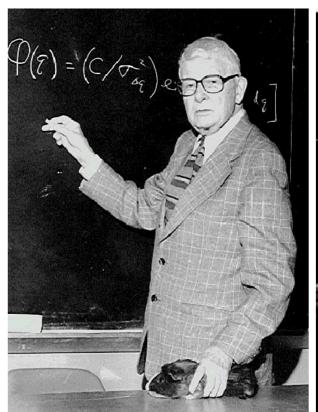
Week 6

Simulation and Modeling Evolution

Population genetics

Sewell Wright J.B.S. Haldane

- Microevolution
- Change in the genetic make up of populations $p_t \xrightarrow{\text{evolution}} p_{(t+1)}$
- Evolutionary forces
- Deterministic forces
 - Selection
 - Migration
 - [Mutation]
- Stochastic forces
 - Genetic drift
 - [Recombination]
- Population genetics as a balance of interacting forces







What do Mendelian alleles do in a population?



Hardy-Weinberg Equilibrium



Wilhelm Weinberg (1862 — 1937)

Godfrey Harold Hardy (1877 – 1947)

These two gentlemen figured it out.

Minding Your Ps and Qs

Genotype:

 $A_1A_1 \quad A_1A_2 \quad A_2A_2$

Relative Frequency: x_{11} x_{12}

Constraint:

$$x_{11} + x_{12} + x_{22} = 1$$

Treat genotype/allele frequencies as random variables

Minding Your Ps and Qs

First calculate alleles freqs

Freq A₁ allele

Freq A₂ allele

$$p = x_{11} + \frac{1}{2}x_{12}$$

$$q = 1 - p = x_{22} + \frac{1}{2}x_{12}$$

Where is this coming from?

Minding Your Ps and Qs Numerical Example

Sickle Cell vs. Normal Hemoglobin in Sub Saharan Village

Genotype: A_1A_1 A_1A_2 A_2A_2 Observed Numbers: 411 1404 185 Relative Frequencies: 0.2055 0.702 0.0925

Calculate the frequency of A₁ allele

Minding Your Ps and Qs Numerical Example

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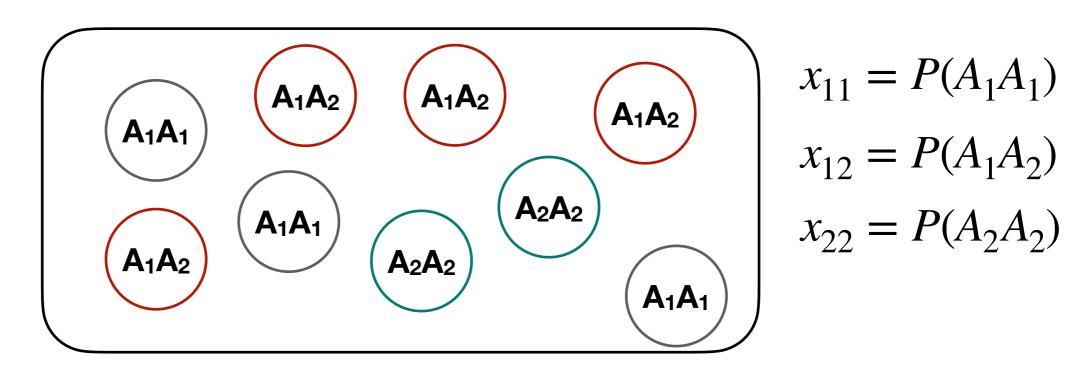
Calculate the frequency of A₁ allele

$$p = 0.2055 + (\frac{1}{2} \times 0.702) = 0.5565$$

Minding Your Ps and Qs

Consider this "experiment":

- 1) Sample a genotype from popn
- 2) Sample an allele from that genotype



Probability of getting A₁ allele, p, is equal to

$$p = (x_{11} \times 1) + (x_{12} \times \frac{1}{2}) + (x_{22} \times 0)$$

The Hardy-Weinberg Law

Assumptions:

- Diploid sexual population
- Infinite population size
- Random mating
- no selection
- no migration
- no mutation

This is a Null model. Why is this useful?

Hardy-Weinberg

Write down genotype freqs in terms of allele freqs

Genotype:
$$A_1A_1$$
 A_1A_2 A_2A_2
H-W Frequency: p^2 $2pq$ q^2

$$p^2 + 2pq + q^2 = 1$$

Again ask yourself, where is this coming from?

Hardy-Weinberg

Write down genotype freqs in terms of allele freqs

```
Genotype: A_1A_1 A_1A_2 A_2A_2 H-W Frequency: p^2 2pq q^2

Prob(A<sub>1</sub> sperm & A<sub>1</sub> egg)
Prob(A<sub>2</sub> sperm & A<sub>2</sub> egg)

+ Prob(A<sub>2</sub> sperm & A<sub>1</sub> egg)
```

Hardy-Weinberg Numerical Example

Back to sickle cell anemia...

Genotype:	A_1A_1	A_1A_2	A_2A_2
H-W Frequency:	p^2	2pq	q^2
Observed Frequencies:	0.2055	0.702	0.0925
H-W Expected Frequencies:	0.309	0.494	0.197

Hardy-Weinberg Numerical Example

Back to sickle cell anemia...

Genotype:	A_1A_1	A_1A_2	A_2A_2
H-W Frequency:	p^2	2pq	q^2
Observed Frequencies:	0.2055	0.702	0.0925
H-W Expected Frequencies:	0.309	0.494	0.197

Pretty big deviations, could assess how big using statistics!

Heterozygosity

"temperature of a population"

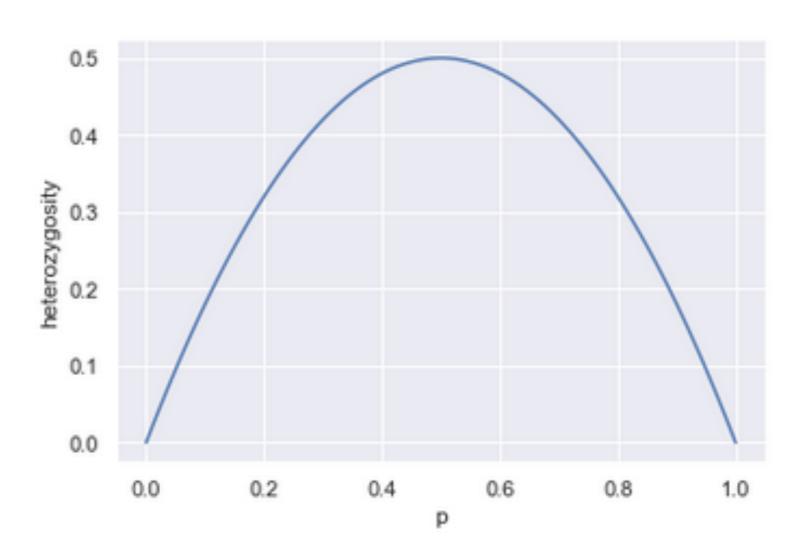
Genotype:
$$A_1A_1$$
 A_1A_2 A_2A_2
H-W Frequency: p^2 $2pq$ q^2

Call heterozygosity the probability of sampling an individual that is heterozygous

$$\hat{H} = 2pq = 2p(1-p)$$

Heterozygosity

"temperature of a population"



$$\hat{H} = 2pq = 2p(1-p)$$

The Hardy-Weinberg Law

Assumptions:

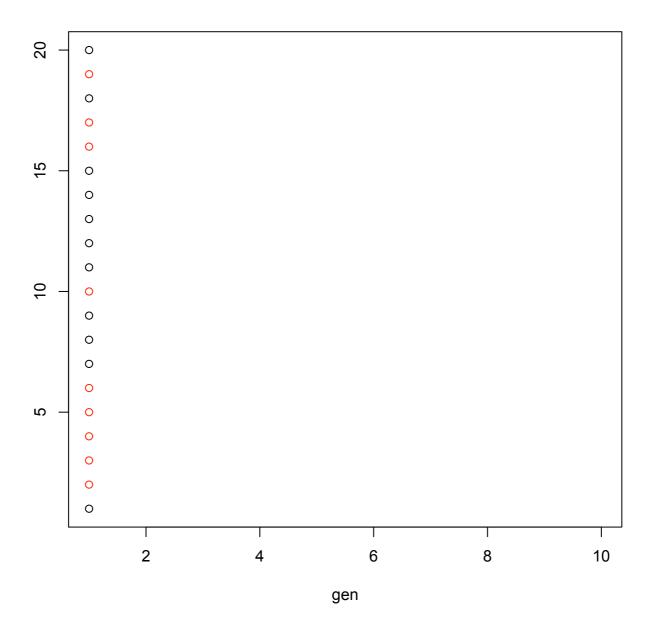
- Diploid sexual population
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This is a Null model. Why is this useful?

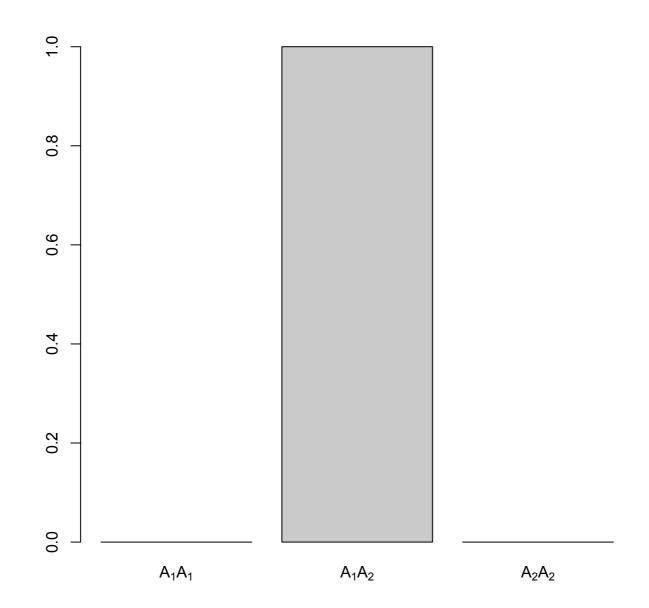
Genetic Drift: the algorithm

- 1. Choose an allele at random from the 2N alleles in the parental generation
- 2. Make an exact copy of the allele
- 3. Place the copy of the allele in the next generation
- 4. Go back to 1 until next generation has 2N alleles

Genetic Drift: the algorithm



Drift in population of size 1



What is probability of being heterozygote in next generation?

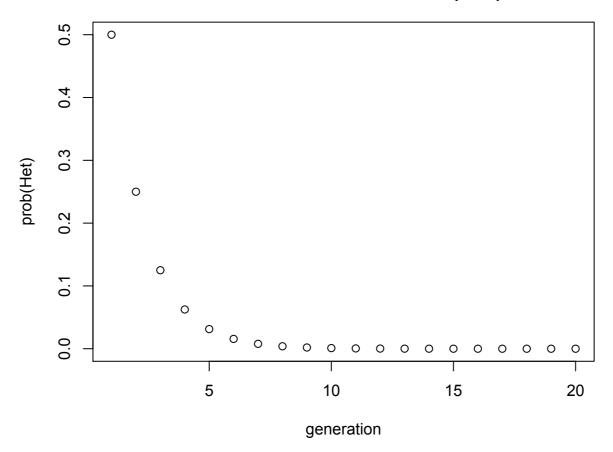
Drift in population of size 1

What is probability of being heterozygote in next generation?

$$Prob(Heterozygote) = \frac{1}{2}$$

$$Prob(Het|t) = \left(\frac{1}{2}\right)^t$$

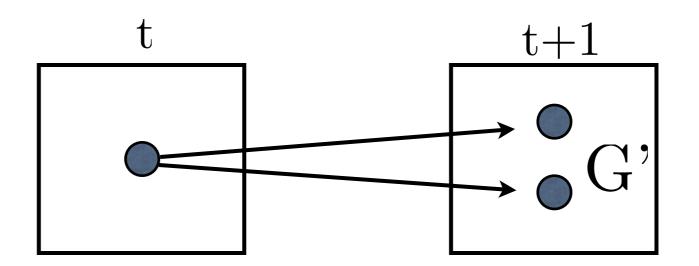
$$Prob(Het|t) = \left(\frac{1}{2}\right)^t$$



Question: How many generations until fixation on average?

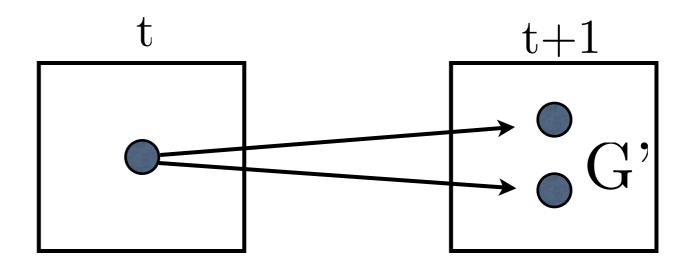
Identity by origin: two alleles that are from same locus on the **same** chromosome

Identity by state: two alleles that are of the same form (e.g. same DNA sequence)



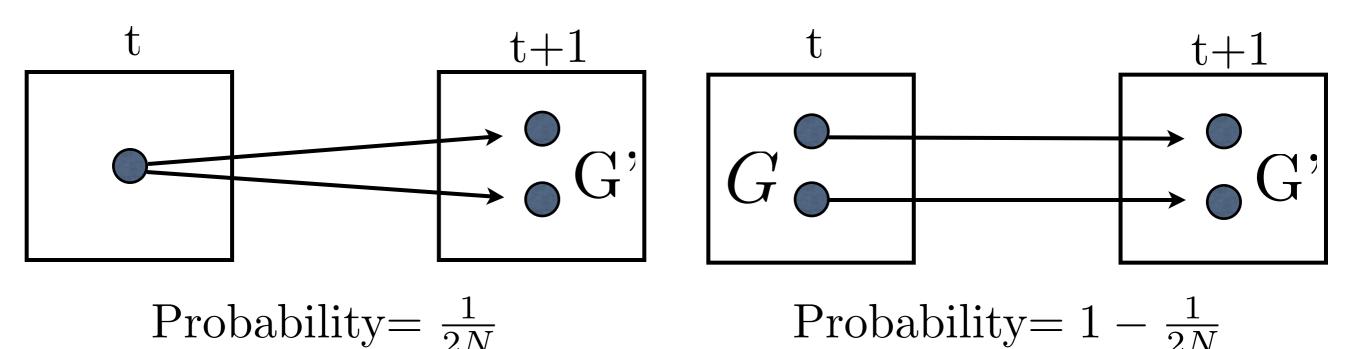
Probability that two alleles chosen at random are identical by state

No variation G = 1Every allele unique G = 0



Probability that two alleles chosen at random are identical by state

$$G' = \frac{1}{2N} + \left(1 - \frac{1}{2N}\right)G$$



$$G' = \frac{1}{2N} + \left(1 - \frac{1}{2N}\right)G$$

Probability that two alleles chosen at random are different by state

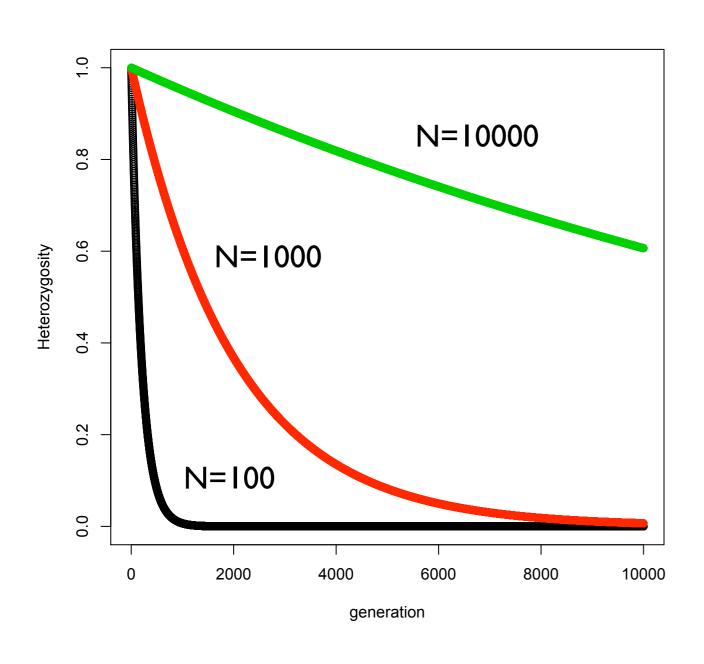
$$H = 1 - G$$

$$H' = 1 - G' = \left(1 - \frac{1}{2N}\right)H$$

$$\Delta_N H = H' - H$$

$$= \left(1 - \frac{1}{2N}\right)H - H$$

$$= -\frac{1}{2N}H$$



Difference Equation

$$H_t = H_0 \left(1 - \frac{1}{2N} \right)^t$$

Ultimately all Heterozygosity is lost!

So who fixes?

2N different alleles:
$$Prob(fix) = \frac{1}{2N}$$

i copies of an allele:
$$Prob(fix) = \frac{i}{2N}$$

So for neutral alleles: Prob(fix|p) = p