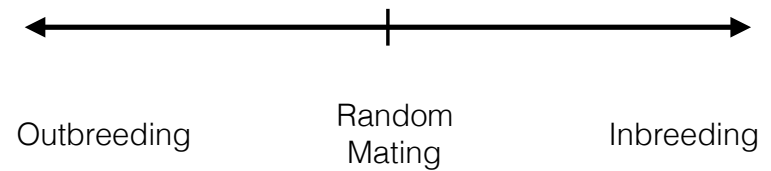




Non-Random Mating



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Loss of Genotypes

	A	B
A	AA	AB
B	AB	BB

Allele frequencies stay the same!

3

Allele Identity

Autozygous - Two alleles are the same because they can be traced directly back to a common ancestor.

$$pF$$

4

Expected Genotype Frequency

$$E[AA] = p^2(1 - F) + pF$$

Diagram illustrating the expected genotype frequency $E[AA]$ based on the inbreeding coefficient F :

- When $F = 0$, $E[AA] = p^2$.
- When $F = 1$, $E[AA] = p$.
- When $F = -1$, the result is unknown (indicated by a question mark).

5

Estimation of F

$$F = \frac{H_E - H_O}{H_E}$$

$$= 1 - \frac{H_O}{H_E}$$

Estimate of F is 'relative' to the expected frequency of heterozygotes under HWE

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Example from `arapat`

Complete Selfing

Mating Frequencies

$$P = f(AA)$$

$$Q = f(AB)$$

$$R = f(BB)$$

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Mating Frequencies

Parental Genotype	Offspring Genotype	Frequency
AA	AA	P
AB	1/4 AA	Q/4
	1/2 AB	Q/2
	1/4 BB	Q/4
BB	BB	R

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$$P_{t+1} = P_t + \frac{Q_t}{4}$$

Parental Genotype	Offspring Genotype	Frequency
AA	AA	P
AB	1/4 AA	Q/4
	1/2 AB	Q/2
	1/4 BB	Q/4
BB	BB	R

$$Q_{t+1} = \frac{Q}{2}$$

$$R_{t+1} = R_t + \frac{Q_t}{4}$$

$$\begin{aligned}
 p_{t+1} &= P_{t+1} + \frac{1}{2}Q_{t+1} \\
 &= \left(P_t + \frac{1}{4}Q_t\right) + \frac{1}{2}\left(\frac{1}{2}Q_t\right) \\
 &= P_t + \frac{1}{2}Q_t \\
 &= p_t
 \end{aligned}$$

Inbreeding **DOES NOT** change allele frequencies,
only genotype frequencies!

Generational Changes in F

$$F_1 = 1 - \frac{H_O}{H_E} = 1 - \frac{Q_1}{2pq}$$

$$F_2 = 1 - \frac{\frac{Q_1}{2}}{2pq}$$

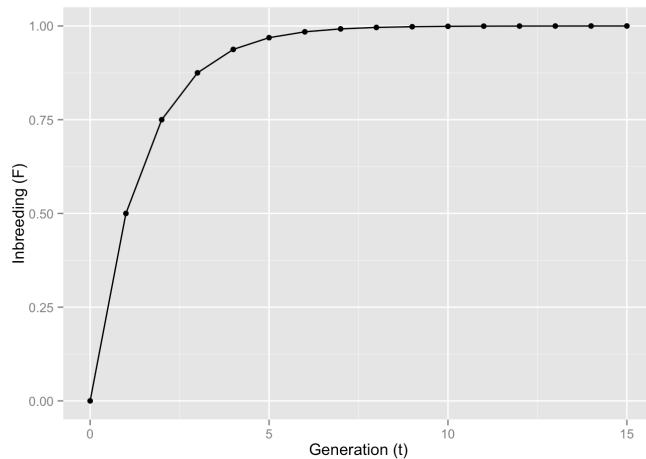
$$F_3 = \frac{\frac{Q_2}{2}}{2pq} = \frac{\frac{Q_1}{2}}{2pq}$$

$$F_4 = \frac{\frac{Q_3}{2}}{2pq} = \frac{\frac{Q_2}{2}}{2pq} = \frac{\frac{Q_1}{2}}{2pq}$$

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$$F_{t+1} = \frac{1}{2} + \frac{1}{2}F_t$$

$$F_t = 1 - \left(\frac{1}{2}\right)^t (1 - F_O)$$

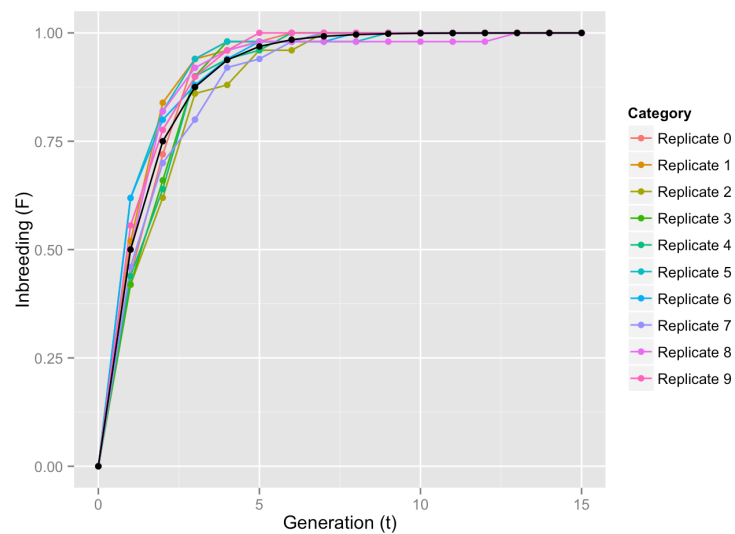


```
t <- 1:20
F <- 1 - 0.5^t
df <- data.frame( t, F)
ggplot(df,aes(t,F)) + geom_line() + geom_point() + xlab("Generation (t)") + ylab("Inbreeding (F)")
```

```
require(gstudio)
AA <- locus( c("A","A") )
AB <- locus( c("A","B") )
BB <- locus( c("B","B") )
pop <- data.frame(ID=1:100, Locus1=c( rep(AA,25), rep(AB,50), rep(BB,25) ) )

genetic_diversity(pop,mode="Fis")
## Locus Fis
## 1 Locus1 0

T <- 1:15
df$Category = "Expectations"
for( rep in 0:9 ) {
  data <- pop
  F <- rep(0, length(T) )
  for(t in T){
    # estimate F
    F[(t+1)] <- genetic_diversity(data,mode="Fis")$Fis[1]
    # self all adults to make offspring
    data <- mate( data, data, N=1 )
  }
  df.rep <- data.frame( T, F, Category=paste("Replicate",rep))
  df <- rbind( df, df.rep )
}
```



Mixed Mating Systems

Category	Mating	Frequency	E[AA]	E[AB]	E[BB]
Selfed (s)	AA x AA	sP	sP		
	AB x AB	sQ	sQ/4	sQ/2	sQ/4
	BB x BB	sR			sR
Outcross (1-s)	AA x AA	(1-s)P ²	(1-s)P ²		
	AA x AB	(1-s)2PQ	(1-s)PQ	(1-s)PQ	
	AA x BB	(1-s)2PR		(1-s)2PR	
	AB x AB	(1-s)Q ²	(1-s)Q ² /4	(1-s)Q ² /2	(1-s)Q ² /4
	AB x BB	(1-s)2QR		(1-s)QR	(1-s)QR
	BB x BB	(1-s)R ²			(1-s)R ²

$$\begin{aligned}
 E[\text{AA}]_{t+1} &= sP_t + s\frac{Q_t}{4} + (1-s)P_t^2 + (1-s)P_tQ_t + (1-s)\frac{Q_t^2}{4} \\
 &= \dots \\
 &= s\left[P_t + \frac{Q_t}{4}\right] + (1-s)p_t^2
 \end{aligned}$$

$$E[\text{AB}]_{t+1} = s\frac{Q_t}{2} + (1-s)2p_tq_t$$

$$E[\text{BB}]_{t+1} = s\left[R_t + \frac{Q_t}{4}\right] + (1-s)q_t^2$$

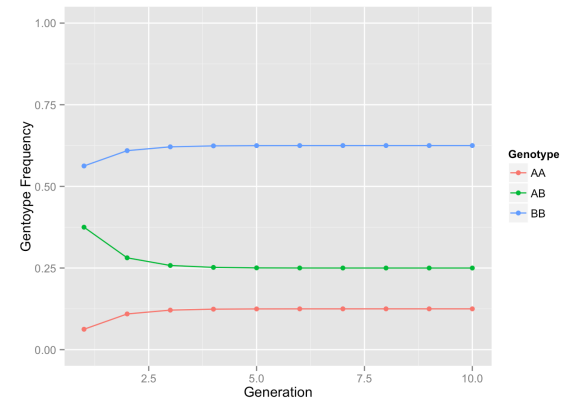
```

p <- fAA <- fAB <- fBB <- rep(NA,10)
p[1] <- 0.25
fAA[1] <- p[1]^2
fAB[1] <- 2*p[1]*(1-p[1])
fBB[1] <- (1-p[1])^2
cbind(p,fAA,fAB,fBB)
##      p      fAA      fAB      fBB
## [1,] 0.25 0.0625 0.375 0.5625
## [2,] NA      NA      NA      NA
## [3,] NA      NA      NA      NA
## [4,] NA      NA      NA      NA
## [5,] NA      NA      NA      NA
## [6,] NA      NA      NA      NA
## [7,] NA      NA      NA      NA
## [8,] NA      NA      NA      NA
## [9,] NA      NA      NA      NA
## [10,] NA      NA      NA      NA

s <- 0.5
for(i in 2:10){
  fAA[i] <- s*(fAA[i-1] + fAB[i-1]/4) + (1-s)*p[i-1]^2
  fAB[i] <- s*fAB[i-1]/2 + (1-s)*2*p[i-1]*(1-p[i-1])
  fBB[i] <- s*(fBB[i-1] + fAB[i-1]/4) + (1-s)*(1-p[i-1])^2
  p[i] <- fAA[i] + fAB[i]/2
}

```

Equilibrium Genotype Frequencies (s=0.5)



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Equilibrium Heterozygosity

$$\hat{Q} = s \frac{\hat{Q}}{2} + (1-s)2pq$$

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Equilibrium F

$$\hat{Q} = \frac{(1-s)4pq}{2-s}$$

$$F = 1 - \frac{H_O}{H_E}$$

$$\hat{F} = \frac{s}{2-s}$$

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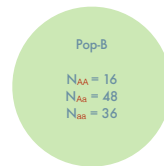
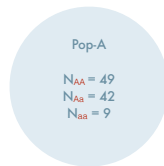
Expected F @ t

$$F_t = \frac{s}{2-s} \left[1 - \frac{s^t}{2} \right] + \left[\frac{s}{2} \right]^t F_0$$

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Wahlund Effects

Unknown Partitioning



1. What is F for each population?
2. What is F if you combined populations?

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