§5: Nonrandom Mating

- In this chapter, 2 ways

  1.) Inbreeding - more likely to mate w/ relatives
  2) Population subdivision (aka "structure")

- Genotype Frequencies

$A_1 A_1$	$p^2(1-F) + pF$	x_{11}
$A_1 A_2$	$2p(1-p)(1-F)$	x_{12}
$A_2 A_2$	$(1-p)^2(1-F) + (1-p)F$	x_{22}

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

- How many df for general genotype frequencies? 2

- How many df for model w/ param F? 2

- When is HWE reached? $F = 0$

- For $0 < F \leq 1$, more or less homozygotes? More

- For $F < 0$, more or less homozygotes? Less

- If $0 \leq F \leq 1$, then F is interpreted as the probability of homozygosity due to special circumstances (PHSC)
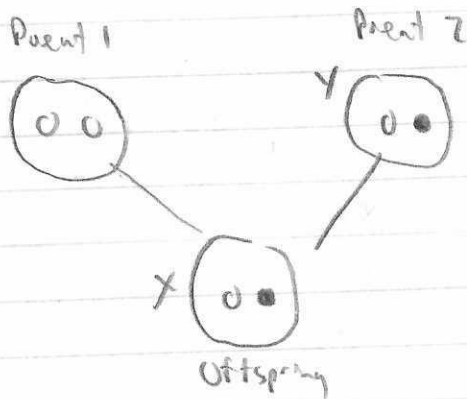
- $Pr(A_1 A_1) = \underbrace{p}_{Pr(A_1)} \left(\underbrace{F}_{PHSC} + \underbrace{(1-F)}_{Not\ PHSC} \underbrace{p}_{Pr(A_1)} \right)$

- "Special circumstances" = Inbreeding and subdivision.

- Describing Relationships
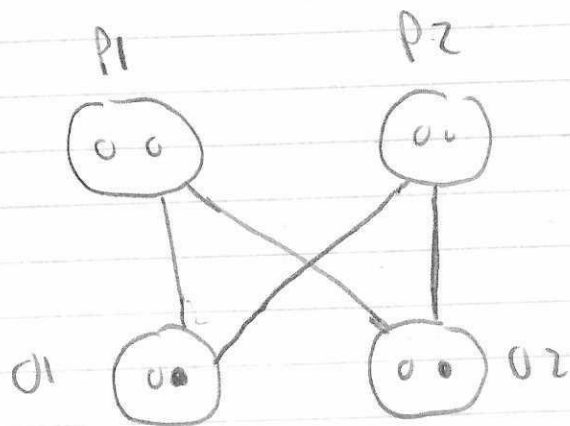- Kinship coefficient = $Pr(2 \text{ alleles are IBD})$

Parent / offspring

Parent 1   Parent 2

X ... Offspring

Kinship between Offspring X and Parent Y?

1) Choose 2 alleles at random from each individual
2) Calculate $Pr(IBD)$

In this case $Pr(IBD) = \frac{1}{4} = \underbrace{Pr(\text{allele from } Y)}_{\frac{1}{2}} \underbrace{Pr(\text{same allele } | ...}_{\frac{1}{2}}$

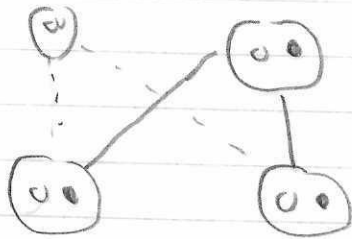Full sibs

P1   P2

O1   O2

$$\underbrace{Pr(\text{Both from } P1)}_{\frac{1}{4}} \underbrace{Pr(\text{sae} \mid p1)}_{\frac{1}{2}} + \underbrace{Pr(\text{Both} \sim P2)}_{\frac{1}{4}} \underbrace{Pr(\text{Sae} \mid P2)}_{\frac{1}{2}}$$
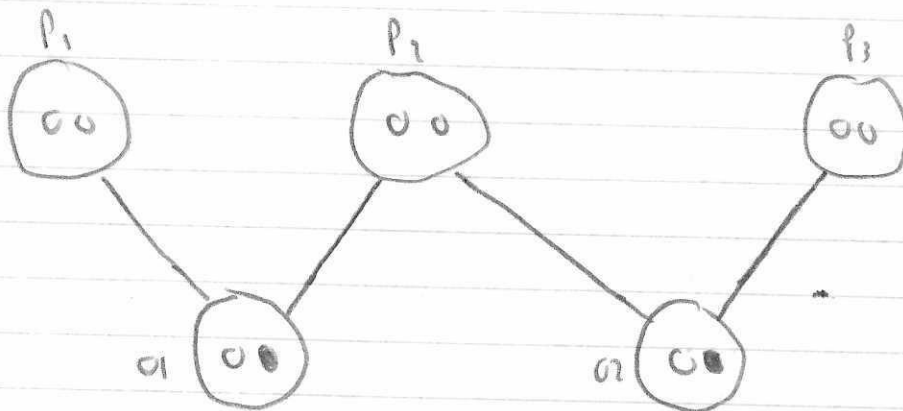
$$= \frac{1}{4}$$

- Anotur way: WLOG, choose whch puent allele it comes to

$\hookrightarrow$ Now sae calculaton as 1 poent $\left(\frac{1}{4}\right)$
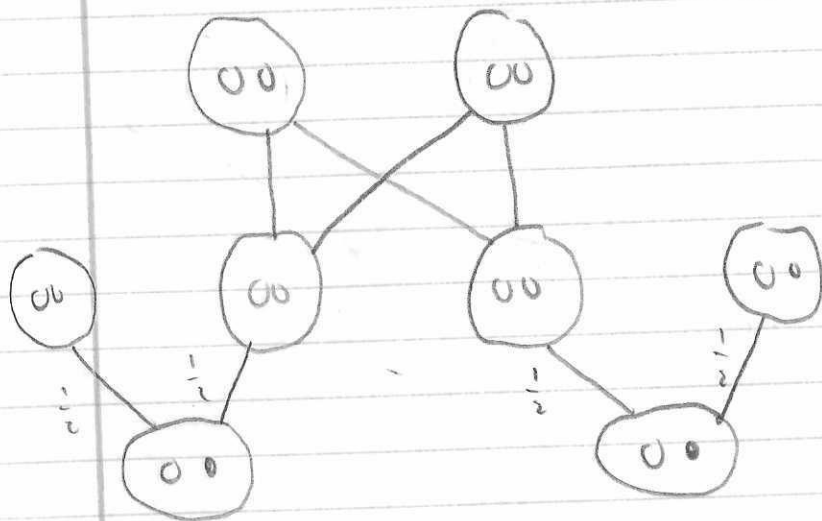
- Exercise: half sibs

$$\underbrace{Pr(\text{Both from } P1)}_{\frac{1}{4}} \underbrace{Pr(\text{Sae} \mid \text{Both } P1)}_{\frac{1}{2}}$$

$$= \frac{1}{8}$$

Exercida: First Cousins

$$\frac{1}{4} \cdot P_r(IBD \mid full \; sibs) = \frac{1}{4} \cdot \frac{1}{4} = \frac{1}{16}$$

- Let r_0, r_1, r_2 be Prob share $0, 1, or \; 2$ copies

- Parent / offspring:
$$r_0 = 0$$
$$r_1 = 1$$
$$r_2 = 0$$

- Full sibs:
$$r_0 = \frac{1}{4} \quad (Prob \; the \; other \; 2)$$
$$r_1 = \frac{1}{2}$$
$$r_2 = \frac{1}{4}$$

Kinship: $f_{xy} = r_0 \cdot 0 + r_1 \cdot \frac{1}{4} + r_2 \cdot \frac{1}{2}$

$$\underbrace{\qquad}_{Pr(same \mid share 1)} \quad \underbrace{\qquad}_{Pr(same \mid share 2)}$$

- Inbreeding Coefficient: $F_I = \Pr(2 \text{ alleles in same individual are identical by descent})$

= Kinship of individual's parents

- $\Pr(A_1 A_1) = \underbrace{F_I}_{\Pr(IBD)} \underbrace{p}_{(A_1 | IBD)} + \underbrace{(1-F_I)}_{\Pr(!IBD)} \underbrace{p^2}_{\Pr(A_1 | !IBD)}$

- F_I is same as generalized HwE
  - { So F_I can be interpreted as $\Pr(IBD)$

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§5.5: Genetic Subdivision:

Group 1 in HwE

$p = \frac{1}{4}$

Group 2 in HwE

$p = \frac{3}{4}$
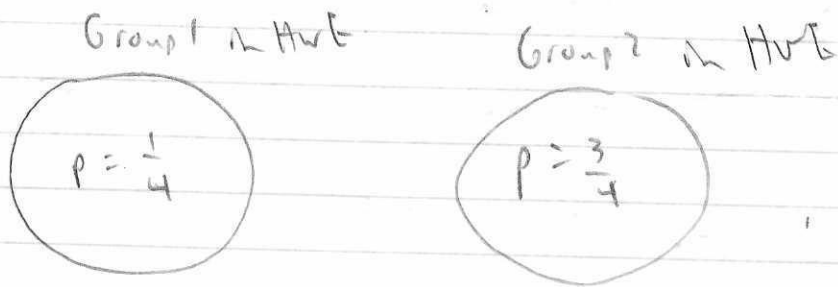
	A_1	$A_1 A_1$	$A_1 A_2$	$A_2 A_2$
G1	$\frac{1}{4}$	$1/16$	$3/8$	$9/16$
G2	$\cdot 3/4$	$9/16$	$3/8$	$4/16$
Species	$1/2$	$5/16$	$3/8$	$5/16$
HwE	$1/2$	$1/4$	$1/2$	$1/4$

} excess homozygosity

Here, $F_{ST} = 1/4$

$2p(1-p)(1-F) = 3/8$

$\Rightarrow 2 \cdot \frac{1}{2} \cdot \frac{1}{2}(1-F) = 3/8$

$\Rightarrow 1-F = 3/4$

$\Rightarrow F = 1/4$

- F_{ST} = amount deviate from HWE due to structure
  F_I = amount deviate from HWE due to inbreeding

- In practice, can't tell if it is due to structure or inbreeding.

- Another view of F_{ST}; c_i = Proportion species from patch i

Genotype	$A_1 A_1$	$A_1 A_1$	$A_2 A_2$
In ith Patch	p_i^2	$2p_i(1-p_i)$	$(1-p_i)^2$
In Species	$\sum c_i p_i^2$	$\sum c_i 2p_i(1-p_i)$	$\sum c_i (1-p_i)^2$
In Species	$p^2(1-F_{ST}) + pF_{ST}$	$2p(1-p)(1-F_{ST})$	$(1-p)^2(1-F_{ST}) + (1-p)F_{ST}$

$\Rightarrow 2p(1-p)(1-F_{ST}) = \sum c_i 2p_i(1-p_i)$

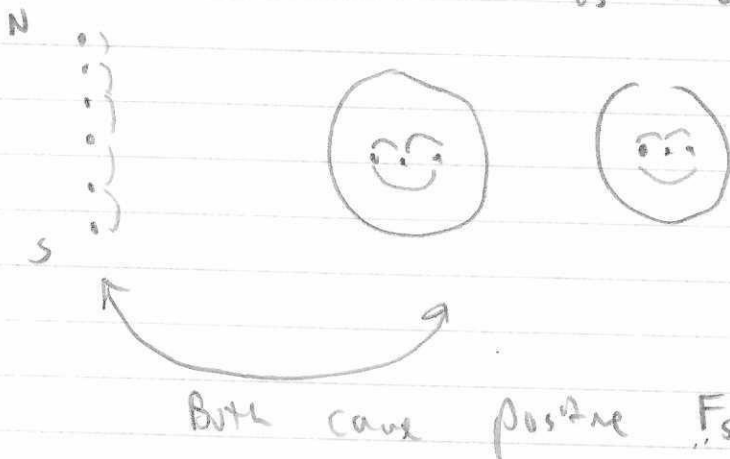$\Rightarrow F_{ST} = \dfrac{2p(1-p) - \sum c_i 2p_i(1-p_i)}{2p(1-p)}$

$= \dfrac{\sum c_i (p_i^2 + (1-p_i)^2) - p^2 - (1-p)^2}{1 - p^2 - (1-p)^2}$
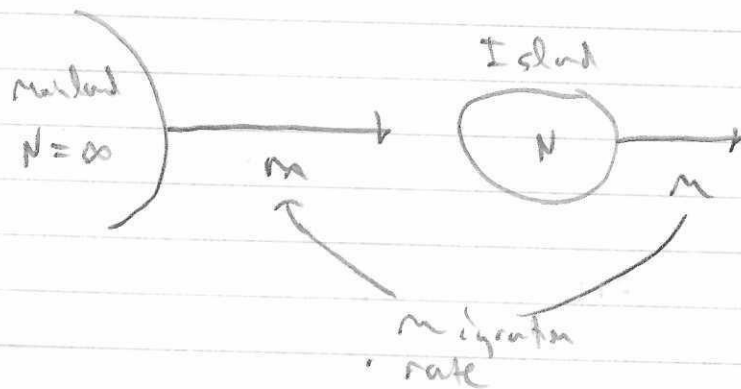
$= G_S - G_T$

$$G_T = p^2 + q^2 = Pr(\text{identical by state})$$

$$G_S = Pr(\text{identical by state | same patch})$$

- F_{ST}: How much higher G_S is to G_T

- Excess homozygosity caused by structure is called "Wahlund's effect"

- F_{ST} does not tell us much about structure

Both cause positive F_{ST}

- <u>F_{ST} and The Island Model</u>

migration rate

different alleles in Island each generation $= 2Nm$

- Only $\underbrace{\text{genetic drift}}_{\text{removes variation}}$ and $\underbrace{\text{migration.}}_{\text{adds variation}}$ They eventually reach equilibrium.

- What is heterozygosity at equilibrium (if each migrant allele is unique)

$$\mathcal{H} = \frac{4Nm}{1 + 4Nm}$$

$$\Rightarrow \mathcal{G} = \frac{1}{1 + 4Nm}$$

$$\Delta_m \mathcal{H} = 2m(1 - \mathcal{H})$$

$\underbrace{}$
change due
to migration

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

$\underbrace{}$
change due to
drift

- $4Nm \approx 0 \Rightarrow \mathcal{G} \approx 1$ (large structure effects)
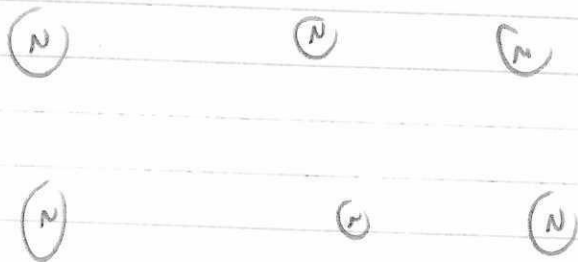 $4Nm \gg 1 \Rightarrow \mathcal{G} \approx 0$ (same as large island)

  If $m > \mathcal{O}\left(\frac{1}{4N}\right)$ then effects of migration negligible
  $\underset{\uparrow}{}$ balance out

  $\Rightarrow 2Nm > \frac{1}{2}$

  [s. one migrant every other generation is enough to

- <u>Message</u>: Weak migration is enough to counteract subdivision

- Island Model

Each island chooses $2Nm$ of folks from other islands.

$\hookrightarrow$ definitely many islands.

$\hookrightarrow$ for each island, every other island combined is the "mainland".

$$G_S = \frac{1}{1 + 4Nm} \quad \text{for } \underline{each} \text{ island} \quad \left(\begin{array}{l}\text{within island}\\ \text{homozygosity}\end{array}\right)$$

Overall homozygosity is $G_T = 0$ (definite pop)

$$F_{ST} = \frac{G_S - G_T}{1 - G_T} = \frac{1}{1 + 4Nm}$$

$\hookrightarrow$ know F_{ST} and N $\Rightarrow$ know m