Natural Selection

BIOL 1435

April 6, 2023

Overview

1. **Drift (WF Model Review)**

2. **Single Locus Diploid Model**

3. **Selection's Impact on Allele Frequency Trajectories**

4. **Selection + Drift**

Overview

1. Drift (WF Model Review)

Q: Why do we need to model evolution?

A: To assess departures from neutrality.

Assumptions of the Wright Fisher model

Assumptions of the Wright Fisher model

- Panmictic population

Assumptions of the Wright Fisher model

- Panmictic population
- Constant population size of N
- Total of $2N$ allele copies

Assumptions of the Wright Fisher model

- Panmictic population
- Constant population size of N
- Total of $2N$ allele copies
- Discrete time process with non-overlapping generations
- All mutations are neutral
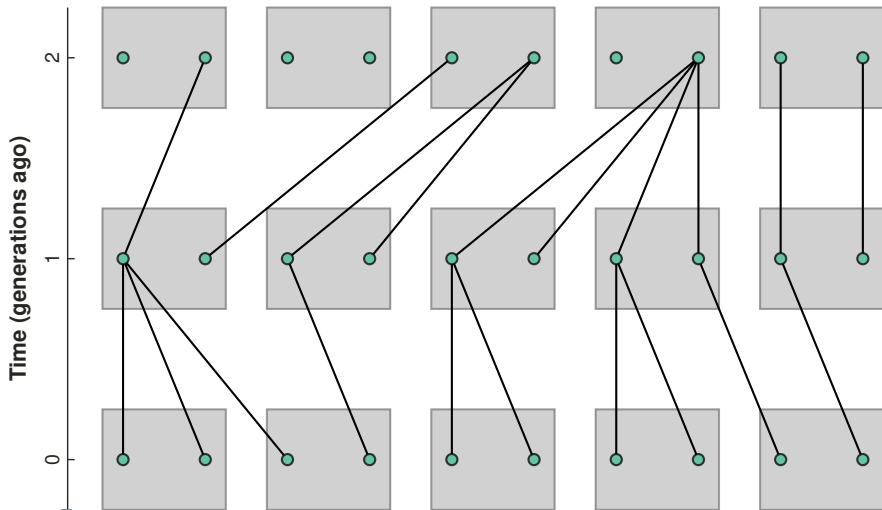
WF population ($N = 5$)

Simulating under the WF model

Simulating Reproduction

Sample with replacement an allelic copy (i) in the current generation (t) with a probability of $\frac{1}{2N}$ to produce an offspring in the next generation ($t+1$), until there are $2N$ allelic copies in the next generation.

WF population ($N = 5$)

WF Model & Genetic Drift

$$Pr(j) = \binom{2N}{j} \left(\frac{j}{2N}\right)^j \left(\frac{2N-j}{2N}\right)^{2N-j} \tag{1}$$

Where j represents the number of allelic copies of a particular allele.

WF Model & Genetic Drift

Definition

$$Pr(j) = \binom{2N}{j} \left(\frac{j}{2N}\right)^j \left(\frac{2N-j}{2N}\right)^{2N-j} \tag{1}$$

Where j represents the number of allelic copies of a particular allele.

$$Pr(k) = \binom{2N}{k} p^k (1-p)^{2N-k} \tag{2}$$

Where k represents the number of offspring with a specific allelic copy and is binomially distributed with $p = \frac{j}{2N}$.
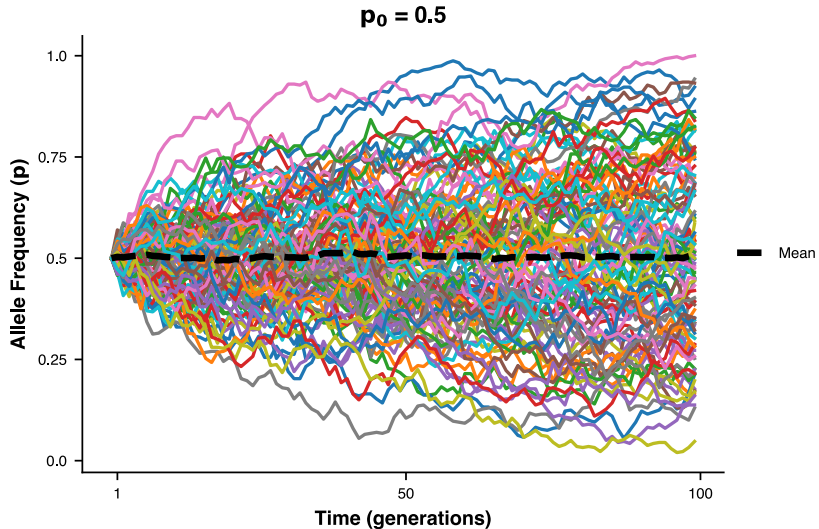
WF Model & Genetic Drift

Definition

$$p' \sim \frac{B(2N, p)}{2N} \tag{3a}$$

$$\mathbb{E}(p') = \frac{2Np}{2N} = p \tag{3b}$$

$$Var(p') = \frac{2Np(1-p)}{2N} = p(1-p) \tag{3c}$$

WF Model & Genetic Drift

$p_0 = 0.5$
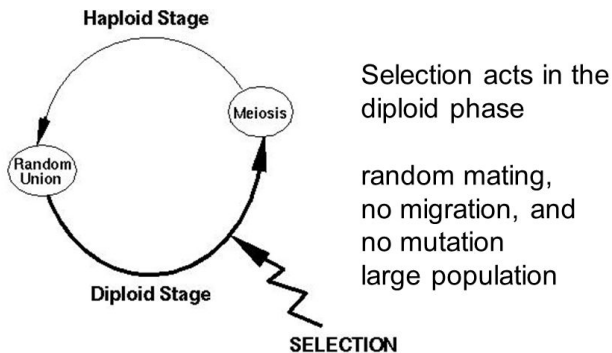
Allele Frequency (p) vs Time (generations)

Mean

Overview

1. Drift (WF Model Review)

2. Single Locus Diploid Model

3. Selection's Impact on Allele Frequency Trajectories

4. Selection + Drift

One-locus diploid model

Selection acts in the diploid phase

random mating, no migration, and no mutation large population

Single Locus Diploid Model

Definition

Genotypes	A_1A_1	A_1A_2	A_2A_2

Single Locus Diploid Model

Definition

Genotypes	A_1A_1	A_1A_2	A_2A_2
Frequency Before Selection	p^2	$2pq$	q^2

Single Locus Diploid Model

Definition

Genotypes	A_1A_1	A_1A_2	A_2A_2
Frequency Before Selection	p^2	$2pq$	q^2
Relative Fitness (Viability)	w_{11}	w_{12}	w_{22}

Single Locus Diploid Model

Definition

Genotypes	A_1A_1	A_1A_2	A_2A_2
Frequency Before Selection	p^2	$2pq$	q^2
Relative Fitness (Viability)	w_{11}	w_{12}	w_{22}
Frequency After Selection	$\frac{p^2 w_{11}}{\bar{w}}$	$\frac{2pq w_{12}}{\bar{w}}$	$\frac{q^2 w_{22}}{\bar{w}}$

Allele Frequency Trajectories

Definition

$$\bar{w} = p^2 w_{11} + 2pq w_{12} + q^2 w_{22} \qquad (4)$$

Population Mean Fitness: $\bar{w} = p^2 w_{11} + 2pq w_{12} + q^2 w_{22}$ (4)

Allele Frequency Trajectories

Definition

$$\text{Population Mean Fitness: } \bar{w} = p^2 w_{11} + 2pq w_{12} + q^2 w_{22} \tag{4}$$

$$\text{Relative Frequencies of Genotypes After Selection: } 1 = \frac{p^2 w_{11}}{\bar{w}} + \frac{2pq w_{12}}{\bar{w}} + \frac{q^2 w_{22}}{\bar{w}} \tag{5}$$

Allele Frequency Trajectories

<div>

Definition

$$\text{Population Mean Fitness: } \bar{w} = p^2 w_{11} + 2pq w_{12} + q^2 w_{22} \tag{4}$$

$$\text{Relative Frequencies of Genotypes After Selection: } 1 = \frac{p^2 w_{11}}{\bar{w}} + \frac{2pq w_{12}}{\bar{w}} + \frac{q^2 w_{22}}{\bar{w}} \tag{5}$$

$$\text{Frequency of the } A_1 \text{ Allele After Selection: } p' = \frac{p^2 w_{11} + pq w_{12}}{\bar{w}} \tag{6}$$

</div>

Allele Frequency Trajectories

Definition

Change in Allele Frequencies due to Selection: $\Delta p = p' - p$ (7a)

$$\Delta p = pq \left(p \left(w_{11} - w_{12} \right) + q \left(w_{12} - w_{22} \right) \right) \times \frac{1}{\bar{w}} \qquad (7b)$$

Allele Frequency Trajectories

Definition

Change in Allele Frequencies due to Selection: $\Delta p = p' - p$ (7a)

$$\Delta p = pq \left(p \left(w_{11} - w_{12} \right) + q \left(w_{12} - w_{22} \right) \right) \times \frac{1}{\bar{w}}$$ (7b)

$$w_1 = pw_{11} + qw_{12}$$ (8a)

$$w_2 = pw_{12} + qw_{22}$$ (8b)

Change in Allele Frequencies due to Selection: $\Delta p = \dfrac{pq \left(w_1 - w_2 \right)}{\bar{w}}$ (9)
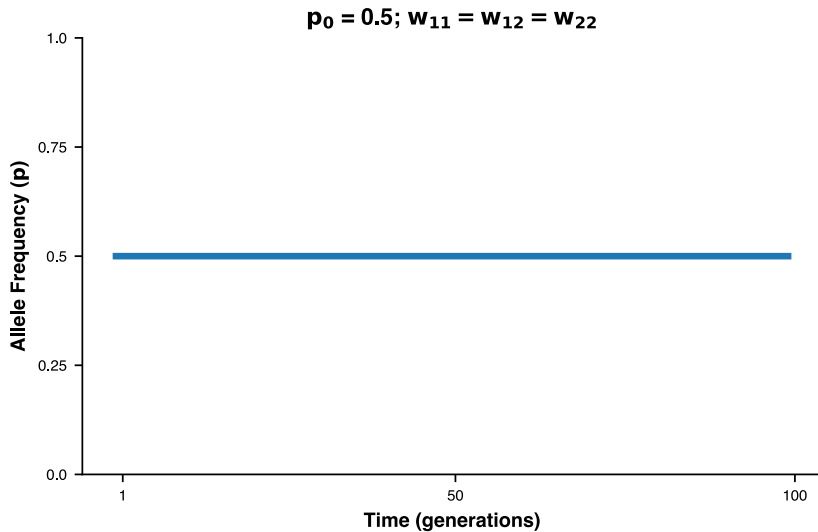
Overview

p' for $w_{11} = w_{12} = w_{22}$

p' for $w_{11} = w_{12} = w_{22}$

$p_0 = 0.5$; $w_{11} = w_{12} = w_{22}$

$p^{'}$ for $w_{11} = 1; w_{12} = 0.95; w_{22} = 0.9$

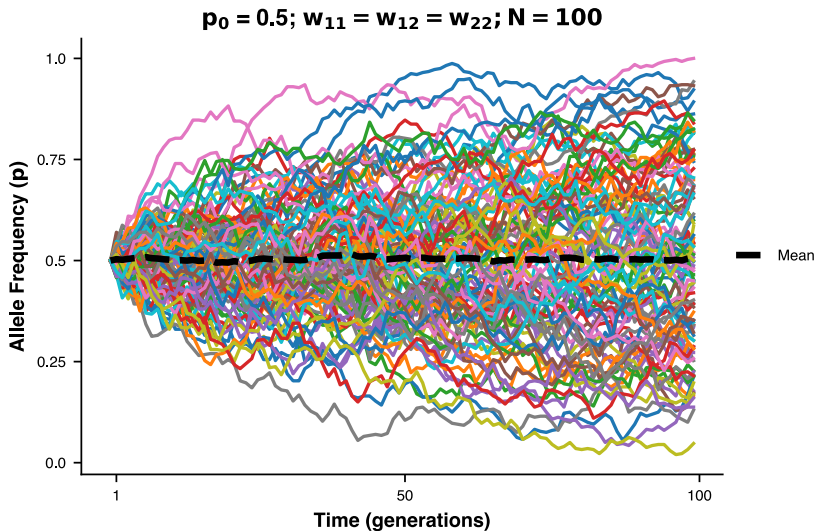# p' for $w_{11} = 1; w_{12} = 0.95; w_{22} = 0.9$
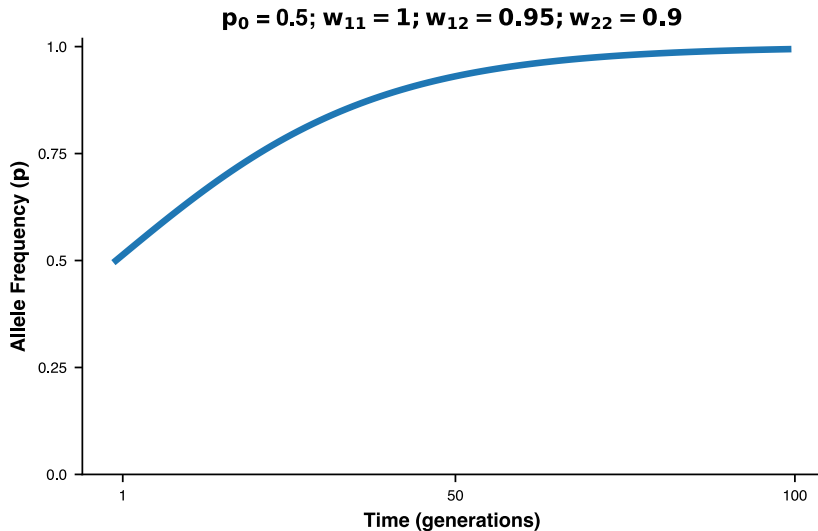
$p_0 = 0.5; w_{11} = 1; w_{12} = 0.95; w_{22} = 0.9$

Overview

A$_1$ Trajectories for $w_{11} = w_{12} = w_{22}$

A_1 Trajectories for $w_{11} = w_{12} = w_{22}$

$p_0 = 0.5; w_{11} = w_{12} = w_{22}; N = 100$

A_1 Trajectories for $w_{11} = 1; w_{12} = 0.95; w_{22} = 0.9$

A$_1$ Trajectories for $w_{11} = 1$; $w_{12} = 0.95$; $w_{22} = 0.9$

$p_0 = 0.5$; $w_{11} = 1$; $w_{12} = 0.95$; $w_{22} = 0.9$; $N = 100$
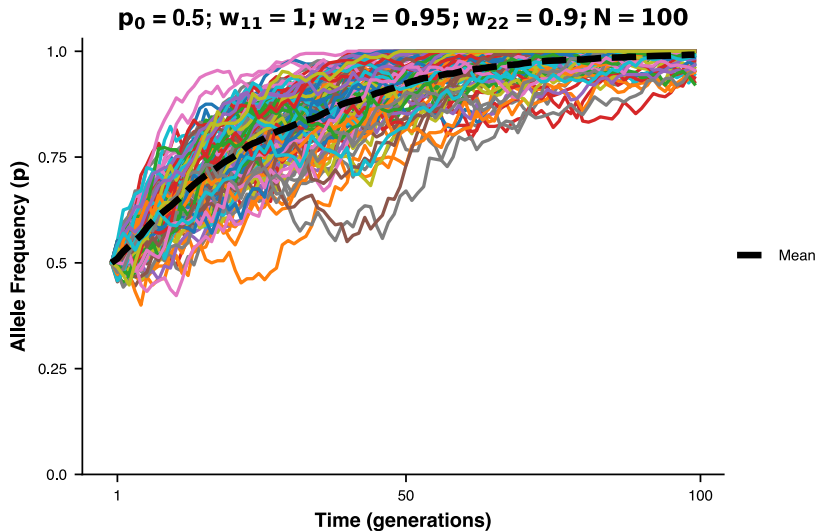
N's Impact on Drift & Selection

N's Impact on Drift & Selection
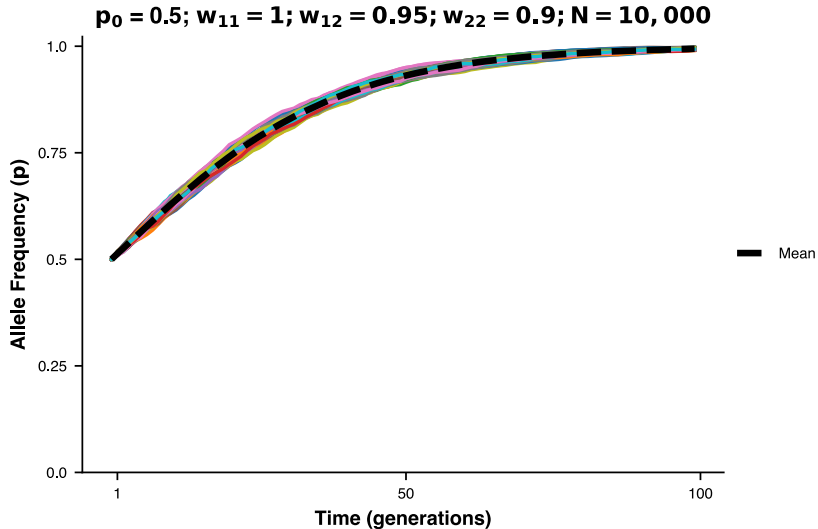
$p_0 = 0.5$; $w_{11} = 1$; $w_{12} = 0.95$; $w_{22} = 0.9$; $N = 10,000$

Dominance

Genotypes	A_1A_1	A_1A_2	A_2A_2
Frequency Before Selection	p^2	$2pq$	q^2
Relative Viability	w_{11}	w_{12}	w_{22}
Relative Fitness	1	$1 - hs$	$1 - s$
Frequency After Selection	$\frac{p^2 w_{11}}{\bar{w}}$	$\frac{2pq w_{12}}{\bar{w}}$	$\frac{q^2 w_{22}}{\bar{w}}$

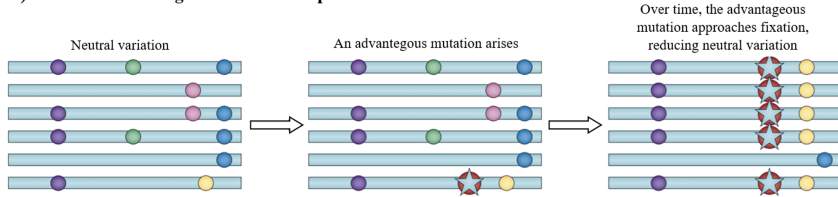Where h is the heterozygous effect and s is the selection coefficient.

Dominance

$p_0 = 0.01; s = 0.01$
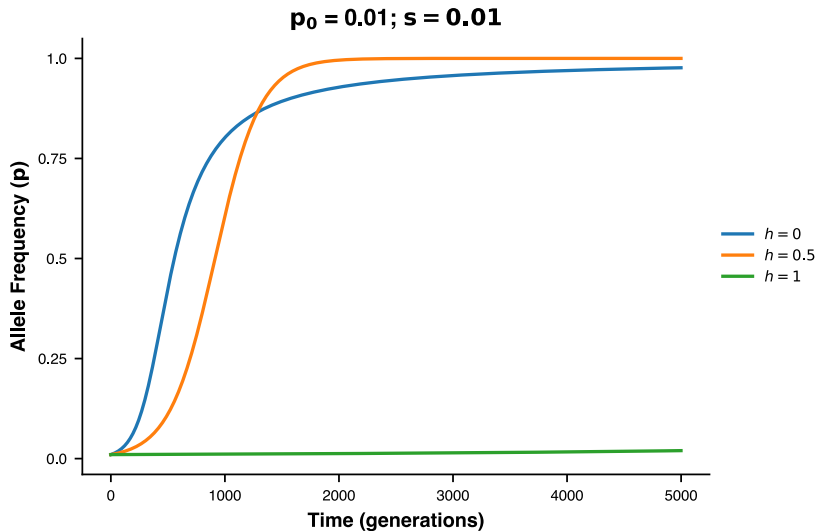
Linked Selection

A) Genetic Hitchhiking or Selective Sweep

Neutral variation

An advantegous mutation arises

Over time, the advantageous mutation approaches fixation, reducing neutral variation

B) Background Selection

Neutral variation

Deleterious mutations arises

Over time, the deleterious mutations, and the neutral variation, are lost