

Extension with covariates X_i

The complete data likelihood is of the form:

$$L_c = \prod_i \{[\pi(X_i)f(Y_i|X_i, D_i = 1)]^{D_i}[(1 - \pi(X_i))f(Y_i|X_i, D_i = 0)]^{1-D_i} f(V_i|X_i, Y_i)\} \quad (1.1)$$

The complete data log likelihood:

$$\begin{aligned} l_c &= \sum_i D_i[\log\pi(X_i) + \log f(Y_i|X_i, D_i = 1)] \\ &+ \sum_i (1 - D_i)[\log(1 - \pi(X_i)) + \log(f(Y_i|X_i, D_i = 0))] \\ &+ \sum_i \log f(V_i|X_i, Y_i). \end{aligned} \quad (1.2)$$

For the case with a covariate X in the model, we need models for:

1. $Y_i|X_i, D_i$, where $Y_i|X_i, D_i \sim N(\mu_d + \phi_d X_i, \Omega)$
(Y, X) is bivariate normal within each disease group ($D = 0, 1$).
2. $V_i|X_i, Y_i$, Here we will use a logistic model:

$$P(V_i = 1|X_i = x, Y_i = y) = \frac{\exp(\theta_0 + \theta_1 y + \theta_2 x)}{1 + \exp(\theta_0 + \theta_1 y + \theta_2 x)} \quad (1.3)$$

3. $D_i|X_i$

$$\pi(x) = P(D_i = 1|X_i = x) = \frac{\exp(\gamma_0 + \gamma_1 x)}{1 + \exp(\gamma_0 + \gamma_1 x)} \quad (1.4)$$

4. if $V_i = 0$ we will replace D_i by:
 $\hat{D}_i = E(D_i|X_i, Y_i, V_i) = E(D_i|X_i, Y_i)$ due to the MAR assumption