IPWE comparison

2020-07-01

Setting: nonstandarized, the predictors have non zero mean values

Simulation

The data sets are generated following the below parameter setting:

$$\mathbf{y_{ki}} = \mathbf{X_i}(\beta_k + \mathbf{b_{ki}} + \Gamma_k(\alpha'\mathbf{x})) + \epsilon_{ki}$$
 (1)

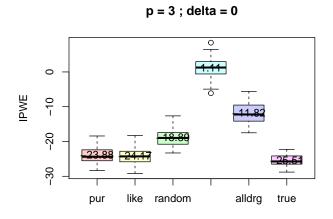
where

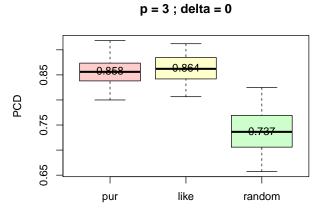
- $\alpha = \alpha_1 + \delta \alpha_2$ - $\alpha_1 = (1, 2, ..., p)';$ - $\alpha_2 = (\alpha_{21}, ..., \alpha_{2p})' \sim Exp(10)$ - $||\alpha||_2^2 = 1$ - when $\delta = 0$, equation (1) is a GEM model while $\delta \neq 0$, equation (1) is a non GEM model
- Suppose we have $k = \{1, 2\}$ treatments. k = 1 represents the placebo group while k = 2 represents the drug group.
- $\mathbf{X_i} = [1, t, t^2]$, and t = [0, 1, 2, 3, 4, 6, 8], which is the design matrix for fixed effect and random effect
- $\beta_1 = \beta_2 = [0, -0.1, -0.05]$
- $\Gamma_1 = [0, \cos(\pi/3)/10, -\sin(\pi/3)/10], \Gamma_2 = [0, \sin(\pi/3)/10, \cos(\pi/3)/10],$

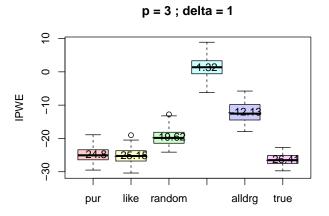
•
$$\mathbf{b_{1i}} \sim N(0, \mathbf{D_1}), \mathbf{b_{2i}} \sim N(0, \mathbf{D_2}), \ \mathbf{D_1} = \mathbf{D_2} = \begin{pmatrix} 1 & 0 & 0 \\ 0 & 0.1 & 0 \\ 0 & 0 & 0.05 \end{pmatrix}$$

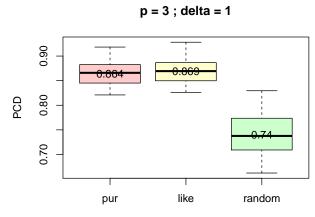
- $\mathbf{x_i} \sim MVN(\mu_x, \Sigma_x)$, $\mu_x = (1, 2, ..., p)$, Σ_x has diagonal equals to 1 and 0.5 everywhere else.
- $\epsilon_1, \epsilon_2 \sim N(0, 1^2)$
- $p = \{3, 10\}$, which is the dimension of the predictors x_i .

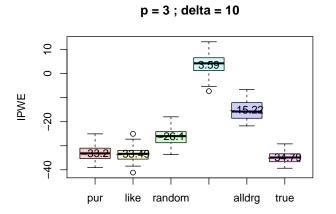
The IPWE are calculated with the estimated treatment assignment by using the purity criterion and by using the log-likelihood criterion. The proportions of correct assignment are also calculated. The whole procedures are repeated for 100 times.

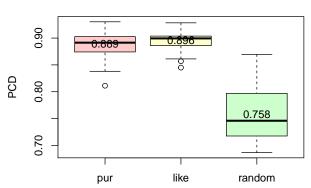












p = 3 ; delta = 10

