Estimators & bias of CTDs and expectations of NTFD parameters

ACE

Estimator

$\hat{V}_A = 2(\hat{CV}_{MZ} - (\hat{V}_{DZ})$

$\hat{V}_C = 2\hat{CV}_{DZ} - \hat{CV}_{MZ}$

Bias

$\hat{V}_A = V_A + \frac{3}{2} V_D$

$\hat{V}_C = V_C - \frac{1}{2} V_D$

New estimator if $V_D = .05$

$\hat{V}_A = 2((\hat{CV}_{MZ} - .05) - (\hat{CV}_{DZ} - .0125))$ (.075 lower than our ACE est.)

$\hat{V}_C = 2(\hat{CV}_{DZ} - .0125) - (\hat{CV}_{MZ} - .05)$ (.025 higher than our ACE est.)

ADE

Estimator

$\hat{V}_A = 4\hat{CV}_{DZ} - \hat{CV}_{MZ}$

$\hat{V}_D = 2\hat{CV}_{MZ} - 4\hat{CV}_{DZ}$

Bias

$\hat{V}_A = V_A + 3V_C$

$\hat{V}_D = V_D - 2V_C$

New estimators if $V_C = .05$

$\hat{V}_A = 4(\hat{CV}_{DZ} - .05) - (\hat{CV}_{MZ} - .05)$ (.15 lower than our ADE est.)

$\hat{V}_D = 2(\hat{CV}_{MZ} - .05) - 4(\hat{CV}_{DZ} - .05)$ (.10 higher than our ADE est.)

In Direct Symmetric approach

In ADE, $\hat{V}_C$ you would have gotten in ACE $= -\frac{1}{2}\hat{V}_D$

In ACE, $\hat{V}_D$ you would have gotten in ADE $= -2\hat{V}_C$

So $\hat{V}_D$ is an estimate of $-2\hat{V}_C$ (so $\hat{V}_C = -\frac{1}{2}\hat{V}_D$)

$\hat{V}_C$ is an estimate of $-\frac{1}{2}\hat{V}_D$ (so $\hat{V}_D = -2\hat{V}_C$)

$\ldots = \frac{1}{2} + \frac{1}{2} + \frac{1}{2}\delta_M^2 = 1 + \delta_M^2$

$g = \frac{1}{2} + 2(\frac{1}{2}g\frac{1}{2}) + a(2\delta m \ldots$

$$x = 2(m\sigma^2_m) + 2(m\sigma^2_\mu \sigma^2_m) = 2m^2\sigma^2(1+\sigma^2_\mu)$$

$$w = 2(\tfrac{1}{2}\delta m) + 2(\tfrac{1}{2}\delta \mu \sigma^2_m) = \delta m(1+\sigma^2_\mu m)$$

$\boxed{\text{NTFD}}$ (see Keller et. al. 2009 in the Answers folder)

$$CV_{DZ} = \frac{1}{4}d^2 + s^2 + f^2 x + \frac{1}{2}a^2[g + \delta^2\mu] + 2awf$$

$$CV_{PO} = \frac{1}{2}a\delta + \frac{1}{2}a\delta\mu\sigma^2 + m\sigma^2 + m\sigma^2 m\sigma^2$$

$$CV_{PO} = \frac{1}{2}a\delta(1+\mu\sigma^2) + m\sigma^2(1+m\sigma^2)$$

$$CV_{PO} = \left(\frac{1}{2}a\delta + m\sigma^2\right)(1+\sigma^2_\mu)$$

$$CV_{spouse} = \sigma^2_\mu \sigma^2$$

$$\delta = cov(A, P) = ga + wf$$

A: additive genetic score

P: phenotype

(δ is just a convenient "shortcut" to make the math look less messy - it is a sub-chain that shows up over and over)

$$V(P) = \sigma^2 = a^2 g + f^2 x + 2awf + d^2 + s^2 + e^2$$

NOTE: we have to arbitrarily fix either m or f to be 1 for identification (this convention isn't an assumption - it's just needed to fit the model - kind of like deciding to fix latent variances to 1 or the path coefficients to 1). I typically set f = 1 & estimate m.