Analysis of paired, screen-positive designs

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1 Model extension to Pepe and Alonzo (2001)

Pepe and Alonzo (2001) show how to fit regression models to paired, screenpositive designs. They use marginal models fitted to all of the data, including those with missing disease status. We propose a simple extension to their framework, where the model is fitted to those individuals with known disease status.

Following the notation used by Pepe and Alonzo (2001), we consider 0/1 tests Y_A and Y_B , with disease status D and covariates Z. Pepe and Alonzo define $\alpha Z = \log P(D=1, Y_B=1|Z)$ and $\alpha Z + \beta Z = \log P(D=1, Y_A=1|Z)$, and use T=1 for test A and T=0 for test B with Y for the test value.

Similar, we define an indicator $S = I(Y_A = 1 \text{ or } Y_B = 1)$ for whether one or either of the tests is positive, such that the disease status is known. Moreover, let $\alpha^*Z = \log P(D=1, Y_B=1|Z, S=1)$ and $\alpha^*Z + \beta^*Z = \log P(D=1, Y_A=1|Z, S=1)$, where we have conditioned on having one or more positive tests. Then, closely following the argument in Pepe and Alonzo (2001),

$$\begin{split} \beta^*Z &= \log \frac{P(D=1,Y_A=1|Z,S=1)}{P(D=1,Y_A=1|Z,S=1)} \\ &= \log \frac{P(Y=1|D=1,Z,T=1,S=1)P(D=1|Z,T=1,S=1)}{P(Y=1|D=1,Z,T=0,S=1)P(D=1|Z,T=0,S=1)} \\ &= \log \frac{P(Y_A=1|D=1,Z,S=1)}{P(Y_B=1|D=1,Z,S=1)} \end{split}$$

where P(D=1|Z,T=1,S=1)=P(D=1|Z,T=0,S=1) for paired data. Noting that

$$P(Y = 1|D = 1, Z, T, S = 1) = \frac{P(Y = 1|D = 1, Z, T) - P(Y = 1|D = 1, Z, T, S = 0)P(S = 0)}{P(S = 1)}$$
$$= \frac{P(Y = 1|D = 1, Z, T)}{P(S = 1)}$$

as P(Y=1|D=1,Z,T,S=0)=0, because no positive tests have S=0, then

$$\beta^* Z = \log \frac{P(Y_A = 1 | D = 1, Z, S = 1)}{P(Y_B = 1 | D = 1, Z, S = 1)}$$
$$= \log \frac{P(Y_A = 1 | D = 1, Z)}{P(Y_B = 1 | D = 1, Z)}$$
$$= \beta Z = \text{rTPF}(Z)$$

In general, α^* does not equal α , as $P(D=1,Y_B=1|Z,S=1)$ may be different to $P(D=1,Y_B=1|Z)$, and the intercept term also be shifted.

Care is further required in using a simplified model. Pepe and Alonzo (2001) fit a reduced PSA model by excluding the main effect due to race. However, [data-driven observation that requires a mathematical derivation], the estimated interaction effect for β^* is then a biased estimate of β .