# Comparison of purity and likelihood criteria in GEM and non GEM models

2020-06-29

### 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

- $\alpha = \alpha_1 + \delta \alpha_2$ -  $\alpha_1 = 1: p$ ; -  $\alpha_2 = (\alpha_{21}, ..., \alpha_{2p}) \sim Exp(4)$ -  $||\alpha||_2^2 = 1$ - when  $\delta = 0$ , equation (1) is a GEM model while  $\delta \neq$ , 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
- $\beta_1 = \beta_2 = [0, -0.1, -0.05]$
- $\Gamma_1 = [0, 1, 0], \Gamma_1 = [0, \cos(\pi/3), \sin(\pi/3)],$

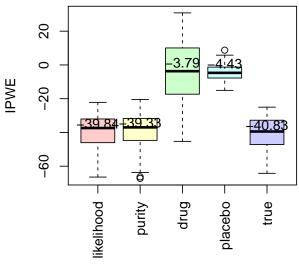
• 
$$\mathbf{b_{1i}} \sim N(0, \mathbf{D_1}), \mathbf{b_{2i}} \sim N(0, \mathbf{D_2}), \mathbf{D_1} = \mathbf{D_2} = \begin{pmatrix} 1 & 0 & 0 \\ 0 & 0.1 & 0.05 \\ 0 & 0.05 & 0.05 \end{pmatrix}$$

- $\mathbf{x_i} \sim MVN(\mu_x, \Sigma_x)$ ,  $\mu_x = \mathbf{0}_p$ ,  $\Sigma_x$  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  $x_i$ .

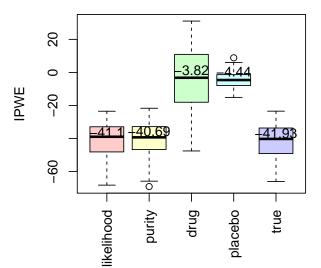
The IPWE are calculated with the estimated treatment assignment by using the purity criterion and by using the log-likelihood criterion. The proportions of correct assignment are also calculated. The whole procedures are repeated for 100 times.

p = 3

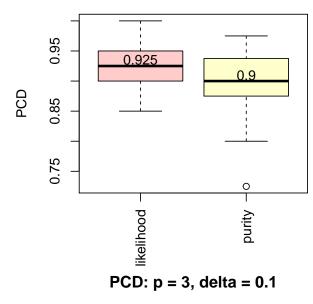
**IPWE:** p = 3, delta = 0

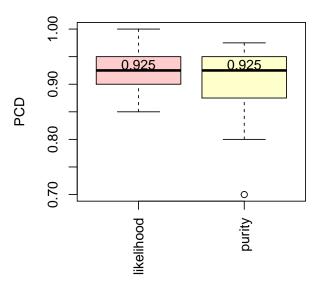


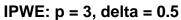
IPWE: p = 3, delta = 0.1

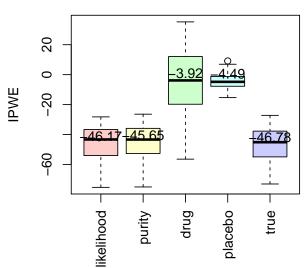


**PCD:** p = 3, delta = 0

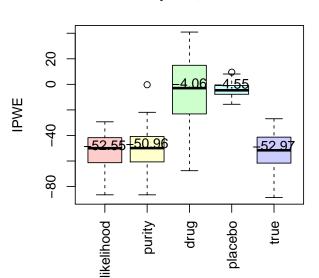




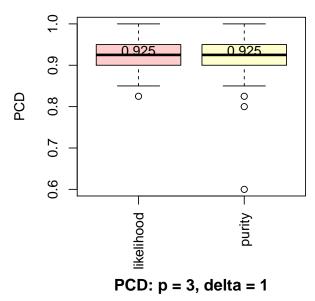


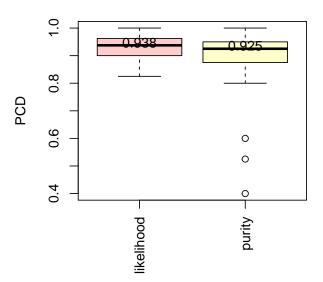


**IPWE:** p = 3, delta = 1

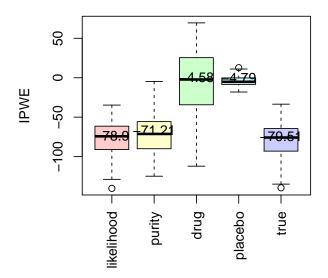


### **PCD:** p = 3, delta = 0.5

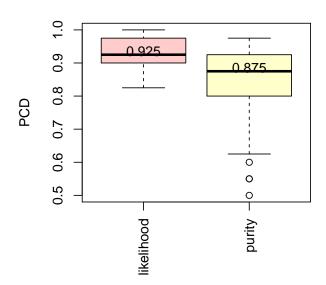




**IPWE:** p = 3, delta = 3

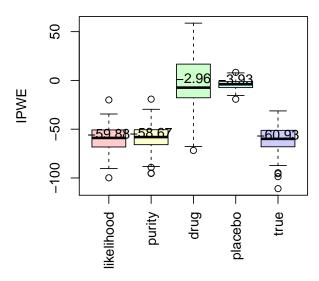


**PCD:** p = 3, delta = 3

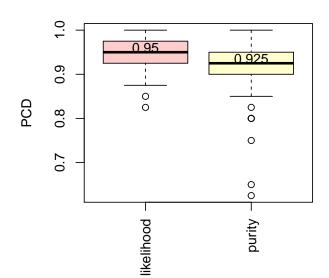


p = 10

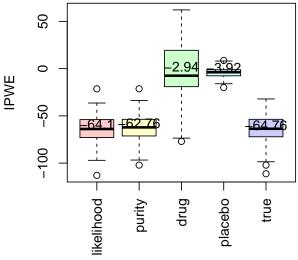
**IPWE:** p = 10, delta = 0



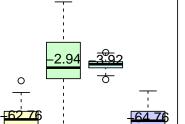
**PCD:** p = 10, delta = 0

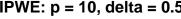


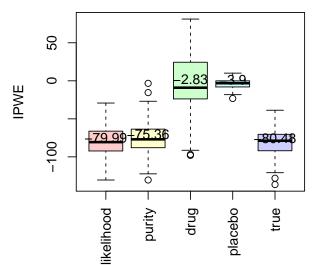
IPWE: p = 10, delta = 0.1



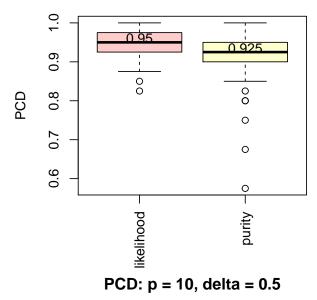
IPWE: p = 10, delta = 0.5

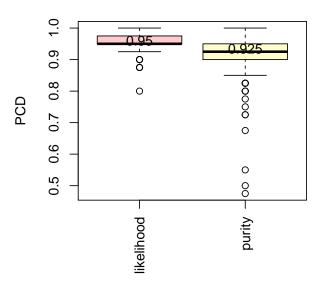


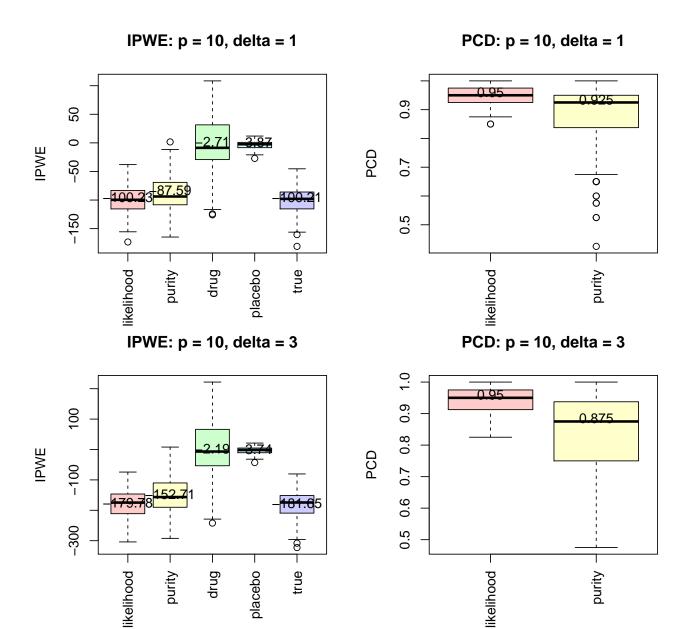




PCD: p = 10, delta = 0.1







## Histogram of purity

purity

# Freduency 0 10 20 30 40 20 0 0 20 30 40 20 0 40 20 30 40 20

## Histogram of likelihood

