

# Introductory Models, Effective Population Size

# Models

- Intentional simplification of complex relationships
  - Eliminate extraneous detail, focus on key parameters
  - Appropriate and useful first approximations
- Evaluate fit of data to model
  - Poor fit may implicate violation of model assumptions
  - Refining of models tells us which parameters most important
- Population genetics relies heavily on mathematical models
  - Specify the mathematical relationships among parameters that characterize a population

# Random Mating

- One of the most important models in population genetics
- Frequency of mating pairs determined by genotype frequencies

Male Genotype

Frequency

$A_1A_1$  ( $P_M$ )

$A_1A_2$  ( $H_M$ )

$A_2A_2$  ( $Q_M$ )

Female Genotype Frequency

$A_1A_1$  ( $P_F$ )

$A_1A_2$  ( $H_F$ )

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$P_M P_F$

$P_M H_F$

$P_M Q_F$

$H_M P_F$

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$H_M Q_F$

$Q_M P_F$

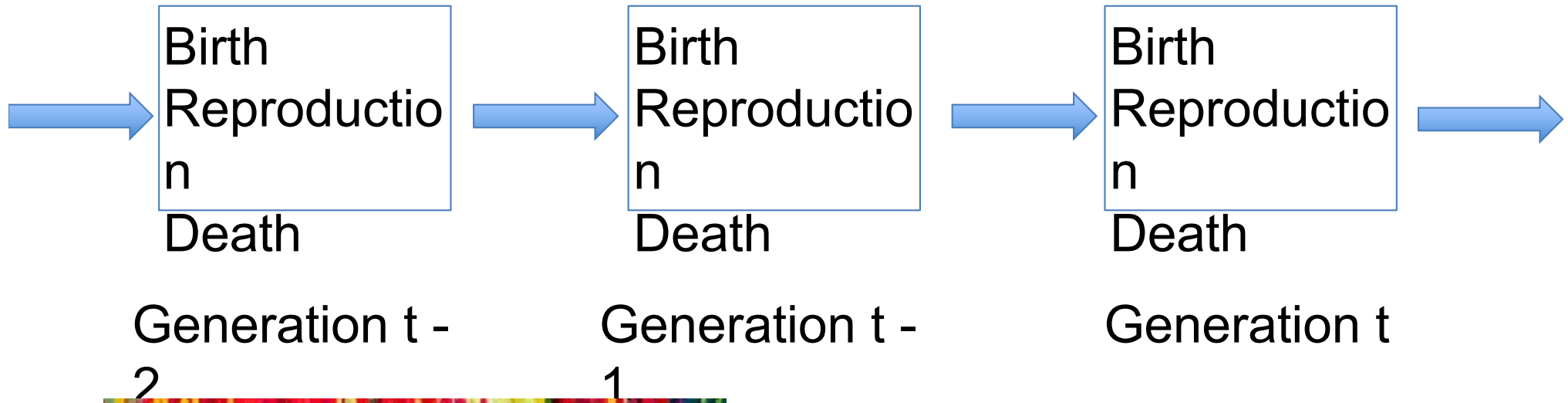
$Q_M H_F$

$Q_M Q_F$

# Random Mating

- One of the most important models in population genetics
- Frequency of mating pairs determined by genotype frequencies
- Also called 'panmictic' model

# Non-overlapping Generations



# Hardy-Weinberg Model

- Both models convenient first approximations for complex populations
- What happens when we combine them?
- What are consequences of random mating in a non-overlapping generation model?



Godfrey Harold Hardy



Wilhelm Weinberg

# HW Model Assumptions

- Discrete generations
- Random mating
- Sexual reproduction
- Diploid
- Bi-allelic locus
- Allele frequencies equal in males, females
- Large population size
- No migration
- No mutation
- No selection



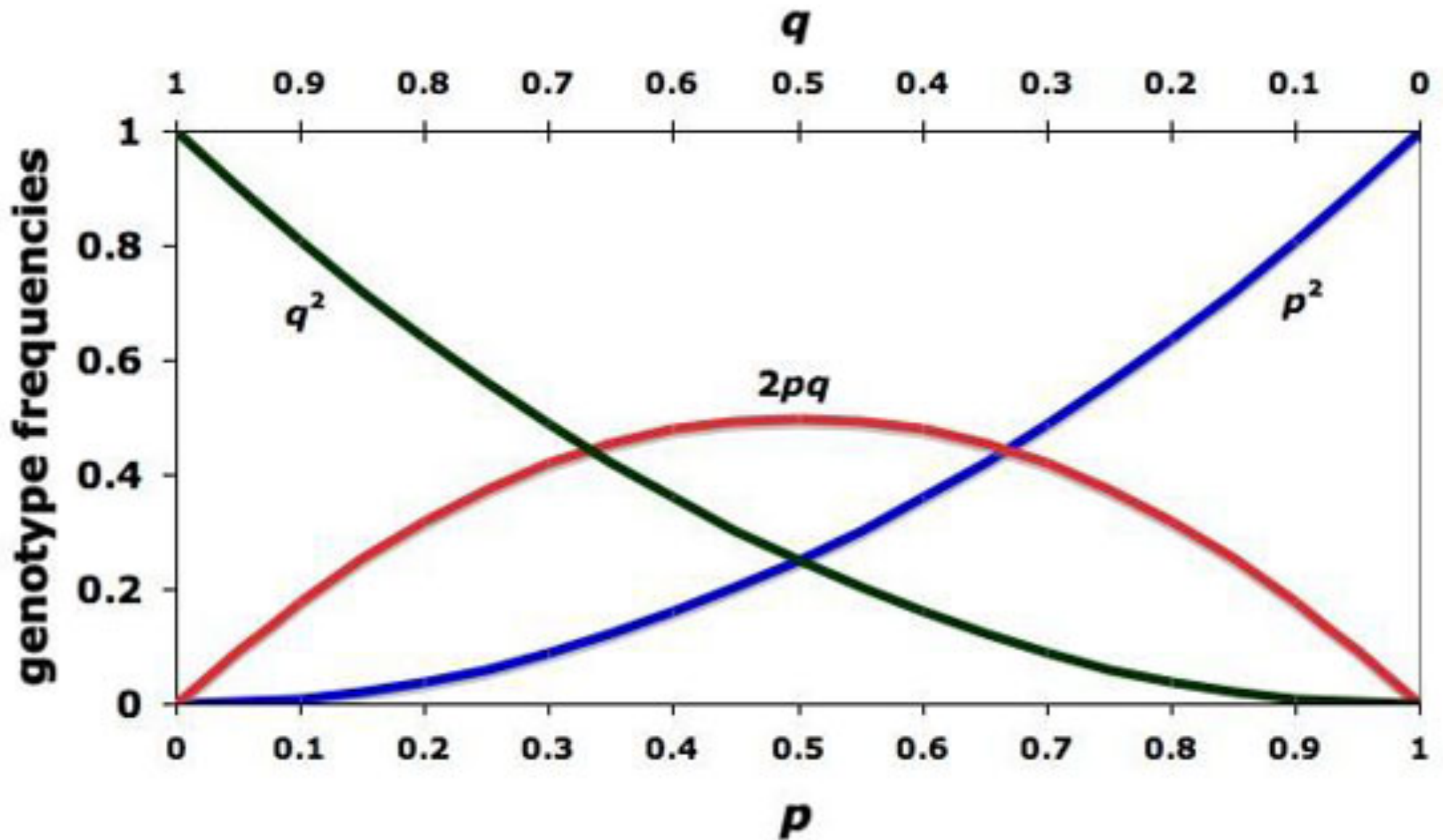
# Hardy-Weinberg Principle

- One of first major principles in population genetics
- Describes relationship between **genotype** frequency and **allele** frequency
  - Equilibrium state
- Autosomal locus with alleles A, a
  - Frequencies of A, a:  $p$ ,  $q$
- Genotypes AA, Aa, aa

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  - HW frequencies:  $p^2$ ,  $2pq$ ,  $q^2$

# HWE Genotype Frequencies



# Hardy-Weinberg Principle

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  - Frequencies of A, a:  $p$ ,  $q$
- Genotypes AA, Aa, aa
  - HW frequencies:  $p^2$ ,  $2pq$ ,  $q^2$
- Once at HWE, allele & genotype freq constant

# Random Genetic Drift

- Hardy-Weinberg equilibrium predicts:
  - 1) Allele frequencies remain constant
  - 2) Genotype frequencies predicted by allele frequencies
- HW model assumes infinite population size
- With **finite** population size, allele frequencies change over time due to sampling
- Random genetic drift: stochastic change in allele frequencies due to finite sampling of gametes

# Random Genetic Drift

- Haploid population of size  $N$
- Two alleles:  $A$ ,  $a$
- At generation  $t$ 
  - Frequency of  $A$  is  $p$
- Frequency of  $a$  is  $q = (1-p)$

What is frequency of  $A$  at generation  $t + 1$ ?

# Random Genetic Drift

In generation  $t$ ,  $\text{freq}(A) = p$ ,  $\text{freq}(a) = (1-p)$

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  - $\text{Pr}(2A) =$

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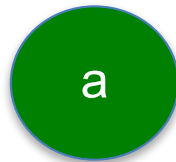
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$$\text{Pr} = p(1 - p)$$



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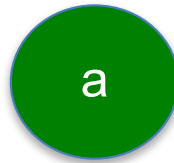
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- Randomly select 2 individuals to be parents
  - $\text{Pr}(2A) = p^2$
  - $\text{Pr}(1A) = 2p(1-p)$
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# Random Genetic Drift

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- Randomly select 3 individuals to be parents

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  - $\text{Pr}(2A) = p^2$
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  - $\text{Pr}(0A) = (1 - p)^2$
- Randomly select 3 individuals to be parents
  - $\text{Pr}(3A) =$
  - $\text{Pr}(2A) =$
  - $\text{Pr}(1A) =$
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# Random Genetic Drift

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  - $\text{Pr}(0A) = (1 - p)^2$
- Randomly select 3 individuals to be parents
  - $\text{Pr}(3A) = p^3$
  - $\text{Pr}(2A) = 3p^2(1 - p)$
  - $\text{Pr}(1A) = 3p(1 - p)^2$
  - $\text{Pr}(0A) = (1 - p)^3$

# Random Genetic Drift

In generation  $t$ ,  $\text{freq}(A) = p$ ,  $\text{freq}(a) = (1-p)$

- Randomly select  $N$  individuals to be parents

$$\Pr(j \text{ alleles of type } A) = \binom{N}{j} p^j (1-p)^{N-j}$$

What is frequency of  $A$  at generation  $t + 1$ ?

# Random Genetic Drift

Frequency of A	Generation(t+1)
0/N	$\binom{N}{0}(p_t)^0(1-p_t)^{N-0}$
1/N	$\binom{N}{1}(p_t)^1(1-p_t)^{N-1}$
2/N	$\binom{N}{2}(p_t)^2(1-p_t)^{N-2}$
.	
.	
.	
N/N	$\binom{N}{N}(p_t)^N(1-p_t)^0$



# Random Genetic Drift

Frequency of A	Generation(t+1)	Generation (t+2)
0/N	$\binom{N}{0}(p_t)^0(1-p_t)^{N-0}$	$\binom{N}{0}(p_{t+1})^0(1-p_{t+1})^{N-0}$
1/N	$\binom{N}{1}(p_t)^1(1-p_t)^{N-1}$	$\binom{N}{1}(p_{t+1})^1(1-p_{t+1})^{N-1}$
2/N	$\binom{N}{2}(p_t)^2(1-p_t)^{N-2}$	$\binom{N}{2}(p_{t+1})^2(1-p_{t+1})^{N-2}$
.		
.		
.		
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# Random Genetic Drift

Frequency of A	Generation(t+1)	Generation (t+2)	Generation(t+3)
0/N	$\binom{N}{0}(p_t)^0(1-p_t)^{N-0}$	$\binom{N}{0}(p_{t+1})^0(1-p_{t+1})^{N-0}$	$\binom{N}{0}(p_{t+2})^0(1-p_{t+2})^{N-0}$
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2/N	$\binom{N}{2}(p_t)^2(1-p_t)^{N-2}$	$\binom{N}{2}(p_{t+1})^2(1-p_{t+1})^{N-2}$	$\binom{N}{2}(p_{t+2})^2(1-p_{t+2})^{N-2}$
.			
.			
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Transitions between states are random, but defined by a probability

Transitions have no memory beyond previous step

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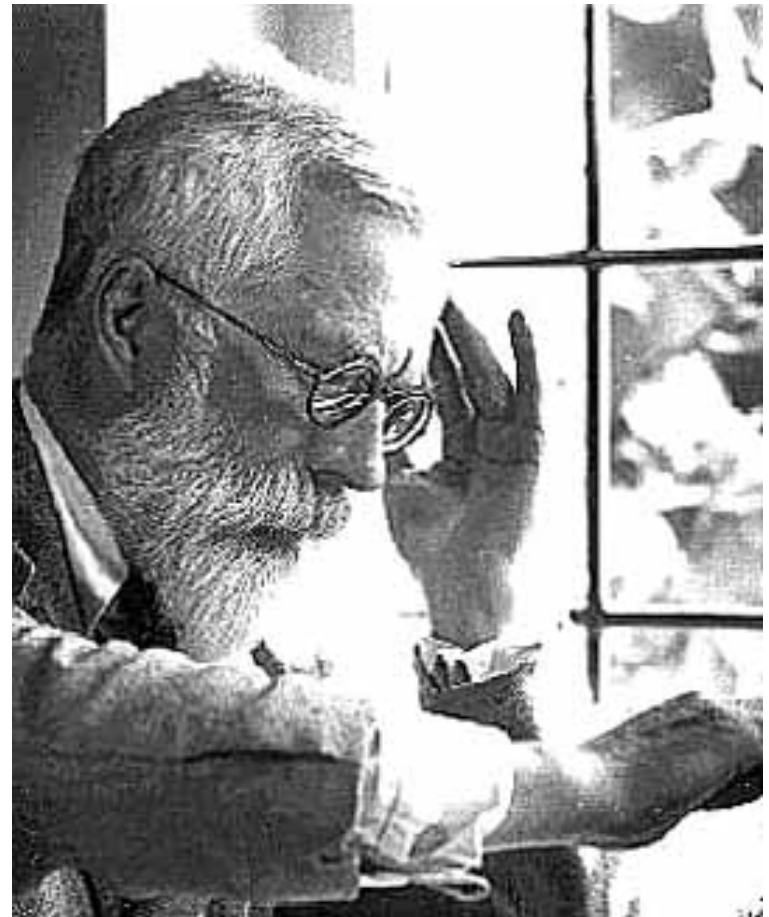
Transitions have no memory beyond previous step

# Diploid Model

- N diploid individuals
  - 2N alleles in population
- Two alleles: A, a (frequencies  $p, q$ )
- Randomly draw 2N gametes to found next generation

$$\Pr(j \text{ alleles of type } A) = \binom{2N}{j} p^j (1-p)^{2N-j}$$

# Wright-Fisher Model



# Wright-Fisher Model

- Assumptions:
  - N diploid organisms (2N alleles)
  - Infinite gametes
  - Discrete Generations
  - Random mating
  - No mutation
  - No selection

$$P_{ij} = \binom{2N}{j} \left(\frac{i}{2N}\right)^j \left(1 - \frac{i}{2N}\right)^{2N-j} = \binom{2N}{j} p^j q^{2N-j}$$

# Time, Probability of fixation

- Alleles are eventually fixed or lost
- $2N$  alleles
  - Each equally likely to fix (selectively equivalent)
  - $\text{Pr}(\text{fixation}) =$

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# Probabilities of fixation, loss

- Alleles are eventually fixed or lost
- $2N$  alleles
  - Each equally likely to fix (selectively equivalent)
  - $\text{Pr}(\text{fixation}) = 1/2N$
  - If  $i$  copies of allele,  $\text{Pr}(\text{fixation}) = i/2N$
- $\text{Pr}(\text{fixation}) = p$
- $\text{Pr}(\text{loss}) = 1-p$

# Times to fixation, loss

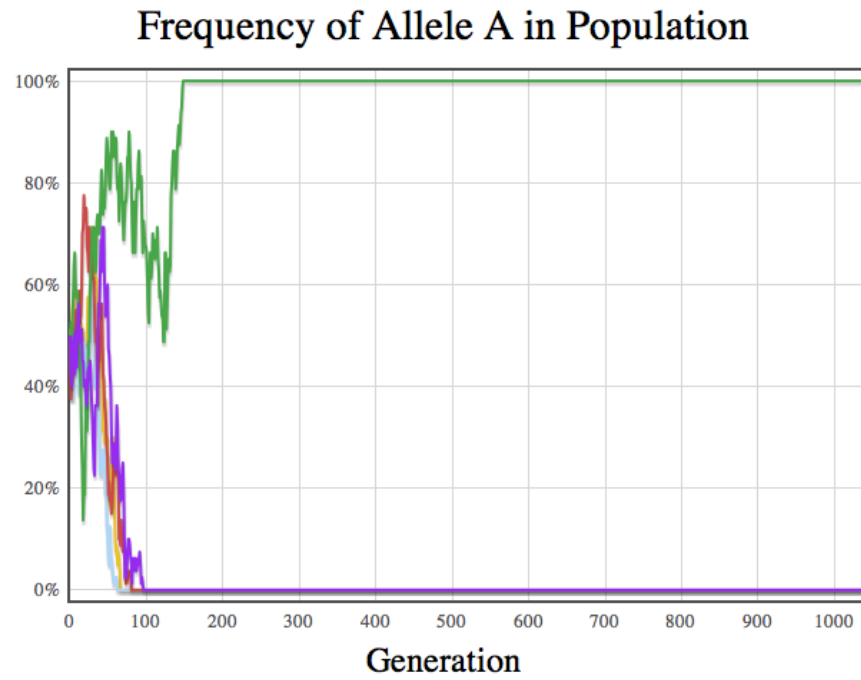
$$t_{fix} = \frac{-4N(1-p)\ln(1-p)}{p}$$

For  $p = 1/2N$ ,  $t_{fix} \approx 4N$

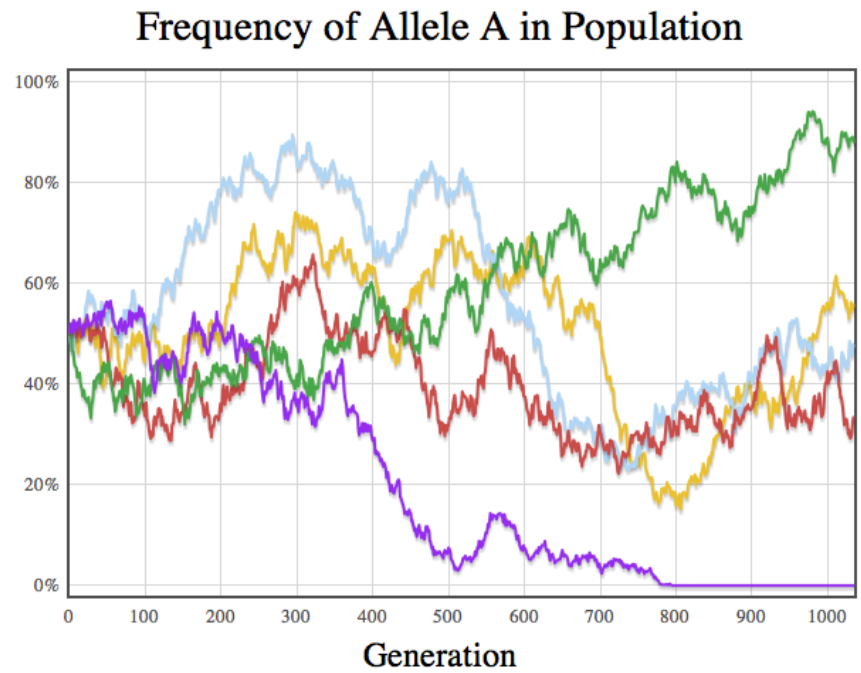
$$t_{loss} = \frac{-4N(p)\ln(p)}{1-p}$$

For  $p = 1/2N$ ,  $t_{loss} \approx 2\ln(2N)$

N = 40

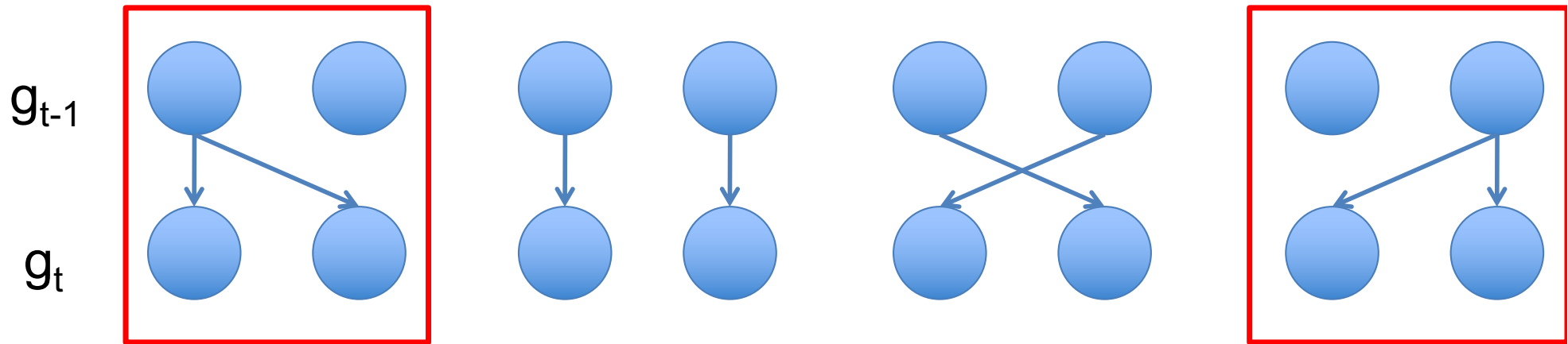


N = 2000



# Decay of Heterozygosity

$$2N=2$$



$$\Pr(\text{IBD}) = 2/4 = 1/2$$

$$\Pr(\text{IBD}) = 1/2N$$

$$\Pr(\text{not IBD}) = 1 - 1/2N$$

$$\Pr(\text{IBD}_t) = F_t = \frac{1}{2N} + \left(1 - \frac{1}{2N}\right)F_{t-1}$$

$$\text{If } F_0 = 0, F_t = 1 - \left(1 - \frac{1}{2N}\right)^t$$

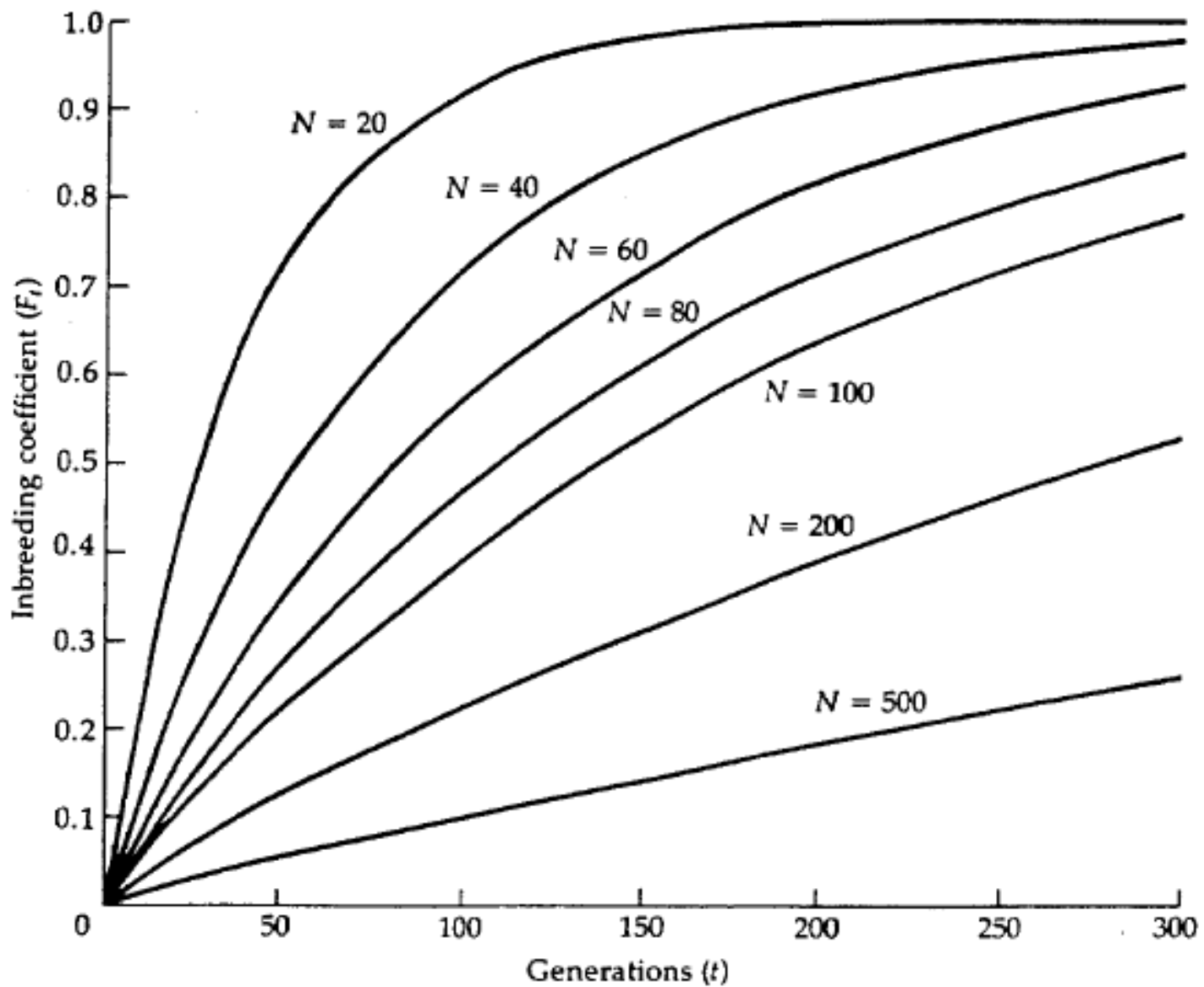


Figure 9. Increase of  $F_t$  in ideal populations as a function of time and effective population size  $N$ .

# Decay of Heterozygosity

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

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



# Summary of Drift

- Stochastic fluctuations in allele frequencies due to sampling in a finite population
- Described by Wright-Fisher model
- Alleles are ultimately fixed or lost from population
  - $\text{Pr}(\text{fix}) = p$ ;  $\text{Pr}(\text{loss}) = 1 - p$
  - $\text{Time}(\text{fix}_{1/2N}) \approx 4N$ ;  $\text{Time}(\text{loss}_{1/2N}) \approx 2\ln(2N)$
- $H$  decreases ( $\sim 1/2N$ ) over time
- Hardy-Weinberg largely still applies
  - Allele frequency changes small
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# Habitat loss

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  - RGD

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- Small, isolated populations are threatened
  - RGD, inbreeding
- Consequences:
  - Reduction in genetic diversity

# Genetically depauperate species

Species	Populations (N)	Individuals (N)	Loci (N)	Poly-morphic loci (%)	Average heterozygosity	Reference
			<i>Allozyme</i>			
<i>Drosophila</i>	43*	> 100	24	43.1	0.140	(10)
<i>Mus musculus</i>	2	87	46	20.5	0.088	(15)
<i>Felis catus</i>	1	56	55	22.0	0.076	(16)
<i>Homo sapiens</i>	Many	> 100	104	31.7	0.063	(43–45)
<i>Acinonyx jubatus</i>	2	55	47	0.0	0.0	



# Genetically depauperate species

**TABLE 2. Distribution and allele frequency of polymorphic allozyme loci in lions**

Population	No. lions scored	Allozyme locus <sup>a</sup>			Percent polymorphic loci	Average Heterozygosity <sup>b</sup>
		<i>IDHI</i>	<i>TF</i>	<i>PTI</i>		
<b>African</b>						
Kruger Park South Africa	15	A = 1.0	a = 0.65 b = 0.35	s = 1.0	7	0.023
Serengeti ecosystem Tanzania, East Africa	27	A = 0.72 B = 0.28	a = 0.52 b = 0.28	s = 1.0	11	0.038
African Zoo lions (Atlas)	18	A = 1.0	a = 0.72 b = 0.28	s = 1.0	7	0.030
<b>Asian</b>						
Indian lions (Gir Forest)	28	B = 1.0	a = 1.0	d = 1.0	0.0	0.0
Indian lions (SSP-studbook)	29	A = 0.72 B = 0.28	a = 0.93 b = 0.07	s = 0.45 d = 0.55	7	0.021



O'Brien et al.

# Genetically depauperate species

Number	Date	Location	Microsatellite locus			mtDNA
			043	090	096	
Contemporary						
14	1980s	Big Cypress Swamp	122/122	121/121	203/203	A
67	1980s	Big Cypress Swamp	122/122	121/121	203/203	A
71	1980s	Big Cypress Swamp	122/130	121/121	203/203	A
422	1980s	Big Cypress Swamp	122/122	121/121	203/203	A
426	1980s	Big Cypress Swamp	122/130	121/121	203/203	A
428	1980s	Big Cypress Swamp	122/122	121/121	203/203	A
Museum						
777	1890s	Florida	–	–	–	C
778	1890s	Florida	–	–	–	C
779	1890s	Florida	–	–	–	C
780	1890s	Immokolee	122/124	127/127	203/203	C
785	1898	Sebastian	134/134	–	–	A
787	1898	Sebastian	104/126	–	–	–
792	1922	Allen's River	–	–	–	B

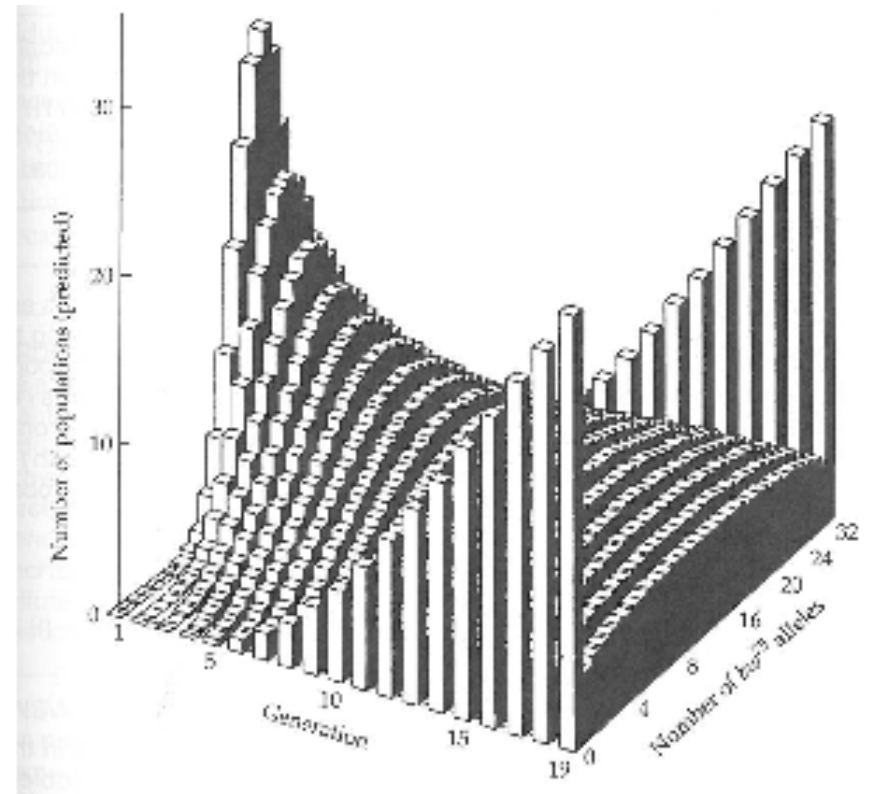
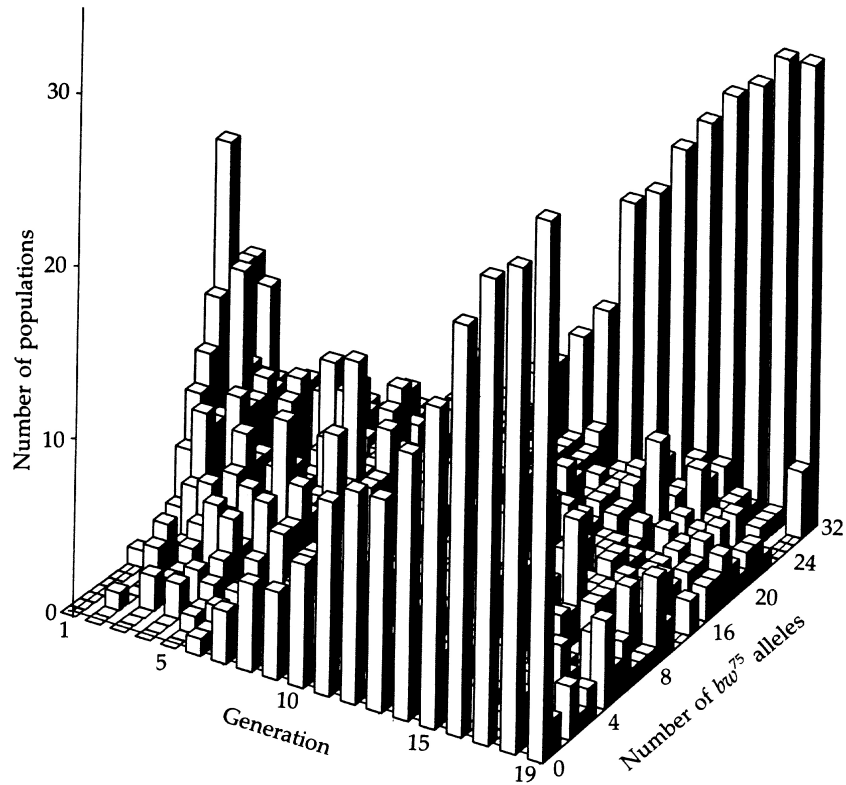


Culver et al. 2008

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  - Allele frequency changes small
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# Effective Population Size





# Effective Population Size

$$\begin{aligned}\text{Var}(p) &= \text{Var}\left(\frac{\#A}{2N}\right) = \left(\frac{1}{2N}\right)^2 \text{Var}(\#A) \\ &= \left(\frac{1}{2N}\right)^2 2Npq \\ &= \frac{pq}{2N}\end{aligned}$$

# Effective Population Size

$$\begin{aligned}\text{Var}(p) &= \text{Var}\left(\frac{\#A}{2N}\right) = \left(\frac{1}{2N}\right)^2 \text{Var}(\#A) \\ &= \left(\frac{1}{2N}\right)^2 2Npq \\ &= \frac{pq}{2N}\end{aligned}$$

- In reality, allele frequency changes  $> pq/2N$ 
  - Fluctuations in population size,  $N_m \neq N_f$ , *etc.*

# Effective Population Size

- Number of individuals in a theoretically ideal population having the same magnitude of drift as the actual population
- Measure 'magnitude' in 3 ways
  - Change in variance of allele frequency (variance  $N_e$ )

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

$$\overline{\text{var}}(p) = \frac{pq}{2N_e}$$

$$N_e = \frac{pq}{2\overline{\text{var}}(p)}$$

# Effective Population Size

- Number of individuals in a theoretically ideal population having the same magnitude of drift as the actual population
- Measure 'magnitude' in 3 ways
  - Change in variance of allele frequency (variance  $N_e$ )
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- Typically smaller than census size  $N$ 
  - Sex ratio
  - Variance in reproductive success
  - Population size changes

# Relating $N$ , $N_e$

- Population size changes

$$\frac{1}{N_e} = \frac{1}{t} \left( \frac{1}{N_0} + \frac{1}{N_1} + \dots + \frac{1}{N} \right)$$

# Relating $N$ , $N_e$

- Population size changes

$$\frac{1}{N_e} = \frac{1}{t} \left( \frac{1}{N_0} + \frac{1}{N_1} + \dots + \frac{1}{N} \right)$$

- Unequal males, females

$$N = N_m + N_f$$

$$N_e = \frac{4N_m N_f}{N_m + N_f}$$



# Hardy-Weinberg Principle

Frequency(A) = p

Frequency(a) = q

Frequency(AA) = P

Frequency(Aa) = H

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## Mating

AA x AA

AA x Aa

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$$q' = Q' + \frac{1}{2}H' = q^2 + \frac{1}{2}2pq = q(q + p) = q$$

- Allele frequency unchanged across generations
  - Mendelian inheritance itself preserves variation
- HWE achieved in ONE generation
  - Equal allele frequencies in males & females, discrete generations