

THE CORRELATION BETWEEN MIDPARENT AND OFFSPRING

Let F be the fraternal trait value, M the maternal trait value, O the offspring trait value, and $\bar{P} = (F + M)/2$. We scale F , M , and O so that each has unit variance. Recall that the covariance between two variables with unit variances is equal to their correlation.

The standard expression for the covariance between parent and offspring attributable to the additive genetic variance is

$$\text{Cov}(F, O) = \text{Cov}(M, O) = \frac{1}{2}(1 + \rho)h^2,$$

where h^2 is the narrow-sense heritability and ρ is the correlation between F and M attributable to assortative mating. The derivation of this expression assumes that mating is not selective; that is, all individuals mate, the only question being with whom. Since in reality mating is selective, the expression must be an approximation.

Let β be the slope in the regression of O on \bar{P} . We have

$$\begin{aligned} \beta &= \frac{\text{Cov}(O, \bar{P})}{\text{Var}(\bar{P})} \\ &= \frac{\text{Cov}(O, \frac{M}{2} + \frac{F}{2})}{\text{Var}(\frac{M}{2} + \frac{F}{2})} \\ &= \frac{\text{Cov}(O, \frac{M}{2}) + \text{Cov}(O, \frac{F}{2})}{\text{Var}(\frac{M}{2}) + \text{Var}(\frac{F}{2}) + 2\text{Cov}(\frac{F}{2}, \frac{M}{2})} \\ &= \frac{\frac{1}{2}\text{Cov}(O, M) + \frac{1}{2}\text{Cov}(O, F)}{\frac{1}{4}\text{Var}(M) + \frac{1}{4}\text{Var}(F) + \frac{1}{2}\text{Cov}(F, M)} \\ &= \frac{\frac{1}{2}(1 + \rho)h^2}{\frac{1}{2} + \frac{1}{2}\rho} \\ &= h^2. \end{aligned}$$

Note that the narrow-sense heritability, h^2 , is not the *correlation* between midparent and offspring. The essential reason for this is that the predictor and outcome variables in this regression have different variances. Recalling that $\text{Corr}(X, Y) = \beta \text{SD}(X)/\text{SD}(Y)$, we find that

$$\text{Corr}(O, \bar{P}) = h^2 \sqrt{\frac{1}{2}(1 + \rho)}.$$

The additional factor means that offspring trait values will be scattered around their expectation even if the heritability is unity. Suppose that each parent is heterozygous (+-) at all trait-affecting loci. Then it is possible in principle for an offspring to be either ++ at all loci or -- at all loci; the trait values of full siblings may differ dramatically even in the absence of environmental or stochastic effects.

Suppose that all measurements are expressed as deviations from the mean. If the trait has a narrow-sense heritability of 0.6 and $\rho = .3$, then the offspring of a couple with an average trait value of 4 will be distributed with a mean of $4 \times .6 = 2.4$ and a standard deviation of $\sqrt{1 - [(1/2)(1 + .3)](.6^2)} = .766$.

Despite earning an honors undergraduate degree in physics from Stanford University, William Shockley's son was called a "regression to the mean" by his father.