Slide 1
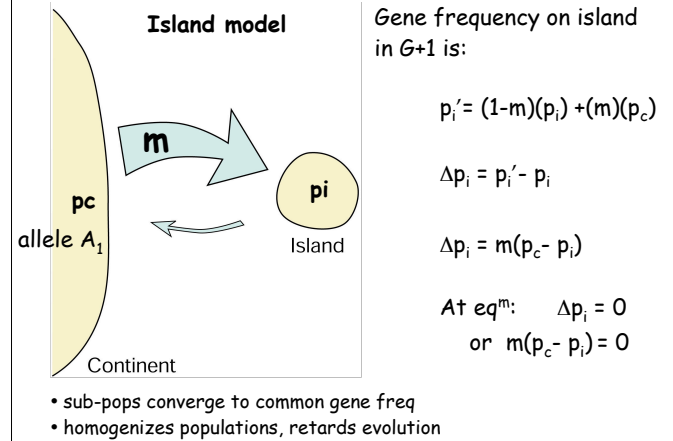
HW Assumptions:

- No selection √
- No mutation √
- No migration
- No random events
- Pop. infinitely large, stable, with equal sex ratio
- Mating within population at random (panmixia)

Migration, Genetic Drift & Inbreeding
or: How does chance influence the direction of evolution?
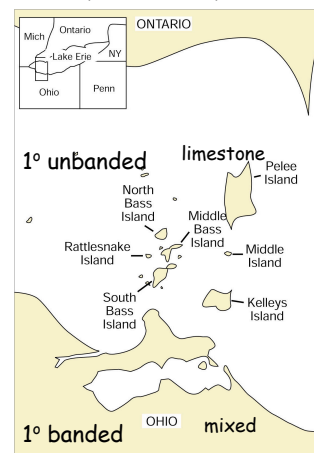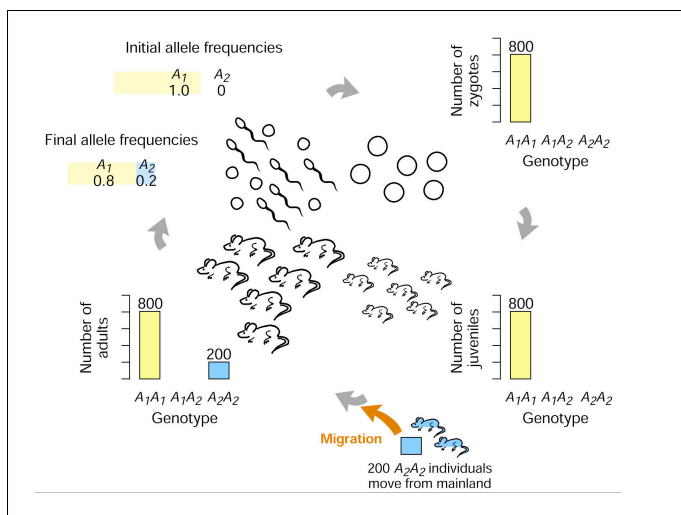
Slide 4

Island model

Gene frequency on island in G+1 is:

$$p_i' = (1-m)(p_i) + (m)(p_c)$$

$$\Delta p_i = p_i' - p_i$$

$$\Delta p_i = m(p_c - p_i)$$

At eq^m: $\Delta p_i = 0$
or $m(p_c - p_i) = 0$

pc
allele A_1
pi
Island
Continent

- sub-pops converge to common gene freq
- homogenizes populations, retards evolution

Slide 2

Migration

Slide 5

An empirical example……

ONTARIO
Mich
Ontario
Lake Erie
NY
Ohio
Penn

1° unbanded
limestone
Pelee Island
North Bass Island
Middle Bass Island
Rattlesnake Island
Middle Island
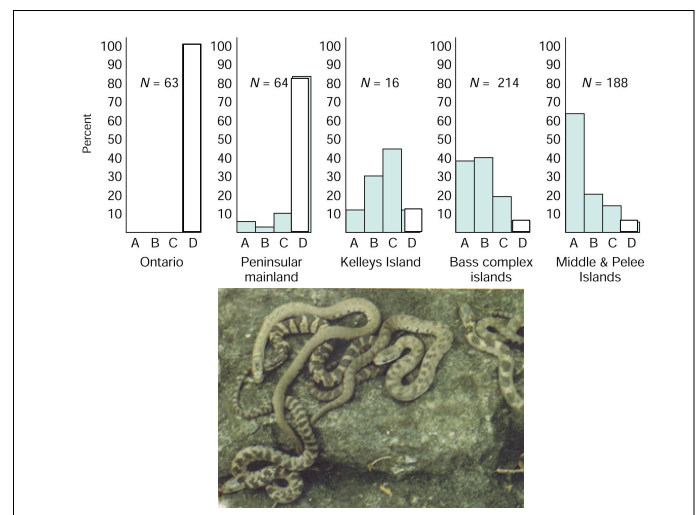South Bass Island
Kelleys Island

1° banded   OHIO   mixed

Nerodia sipedon
- banded more visible on limestone

Coloration - single locus B >> b

Slide 3

Initial allele frequencies
A_1 A_2
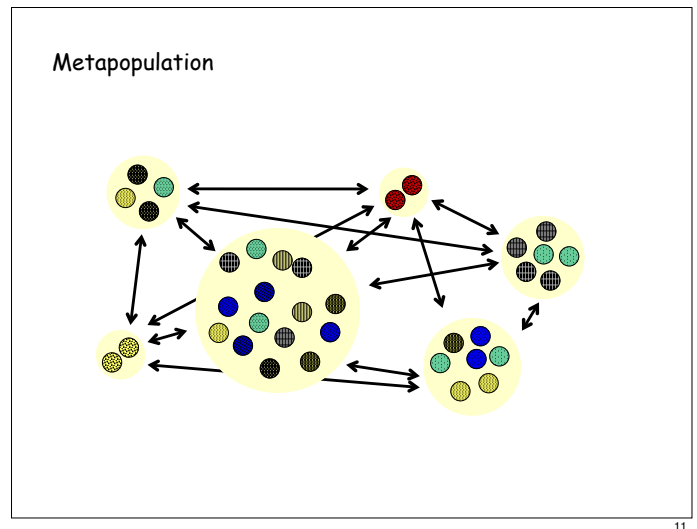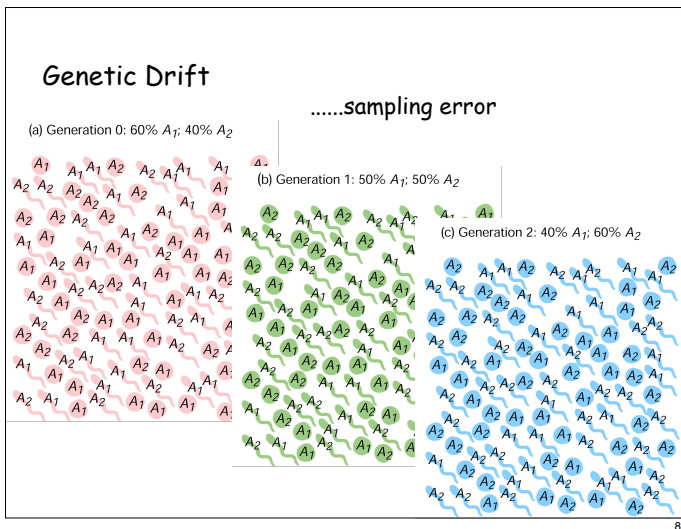1.0   0

Number of zygotes
800
A_1A_1 A_1A_2 A_2A_2
Genotype

Final allele frequencies
A_1 A_2
0.8   0.2

Number of adults
800
200
A_1A_1 A_1A_2 A_2A_2
Genotype

Number of juveniles
800
A_1A_1 A_1A_2 A_2A_2
Genotype

Migration
200 A_2A_2 individuals move from mainland

Slide 6

Percent

N = 63   A B C D   Ontario
N = 64   A B C D   Peninsular mainland
N = 16   A B C D   Kelleys Island
N = 214   A B C D   Bass complex islands
N = 188   A B C D   Middle & Pelee Islands

Slide 7

b

Δq (change in the frequency of A_2 from this generation to the next)

0.04
0.03
0.02
0.01
0
-0.01
-0.02
-0.03

0.2 0.4 0.6 0.8 1

(a) Strong selection, little migration

(b) Moderate selection, moderate migration

(c) Weak selection, much migration

q (frequency of A_2 in this generation)

Slide 10

Population structure

Sewall Wright (1889-1988)

Classic model   Structural model

σ^2_T

σ^2_B

ϖ^2_w

SOCIAL LINEAGES

Slide 8

Genetic Drift

......sampling error

(a) Generation 0: 60% A_1; 40% A_2

(b) Generation 1: 50% A_1; 50% A_2

(c) Generation 2: 40% A_1; 60% A_2

Slide 11

Metapopulation

Slide 9

Genetic Drift
- a mechanism of evolution
- absolutely random
- does <u>not</u> lead to adaptation
- <u>does</u> Δ allele freq
- stems from violation of infinite size HW assumption

House mice, east side barn 2, Austin TX   Selander 1970

Slide 12

1. Coalescence

A_1 A_1 A_1 A_1 A_1 A_1 A_1 A_2 A_2 A_2 A_2 A_2 A_2 A_2

0

Time

t

av. r among indiv incr

fixed with prob = initial freq in the pop, f(A_i)

Mean time to coalescence = 2N gen,

where N is the # of diploid indiv at present

Slide 13
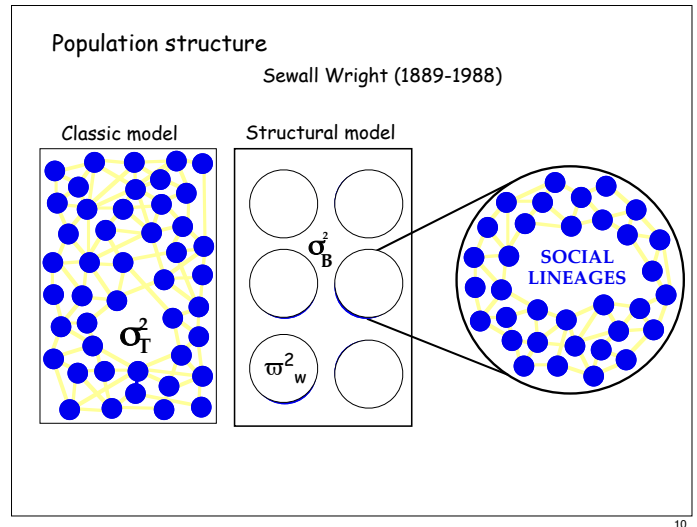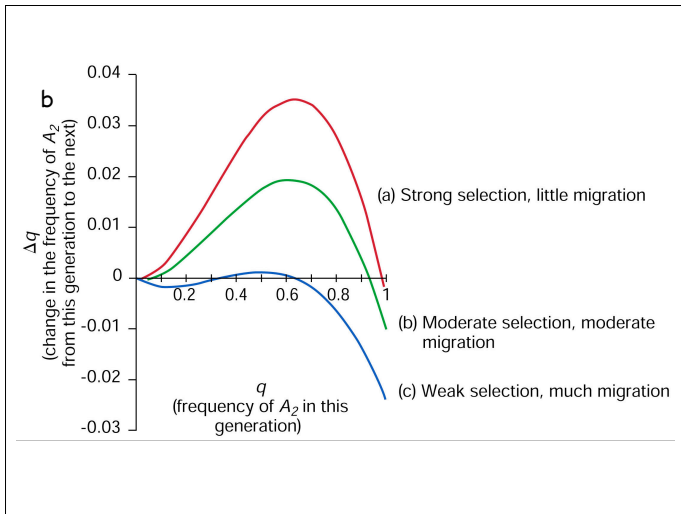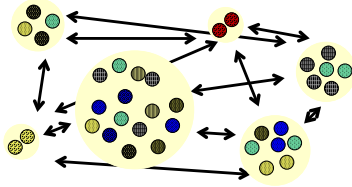
2. Random fluctuations in gene frequency

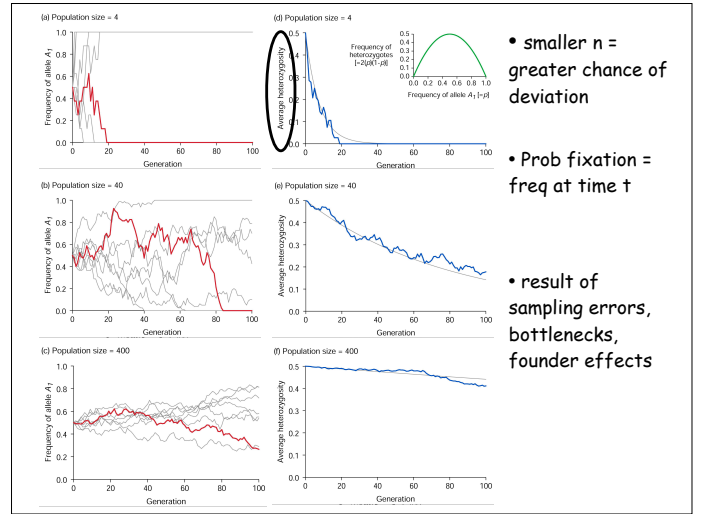Assume $f(A_1)= p$ & $f(A_2)= q$ in some ## of demes (metapopulation), each with N breeding individuals

In each generation, newborns suffer random mortality to leave N adults

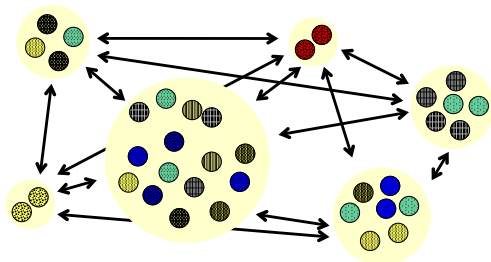But p' varies (binomial probability) 0 - 1, around a mean of p
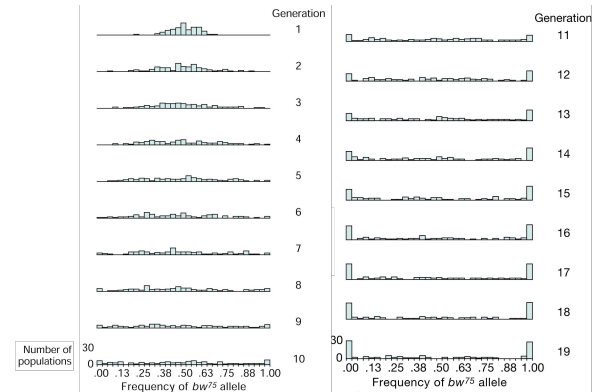
Picture a single deme.....

Slide 16

(a) Population size = 4
(b) Population size = 40
(c) Population size = 400
(d) Population size = 4
(e) Population size = 40
(f) Population size = 400

Frequency of heterozygotes [$=2[p](1-p)$]

Frequency of allele A_1 [$=p$]

• smaller n = greater chance of deviation

• Prob fixation = freq at time t

• result of sampling errors, bottlenecks, founder effects

Slide 14

• Random -> fixation
• Decrease within
• Increase between
• Probability?

Slide 17

Lab demo of drift...
107 pops (8M, 8F)
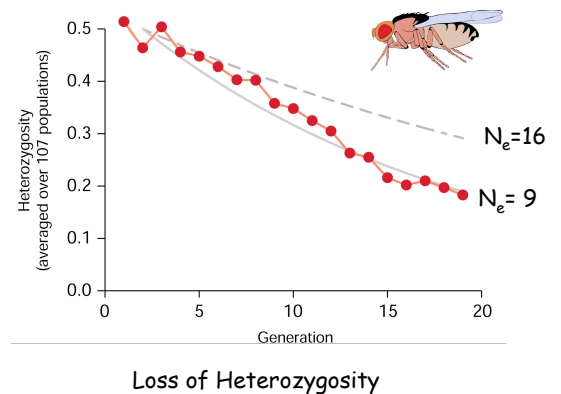Het for eye color (bw^{75}/bw) => initial freq bw^{75} = 0.5

Generation 1–10, 11–19

Number of populations

Frequency of bw^{75} allele

Buri (1956) Drosophila melanogaster

Slide 15

(a) Population size = 4

Frequency of allele A_1

Generation

(d) Population size = 4

Average heterozygosity

Frequency of heterozygotes [$=2[p](1-p)$]

Frequency of allele A_1 [$=p$]

Generation

Slide 18

Heterozygosity (averaged over 107 populations)
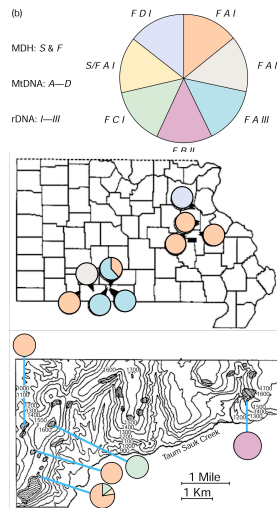
N_e=16

N_e= 9

Generation

Loss of Heterozygosity
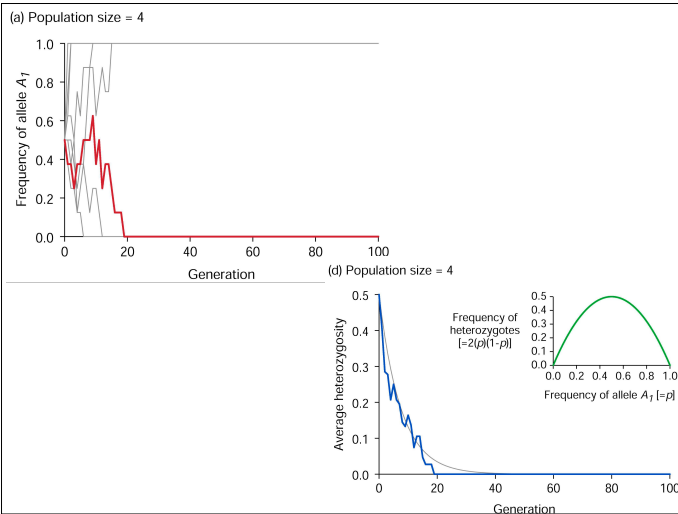
Measuring drift in nature......

- Glades - patchy remnants of desert habitat in Ozark forests

- Small, relict pops of Collared lizard

- No gene flow

- Predicted - strong imprint of genetic drift

Templeton et al (1990)
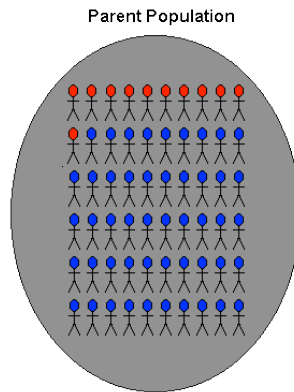
1 Mile
1 Km

Elephant Seals

20 -> 30,000

Genetic Drift

...sampling effects...

associated with....
Bottlenecks & Founder Effects

Parent Population

Type O
Type A

Founder Effect

Pennsylvania Amish

1770: 200 people
1964: 8,000

Ellis-van Creveld allele 7%
U.S. pop. 0.1%

'Six-fingered dwarfism'

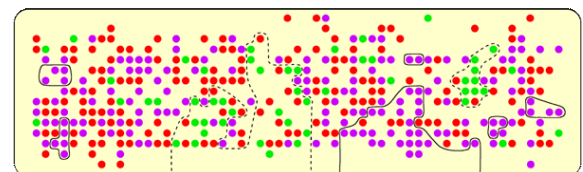Bottlenecks

- loss of alleles reduces individual variation & adaptability

Bottleneck event

Extinction
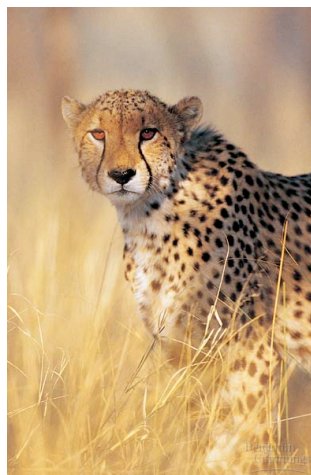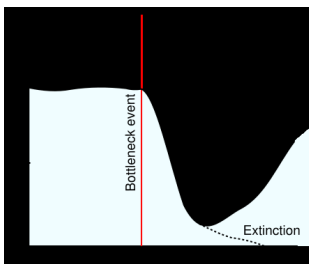
House mice, east side barn 2, Austin TX   Selander 1970
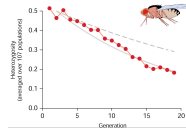
Genetic Drift…..

- a **regular occurrence** of sampling effects
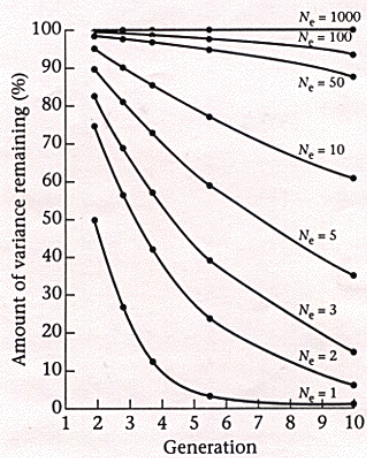- an impt mechanism of evolution

e.g. Buri fly experiment

Role of Effective Population Size N_e

- size of pop (ideal, random mating) losing genetic variation via drift at same rate as observed in actual pop

$$Ne = \frac{4NmNf}{(Nm +Nf)}$$

M	F	Ne
5	5	10
9	1	3.6
1000	1	4

25

26