

# BIOL 432 - Evolution

## Lecture 8

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### Expected Genotype Frequencies in the Absence of Evolution are Determined by the Hardy-Weinberg Equation.

#### Assumptions:

- 1) No mutation
- 2) Random mating
- 3) Infinite population size
- 4) No immigration or emigration
- 5) No selection

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### Random genetic drift



- Evolution = change of allele frequency within a population
- Randomness cannot lead to adaptation
- Can nevertheless be a powerful evolutionary force
- Main mode by which non-coding sequence evolves?

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## Populations

**Population:** Individuals of the same species in a particular area.  
(Geneticists further often assume that mating is random and panmictic)



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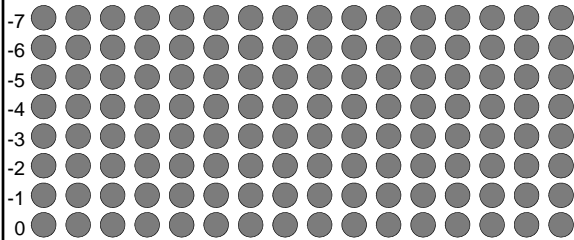
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## Populations have a history



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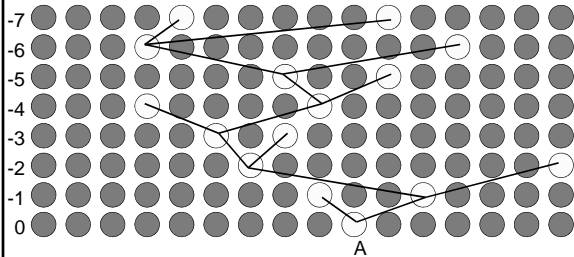
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## Pedigrees



Pedigree showing the ancestors of one individual in generation 1

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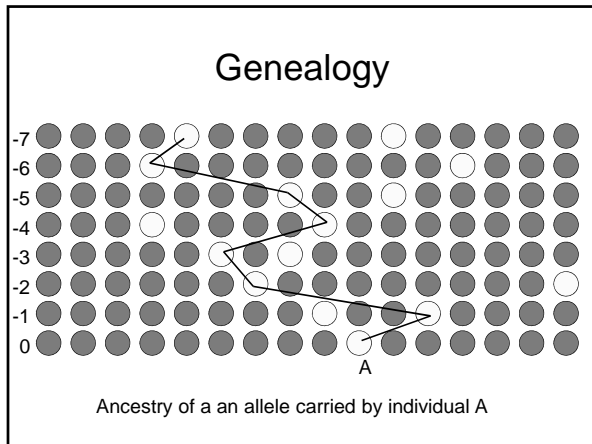
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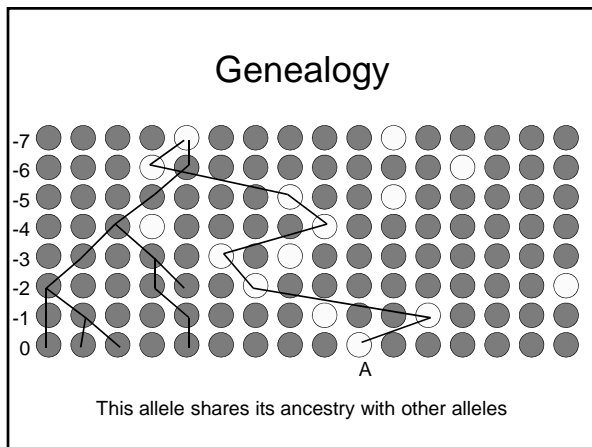
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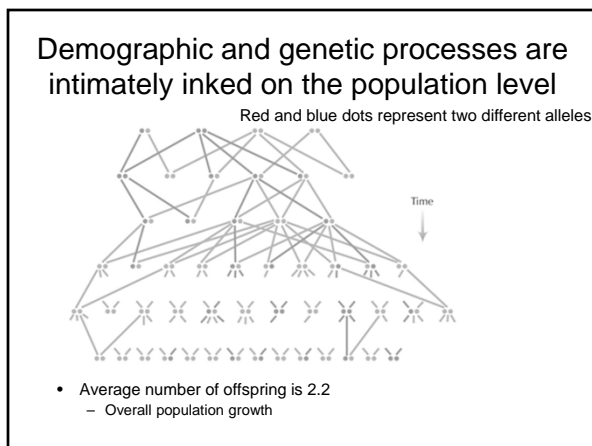
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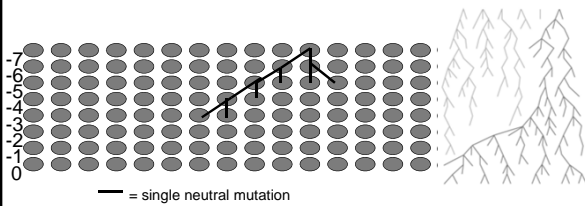
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## The simplest model: A haploid asexual population of constant size

- E.g. an idealized population of bacteria




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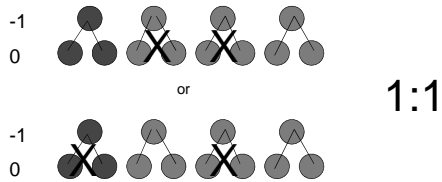
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### Assumptions:

- Mutation is neutral (has no selective advantage or disadvantage)
- Population size is constant
- Two possibilities: fission (i.e. reproduction) or death




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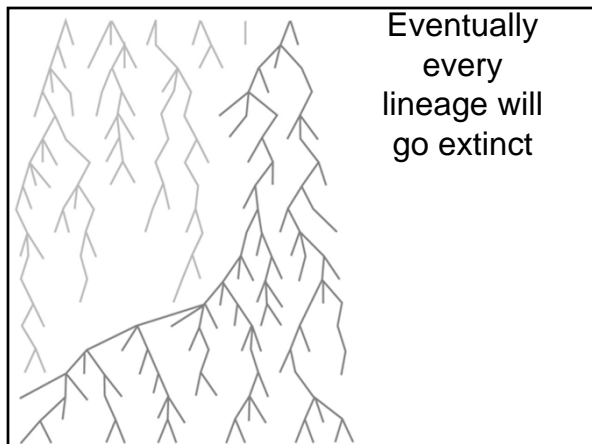
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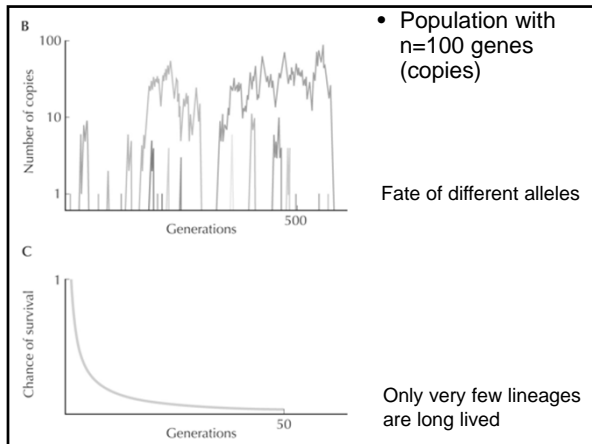
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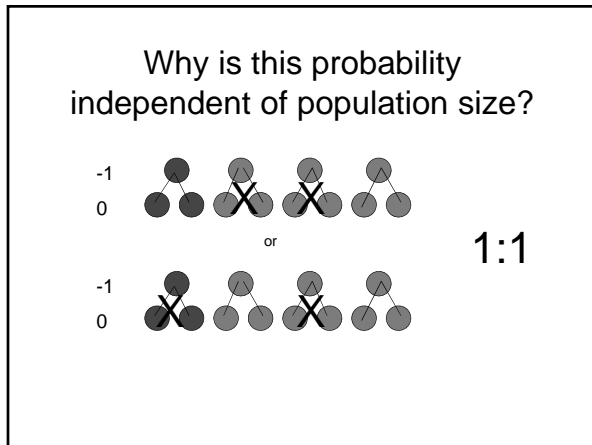
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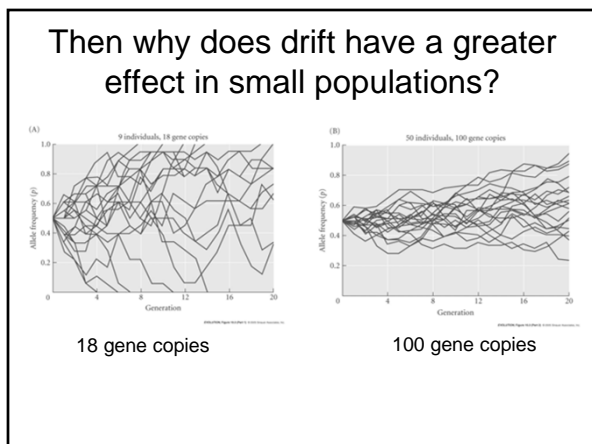
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### Example: cape buffalo in game reserves of different size



- Microsatellite study by Heller et al. 2010

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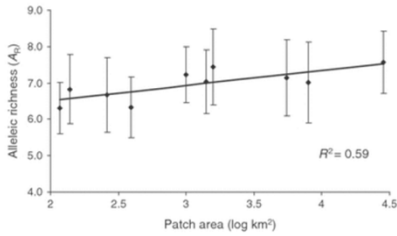
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### Example: cape buffalo in game reserves of different size



- Reserves ranged in size from 100 to 28,000 km<sup>2</sup>

Allelic richness = mean number of alleles across multiple microsatellite loci




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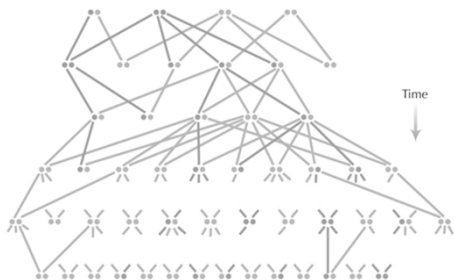
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### In diploid organisms meiosis adds randomness




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### The Wright-Fisher Model

P Q    Q Q    N=2

Frequency P = p = #P/2N = 0.25    Frequency Q = q = #Q/2N = 0.75

- Assumption: Population size is constant
- Assumption: Each individual produces a large number of gametes
- Assumption: Gametes are produced in proportion to parental allele frequencies
- Assumption: Mating of alleles is random
- Assumption: Generation are discrete

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### The Wright-Fisher Model

= 0.75 x 0.75 x 0.75 x 0.75 = 0.32

- 0.32
- Which of the following outcomes is more likely?

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### The Wright-Fisher Model

= 0.75 x 0.75 x 0.75 x 0.25 = 0.105

= 0.75 x 0.75 x 0.75 x 0.25 = 0.105

= 0.75 x 0.75 x 0.75 x 0.25 = 0.105

= 0.75 x 0.75 x 0.75 x 0.25 = 0.105

= 0.422

- 0.422

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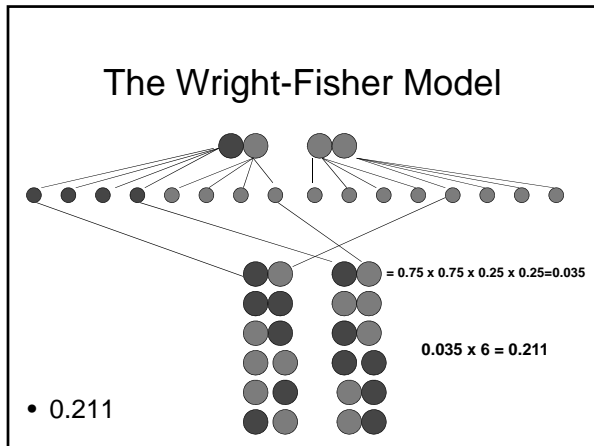
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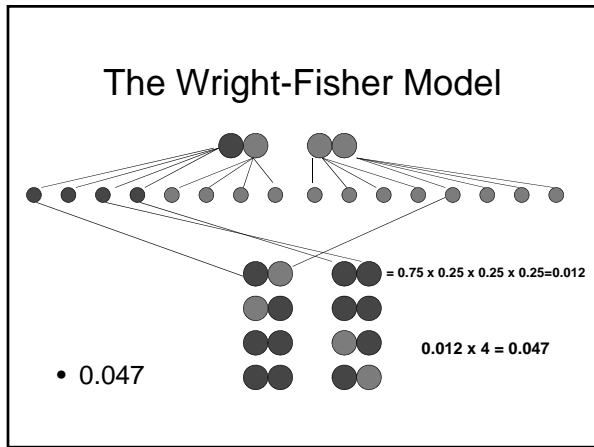
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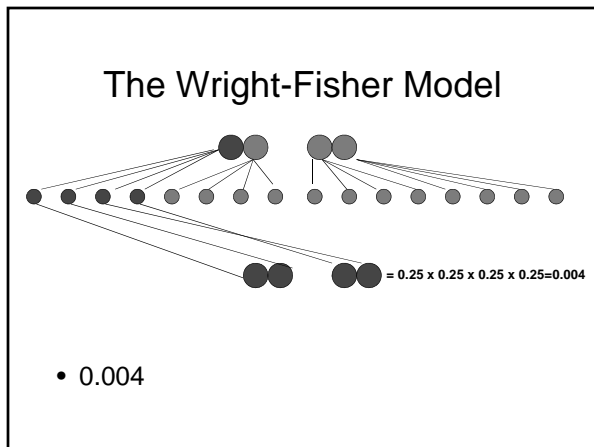
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The outcome of the Wright-Fisher model is described by the binomial distribution

Binomial

$$\frac{n!}{i!(n-i)!} q^{n-i} p^i$$

$$2N = n$$

$$\text{Mean: } 2Np$$

$$\text{Variance: } 2Npq$$

$i$  = outcome with probability  $p$  (e.g. drawing a P allele for the next generation)

- See table 28.1 (online on textbook site)

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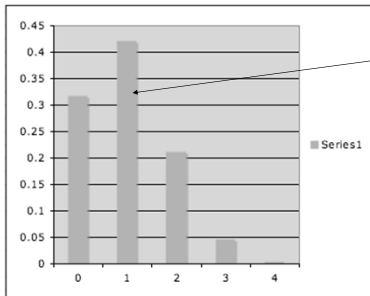
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### The Wright-Fisher model



$$\text{Mean} = 2Np = 2 \cdot 2 \cdot 0.25 = 1$$

$$1/4 = 0.25$$

Mean allele frequency is expected to stay the same

- The probability for each of the 5 outcomes follows the binomial distribution

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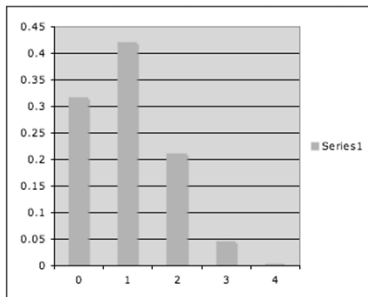
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### The Wright-Fisher model



$$\text{Variance} = 2Npq = 2 \cdot 2 \cdot 0.25 \cdot 0.75 = 0.75$$

$$\text{Variance for allele frequency: } (p \cdot q) / 2N = (0.25 \cdot 0.75) / (2 \cdot 2) = 0.047$$

- The probability for each of the 5 outcomes follows the binomial distribution

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Under the Wright-Fisher model the two alleles behave like competing clones

- <http://www.coalescent.dk/>

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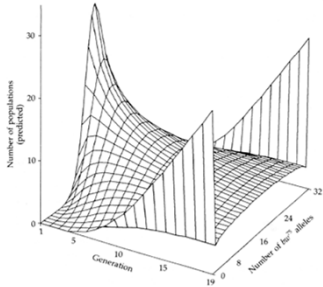
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### The Wright-Fisher Model



- Theoretical expectation for allele frequency if drift continues for several generations

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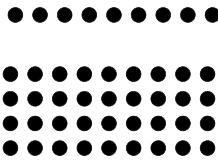
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### An experimental study of genetic drift in *Drosophila*

Generation 0:  
Frequency brown mutation =  $p = 0.5$



8 males x  
8 females



$N = 100$   
populations

t = 19  
generations

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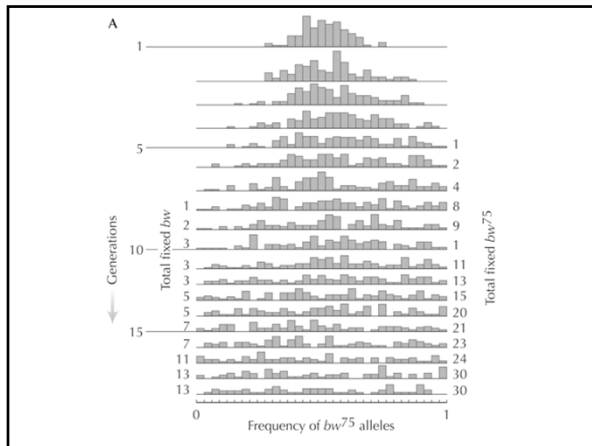
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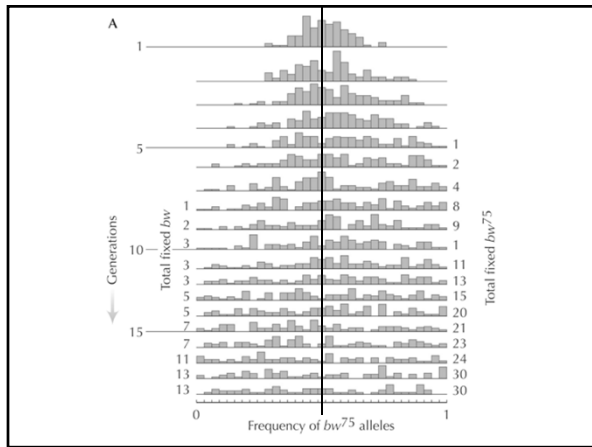
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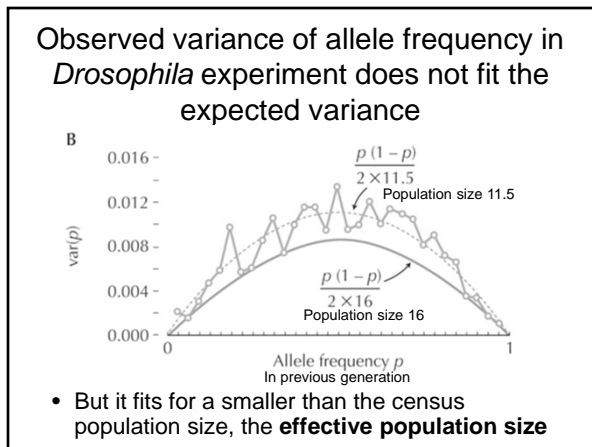
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## Effective Population size

The size of the ideal Fisher-Wright population that would give the same rate of random drift as the actual population

(I.e. if the census population size and the effective population size do not match the population deviates from the Wright-Fisher model)

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## Population Size (N) vs. Effective Population Size ( $N_e$ )

$N_e$  is what determines the strength of genetic drift

Factors that cause  $N_e$  to be less than N

- overlap of generations
- variation among indivs in reproductive success

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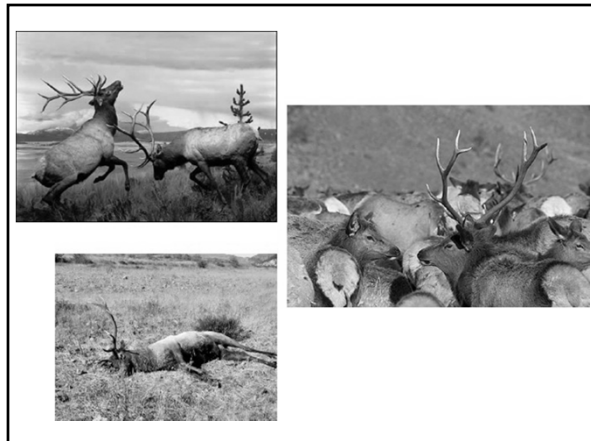
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**Population Size (N) vs. Effective Population Size ( $N_e$ )**

Factors that cause  $N_e$  to be less than N

- overlap of generations
- variation among indivs in reproductive success
- unequal sex ratio

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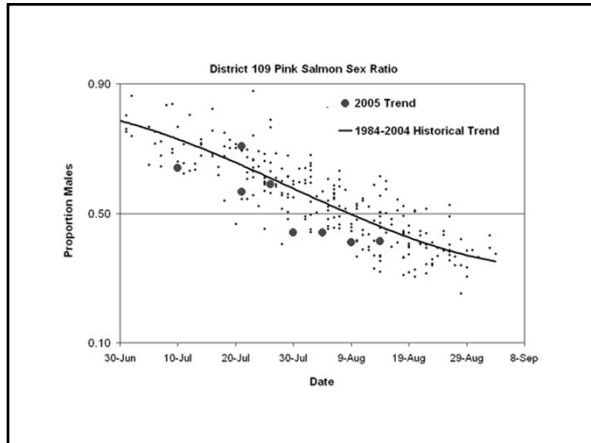
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**Population Size (N) vs. Effective Population Size ( $N_e$ )**

Factors that cause  $N_e$  to be less than N

- overlap of generations
- variation among indivs in reproductive success
- unequal sex ratio
- fluctuations in population size

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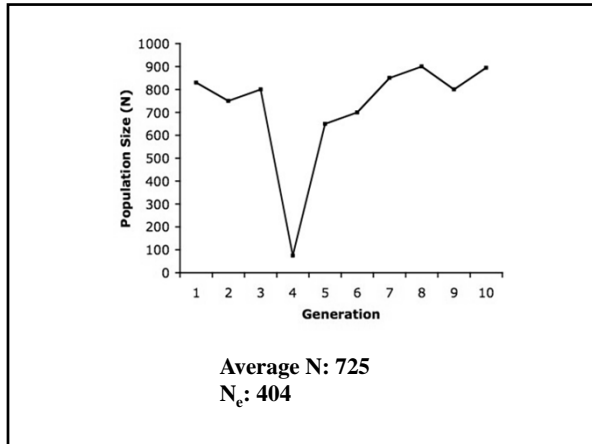
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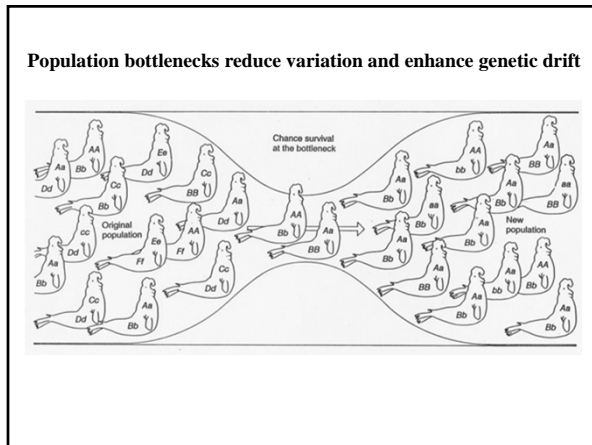
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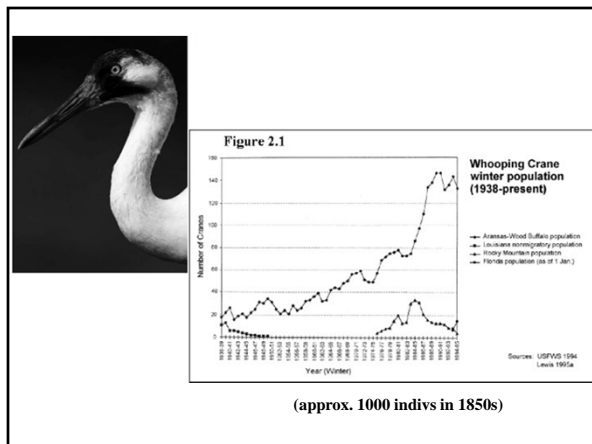
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### mtDNA variation in Whooping Cranes

Haplotype	Pre-bottleneck	Post-bottleneck
1	0	12
2	0	2
3	5	3
4	0	1*
5	1	0
6	1	0
7	2	0
8	1	0
9	1	0

\*Present immediately after the bottleneck (1951), but not today.

Glenn et al. (1999) Conservation Biology 13: 1097-1107.

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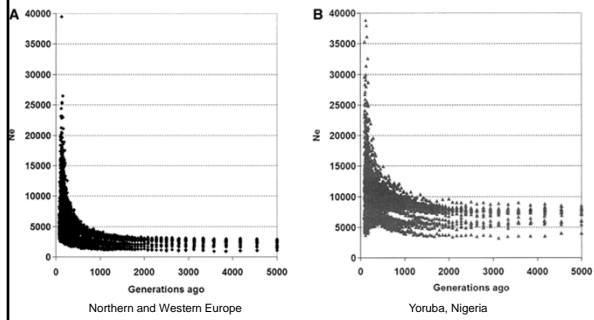
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### Effective population size of humans

Tenesa et al., Genome Res. 2007. 17: 520-526



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How can we know about past effective population size?

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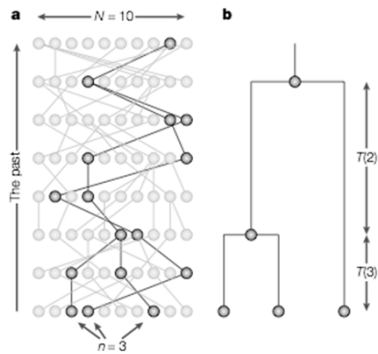
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What is the chance that two random alleles share an ancestor in the previous generation?

$1/2N$



Chances for coalescent event get smaller with fewer lineages sorting

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Branches get longer with fewer remaining lineages, even though N stays the same

Expected times for coalescent events with 6 to 2 lineages remaining

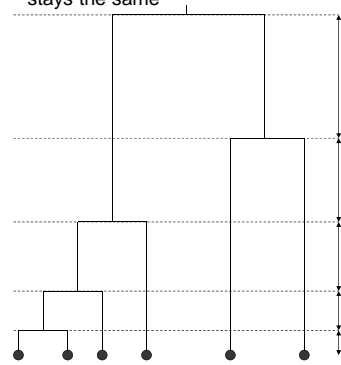
$E(T_2) = 2N/1$

$E(T_3) = 2N/3$

$E(T_4) = 2N/6$

$E(T_5) = 2N/10$

$E(T_6) = 2N/15$




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We can make predictions about the average and variance of coalescent times - but not about specific genealogies



Figure 2 | **Random genealogical trees.** The trees were generated using the same model — the standard coalescent for sample of size ten. Therefore, the variation among the trees reflects chance alone.

- Some potential outcomes of evolution in a Wright-Fisher population

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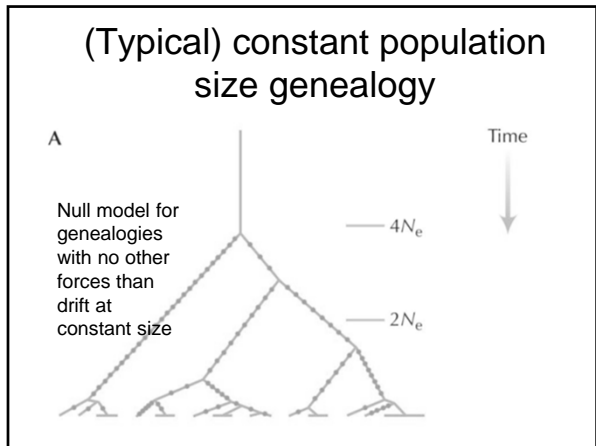
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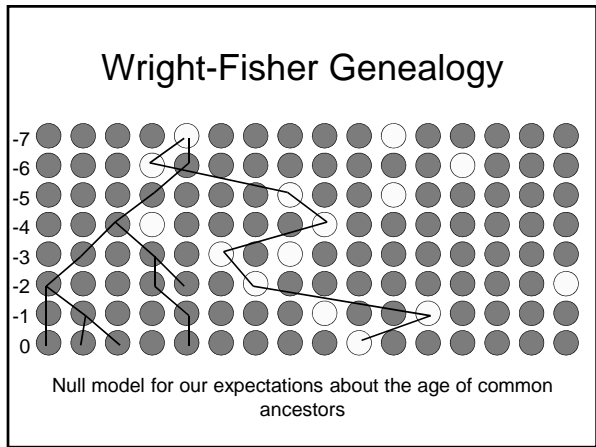
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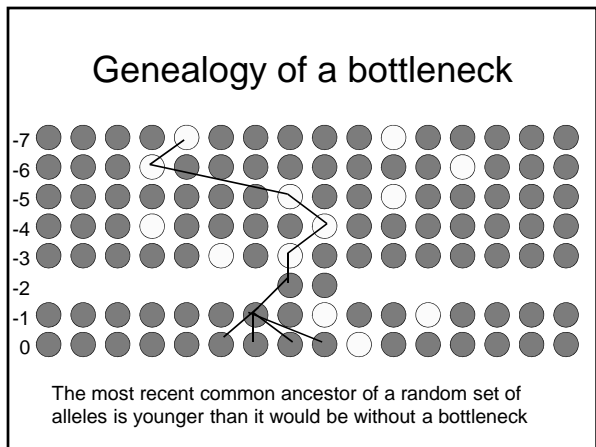
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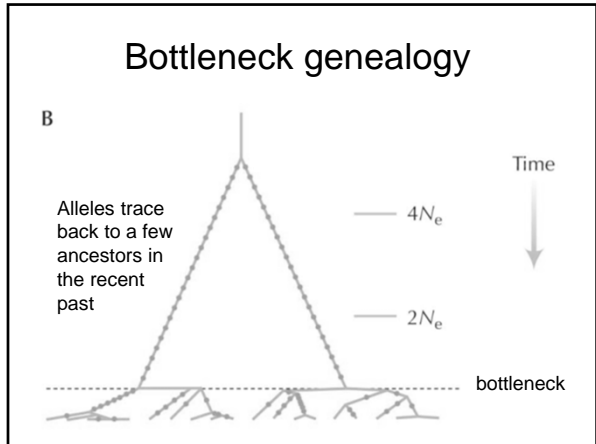
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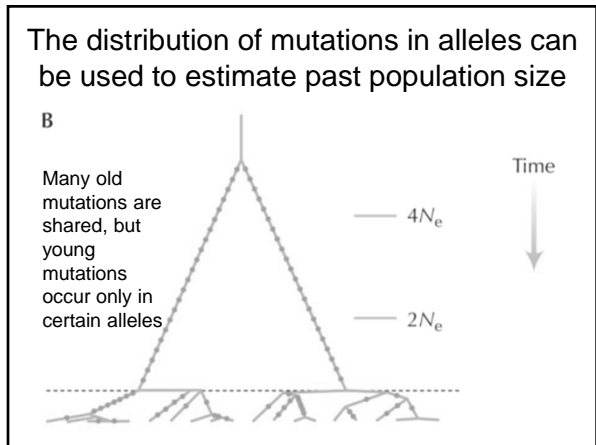
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