

# Genetic Covariance of Trait Values for Relatives

## **Coefficients of Coancestry**



 We previously showed that for a pair of individuals that the kinship coefficient (or coefficient of coancestry) θ can be written in terms of Jacquard's 9 condensed coefficients of identity where

$$\theta = \Delta_1 + \frac{1}{2}(\Delta_3 + \Delta_5 + \Delta_7) + \frac{1}{4}\Delta_8$$

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# Jacquard's (1970) 9 Condensed Coefficients of



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## **Coefficients of Coancestry**



- $\bullet$  Consider an outbred population. For outbred populations we have that  $\Delta_1$  to  $\Delta_6$  are 0.
- it is convenient to let  $k_2$ ,  $k_1$  and  $k_0$  represent the probability that a pair of outbred individuals sharing 2, 1, or 0 alleles IBD, respectively, in lieu of  $\Delta_7$ ,  $\Delta_8$ , and  $\Delta_9$ .
- For outbred populations the kinship coefficient for a pair of individuals can be written as

$$\theta = \frac{1}{2}k_2 + \frac{1}{4}k_1$$

• Note that the kinship coefficient is based on the probability of sharing 0, 1, or 2 alleles IBD. However, at a locus, a pair of individuals actually share either zero, one, or two alleles ibd at a locus.

# **Coefficients of Coancestry**



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- Let  $k_0^*$ ,  $k_1^*$ , and  $k_2^*$  be the actual value at the locus.
- Exactly one of these three quantities is one (for that ibd state being true) and the other two are zero (for those ibd states being false).
- Calculate the following
  - $E[k_i^*]$
  - $Var[k_i^*]$
  - $E[k_i^* k_j^*]$  for  $i \neq j$
  - $Cov[\vec{k_i^*}, k_j^*]$  for  $i \neq j$



• We have the following:

- $E[k_i^*] = k_i$
- $Var[k_i^*] = k_i(1-k_i)$
- $E[k_i^*k_j^*] = 0$  for  $i \neq j$
- $Cov[\tilde{k_i^*}, k_j^*] = -k_i k_j$  for  $i \neq j$



• Now, the actual coancestry at a locus for two noninbred individuals is

$$\theta^* = \frac{1}{2}k_2^* + \frac{1}{4}k_1^*$$

• Calculate  $Var(\theta^*)$ 



$$Var(\theta^*) = \frac{1}{4}Var(k_2^*) + \frac{1}{16}Var(k_1^*) + \frac{1}{4}Cov(k_1^*, k_2^*)$$
$$= \frac{1}{4}k_2(1-k_2) + \frac{1}{16}k_1(1-k_1) - \frac{1}{4}k_2k_1$$

- First cousins have  $k_2 = 0$ ,  $k_1 = .25$  and  $k_0 = .75$ . Calculate the expected value, variance, and standard deviation of actual coancestry for this relative pair type at a locus.
- What is the variance of actual coancestry for parent-offspring?



$$Var(\theta^*) = \frac{1}{4}k_2(1-k_2) + \frac{1}{16}k_1(1-k_1) - \frac{1}{4}k_2k_1$$

- First cousins have  $k_2 = 0$ ,  $k_1 = \frac{1}{4}$  and  $k_0 = \frac{3}{4}$ , so  $\theta = \frac{1}{16} = .0625$ .
- The variance of actual coancestry is  $\left(\frac{1}{16}\right)\left(\frac{1}{4}\right)\left(\frac{3}{4}\right) = \frac{3}{256}$
- The standard deviation is  $\frac{\sqrt{3}}{16} = .10825$
- For parent-offspring, the variance of actual coancestry is 0.

- We will now focus on obtaining the genetic covariance of trait values for two outbred relatives
- Consider a quantitative trait that is influence by a single locus.
- As before, we denote the genetic value for genotype  $A_iA_j$  as

$$G_{ij} = \mu_G + lpha_i + lpha_j + \delta_{ij}$$

where

$$\mu_G = \sum_i \sum_j p_i p_j G_{ij} = G..$$
$$\alpha_i = \sum_j p_j G_{ij} - \mu_G = G_{i.} - G..$$
$$\delta_{ij} = G_{ij} - \mu_G - \alpha_i - \alpha_j = G_{ij} - G_{i.} - G_{j.} + G..$$

 $\mathbf{G}_{ij} = \mathbf{G}_{ij} - \mu_G - \mu_i - \mu_j = \mathbf{G}_{ij} - \mathbf{G}_{i.} - \mathbf{G}_{j.} + \mathbf{G}_{i.}$ 

• These imply that  $\sum_i p_i \alpha_i = 0$  and  $\sum_i p_i \delta_{ij} = 0$ 

- Consider two individuals X and Y. We will calculate the covariance of the genetic values for X and Y.
- Let  $X_1$  and  $X_2$  be the two alleles at the locus for individual X, and let  $Y_1$  and  $Y_2$  be the two alleles for individual Y
- We have the following:

 $Cov(G_{X_{1}X_{2}}, G_{Y_{1}Y_{2}}) =$  $Cov(\mu_{G} + \alpha_{X_{1}} + \alpha_{X_{2}} + \delta_{X_{1}X_{2}}, \mu_{G} + \alpha_{Y_{1}} + \alpha_{Y_{2}} + \delta_{Y_{1}Y_{2}})$  $= Cov(\alpha_{X_{1}}, \alpha_{Y_{1}}) + Cov(\alpha_{X_{1}}, \alpha_{Y_{2}}) + Cov(\alpha_{X_{1}}, \delta_{Y_{1}Y_{2}})$  $+ Cov(\alpha_{X_{2}}, \alpha_{Y_{1}}) + Cov(\alpha_{X_{2}}, \alpha_{Y_{2}}) + Cov(\alpha_{X_{2}}, \delta_{Y_{1}Y_{2}})$  $+ Cov(\delta_{X_{1}X_{2}}, \alpha_{Y_{1}}) + Cov(\delta_{X_{1}X_{2}}, \alpha_{Y_{2}}) + Cov(\delta_{X_{1}X_{2}}, \delta_{Y_{1}Y_{2}})$  $= 4Cov(\alpha_{X_{1}}, \alpha_{Y_{1}}) + 2Cov(\alpha_{X_{1}}, \delta_{Y_{1}Y_{2}}) + 2Cov(\delta_{X_{1}X_{2}}, \alpha_{Y_{1}})$  $+ Cov(\delta_{X_{1}X_{2}}, \delta_{Y_{1}Y_{2}})$ 



- Now let's first focus on the terms involving the covariance of the additive and dominance effects:  $2Cov(\alpha_{X_1}, \delta_{Y_1Y_2})$  and  $2Cov(\delta_{X_1X_2}, \alpha_{Y_1})$
- Let's consider the covariance when X and Y are the monozygotic twins, or the genetic equivalence of X = Y. What do we know about  $Cov(\alpha_{X_1}, \delta_{X_1X_2})$

$$Cov(\alpha_{X_1}, \delta_{X_1X_2}) = E(\alpha_{X_1}\delta_{X_1X_2}) - E(\alpha_{X_1})E(\delta_{X_1X_2})$$
$$= E(\alpha_{X_1}\delta_{X_1X_2}) - 0$$
$$= \sum_i \sum_j p_i p_j \alpha_i \delta_{ij} = \sum_i p_i \alpha_i \sum_j p_j \delta_{ij} = \sum_i p_i \alpha_i (0) = 0$$

• We actually already know this to be true since the additive effects and the dominance effects are uncorrelated!

- It follows that for any pair of individuals X and Y, who obviously must have IBD sharing that is less than or equal to monozygotic twins, that the additive and dominance effects must also have a covariance of 0.
- So we have

$$Cov(G_{X_{1}X_{2}}, G_{Y_{1}Y_{2}}) =$$

$$4Cov(\alpha_{X_{1}}, \alpha_{Y_{1}}) + 2Cov(\alpha_{X_{1}}, \delta_{Y_{1}Y_{2}}) + 2Cov(\delta_{X_{1}X_{2}}, \alpha_{Y_{1}})$$

$$+Cov(\delta_{X_{1}X_{2}}, \delta_{Y_{1}Y_{2}})$$

$$= 4 \operatorname{Cov}(\alpha_{X_1}, \alpha_{Y_1}) + \operatorname{Cov}(\delta_{X_1X_2}, \delta_{Y_1Y_2})$$

• Now take a moment to calculate  $4Cov(\alpha_{X_1}, \alpha_{Y_1})$ . Hint: use the kinship coefficient  $\theta$  for the two individuals for this calculation

• We have

$$Cov(\alpha_{X_1}, \alpha_{Y_1}) = E[\alpha_{X_1}\alpha_{Y_1}] - E[\alpha_{X_1}]E[\alpha_{Y_1}]$$
$$= E[\alpha_{X_1}\alpha_{Y_1}] - 0$$

Now

 $E[\alpha_{X_1}\alpha_{Y_1}] = E[\alpha_{X_1}\alpha_{Y_1}|X_1 \text{ and } Y_1 \text{ are IBD}]P(X_1 \text{ and } Y_1 \text{ are IBD})$  $+E[\alpha_{X_1}\alpha_{Y_1}|X_1 \text{ and } Y_1 \text{ are not IBD}]P(X_1 \text{ and } Y_1 \text{ are not IBD})$  $=E[\alpha_{X_1}^2]\theta + 0(1-\theta)$  $=\frac{1}{2}\sigma_a^2\theta$ 

where  $\sigma_a^2$  is the additive variance for the trait since we previously define  $\sigma_a^2 = 2 \operatorname{Var}(\alpha_i) = 2 \sum_i p_i \alpha_i^2$ 

So we have  

$$Cov(G_{X_1X_2}, G_{Y_1Y_2}) = = 4Cov(\alpha_{X_1}, \alpha_{Y_1}) + Cov(\delta_{X_1X_2}, \delta_{Y_1Y_2})$$

$$= 4(\frac{1}{2}\sigma_a^2) + Cov(\delta_{X_1X_2}, \delta_{Y_1Y_2}) = 2\theta\sigma_a^2 + Cov(\delta_{X_1X_2}, \delta_{Y_1Y_2})$$

• Now take a moment to calculate  $Cov(\delta_{X_1X_2}, \delta_{Y_1Y_2})$ . Hint: condition of the probabilities of the pair sharing zero, one, or two alleles IBD, i.e.,  $k_0, k_1$ , and  $k_2$ 

• We have

Now

$$Cov(\delta_{X_1X_2}, \delta_{Y_1Y_2}) = E[\delta_{X_1X_2}\delta_{Y_1Y_2}] - E[\delta_{X_1X_2}]E[\delta_{Y_1Y_2}]$$
$$= E[\delta_{X_1X_2}\delta_{Y_1Y_2}] - 0$$
$$E[\delta_{X_1X_2}\delta_{Y_1Y_2}] =$$

$$\begin{split} E[\delta_{X_1X_2}\delta_{Y_1Y_2}|X \text{ and } Y \text{ share 2 alleles IBD}] \times \\ P(X \text{ and } Y \text{ share 2 alleles IBD}) \\ + E[\delta_{X_1X_2}\delta_{Y_1Y_2}|X \text{ and } Y \text{ share 1 allele IBD}] \times \\ P(X \text{ and } Y \text{ share 1 alleles IBD}) \\ + E[\delta_{X_1X_2}\delta_{Y_1Y_2}|X \text{ and } Y \text{ share 0 alleles IBD}] \times \\ P(X \text{ and } Y \text{ share 0 alleles IBD}) \end{split}$$

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• We have that

 $E[\delta_{X_1X_2}\delta_{Y_1Y_2}|X \text{ and } Y \text{ share 2 alleles IBD}] \times$ 

 $P(X \text{ and } Y \text{ share 2 alleles IBD}) = E[\delta_{X_1X_2}^2]k_2$ 

We also have that

 $E[\delta_{X_1X_2}\delta_{Y_1Y_2}|X \text{ and } Y \text{ share 1 allele IBD}] \times$   $P(X \text{ and } Y \text{ share 1 alleles IBD}) = k_1 \sum_{l} \sum_{i} \sum_{j} p_l p_i p_j \delta_{il} \delta_{jl}$   $= k_1 \sum_{l} p_l \sum_{i} p_i \delta_{il} \sum_{j} p_j \delta_{jl}$   $= k_1 \sum_{l} p_l(0)(0)$ 

since  $\sum_{i} p_i \delta_{ij} = 0$ .

• Finally, we have that

 $E[\delta_{X_1X_2}\delta_{Y_1Y_2}|X \text{ and } Y \text{ share 0 alleles IBD}] \times$  $P(X \text{ and } Y \text{ share 0 alleles IBD}) = E[\delta_{X_1X_2}]E[\delta_{Y_1Y_2}]k_0$  $= (0)(0)k_0 = 0$ 

• So, putting the three terms together we have that

$$Cov(\delta_{X_1X_2}, \delta_{Y_1Y_2}) = E[\delta_{X_1X_2}^2]k_2 + (0)k_1 + (0)k_0 = \sigma_d^2k_2$$

where  $\sigma_d^2$  is the dominance variance for the trait that we previously define as

$$\sigma_d^2 = Var(\delta_{ij}) = E[\delta_{ij}^2] = \sum_{ij} p_{ij} \delta_{ij}^2$$



• So we have

$$Cov(G_{X_1X_2}, G_{Y_1Y_2}) =$$
  
= 4Cov(\alpha\_{X\_1}, \alpha\_{Y\_1}) + Cov(\delta\_{X\_1X\_2}, \delta\_{Y\_1Y\_2})  
= 2\theta \sigma\_a^2 + k\_2 \sigma\_d^2

• For inbred individuals, obtaining genetic covariance is a bit more complicated, but one can show that for X and Y inbreed we have

$$Cov(G_{X_1X_1}, G_{Y_1Y_2}) =$$

$$= 2\theta \sigma_a^2 + \Delta_7 \sigma_d^2$$

$$+ D_1(4\Delta_1 + \Delta_3 + \Delta_5) + D_2\Delta_1 + H^2(\Delta_1 + \Delta_2 - F_X F_Y)$$

# Terminology and Expressions for Variance of Trans

Components	Multi-allelic	Bi-allelic
Additive Variance	$\sigma_A^2 = 2\sum_i p_i \alpha_i^2$	$\sigma_A^2 = 2pq\alpha^2$
Dominance Variance	$\sigma_D^2 = \sum_i \sum_j p_i p_j \delta_{ij}^2$	$\sigma_D^2 = (2pqd)^2$
Inbreeding depression	$H = \sum_{i} p_i \delta_{ii}$	H=-2qpd
Covariance of $\alpha_i$ 's and $\delta_{ii}$ 's	$D_1 = \sum_i p_i \alpha_i \delta_{ii}$	$D_1 = 2pqd\alpha(p-q)$
Variance of $\delta_{ii}$ 's	$D_2 = \sum_i p_i \delta_{ii}^2 - H^2$	$D_2 = 4pq(1-4pq)d^2$