

## Gillespie Ch 1:

- Nucleotides -- ATGC --

- Must DNA similar b/t species

-- TAA **G**A A T --- Copy 1 ← each are also a double helix  
-- TAA **T**A A T --- Copy 2 ←  
↑

- Variant = "segregating site" = "polymorphic site"  
= location where differences occur

- SNP = single nucleotide polymorphism: location where difference is a single nucleotide

- Allele = type of difference  
E.g. above we have "G" allele and "T" allele

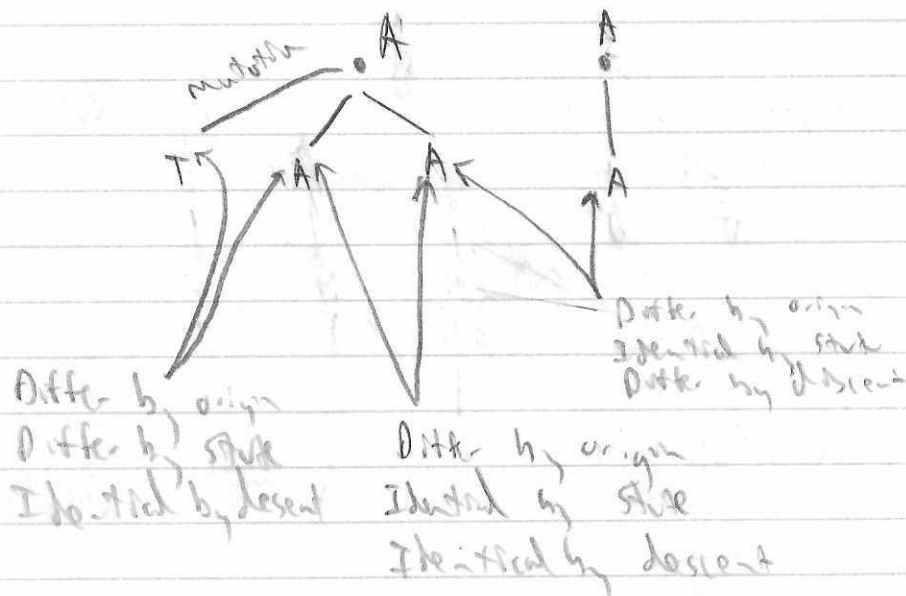
- Genotype = all copies of alleles  
E.g. "GT" for that individual

- Note: Sometimes Gillespie uses "Allele" to mean a different sequence at Alcohol Dehydrogenase (ADH) but many different SNPs together is just a type of difference "Allele", some folks would call this a haplotype.

- Locus = location on genome (plural, loci)

- Allele differs by origin if on different chromosomes
- Differ by state if different sequence
- Differ by descent if allele does not share common ancestor.

Ex.)



Identical by origin  $\Rightarrow$  Identical by state and descent

Identical by state  $\Rightarrow$  (usually) identical by descent  
 $\uparrow$  mutation is rare

Identical by descent  $\nRightarrow$  identical by state  
 Identical by state  $\nRightarrow$  identical by origin

<sup>Diploid</sup>  
• Homozygous: Individual has both alleles identical by state

• Heterozygous: Diploid individual's alleles differ by state.

• Allele frequency: Proportion of genes that have an allele

• Genotype frequency: Proportion of individuals that have a genotype.

Ex.) AA, AT, TT, AT, AA

$$A \text{ allele frequency} = \frac{6}{10}$$

$$AT \text{ genotype frequency} = \frac{2}{5}$$

Let's call one allele  $A_1$  and the other  $A_2$  that differ by state

|                    |          |          |          |          |
|--------------------|----------|----------|----------|----------|
| Genotypes          | $A_1A_1$ | $A_1A_2$ | $A_2A_1$ | $A_2A_2$ |
| Genotype frequency | $x_{11}$ | $x_{12}$ |          | $x_{22}$ |

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

Allele frequency

$$\text{of } A_1: p = x_{11} + \frac{1}{2} x_{12}$$

$$\text{of } A_2: q = 1 - p = x_{22} + \frac{1}{2} x_{12}$$

$$p = \begin{matrix} \text{pick } A_1 A_1 & \text{pick } A_1 & \text{pick } A_1 A_2 & \text{pick } A_1 & \text{pick } A_2 A_2 & \text{pick } A_1 \\ \downarrow & \downarrow & \downarrow & \downarrow & \downarrow & \downarrow \\ X_{11} \cdot 1 & + & X_{12} \cdot \frac{1}{2} & + & X_{22} \cdot 0 \end{matrix}$$

$$1.1.) \quad \binom{n}{2} + n = \frac{n(n-1)}{2} + n = \frac{n(n+1)}{2}$$

$$1.2.) \quad S: \frac{2 \cdot 141 + 111 + 32}{2 \cdot 332} = 0.6401$$

$$F: \frac{2 \cdot 28 + 111 + 15}{2 \cdot 332} = 0.2741$$

$$I: \frac{2 \cdot 5 + 15 + 32}{2 \cdot 332} = 0.08584$$

HWE: Consider  $A_i$  to be a success  
 $X = \#$  of  $A_i$ 's in a randomly sampled individual

If alleles are independent, then  $X \sim \text{Bin}(2, p)$

Independent: Large population size  
 Random mating  
 No selection  
 No migration

genotype frequencies

$$\begin{aligned}
 P_r(X=2) &= p^2 &= & x_{22} \\
 P_r(X=1) &= 2p(1-p) &= & x_{12} \\
 P_r(X=0) &= (1-p)^2 &= & x_{11}
 \end{aligned}$$

• HWE is reached in one generation in hermaphrodites

$$P_r(A_1A_1) = \underbrace{P_r(Egg=A_1)}_p \cdot \underbrace{P_r(Sperm=A_1)}_p = p^2$$

$$P_r(A_2A_2) = (1-p)^2$$

$$\begin{aligned}
 P_r(A_1A_2) &= \underbrace{P_r(Egg=A_1)}_p \cdot \underbrace{P_r(Sperm=A_2)}_{1-p} + \underbrace{P_r(Egg=A_2)}_{1-p} \cdot \underbrace{P_r(Sperm=A_1)}_p \\
 &= 2p(1-p)
 \end{aligned}$$

Note: ① Allele frequencies do not change under random mating

② In 2-sex species, it takes 2 generations

③ only need allele freq to get genotype freq.

1.3.) Female genotype freqs:  $x_{11}, x_{12}, x_{22}$   
 male genotype freqs:  $y_{11}, y_{12}, y_{22}$

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

$P_r(A_1A_1) = pq$

$P_r(A_1A_2) = p(1-q) + q(1-p)$

$P_r(A_2A_2) = (1-p)(1-q)$

↑ Genotype freq for all individuals, regardless of sex  
 ↑ so by previous argument, next generation is HWE

1.4.) See R

• Ratio of  $A_1A_2$  frequency to  $A_2A_2$  freq

$$\frac{P_r(A_1A_2)}{P_r(A_2A_2)} = \frac{2pq}{q^2} = \frac{2p}{q} \approx \frac{2}{q}$$

↑  
for small  $q$

• If have alleles  $A_1, \dots, A_n$  w/ allele freqs  $p_1, \dots, p_n$

Under HWE:  $P_r(A_iA_i) = p_i^2$   
 $P_r(A_iA_j) = 2p_i p_j$

homozygote

$G = P_r(\text{homo}) = \sum_{i=1}^n p_i^2$

heterozygote

$H = P_r(\text{hetero}) = 1 - G = 1 - \sum_{i=1}^n p_i^2$

only under H<sub>0</sub>

Heterozygosity = frequency of heterozygotes

but this is used more generally

$$\sum \frac{(\text{Obs} - \text{Exp})^2}{\text{Obs}}$$

| Obs | Exp |
|-----|-----|
| 141 |     |
| 111 |     |
| 28  |     |
| 32  |     |
| 15  |     |
| 5   |     |

1.7.)  $p_f = A_1$  frequency for females  
 $p_m = A_1$  frequency males

Males only have one copy



Men:  $P(A_1) = p_f$

females:  $P(A_1 A_1) = p_f p_m$   
 $P(A_1 A_2) = p_f(1-p_m) + (1-p_f) p_m$   
 $P(A_2 A_1) = (1-p_f)(1-p_m)$

Ne  $p_f = p_f p_m + \frac{1}{2} p_f + \frac{1}{2} p_m - \frac{1}{2} p_f p_m + \frac{1}{2} p_m - \frac{1}{2} p_f p_m$   
 $= \frac{1}{2} (p_f + p_m)$

Each generation:

$$p_m^{(old)} = p_f^{(old)}$$

$$p_f^{(new)} = \frac{1}{2} (p_m^{(old)} + p_f^{(old)})$$

$$p_f^{(1)} = p_f$$

$$p_m^{(1)} = p_m$$

$$p_f^{(2)} = \frac{1}{2} (p_m + p_f)$$

$$p_m^{(2)} = p_f$$

$$p_f^{(3)} = \frac{1}{2} \left( p_f + \frac{1}{2} (p_m + p_f) \right)$$

$$= \frac{3}{4} p_f + \frac{1}{4} p_m$$

$$p_m^{(3)} = \frac{1}{2} (p_m + p_f)$$

$$p_f^{(4)} = \frac{1}{2} \left( \frac{1}{2} p_m + \frac{1}{2} p_f + \frac{3}{4} p_f + \frac{1}{4} p_m \right)$$

$$= \frac{5}{8} p_f + \frac{3}{8} p_m$$

$$p_m^{(4)} = \left( \frac{3}{4} p_f + \frac{1}{4} p_m \right)$$

$$x_i = \frac{1}{2} (x_{i-2} + x_{i-1})$$

$$x_0 = p_m$$

$$x_1 = p_f$$