Derivation for Inflation of Heritability by Parentally-Imbalanced VCT

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Background

Define the phenotype as

$$P = A + C + \epsilon$$

where A is the additive genetic value, C is the vertically culturally transmitted trait value, and ϵ is i.i.d. Gaussian noise. $\text{Var}(P)$ is normalized to 1, so $\text{Var}(A) = h^2$, $\text{Var}(C) = b^2$, and $\text{AVar}(\epsilon) = 1 - h^2 - b^2$.

In the original model, we assumed that C for any given offspring would simply be the mean of the parental values:

$$C_i = \frac{C_p + C_m}{2} + \epsilon$$

However, this can be generalized to a weighted sum over both parents, where the father contributes variance

$$b_p^2 = wb^2$$

and the mother

$$b_m^2 = (1 - w)b^2$$

Crucially, by the properties of ratios, this means that if $w = 0.75$, then the ratio of contributions will be

$$\frac{b_p^2}{b_m^2} = \frac{w}{1 - w} = (0.75)(0.25) = 3$$

In the parental mean case where $w = 0.5 = 1 - w$:

$$\frac{b_p^2}{b_m^2} = \frac{w}{1 - w} = 1$$

(John, I believe this is the point you were making at our meeting, but forgive me if I misinterpreted your words).

The interesting empirical result is that the average phenotypic covariance $\text{Cov}(P_i, P_j)$ for a given (h^2, b^2) parameter set appears to be higher as w moves away from 0.5 and toward 0 or 1.

Theory

Here I present a small derivation attempting to explain this result analytically. The VCT value for one individual:

$$c_i = \sum_j^2 w_j c_j = wc_p + (1 - w)c_m$$

For siblings sharing parents:

$$\begin{aligned}
\mathrm{Cov}(c_i, c_j) &= \mathrm{Cov}\left(wc_p + (1-w)c_m + \epsilon_i, wc_p + (1-w)c_m + \epsilon_j\right) \\
&= \mathrm{Cov}\left(wc_p + (1-w)c_m, wc_p + (1-w)c_m\right) \\
&= \mathrm{Var}\left(wc_p + (1-w)c_m\right) \\
&= w^2\mathrm{Var}(c_p) + (1-w)^2\mathrm{Var}(c_m) \\
&= b^2(w^2 + (1-w)^2)
\end{aligned}$$

This is a polynomial $f(w)$ in w.

The total phenotype correlation is

$$\mathrm{Cov}(P_i, P_j) = \mathrm{Cov}(a_i, a_j) + \mathrm{Cov}(c_i, c_j)$$

$$\mathrm{Cov}(a_i, a_j) = 2k_{ij}h^2$$

where k_{ij} is the kinship coefficient.

Therefore:

$$\mathrm{Cov}(P_i, P_j) = 2k_{ij}h^2 + b^2(w^2 + (1-w)^2)$$

$\mathrm{Cov}(P_i, P_j)$ is therefore a second-degree polynomial w with a minimum at $w = 0.5$, and with a minimum value and intercept determined by k_{ij} and h^2.

Initially, it would seem like this is also a full expression for phenotype covariance for arbitrary relatives, but I believe that the earlier assumption that $\mathrm{Cov}(c_i, c_j) = \mathrm{Var}(c_i)$ only holds for the case of sampling from the same parents, i.e. full siblings. In the more general case, we'd need an expression for the expected parental c values given the distance between parent sets.

```r
phenotype_cov <- function(w, b2, k = 0.5, h2 = 0.2) {
  return(2 * k * h2 + b2 * ((w^2) + (1 - w)^2))
}

w_vals <- seq(0, 1, length.out = 100)
b2_vals <- seq(0, 0.8, by = 0.2)

p_covariances_matrix <- sapply(
  X = b2_vals,
  FUN = phenotype_cov,
  w = w_vals,
  h2 = 0.2,
  k = 0.5
)

colors <- c("black", "red", "blue", "purple", "lightblue")
matplot(
  x = w_vals,
  y = p_covariances_matrix,
  xlab = bquote(w),
  ylab = bquote(Cov(P[i], P[j])),
  col = colors,
  type = "l",
  lty = "solid",
  lwd = 2
)
legend(
```

```
    "top",
    legend = paste("w =", b2_vals),
    fill = colors
)
```