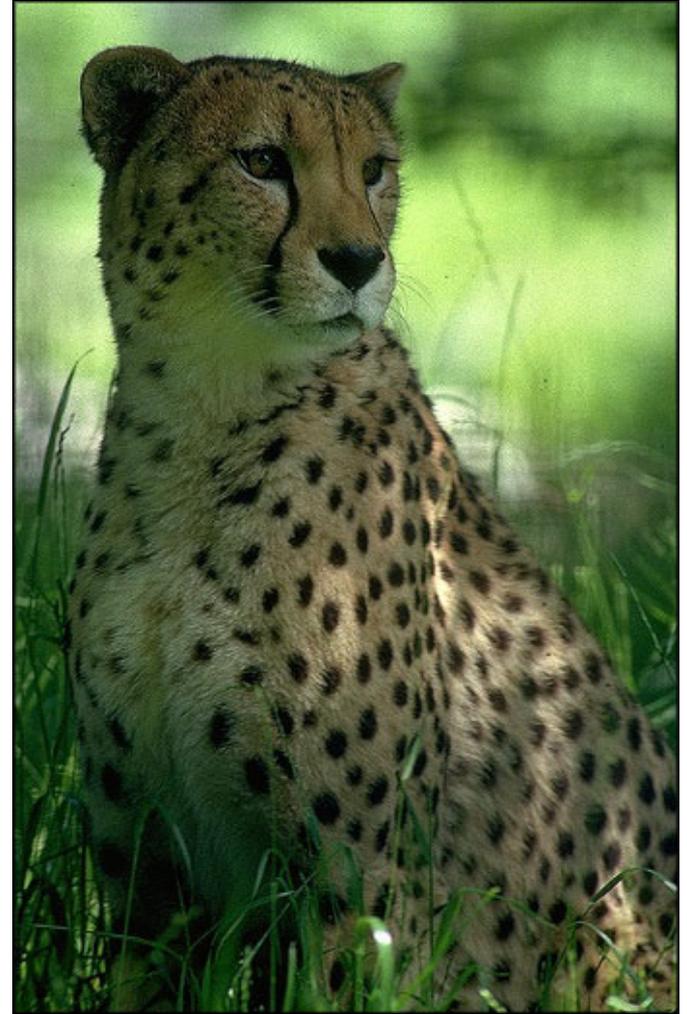


Genetic Drift Lecture outline

1. Founder effect
2. Genetic drift consequences
3. Population bottlenecks
4. Effective Population size

Odd populations

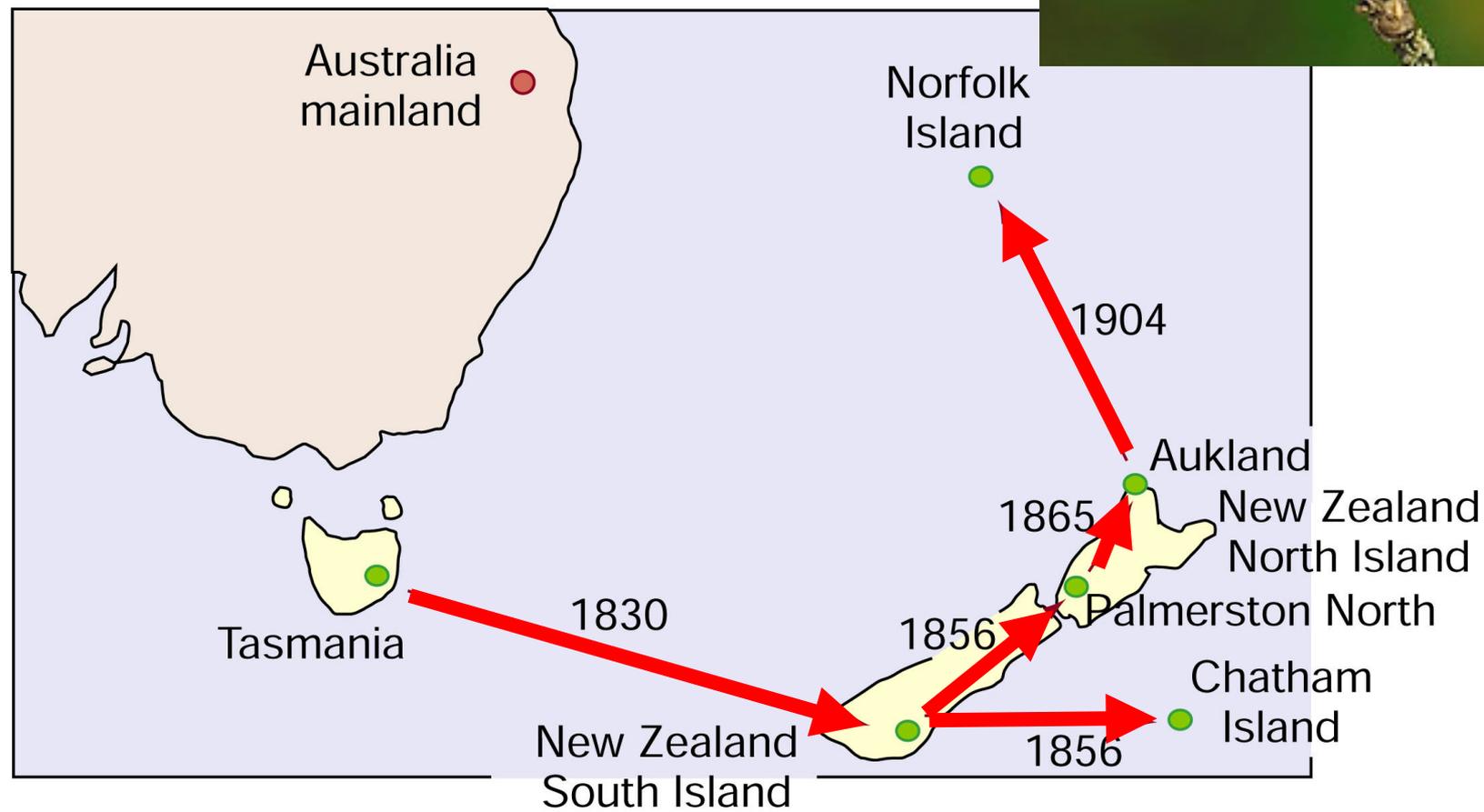
Deer at Seneca Army Depot

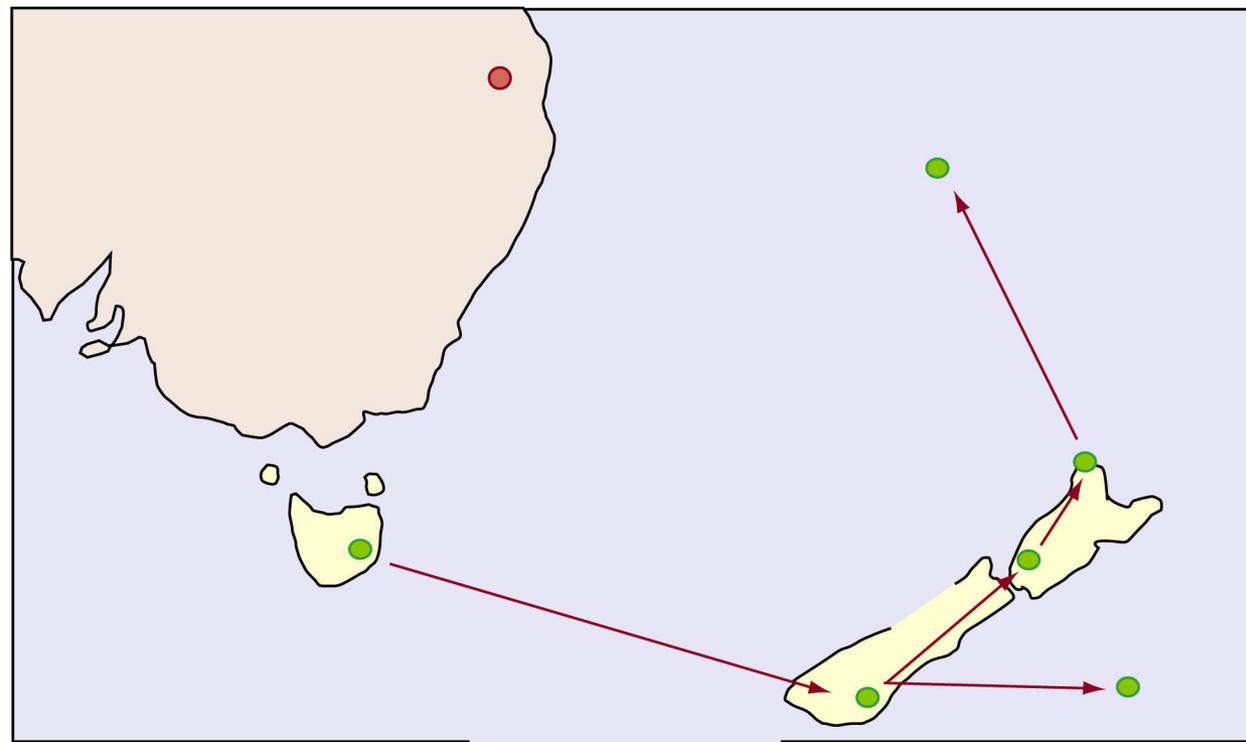


Cheetah

Silvereyes (*Zosterops lateralis*)

(example of sampling error)





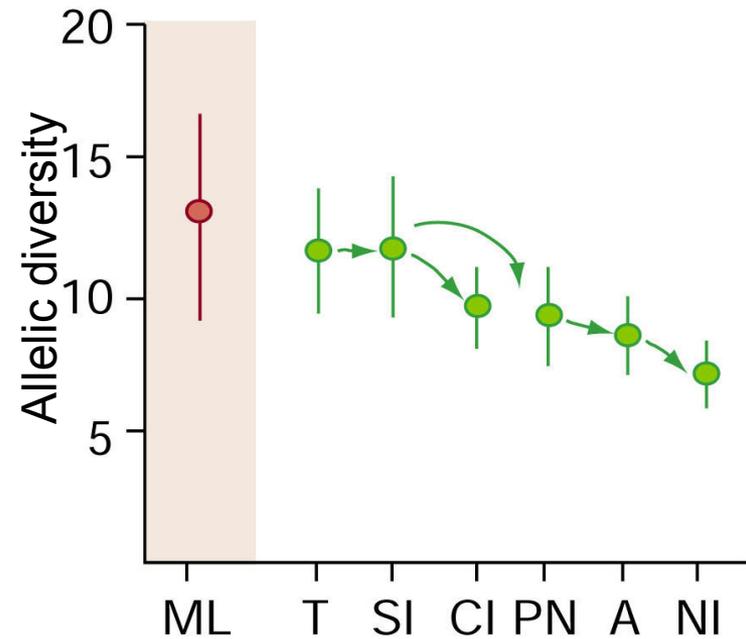
Can result in:
 Change in allelic composition
 (loss of diversity)

Allelic diversity
 Average number of alleles found per locus

Founder Effect

What happens when a small number of individuals start a new populations?

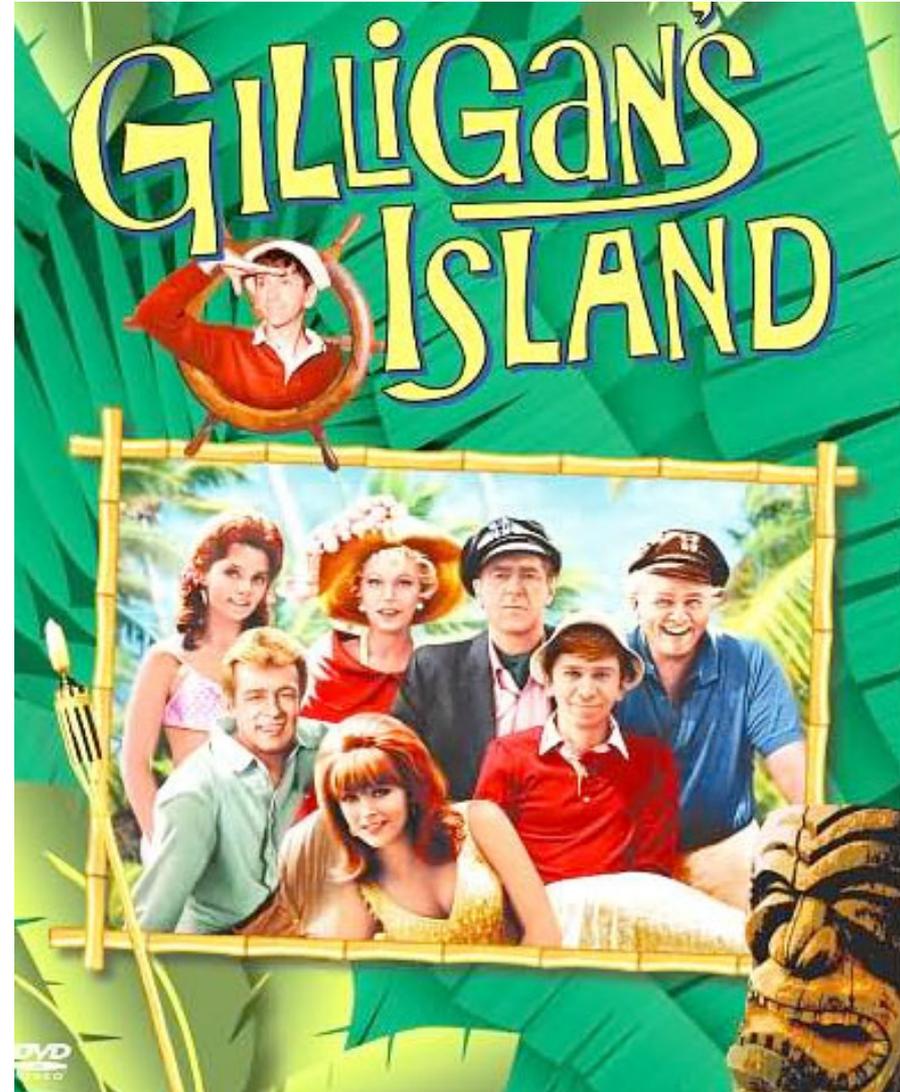
Predict a decay in allelic diversity



Sampling Error and Evolution

Founder effect

- Reduced diversity
- Change in allele frequencies



A review of Hardy-Weinberg assumptions

- No selection (random fitness)
- No mutation
- No immigration or emmigration
- Random mating
- Large population size

Large Population Size?

Question:

What happens if the population has a small size?

Answer:

Genetic Drift

The role of **Random Chance**

Genetic Drift: change in frequencies of alleles in a population resulting from sampling error

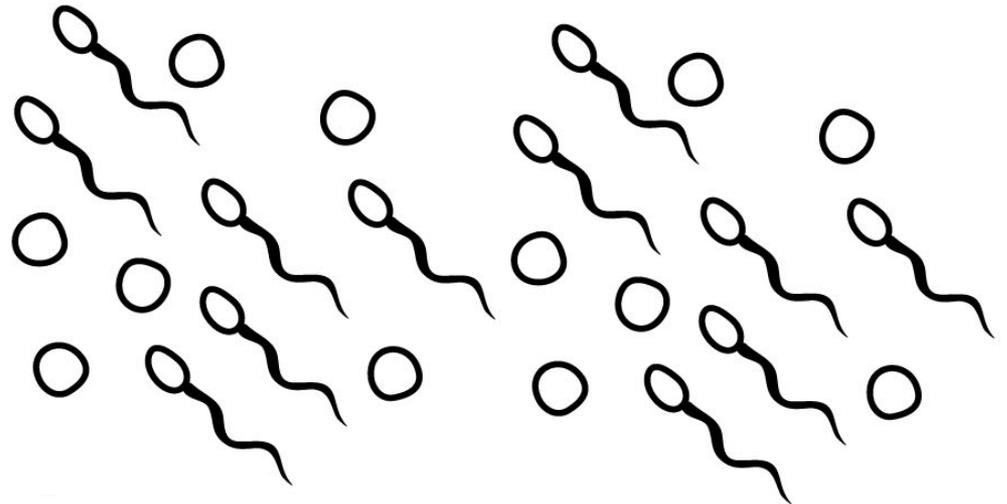
Does not lead to adaptation!

A toy (mouse) example

- Population size
 - 10 mice
- Initial allele frequencies
- Generate gametes based on these frequencies

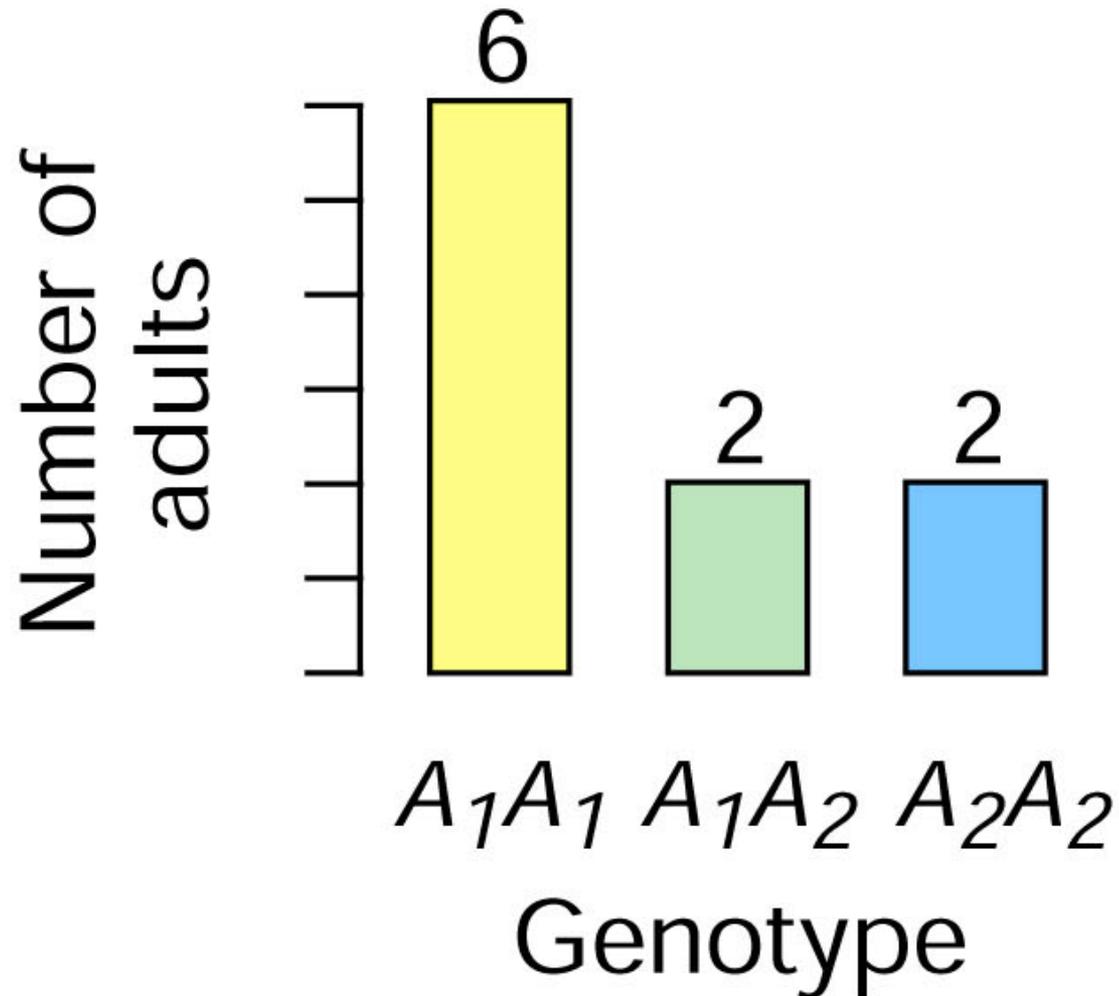


A_1	A_2
0.6	0.4



Next generate 10 new individuals

New population of 10 mice



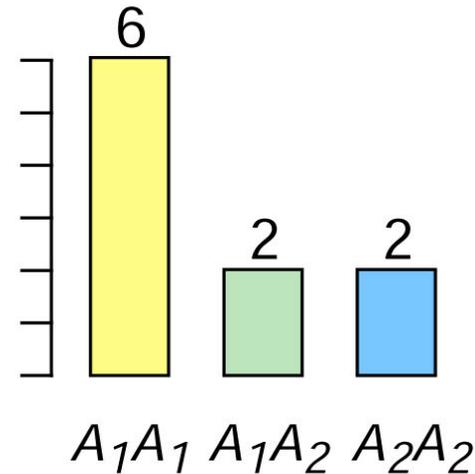
Calculate new Allele Frequencies

Genotype Frequencies

$$A_1A_1 = 6/10 = 0.6$$

$$A_1A_2 = 2/10 = 0.2$$

$$A_2A_2 = 2/10 = 0.2$$



New Allele frequencies

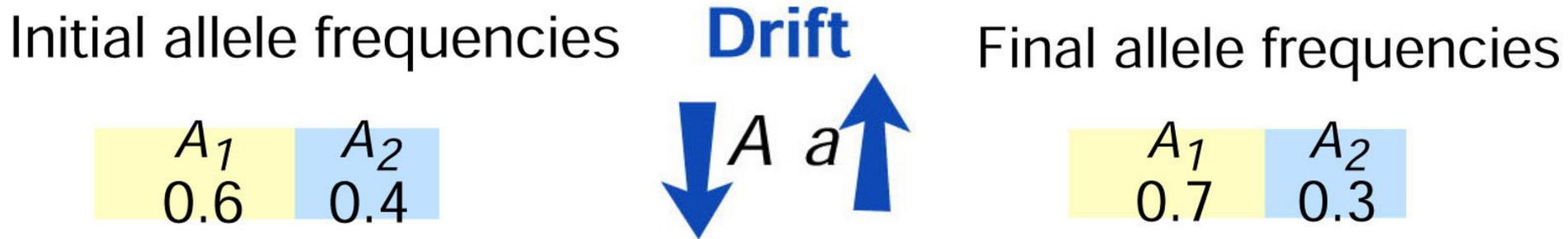
$$\text{Freq}(A_1) = 1 * \text{Freq}(A_1A_1) + \frac{1}{2} * \text{Freq}(A_1A_2)$$

$$\text{Freq}(A_1) = 1 * 0.6 + \frac{1}{2} * 0.2 = 0.7$$

$$\text{Freq}(A_2) = 1 * \text{Freq}(A_2A_2) + \frac{1}{2} * \text{Freq}(A_1A_2)$$

$$\text{Freq}(A_2) = 1 * 0.2 + \frac{1}{2} * 0.2 = 0.3$$

Result of Drift

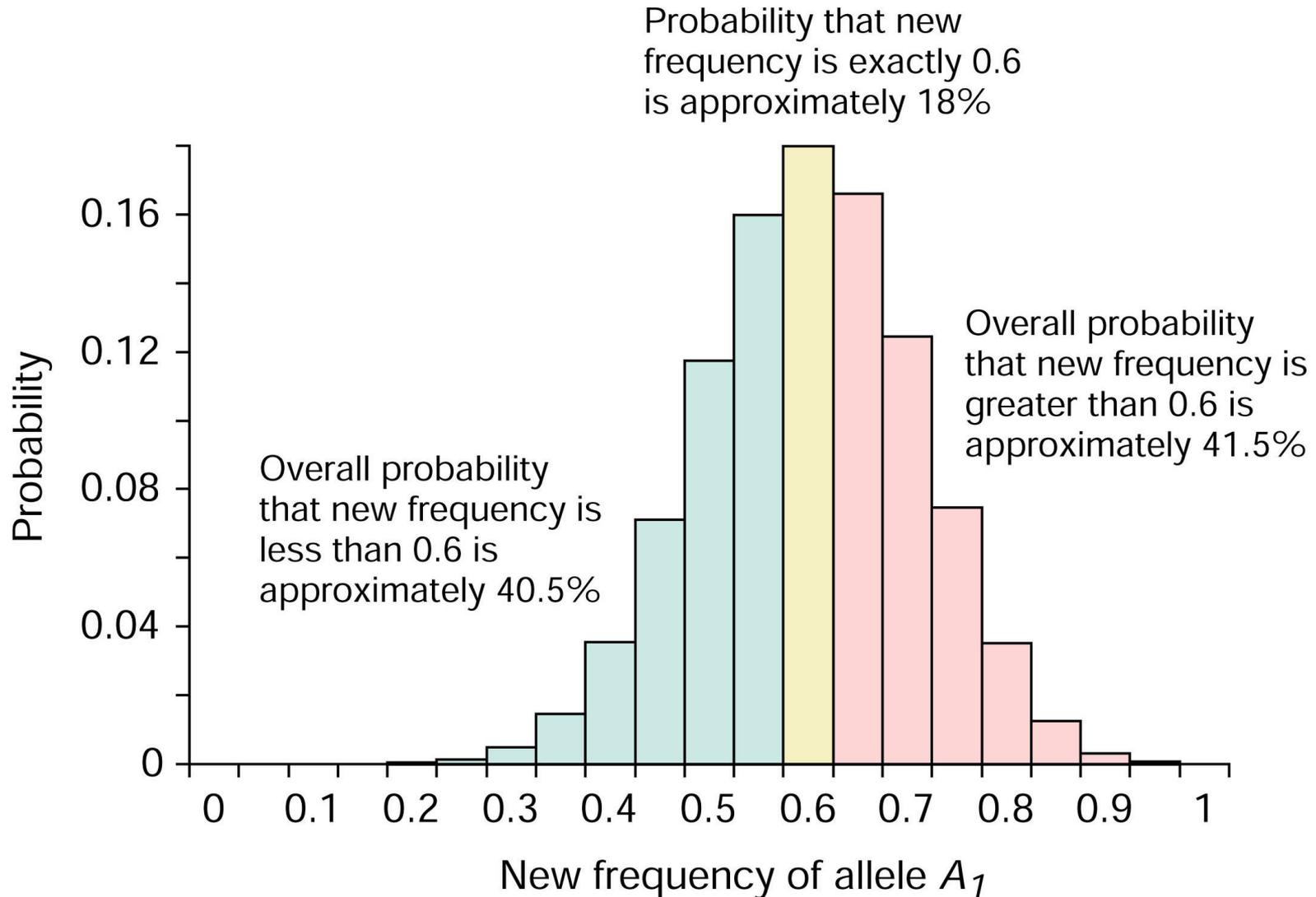


Random change in allele frequencies

What are the HW equilibrium values?

Imagine 1000 replicate populations

what's the distribution of new allele frequencies?



What happens in the future?

- We've just measured the change across one generation.
- How does the allele frequency change through time?
- Can it be predicted?

Random fixation of alleles

BUT...

Given enough time

what's the **probability** that an allele goes to fixation?

Each **copy** of an allele has an equal chance of becoming fixed

Each copy of A1 has this chance.

Suppose there **x copies** in the population

$$x \times \frac{1}{2N} = \frac{x}{2N} = \textit{freq}(x) = p$$



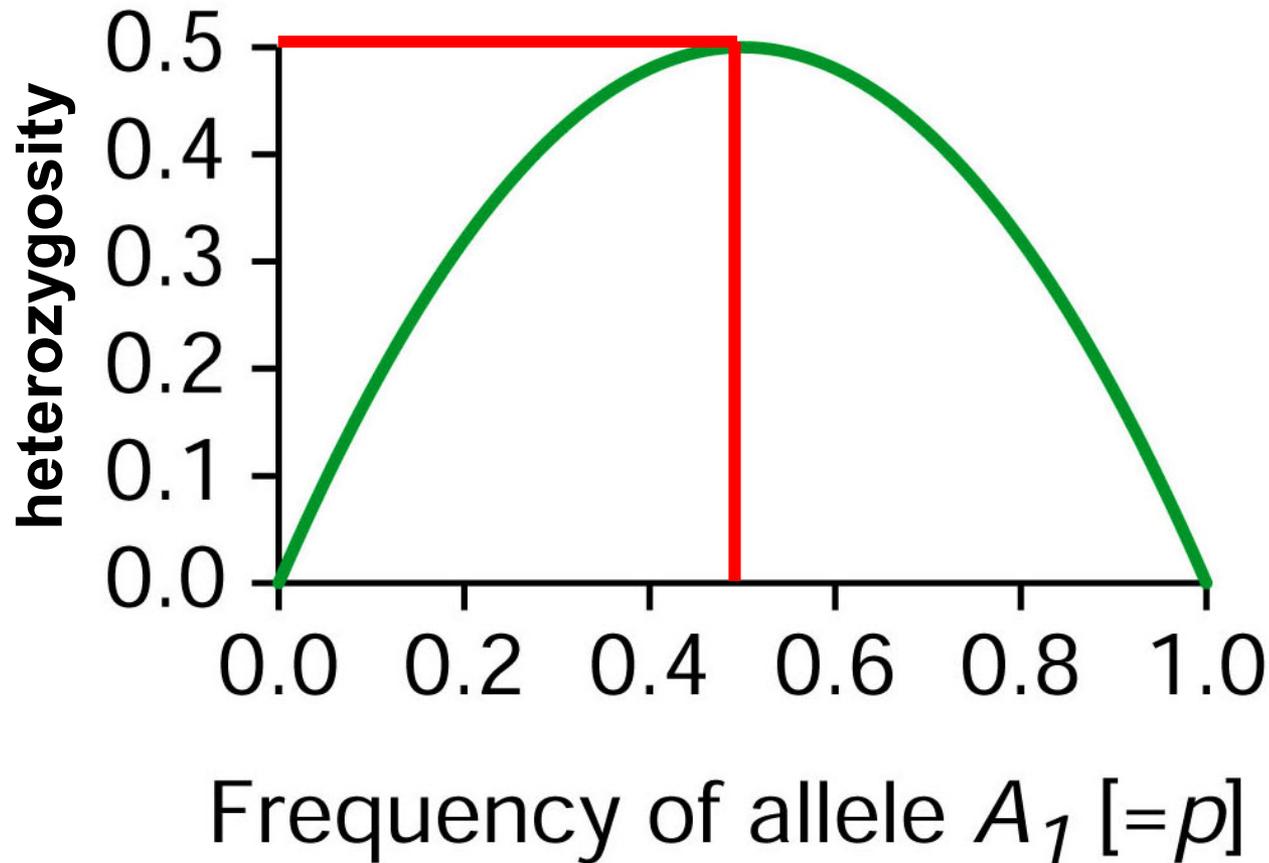
Number of copies
of allele



Chance of each copy becoming fixed

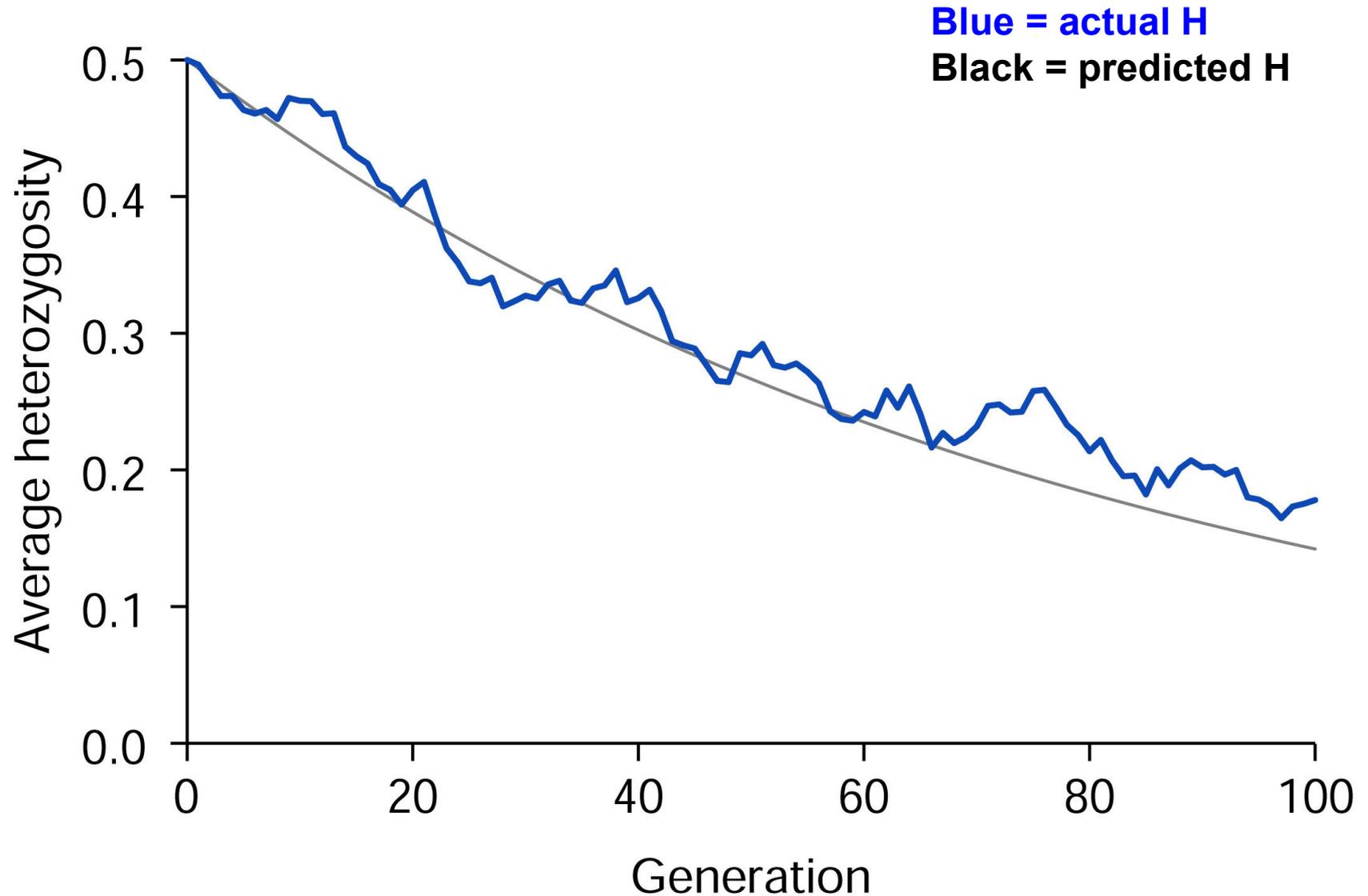
Heterozygosity

Frequency of heterozygotes in the population ($H = 2pq$)



Heterozygosity

(e) Population size = 40



Loss of heterozygosity

Heterozygosity in next generation

Heterozygosity in current generation

$$H_{g+1} = H_g \left[1 - \frac{1}{2N} \right]$$

Reduced by this much

Consequences of Genetic Drift

Over time:

1. Random fixation of alleles

- Allelic diversity within populations decreases

2. Loss of heterozygosity

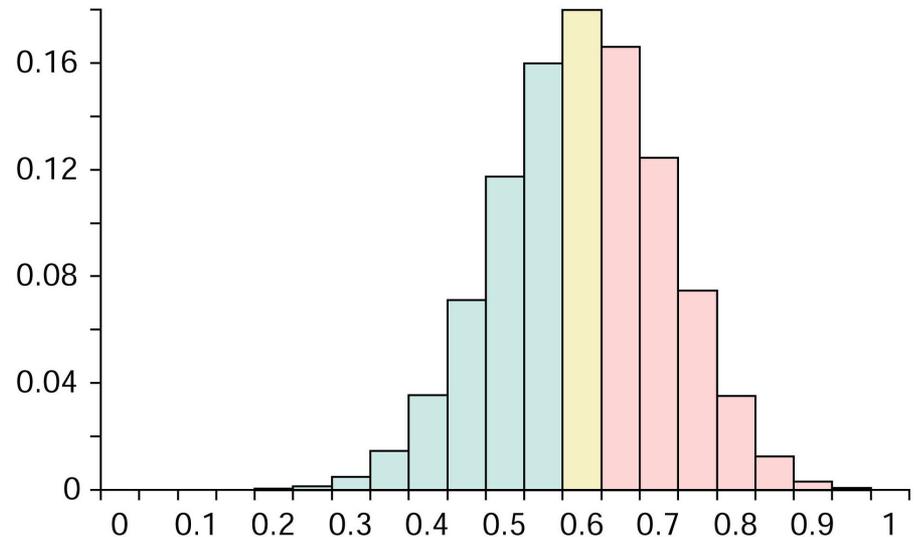
3. Variance among populations increases

- Proportion of shared alleles between populations decreases

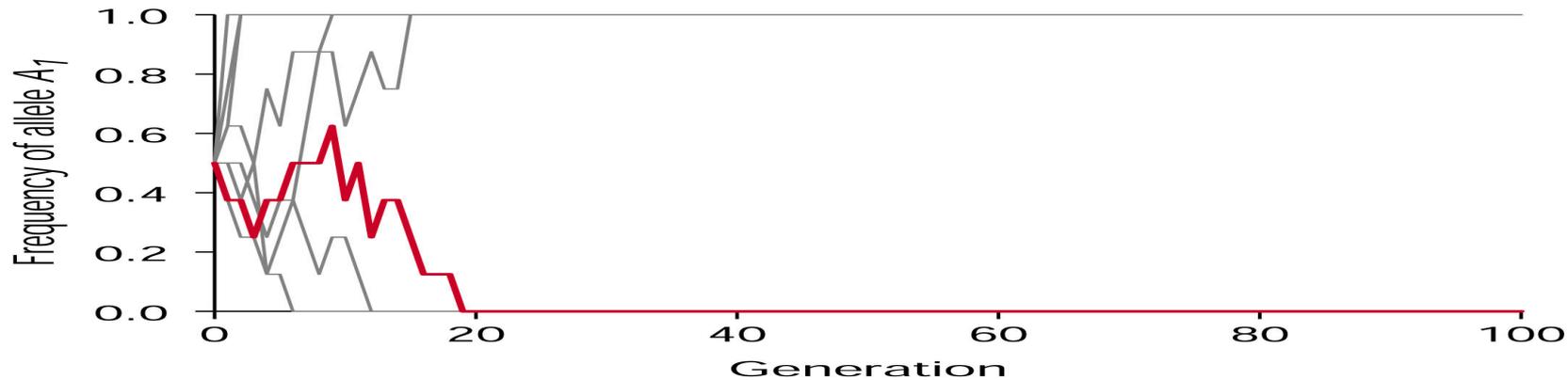
Genetic Drift and Population Size

How does the effect of genetic drift change with the population size?

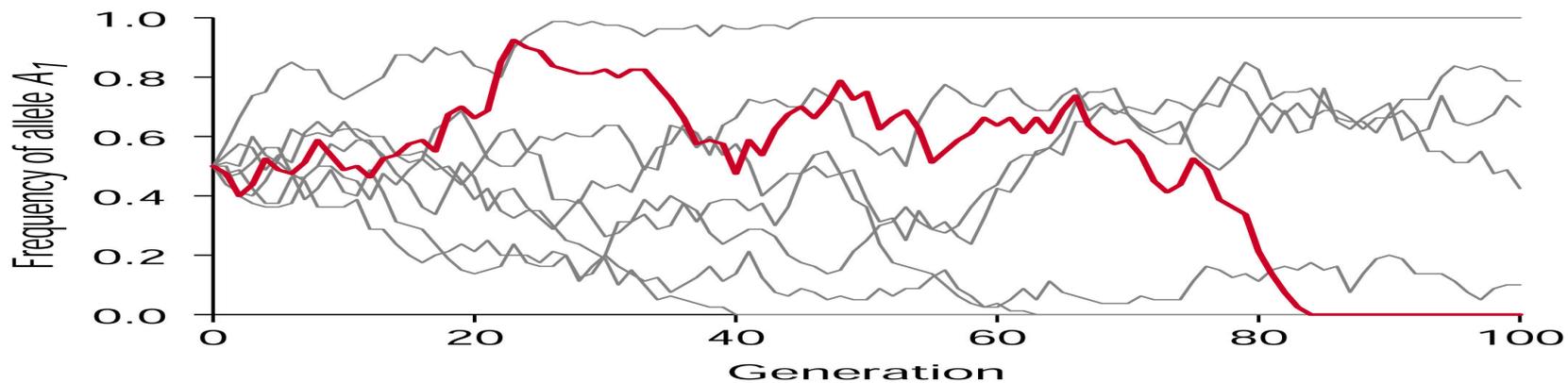
Recall distribution of allele frequencies for population of size 10



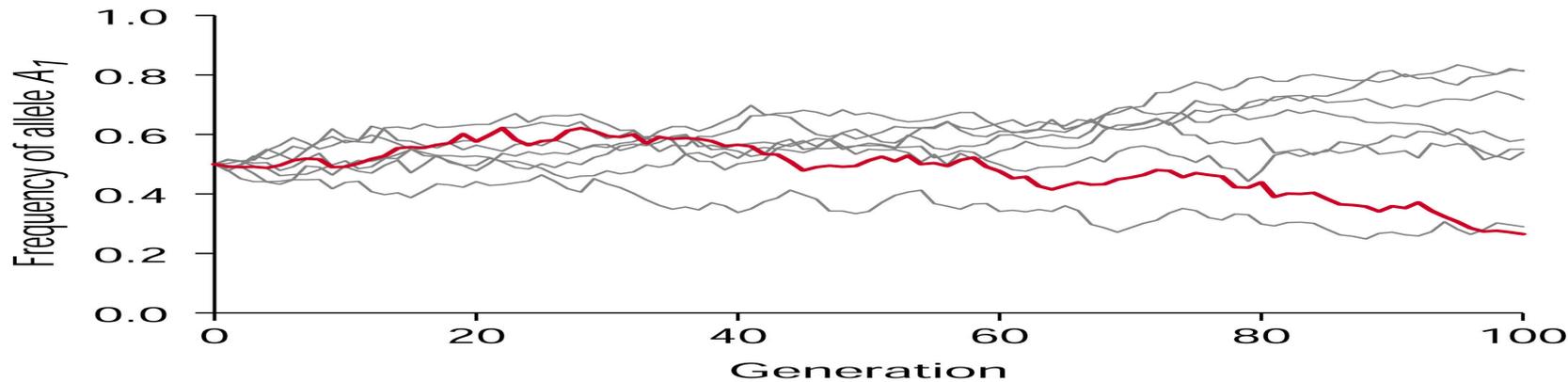
(a) Population size = 4



(b) Population size = 40

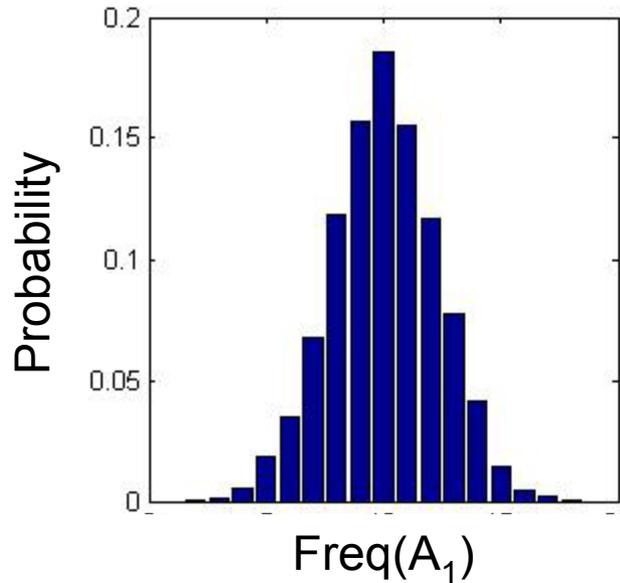


(c) Population size = 400

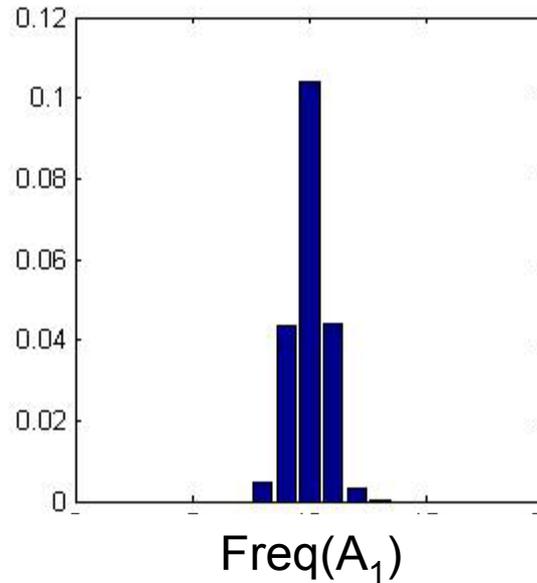


Genetic Drift and Population Size

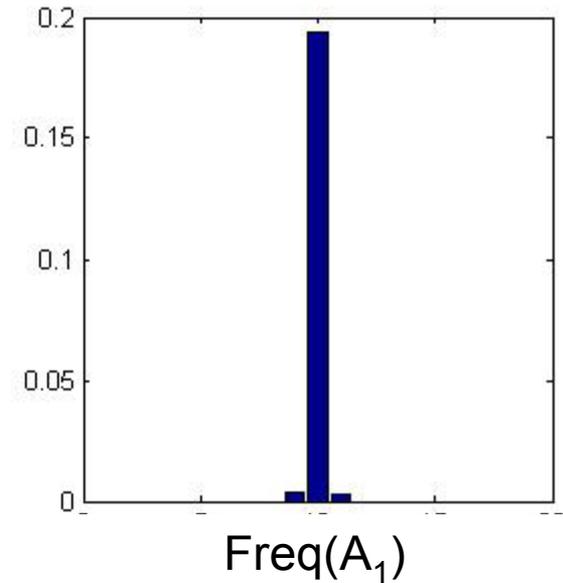
N = 10



N = 100



N = 1000



Var(p):

describes the range of expected allele frequencies.

$$\text{var}(p) = \frac{p(1-p)}{2N}$$

What happens to var(p) value as N increases?

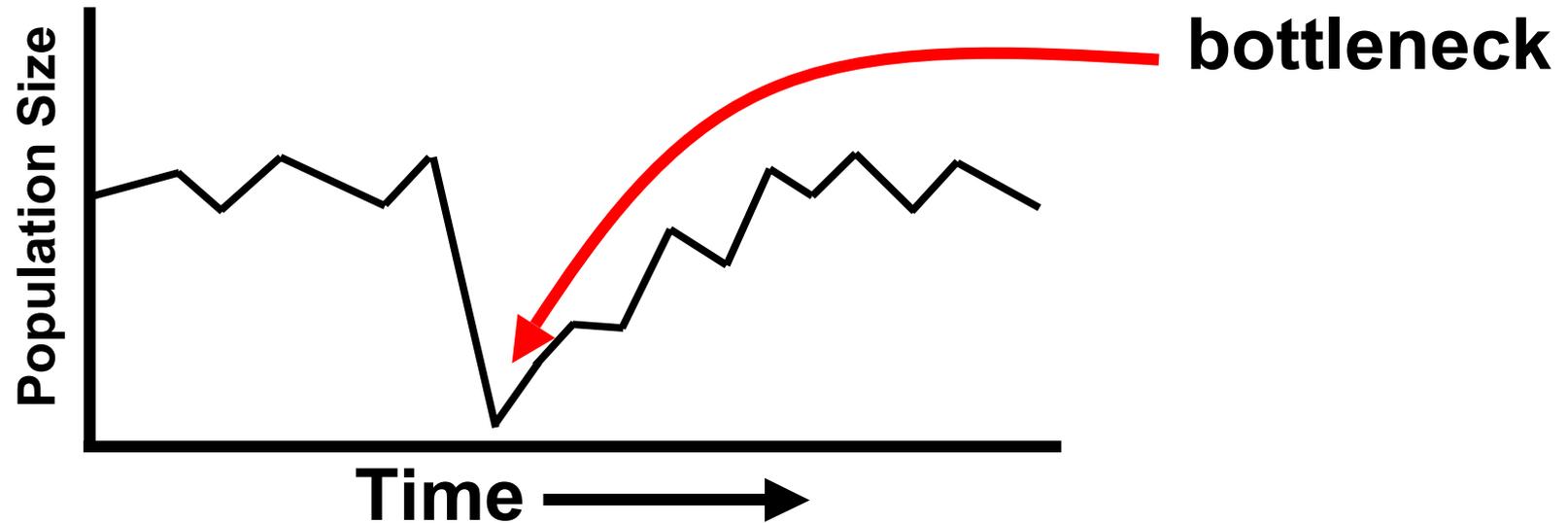
Genetic Drift and Population Size

- Fixation of alleles and Loss of heterozygosity
 - **Rapid in small populations**
 - **Slow in large populations**

Results of Genetic Drift

1. Allele frequencies fluctuate randomly from one generation to the next
2. Eventually one of the starting alleles is fixed and others are lost
3. Expected heterozygosity declines over time
4. Rate of drift is directly related to population size

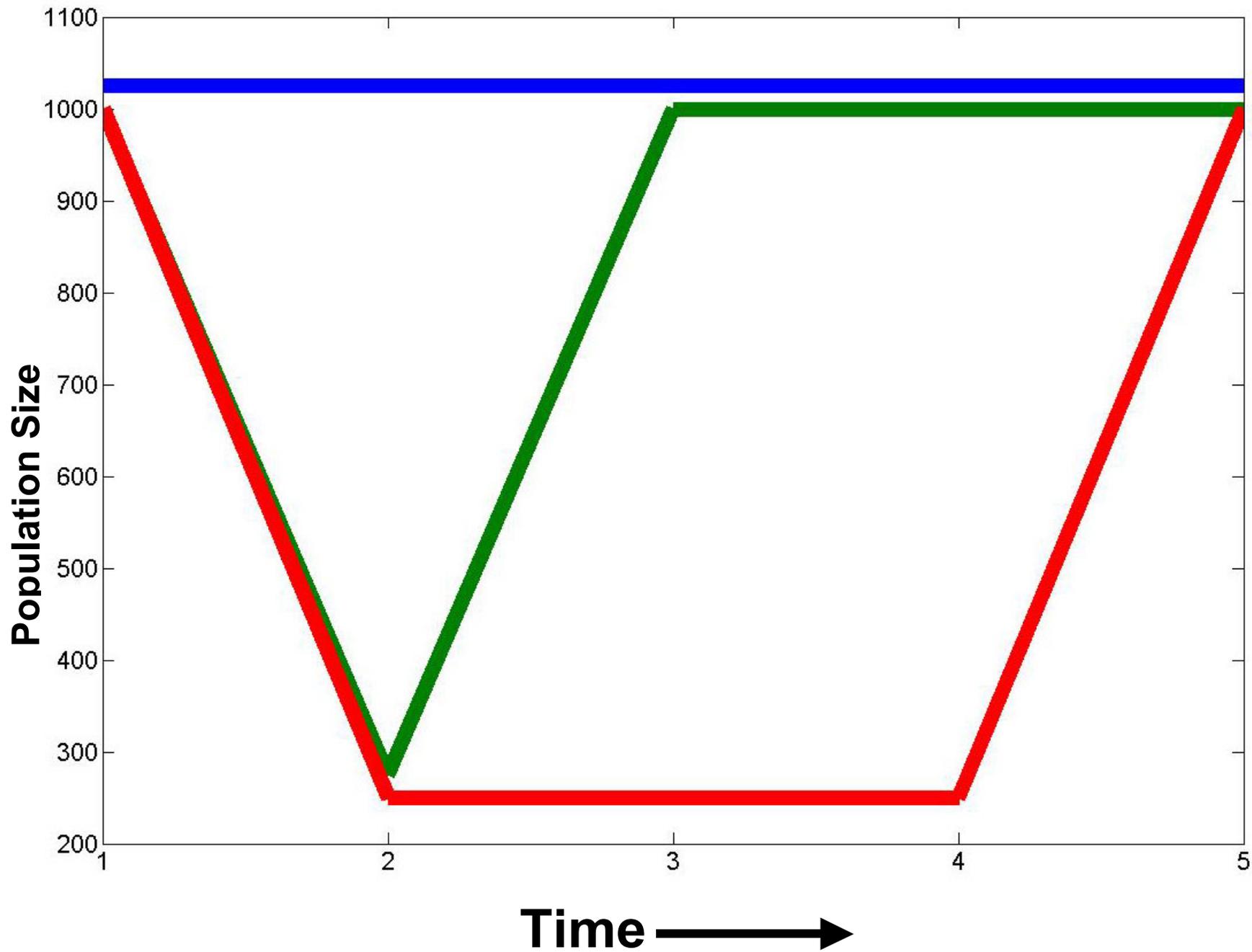
Change in population size over time



We need a measure of N that accounts for this change over time

N_e : Effective population size

Size of a theoretical population that would lose heterozygosity at the same rate as the actual population



Population bottlenecks

Harmonic mean of N

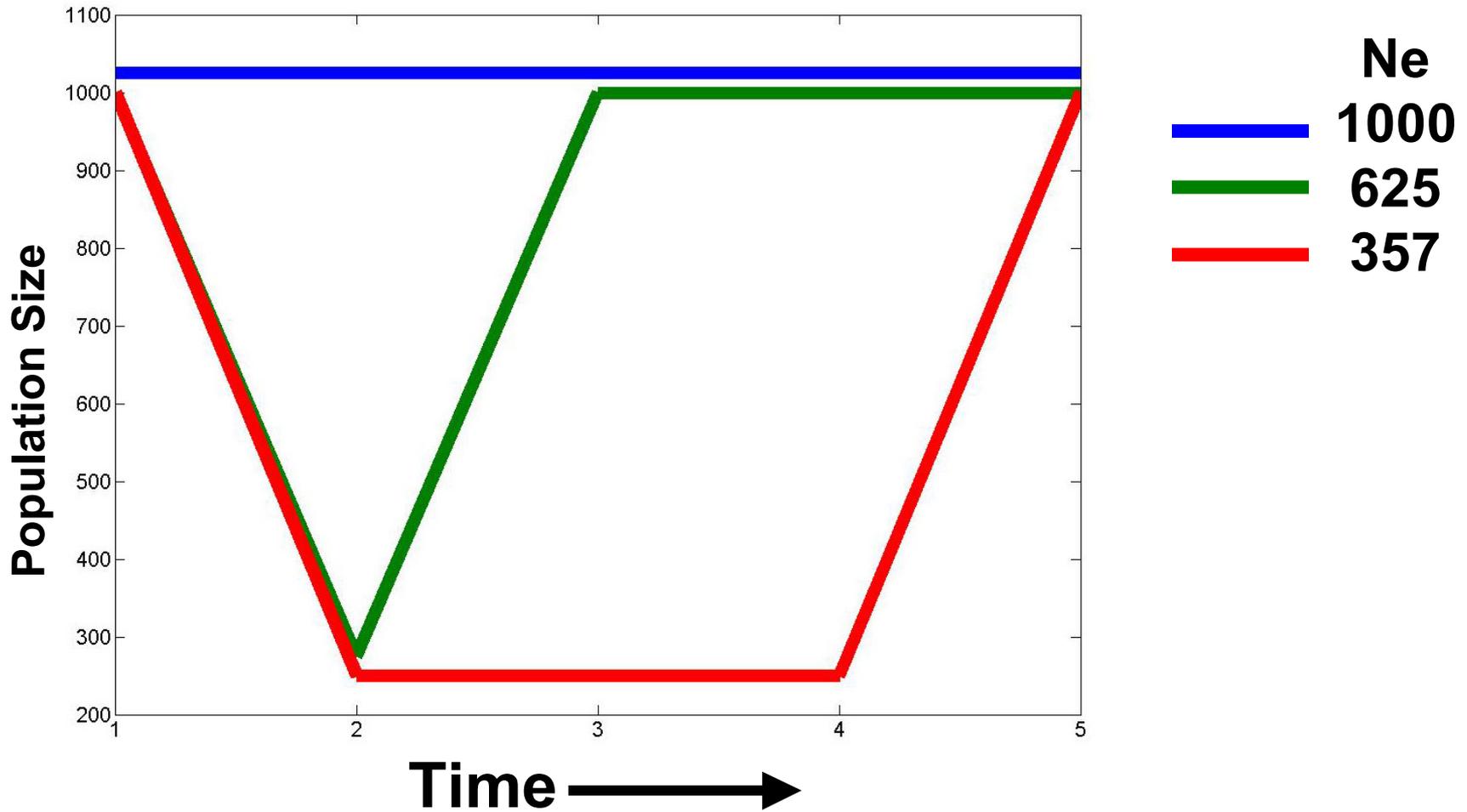
$$N_e = \frac{t}{\sum_{i=1}^t \frac{1}{N_i}}$$

	1	2	3	4	5
Constant	1000	1000	1000	1000	1000
Short	1000	250	1000	1000	1000
Long	1000	250	250	250	1000

$$N_e = \frac{5}{\frac{1}{1000} + \frac{1}{1000} + \frac{1}{1000} + \frac{1}{1000} + \frac{1}{1000}} = \frac{5}{.005} = 1000$$

$$N_e = \frac{5}{\frac{1}{1000} + \frac{1}{250} + \frac{1}{1000} + \frac{1}{1000} + \frac{1}{1000}} = \frac{5}{.008} = 625$$

$$N_e = \frac{5}{\frac{1}{1000} + \frac{1}{250} + \frac{1}{250} + \frac{1}{250} + \frac{1}{1000}} = \frac{5}{.014} = 357$$



Effect on N_e depends:

1. Magnitude of bottleneck
2. Duration of bottleneck