chance effects

random genetic drift

- populations are not infinitely large
- reproduction is a probabalistic process
  - the number of offspring is different by chance
  - genes in one generation are represented by a chance number of copies of the gene in the next
- **Stochastic** changes in populations

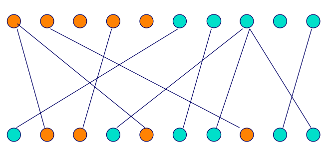
random genetic drift simple model - assumptions

- monoecious diploid organisms
  - allows for self-fertilization
- sexual reproduction

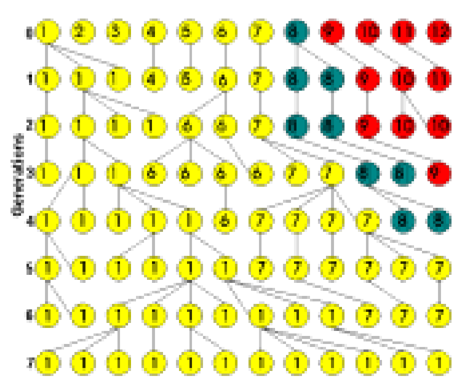
random genetic drift simple model - assumptions

- non-overlapping generations
- no mutation
- no selection

random genetic drift simple model - assumptions

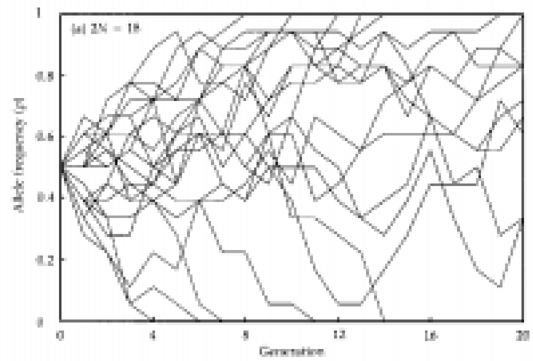


some genes represented more
some genes represented less
some represented as same number

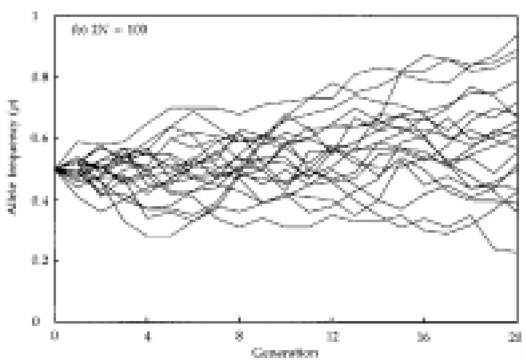


random genetic drift
simple model - assumptions

- rate of genetic drift depends on the size of the population - 2N
  - **genetic drift faster when N is smaller**



Hartl & Clark, 1989



simulation results

Hartl & Clark, 1989

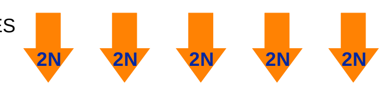
random genetic drift
simple model - assumptions

- Many independent subpopulations
  - each of constant size N
  - random mating within each subpopulation

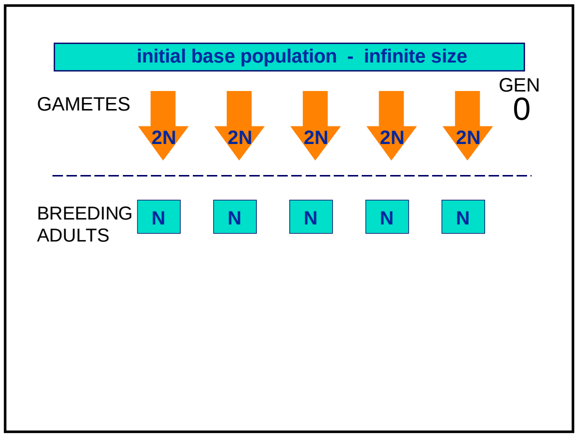
initial base population - infinite size

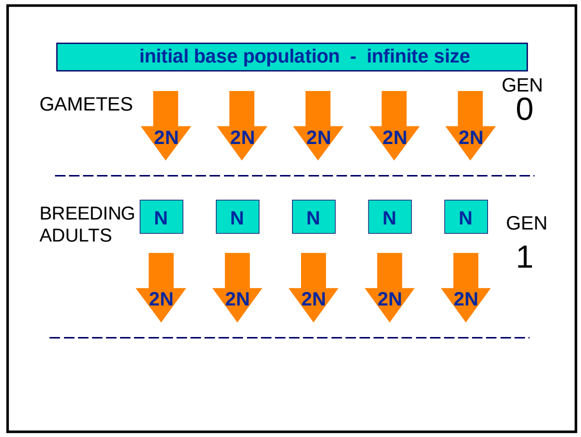
initial base population - infinite size

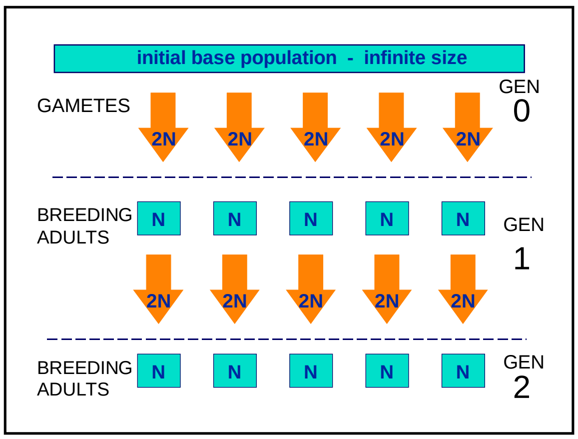
GAMETES



GEN
0

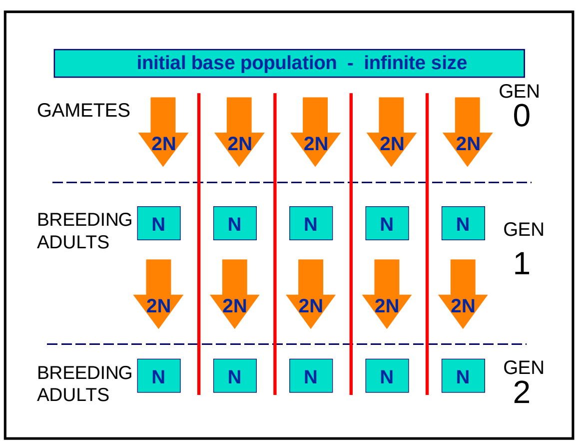






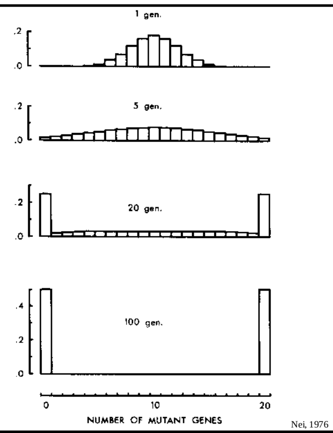
random genetic drift simple model - assumptions

- Many independent subpopulations
  - no migration between subpopulations



random genetic drift simple model - assumptions

- Follow the allelic state of each subpopulation in each generation and record the frequency of particular discrete classes



Nei, 1976

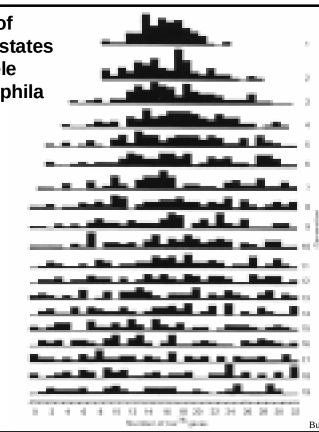
random genetic drift
an experimental model

- Buri, 1956
  - used Drosophila
  - follow the frequency of eye color, bw^{75}
    - bw75 homzygote = light brown eye
    - heterozygote = red eye
    - bw homozygote = brown eye
  - keep population size fixed
    - 8 males
    - 8 females

random genetic drift
an experimental model

- Buri, 1956
  - allow flies to reproduce; remove adults
  - from progeny group randomly pick new group of 16 flies
    - record genotypes
    - determine number of bw75 alleles
    - repeat

distribution of segregating states for bw75 allele in 107 Drosophila populations



N = 16 in each population

Buri, 1956

random genetic drift
an experimental model

- subpopulations spread out to occupy all states
  - population distribution starts out bell-shaped
  - as time proceeds, distribution becomes flat

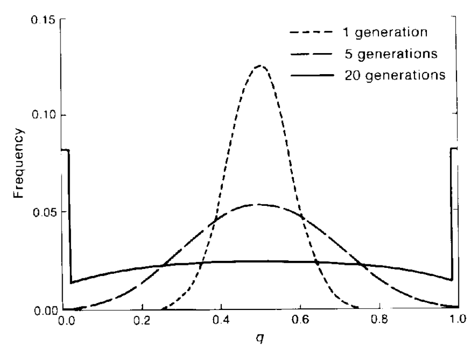


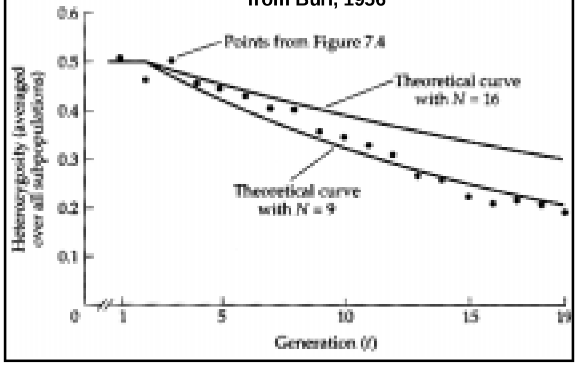
Figure 7.5. The smoothed distribution of allelic frequency for a population of size 20 and an initial allelic frequency of 0.5 after 1, 5, and 20 generations.

Hedrick, 1985

random genetic drift
an experimental model

- fixation and loss
  - after a few generations, some populations become fixed for bw75
  - after a few generations, some populations lose bw75
  - proportion of segregating population declines

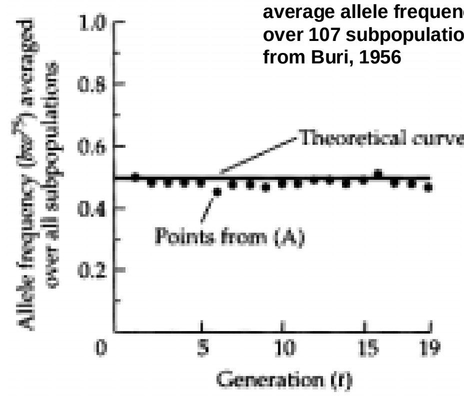
decay in total heterozygosity averaged over 107 subpopulations from Buri, 1956



random genetic drift
an experimental model

- sub populations spread out to occupy all states
- considering the total population, average allele frequency remains unchanged

average allele frequency over 107 subpopulations from Buri, 1956



change in gene frequency under genetic drift

- change in gene frequency from one generation to the next
  - can be described by a binomial distribution

how do we measure the probability of change in allele frequency?

What is the probability that there will be

exactly x copies of the allele present in the progeny group,

given that the

frequency of the allele was p in the parental group

and that

the number of genes sampled is 2N

example

- what if the population is made up of two plants (monoecious)
  - and we start out with two heterozygotes for the allele that we are following

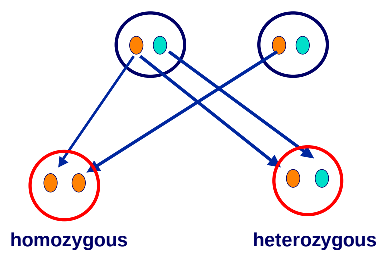
example

- what if the population is made up of two plants (monoecious)
  - and we start out with two heterozygotes for the allele that we are following
- what is the probability that the allele frequency will be 0.25 in the progeny group?
  - given that we sample 2N = 4 genes

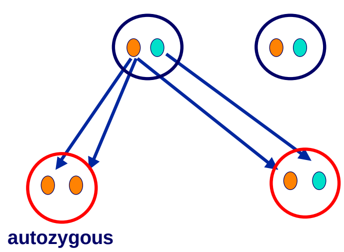
possible outcomes?

- five classes
- any # of alleles, i, from 0 ---> 4
  - 0
  - 1
  - 2
  - 3
  - 4

example



example



binomial probability distribution

$$P(i) = \binom{2N}{i} p^i q^{2N-i}$$

number of combinations of i copies of an allele drawn from 2N possible copies where there are two possible outcomes

binomial probability distribution

$$P(i) = \frac{2N!}{i!(2N-i)!} p^i q^{2N-i}$$

number of combinations of i copies of an allele drawn from 2N possible copies where there are two possible outcomes

binomial probability distribution

$$P(1) = \frac{4!}{1!\,3!} p^1 q^3$$

but, what do we use for p and q?

binomial probability distribution

$$P(1) = \frac{4!}{1!\,3!} (.5)^1 (.5)^3$$

p = frequency of the allele in the parental generation

0.5

and q = (1 - p)

binomial probability distribution

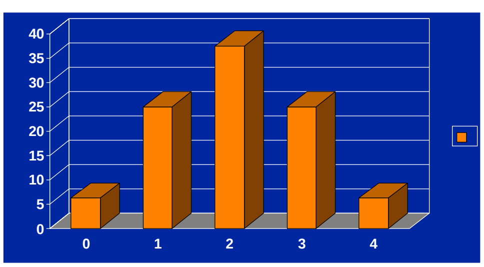
$$P(1) = \frac{4!}{1!\,3!} (.5)^1 (.5)^3 \quad \mathbf{= 0.25}$$

p = frequency of the allele in the parental generation

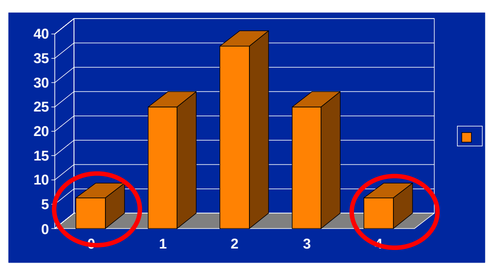
0.5

and q = (1 - p)

probability of being in a state



probability of being in a state



absorbing classes

absorbing state

- 0.0 or 1.0 class
  - allele frequency cannot change any more in the absence of mutation

how do we describe how the population will change into the future

- determine a transition probability matrix for population size 2N genes

transition probability matrix

FROM \ TO	0	1	2	3	4
0	1	0	0	0	0
1	0.3165	0.4225	0.2115	0.0475	0.0045
2	0.0625	0.25	0.375	0.25	0.0625
3	0.0045	0.0475	0.2115	0.4225	0.3165
4	0	0	0	0	1

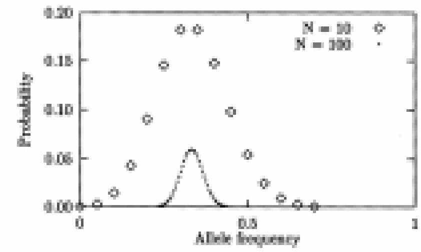
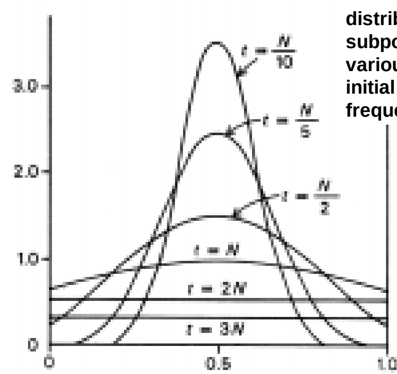


Figure 2.8: The probabilities of allele frequencies after one round of random mating for population sizes of $N = 10$ and $N = 100$ and initial allele frequency $p = 1/3$.

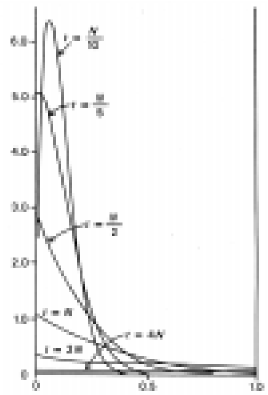
behavior of the population depends on the starting point

- $p_0 = 0.5$ results in a symmetry of future population changes
- p_0 near 0 or 1 shows asymmetry



distribution of subpopulations at various times. initial allele frequency = 0.5

Kimura, 1955



distribution of subpopulations at various times. initial allele frequency = 0.1

Kimura, 1955