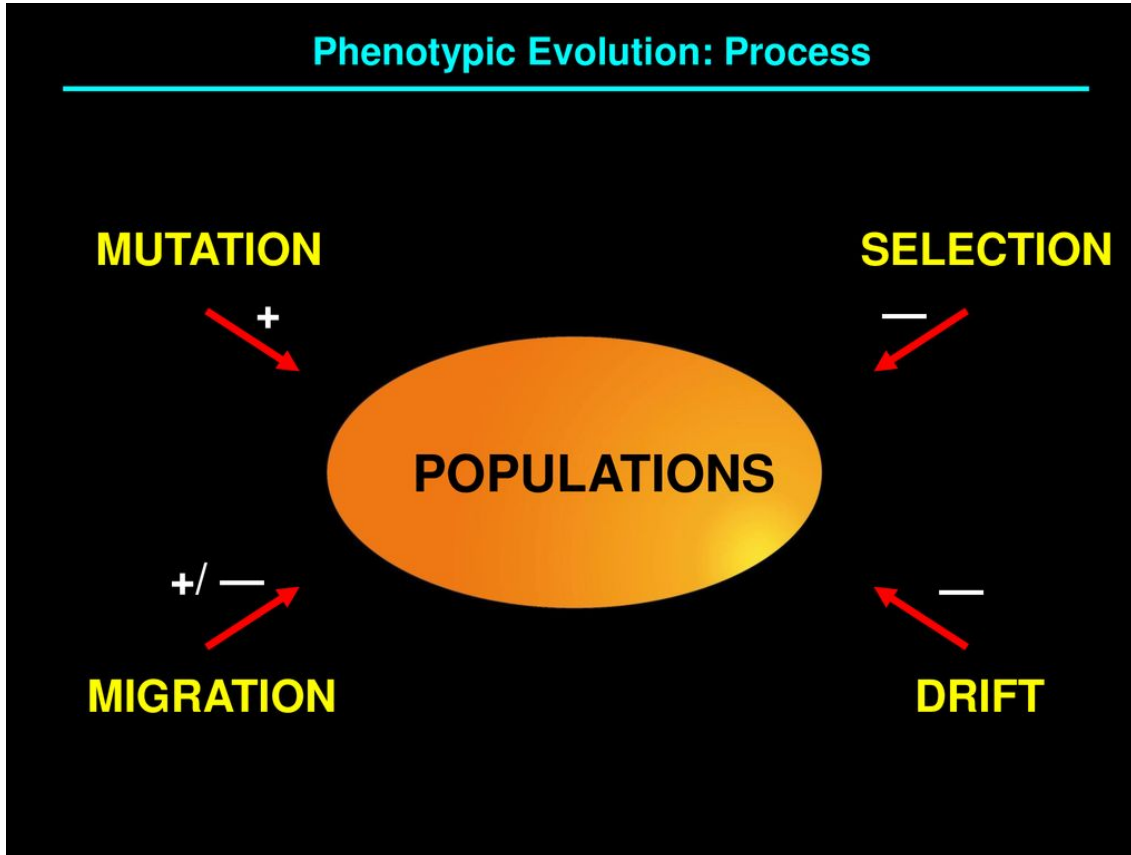
✉ dpadil10@asu.edu | 🔗 <https://dylanpadilla.netlify.app/>

Outline

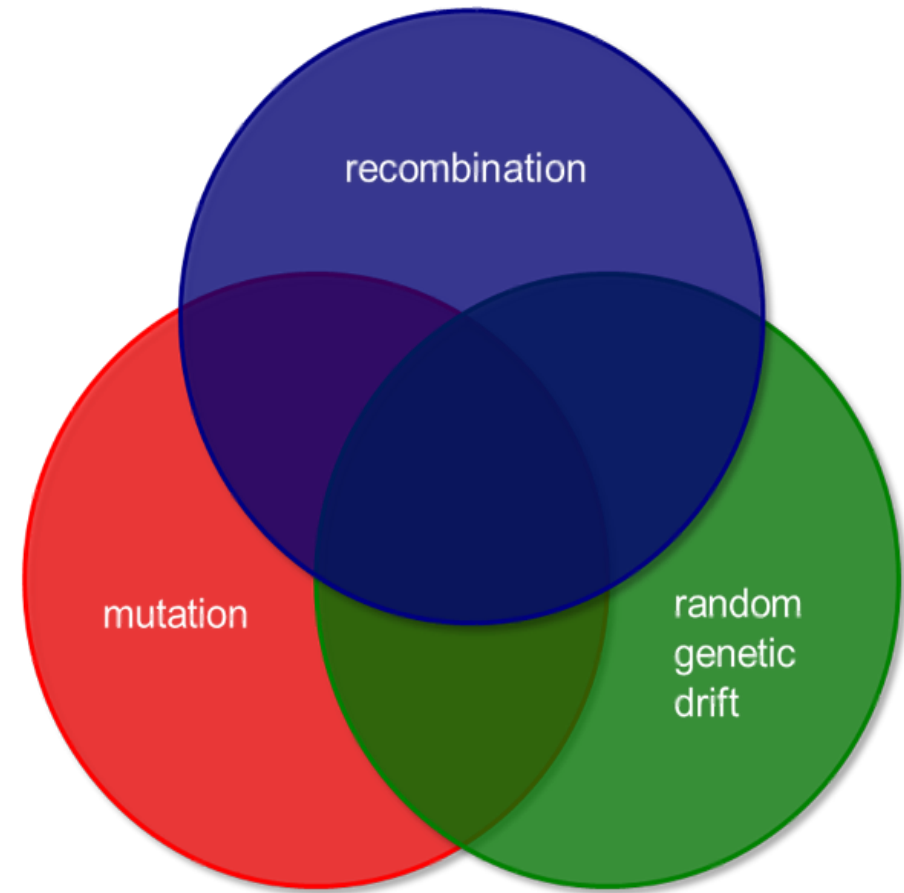
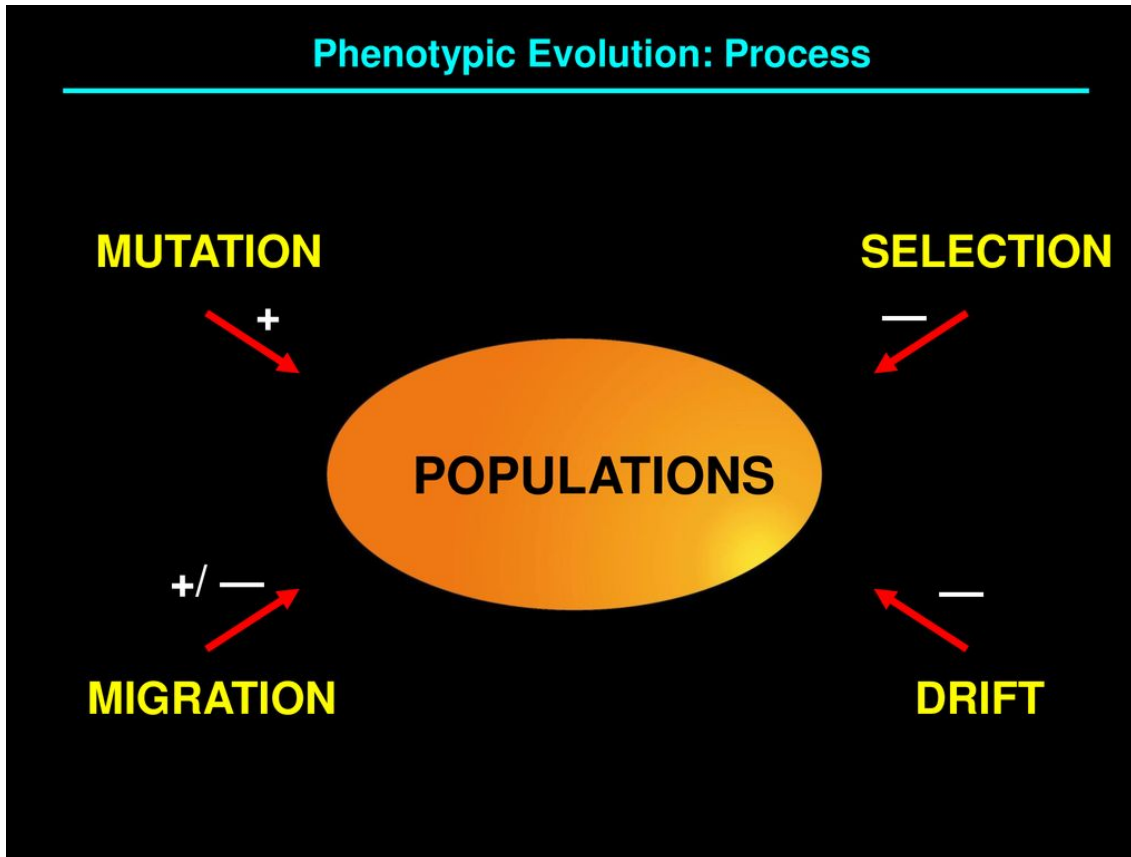
- Mechanisms of evolution
- Hardy-Weinberg equilibrium
- Discuss genetic drift
- Genetic drift examples

What is Evolution?

What is Evolution?

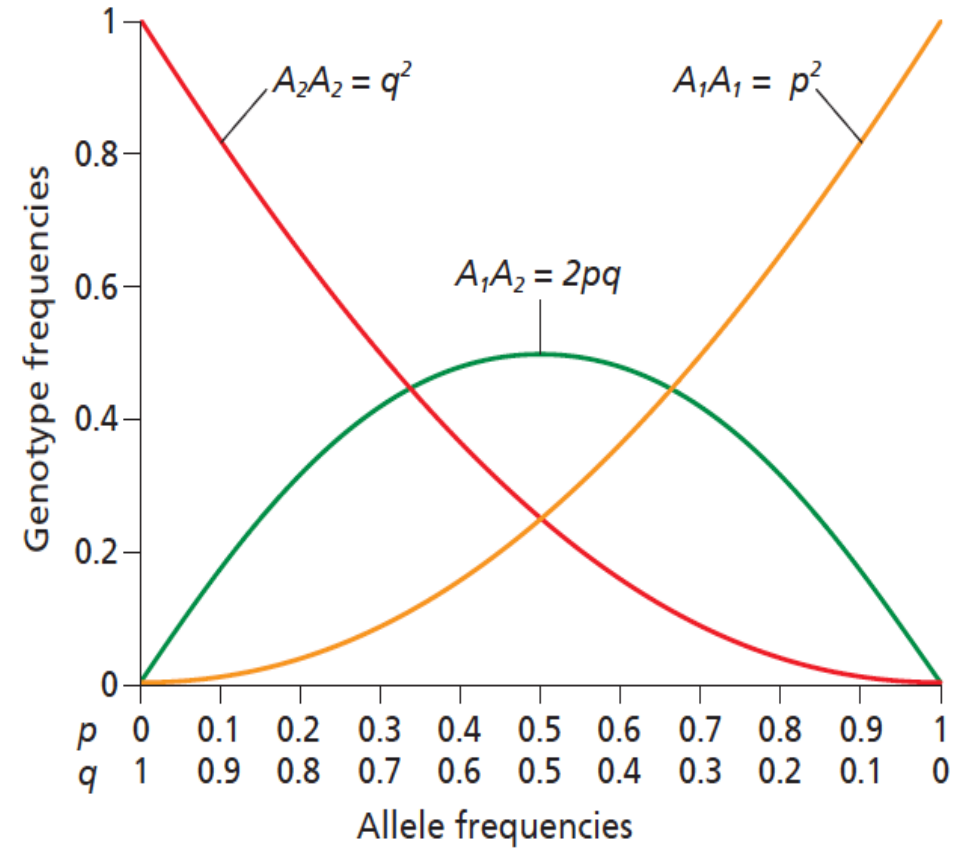


What is Evolution?



Hardy-Weinberg Equilibrium

What happens when nothing is happening?



Hardy-Weinberg Equilibrium

Table 20.1

The Hardy-Weinberg Equilibrium

Assumptions

1. Population size is infinite.
2. Random mating occurs in the population, allowing genotype frequencies to be predicted by allele frequencies.
3. Natural selection does not operate.
4. Migration (gene flow) does not introduce new alleles.
5. Mutation does not introduce new alleles.
6. Genetic drift does not occur.

Predictions

1. Allele frequencies remain stable over time.
2. Allele distribution into genotypes is predictable.
3. Stable equilibrium frequencies of alleles and genotypes are maintained.
4. Evolutionary and nonrandom mating effects are predictable.

Hardy-Weinberg Equilibrium

Table 20.1

The Hardy-Weinberg Equilibrium

Assumptions

1. Population size is infinite.
2. Random mating occurs in the population, allowing genotype frequencies to be predicted by allele frequencies.
3. Natural selection does not operate.
4. Migration (gene flow) does not introduce new alleles.
5. Mutation does not introduce new alleles.
6. Genetic drift does not occur.

Predictions

1. Allele frequencies remain stable over time.
2. Allele distribution into genotypes is predictable.
3. Stable equilibrium frequencies of alleles and genotypes are maintained.
4. Evolutionary and nonrandom mating effects are predictable.

These assumptions are not met by real populations, but reality is often close enough to the theory to allow accurate predictions to be made based on the H-W equilibrium

Hardy-Weinberg Equilibrium

With random mating and no evolution, allele frequencies do not change from one generation to the next

		Male gametes	
		A_1 0.60	A_2 0.40
Female gametes	A_1 0.60	A_1A_1 0.36	A_1A_2 0.24
	A_2 0.40	A_1A_2 0.24	A_2A_2 0.16

Binomial expansion:

$$(0.60 + 0.40)(0.60 + 0.40) = 0.36 + 0.24 + 0.24 + 0.16 = 1.00$$

Genotype frequencies:

$$A_1A_1 = 0.36$$

$$A_1A_2 = 0.48$$

$$A_2A_2 = 0.16$$

$$\text{Total} = 1.00$$

$$f(A_1) = 36\% + 24\% = 60\%$$

$$f(A_2) = 16\% + 24\% = 40\%$$

Expressed as ' p and q ':

$$f(A_1) = p^2 + pq$$

$$f(A_2) = q^2 + pq$$

Genetic drift

- Changes in allele frequency that results from the random sampling of individuals from generation to generation in a finite population
- Increases the homozygosity of a population (i.e., increases AA or aa , decreases Aa)
- Reduction of genetic variation within a given population can increase the differences between populations of the same species

Why is drift very important?

The neutral theory of evolution



Motoo Kimura

1. "claims that most of DNA sequence difference between alleles within a population or between species are due to neutral mutations"
2. Under this model, genetic mutations insert genetic variation into populations and are countered by the process of genetic drift which eliminates genetic variation from populations

Let's see an example

```
Ne <- c(60, 64, 48, 34, 22, 60, 46, 38, 24, 10)
chrom <- 2 * Ne
p = .6
q = 1 - p
gen <- 100
matrix <- array(NA, dim = c(100, 10))
```

```
head(matrix)
```

	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]	[,8]	[,9]	[,10]
[1,]	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
[2,]	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
[3,]	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
[4,]	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
[5,]	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
[6,]	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA

```
matrix[1, ] <- round(rep(chrom*p, 1))
```

```
head(matrix)
```

	[,1]	[,2]	[,3]	[,4]	[,5]	[,6]	[,7]	[,8]	[,9]	[,10]
[1,]	72	77	58	41	26	72	55	46	29	12
[2,]	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
[3,]	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
[4,]	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
[5,]	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
[6,]	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA

```
for(i in 2:gen){  
  for(j in 1:10){  
    matrix[i, j] <- rbinom(n = 1, size = chrom, prob = matrix[i-1, j]/chrom)  
  }  
}  
  
dat <- as.data.frame(matrix)  
  
head(dat)
```

	V1	V2	V3	V4	V5	V6	V7	V8	V9	V10
1	72	77	58	41	26	72	55	46	29	12
2	66	72	62	40	18	68	55	46	37	13
3	73	68	73	37	16	70	58	43	41	6
4	70	63	75	25	17	68	67	38	51	7
5	71	64	59	21	19	68	55	40	58	8
6	67	67	59	32	17	74	50	50	60	14

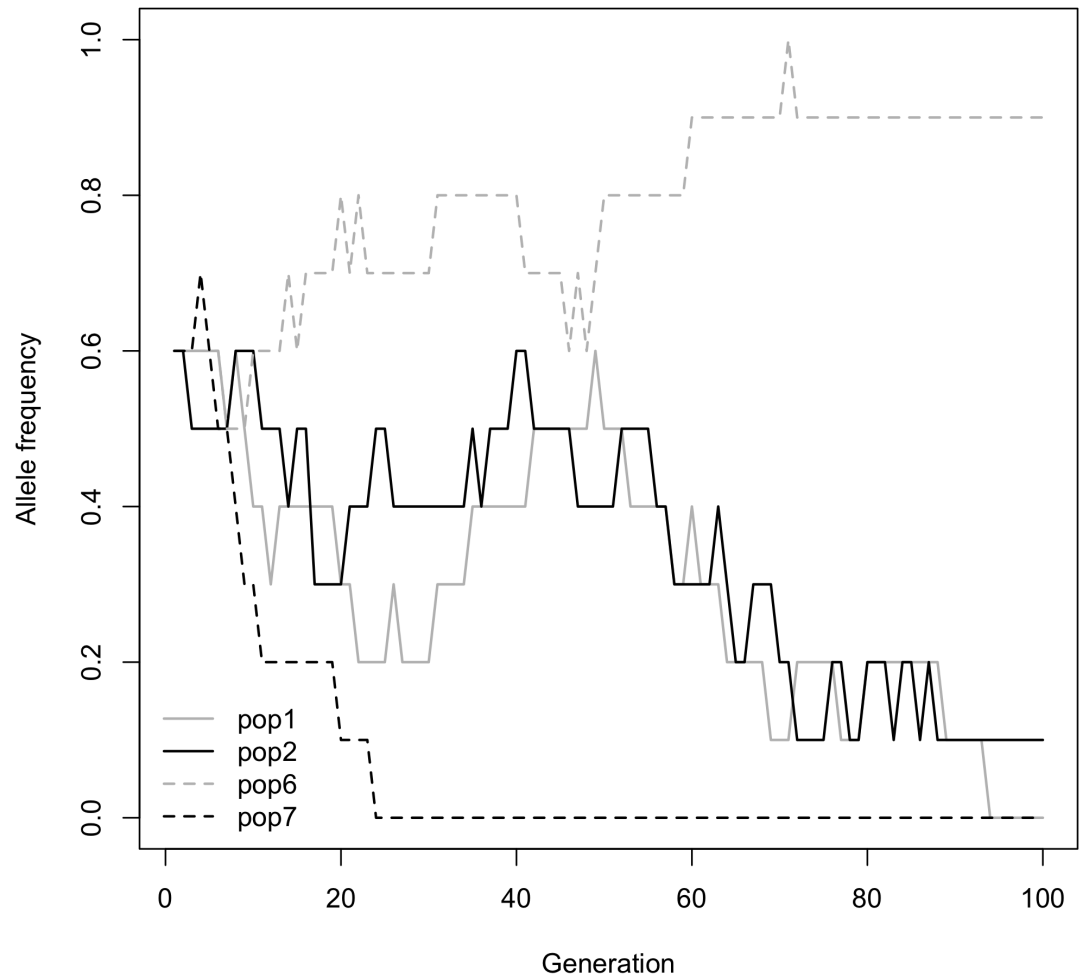
```
for(i in 1:ncol(dat)){  
  dat[, i] <- round(dat[i]/chrom[i], 1)  
}
```

```
head(dat)
```

	V1	V2	V3	V4	V5	V6	V7	V8	V9	V10
1	0.6	0.6	0.6	0.6	0.6	0.6	0.6	0.6	0.6	0.6
2	0.6	0.6	0.6	0.6	0.4	0.6	0.6	0.6	0.8	0.7
3	0.6	0.5	0.8	0.5	0.4	0.6	0.6	0.6	0.9	0.3
4	0.6	0.5	0.8	0.4	0.4	0.6	0.7	0.5	1.1	0.3
5	0.6	0.5	0.6	0.3	0.4	0.6	0.6	0.5	1.2	0.4
6	0.6	0.5	0.6	0.5	0.4	0.6	0.5	0.7	1.2	0.7

```
dat$gen <- 1:100
```

```
plot(rep(NA, 100), type = "n", ylim = c(0, 1), ylab = "Allele frequency",
     lines(V1 ~ gen, data = dat, type = "l", lwd = 1.5, col = "black"),
     lines(V2 ~ gen, data = dat, lwd = 1.5, col = "gray"),
     lines(V6 ~ gen, data = dat, lwd = 1.5, col = "gray", lty = 2),
     lines(V7 ~ gen, data = dat, lwd = 1.5, lty = 2),
     legend("bottomleft", legend = c("pop1", "pop2", "pop6", "pop7"))
```



Summary

- Though natural selection is a major driver of evolution in populations, there are other processes that result in genetic changes as well
- Genetic drift is a random process meaning that there is no selective pressure needed for certain alleles to increase or decrease in a population
- Large fluctuations in allele frequencies are more common in small populations
- Genetic drift can have major effects when a population is sharply reduced in size by a natural disaster (bottleneck effect) or when a small group splits off from the main population to found a colony (founder effect)



Online simulation

[click here to follow along](#)

