Migration, drift, and non-random mating
Hardy-Weinberg conditions

- No mutation
- No selection
- No migration
- No genetic drift
- No non-random mating
If Hardy-Weinberg holds, then…

• No allele frequency change
  \[ p = \text{frequency of allele A} \]
  \[ q = \text{frequency of allele a} \]

• Genotype frequencies follow from
  \[ p^2 + 2pq + q^2 \]
Migration

• Not seasonal movement
  – E.g. birds

• Movement of alleles form one population to another
  – Called ‘gene flow’

• Makes populations more similar to each other
Migration

- 200 $A_2A_2$ individuals migrate from mainland
- Initial allele frequencies: $A_1 = 1.0$, $A_2 = 0$
- Number of individuals:
  - $A_1A_1$: 800
  - $A_1A_2$: 800
- Final allele frequencies: $A_1 = 0.8$, $A_2 = 0.2$
- Genotype frequencies:
  - $A_1A_1$, $A_1A_2$, $A_2A_2$
Nerodia sipedon
Selection on banding pattern

• Mainland
  – Banded snakes favored (dappled light)

• Islands
  – Unbanded snakes favored
    • Barren limestone basking surfaces

• Banded alleles on island persist due to migration from mainland
Migration of alleles

• Changes allele frequencies
• Can alter genotype frequencies
• Makes populations more similar
Measuring genetic similarity of populations

• Fst statistic ranges from 0 to 1
• Measures variation among subpopulations relative to the total variation (s and t)
• Fst high, then subpopulations pretty distinct
• Fst low, subpopulations homogenous
Silene dioica Swedish islands

- Colonize young island
  - Genes that get to any specific island mostly a matter of chance
- Pollination by insects
  - Over time, genes get spread from island to island (migration of alleles)
- Die off through ecological succession
  - Old populations survivors stochastic
Giles and Goulet, 1997

(a)

(b)

Variation in allele frequencies among populations ($F_{ST}$)

0.09

0.08

0.07

0.06

0.05

0.04

0.03

0.02

0.01

0

Young populations ($N = 13$)

Intermediate populations ($N = 30$)

Old populations ($N = 30$)
Genetic drift

• In Giles and Goulet’s study, what accounts for the high Fst values for young populations?

• Chance founder events
  – Populations drawn from small potential pool
Population size and genetic drift

• Flip a coin, odds are even (50:50) heads or tails
• If you flip the coin 10,000,000 times
  – You’d better get really close to 50:50
• If you flip the coin only 4 times, you have a good chance of getting either all heads or all tails
  12.5% chance, even if the coin is a fair coin
Sampling error in small populations
Chance of random allele frequency change, $N = 10$ zygotes

Probability that new frequency is exactly 0.6 is approximately 18%

Overall probability that new frequency is greater than 0.6 is approximately 41.5%

Overall probability that new frequency is less than 0.6 is approximately 40.5%
Drift versus sample size

- 3 runs of a simulation model
- True allele frequency 60:40
Drift as an evolutionary force

• Drift not an important evolutionary force in large populations
• Can be important in small populations
  – Founding of new populations
  – Fixation of alleles, loss of heterozygosity
Founder effect

- High Fst in *Silene dioica* young populations
- In humans,
  - Ellis-van-Creveld syndrome
    - Rare form of Dwarfism
    - Allele frequency around 0.001 in most populations
    - But found at 0.07 in Pennsylvania Amish descended from 200 founding individuals
Drift and allele frequency change

• small populations over many generations
• Fixation: an allele is *fixe* at a locus if it is at a frequency of 100%
• Heterozygosity decrease as alleles becomes rarer

Note: \[2(p)(1-p)\]

\[= 2pq\]
Fixation of alleles

• If allele frequency goes to 1 it is fixed
• If it goes to 0 the allele is lost, and the alternative allele is fixed (if there are only two alleles)
• Probability that an allele goes to fixation equal to its initial frequency
  – With drift alone that is (no mutation, no selection, etc.)
Loss of heterozygosity

- Heterozygote frequency = 2 pq
  - Alternatively 2p(1-p)
  - At a maximum when p = 0.5
- Buri *Drosophila* experiment
- 107 lines of 8 females 8 males
- Start p = q = 0.5
- Qualitative: heterozygosity decrease
- Quantitative: for population with size 16, heterozygosity should follow dashed line; instead followed solid gray line - the prediction for n = 9
Effective population size

• Buri’s fly populations lost heterozygosity as predicted IF the population size was 9 not 16
• If some died, or failed to reproduce, then the effective population size can be smaller than the actual population size

\[ \text{Ne} = \frac{4 \times Nm \times Nf}{Nm + Nf} \]

Nm = number of sexually reproductive males
Nf = number of sexually reproducing females

• 5 males 5 females, Ne = 10
• 1 male 9 females, Ne = 3.6
Drift and the neutral theory

• Alleles that have no fitness effect called neutral
• Allelic substitution can be by drift or selection
• If most mutations produce selectively neutral alleles, the fate of those alleles will be governed mostly by drift
  – Basis of idea behind molecular clock
Genetic drift summary

• Random effects
• Importance highly dependent on population size
  – Effective population size even smaller
• Can allow a neutral allele to replace another simply by chance
• Decreases allelic diversity and heterozygosity
Non-random mating

• Obviously individuals do not mate randomly
  – Really, would you want to mate randomly?

• We are talking about random mating with respect to particular alleles

• Not non-random mating with respect to money, sexiness, or ability to make your heart go pitter-patter
  – That is sexual selection, a form of natural selection
Non-random mating with respect to alleles

• Positive assortative mating
  – Like mates with like

• Mating among genetic relatives called *Inbreeding*
Inbreeding and heterozygosity

• Imagine extreme inbreeding
• Self fertilization
• Homozygotes produce all homozygotes
• Heterozygotes produce 1/2 homozygotes and 1/2 heterozygotes
• Proportion of heterozygotes decreases by 1/2 each generation
Selfing and heterozygosity

Table 6.1  Changes in genotype frequencies with successive generations of selfing

The frequency of allele $A_1$ is $p$ and the frequency of allele $A_2$ is $q$. Note that allele frequencies do not change from generation to generation—only the genotype frequencies. After Crow (1983).

<table>
<thead>
<tr>
<th>Generation</th>
<th>$A_1A_1$</th>
<th>Frequency of $A_1A_2$</th>
<th>Frequency of $A_2A_2$</th>
</tr>
</thead>
<tbody>
<tr>
<td>0</td>
<td>$p^2$</td>
<td>2pq</td>
<td>$q^2$</td>
</tr>
<tr>
<td>1</td>
<td>$p^2 + (pq/2)$</td>
<td>$pq$</td>
<td>$q^2 + (pq/2)$</td>
</tr>
<tr>
<td>2</td>
<td>$p^2 + (3pq/4)$</td>
<td>$pq/2$</td>
<td>$q^2 + (3pq/4)$</td>
</tr>
<tr>
<td>3</td>
<td>$p^2 + (7pq/8)$</td>
<td>$pq/4$</td>
<td>$q^2 + (7pq/8)$</td>
</tr>
<tr>
<td>4</td>
<td>$p^2 + (15pq/16)$</td>
<td>$pq/8$</td>
<td>$q^2 + (15pq/16)$</td>
</tr>
</tbody>
</table>
Inbreeding produces excess homozygotes

• More homozygotes than predicted by Hardy-Weinberg suggests something, perhaps inbreeding is going on

• One generation of random mating re-establishes Hardy-Weinberg genotype frequencies
Inbreeding depression

• Does not mean you are sad you kissed your cousin
• Inbreeding produces a deficit of heterozygotes and a surplus of homozygotes
• What if those homozygotes are of deleterious recessive alleles?
Inbreeding reduces fitness: humans

![Graph showing the relationship between inbreeding and mortality rate among children](image)
Also, plants, non-human animals

Blue outcrossed controls; red selfed
Conservation Genetics: the case of the greater prairie chicken in Illinois
Movie time
Decline

• Millions pre-1837 steel plow
• 25000 in 1933
• 2000 in 1962
• 500 in 1972
• 76 in 1990
• 50 or less 1994
Habitat loss: steel plow 1837

Two remaining habitats protected in 1962 and 1967
Protection and population decline
Why the post mid 1970’s decline?

• Migration
• Drift
• Inbreeding
### Allelic diversity

**Table 6.4** Number of alleles per locus found in each of the current populations of Illinois, Kansas, Minnesota, and Nebraska and estimated for the Illinois prebottleneck population

<table>
<thead>
<tr>
<th>Locus</th>
<th>Illinois</th>
<th>Kansas</th>
<th>Minnesota</th>
<th>Nebraska</th>
<th>Illinois prebottleneck*</th>
</tr>
</thead>
<tbody>
<tr>
<td>ADL42</td>
<td>3</td>
<td>4</td>
<td>4</td>
<td>4</td>
<td>3</td>
</tr>
<tr>
<td>ADL23</td>
<td>4</td>
<td>5</td>
<td>4</td>
<td>5</td>
<td>5</td>
</tr>
<tr>
<td>ADL44</td>
<td>4</td>
<td>7</td>
<td>8</td>
<td>8</td>
<td>4</td>
</tr>
<tr>
<td>ADL146</td>
<td>3</td>
<td>5</td>
<td>4</td>
<td>4</td>
<td>4</td>
</tr>
<tr>
<td>ADL162</td>
<td>2</td>
<td>5</td>
<td>4</td>
<td>4</td>
<td>6</td>
</tr>
<tr>
<td>ADL230</td>
<td>6</td>
<td>9</td>
<td>8</td>
<td>10</td>
<td>9</td>
</tr>
<tr>
<td>Mean</td>
<td>3.67</td>
<td>5.83</td>
<td>5.33</td>
<td>5.83</td>
<td>5.12</td>
</tr>
<tr>
<td>SE</td>
<td>0.56</td>
<td>0.75</td>
<td>0.84</td>
<td>1.05</td>
<td>0.87</td>
</tr>
<tr>
<td>Sample size</td>
<td>32</td>
<td>37</td>
<td>38</td>
<td>20</td>
<td>15</td>
</tr>
</tbody>
</table>

*Note:* SE indicates standard error of mean number of alleles per locus. The Illinois population in column 1 shows significantly less allelic diversity than the rest of the populations ($P < 0.05$).

*Number of alleles in the Illinois prebottleneck population include both extant alleles that are shared with the other populations and alleles detected in the museum collection.

*Source:* From Bouzat et al. (1998).
Egg viability
Evolutionary forces

• Drift
  – Small population
  – Even smaller effective population size
    • Lek mating system

• Low allelic diversity, low heterozygosity

• Migration reintroduces new alleles
  – Gene flow