Lecture 3
Covariance Between Relatives

• Needed for
  – Estimation of Genetic Parameters
    • Heritabilities
    • Genetic Correlations
  – Estimation of Breeding Values
    • Information on relatives

Parent Offspring Regression

Obvious method to determine heritability

\[ h^2 = \frac{\text{Cov}(o, P)}{\text{Var}(P)} \]

Offspring Height vs. Parents Height

How does this data give an indication of heritability
What pattern would you expect? Between and within family?
Which Trait has Higher Heritability?

Situation 1
- Family
- Trait Value
- Var(B)=2.5
- Var(W)=.5
- Vp=Var(B)+Var(W)=3

Situation 2
- Family
- Trait Value
- Var(B)=0
- Var(W)=3
- Vp=Var(B)+Var(W)=3

Partitioning Variation

Between vs within Family

Case 1
\[ \frac{\text{Var}(B)}{V_p} = \frac{2.5}{3} = .83 \]

Case 2
\[ \frac{\text{Var}(B)}{V_p} = \frac{0}{3} = 0 \]

Which of these situations is indicative of a high genetic component?

Var(B)=variation among group, group are full sib groups

Genetic Covariance

- Relatives are more likely to share alleles than non-relatives
  - Sharing Alleles = Identical by Descent (IBD)
    - Identically same allele can be traced to an ancestor
  - Not to be confused with Alike in State
    - Same allele but not IBD

Example IBD alleles

A_1A_2

A_1A_3

S_1

S_2

S_0
**Single Parent-offspring Covariance**

1. **Gp** = \( \alpha_1 + \alpha_2 + \delta_{12} \)  
   100% of the time parent and offspring will share one and only one allele

2. **Go** = \( \alpha_1 + \alpha_x + \delta_{1x} \)

3. \( \text{Cov}(G_p, G_o) = \text{Cov}(\alpha_1, \alpha_2) + \text{Cov}(\alpha_1, \alpha_x) + \text{Cov}(\alpha_1, \delta_{12}) + \text{Cov}(\alpha_x, \alpha_1) + \text{Cov}(\alpha_x, \alpha_x) + \text{Cov}(\alpha_x, \delta_{1x}) + \text{Cov}(\delta_{12}, \alpha_1) + \text{Cov}(\delta_{12}, \alpha_x) + \text{Cov}(\delta_{12}, \delta_{1x}) \)

Because

\( \text{Var}(\alpha_1 + \alpha_2) = \frac{1}{2} \sigma_A^2 + \frac{1}{2} \sigma_A^2 \)

\( \text{Var}(\alpha_x) = \frac{1}{2} \sigma_A^2 \)

**In General: Covariance between effects**

\[
\text{Cov}(\alpha_i, \alpha_j) = \begin{cases} 
0 & \text{if } i \neq j, \text{i.e. not IBD} \\
\frac{1}{2} \sigma_A^2 & \text{if } i = j, \text{i.e. IBD}
\end{cases}
\]

Additivity is a function of single alleles

\[
\text{Cov}(\alpha_i, \delta_{ij}) = 0 \quad \text{By construct}
\]

\[
\text{Cov}(\delta_{ij}, \delta_{km}) = \begin{cases} 
0 & \text{if } i \neq km, \text{i.e. both not IBD} \\
\sigma_D^2 & \text{if } i = km, \text{i.e. both IBD}
\end{cases}
\]

Dominance if a function of both alleles at a locus, it is predicted as the failure of both alleles at that locus to be additive

**Summary**

<table>
<thead>
<tr>
<th>Number of IBD alleles</th>
<th>Probability of Sharing</th>
<th>Contribution to variances</th>
</tr>
</thead>
<tbody>
<tr>
<td>0</td>
<td>0</td>
<td>( \frac{1}{2} \sigma_A^2 )</td>
</tr>
<tr>
<td>1</td>
<td>1</td>
<td>( \frac{1}{2} \sigma_A^2 + \sigma_D^2 )</td>
</tr>
<tr>
<td>2</td>
<td>0</td>
<td>( \sigma_A^2 + \frac{1}{2} \sigma_D^2 )</td>
</tr>
</tbody>
</table>

Total covariance = Sum Probability x contribution

\[
(1) \frac{1}{2} \sigma_A^2 + (0)(\sigma_A^2 + \sigma_D^2) = \frac{1}{2} \sigma_A^2
\]
Midparent-Offspring

\[ Cov(O, MP) = Cov(\sigma, \frac{P_m + P_f}{2}) = Cov(\sigma, P_m/2) + Cov(\sigma, P_f/2) = \frac{1}{2} \sigma_d^2 + \frac{1}{2} \sigma_d^2 = \sigma_d^2 \]

Collateral: Number of IBD Alleles

<table>
<thead>
<tr>
<th>Sib O₁ possible genotypes</th>
<th>A₃A₃</th>
<th>A₃A₅</th>
<th>A₅A₅</th>
<th>A₅A₅</th>
</tr>
</thead>
<tbody>
<tr>
<td>A₃A₅, 0.25</td>
<td>1/4</td>
<td>1/4</td>
<td>1/4</td>
<td>1/4</td>
</tr>
<tr>
<td>A₃A₆, 0.25</td>
<td>1/4</td>
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</table>

Collateral: Half sibs

\[ Cov(G_{O₁}, G_{O₂}) \]

Collateral: Half sibs

Number of IBD | Probability of Sharing | Contribution to variances
---------------|------------------------|--------------------------
0 IBD alleles  | 8/16                   | 0 \(\sigma_d^2\)          |
1 IBD alleles  | 8/16                   | \(\frac{1}{2} \sigma_d^2\) + \(\frac{1}{2} \sigma_d^2\) |
2 IBD alleles  | 0                      | \(\sigma_d^2 + \sigma_d^2\) |

Total covariance=Sum Probability x contribution= \(\frac{1}{16} \times \frac{1}{2} \sigma_d^2 + \frac{1}{16} \times \frac{1}{2} \sigma_d^2 = \frac{1}{4} \sigma_d^2 \)
Collateral: Full sibs

\[ \text{Cov}(G_{O_1}, G_{O_2}) \]

Collateral: Number of IBD Alleles

<table>
<thead>
<tr>
<th>Sib O₁ possible genotypes</th>
<th>A₁A₃</th>
<th>A₁A₄</th>
<th>A₂A₃</th>
<th>A₂A₄</th>
</tr>
</thead>
<tbody>
<tr>
<td>1/4 A₁A₃</td>
<td>2</td>
<td>1</td>
<td>1</td>
<td>0</td>
</tr>
<tr>
<td>1/4 A₁A₄</td>
<td>1</td>
<td>2</td>
<td>0</td>
<td>1</td>
</tr>
<tr>
<td>1/4 A₂A₃</td>
<td>1</td>
<td>0</td>
<td>2</td>
<td>1</td>
</tr>
<tr>
<td>1/4 A₂A₄</td>
<td>0</td>
<td>1</td>
<td>1</td>
<td>2</td>
</tr>
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</table>

Collateral: Full sibs

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<th>Number of IBD alleles</th>
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<th>Contribution to variances</th>
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</thead>
<tbody>
<tr>
<td>0 IBD alleles</td>
<td>4/16</td>
<td>0</td>
</tr>
<tr>
<td>1 IBD alleles</td>
<td>8/16</td>
<td>( \frac{1}{2} \sigma_D^2 )</td>
</tr>
<tr>
<td>2 IBD alleles</td>
<td>4/16</td>
<td>( \sigma_A^2 + \sigma_D^2 )</td>
</tr>
</tbody>
</table>

\[ \text{Cov}(G_{O_1}, G_{O_2}) = \text{Total covariance} = \text{Sum Probability x contribution} = \]

\[ \left( \frac{4}{16} \right) \left( \frac{1}{2} \sigma_D^2 \right) + \left( \frac{8}{16} \right) \left( \sigma_A^2 + \sigma_D^2 \right) = \frac{1}{2} \sigma_A^2 + \frac{1}{2} \sigma_D^2 \]

Collateral: Number of IBD Alleles

<table>
<thead>
<tr>
<th>Sib O₂ possible genotypes</th>
<th>A₁A₃</th>
<th>A₁A₄</th>
<th>A₂A₃</th>
<th>A₂A₄</th>
</tr>
</thead>
<tbody>
<tr>
<td>A₁A₃ 1/4</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>A₁A₄ 1/4</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>A₂A₃ 1/4</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>A₂A₄ 1/4</td>
<td></td>
<td></td>
<td></td>
<td></td>
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</table>

Covariance Between Relatives in General

\[ \text{Cov}(G_x, G_y) \]

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<tr>
<th>Number of IBD alleles</th>
<th>Probability of Sharing</th>
<th>Contribution to variances</th>
</tr>
</thead>
<tbody>
<tr>
<td>1 IBD alleles</td>
<td>( \text{Pr}(1)_{xy} )</td>
<td>( \frac{1}{2} \sigma_A^2 )</td>
</tr>
<tr>
<td>2 IBD alleles</td>
<td>( \text{Pr}(2)_{xy} )</td>
<td>( \sigma_A^2 + \sigma_D^2 )</td>
</tr>
</tbody>
</table>

Let \( r_{xy} = \frac{1}{2} \text{Pr}(1)_{xy} + \text{Pr}(2)_{xy} \) \( u_{xy} = \text{Pr}(2)_{xy} \)

Total covariance = Sum Probability x contribution =

\[ \text{Cov}(G_x, G_y) = r_{xy} \sigma_A^2 + u_{xy} \sigma_D^2 \]

With higher order effects (epistasis)

\[ \text{Cov}(G_x, G_y) = r_{xy} \sigma_A^2 + u_{xy} \sigma_D^2 + r_{xy}^2 \sigma_{A4}^2 + r_{xy}^2 u_{xy} \sigma_{A3D}^2 + u_{xy}^2 \sigma_{D4}^2 + ... \]
Covariance Between Relatives
Common Environmental Causes  Ec

Common Farm

Common Maternal

Common Cage or Pen

Specific Environmental Effects  Es

Environmental Effects
Common Environmental Effects Ec contribute to resemblance of sibs
Specific Environmental effect: Es
Causes correlation among sequential records from same animal

Summary Resemblance Among Relatives

<table>
<thead>
<tr>
<th>Relative Pair</th>
<th>Cov</th>
<th>Relative to Phenotypic Variance</th>
<th>$h^2$</th>
</tr>
</thead>
<tbody>
<tr>
<td>Parent-Offspring</td>
<td>$\frac{1}{2}\sigma_A^2$</td>
<td>$b_{o,p} = \frac{1}{2}\sigma_A^2 / \sigma_P^2$</td>
<td>$h^2 = 2b_{o,p}$</td>
</tr>
<tr>
<td>Midparent-Offspring</td>
<td>$\frac{1}{2}\sigma_A^2$</td>
<td>$b_{o,p} = \left(\frac{1}{2}\sigma_A^2 / \sigma_P^2\right)$</td>
<td>$h^2 = b_{o,p}$</td>
</tr>
<tr>
<td>Half-Sib</td>
<td>$\frac{1}{2}\sigma_A^2$</td>
<td>$t_{HS} = \left(\frac{1}{2}\sigma_A^2 / \sigma_P^2\right)$</td>
<td>$h^2 = 4t_{HS}$</td>
</tr>
<tr>
<td>Full-Sib</td>
<td>$\frac{1}{2}\sigma_A^2 + \frac{1}{2}\sigma_D^2 + \sigma_E^2$</td>
<td>$t_{HS} = \left(\frac{1}{2}\sigma_A^2 + \frac{1}{2}\sigma_D^2 + \sigma_E^2 / \sigma_P^2\right)$</td>
<td>$h^2 \leq 2t_{FS}$</td>
</tr>
</tbody>
</table>

$Var(MP) = Var\left(\frac{P_m + P_f}{2}\right) = \frac{1}{2}(Var(P_m + P_f)) = \frac{1}{2}(\sigma_A^2 + \sigma_D^2) = \frac{1}{4}\sigma_P^2$
Problem set 3

• Recall Problem 1 of Set 2: Falconer (1981) reported a partially dominant gene in the mouse called pg “pygmy.” At six weeks of age, they produce the following average weight phenotypes in grams (the actual weight of the heterozygote was 12, but it was reduced to 10 for this example):
  • + / + : 14, + / pg : 10, pg / pg : 6
• If the population of mice is randomly mating with \( p^+ = 0.3, q_n = 0.7 \)
• Assume an Environmental variance of 7 and no environmental effects common to families. Compute the regression or intraclass correlation for the following
  -- a) one parent-offspring
  -- b) half-sib
  -- c) Full-sib
  -- d) If the frequency of the wild allele (+) increased to .5, would you expect these values to increase, decrease, or remain the same, Why (?)