

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

2020-06-30

## Simulation

The data sets are generated following the below parameter setting:

$$\mathbf{y}_{\mathbf{ki}} = \mathbf{X}_{\mathbf{i}}(\beta_{\mathbf{k}} + \mathbf{b}_{\mathbf{ki}} + \mathbf{\Gamma}_{\mathbf{k}}(\alpha' \mathbf{x})) + \epsilon_{\mathbf{ki}} \quad (1)$$

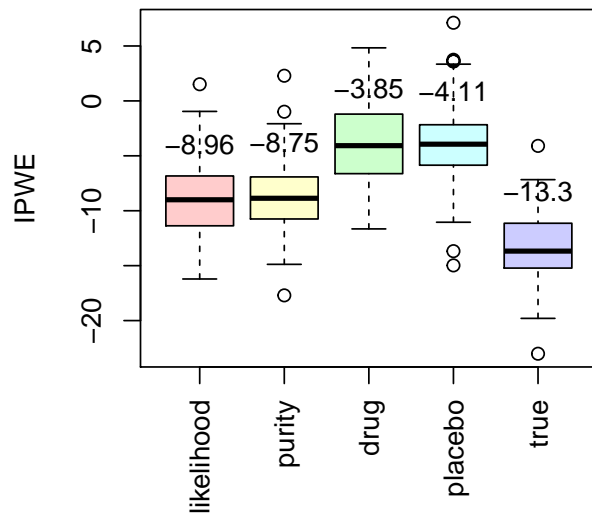
where

- $\alpha = \alpha_1 + \delta \alpha_2$ 
  - $\alpha_1 = (1, 2, \dots, p)'$ ;
  - $\alpha_2 = (\alpha_{21}, \dots, \alpha_{2p})' \sim \text{Exp}(10)$
  - $\|\alpha\|_2^2 = 1$
  - 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.
- $\mathbf{X}_{\mathbf{i}} = [1, t, t^2]$ , and  $t = [0, 1, 2, 3, 4, 6, 8]$ , which is the design matrix for fixed effect and random effect
- $\beta_1 = \beta_2 = [0, -0.1, -0.05]$
- $\mathbf{\Gamma}_1 = [0, \cos(\pi/3), -\sin(\pi/3)]/10$ ,  $\mathbf{\Gamma}_2 = [0, \sin(\pi/3), \cos(\pi/3)]/10$ ,
- $\mathbf{b}_{1i} \sim N(0, \mathbf{D}_1)$ ,  $\mathbf{b}_{2i} \sim N(0, \mathbf{D}_2)$ ,  $\mathbf{D}_1 = \mathbf{D}_2 = \begin{pmatrix} 1 & 0 & 0 \\ 0 & 0.1 & 0.05 \\ 0 & 0.05 & 0.05 \end{pmatrix}$
- $\mathbf{x}_i \sim MVN(\mu_x, \Sigma_x)$ ,  $\mu_x = \mathbf{0}_p$ ,  $\Sigma_x$  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  $x_i$ .

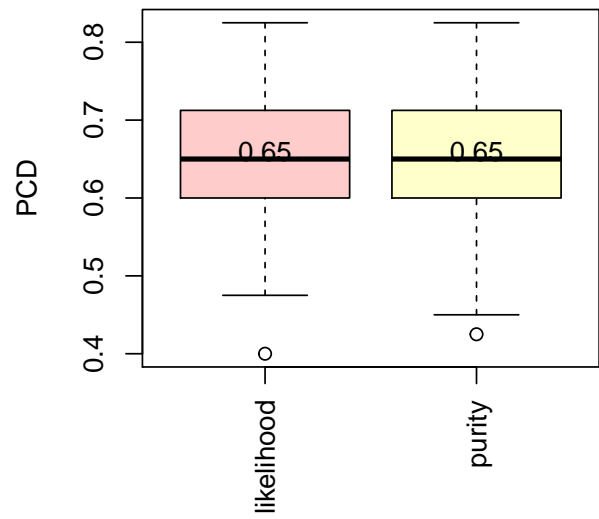
The IPWE are calculated with the estimated treatment assignment by using the purity criterion and by using the log-likelihood criterion. The proportions of correct assignment are also calculated. The whole procedures are repeated for 100 times.

**When dimension  $p = 3$**

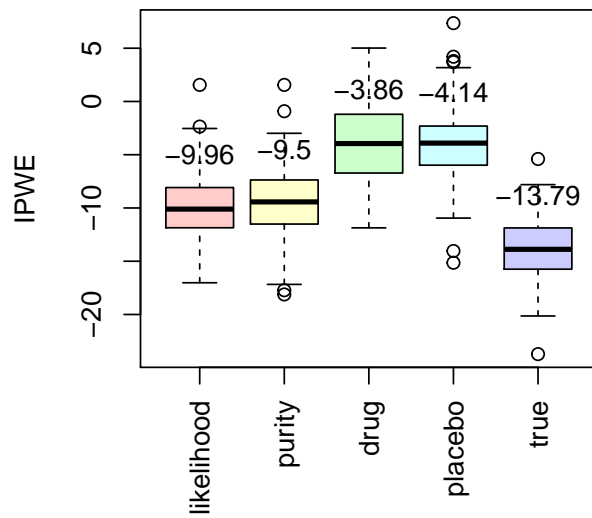
**IPWE:  $p = 3$ ,  $\delta = 0$**



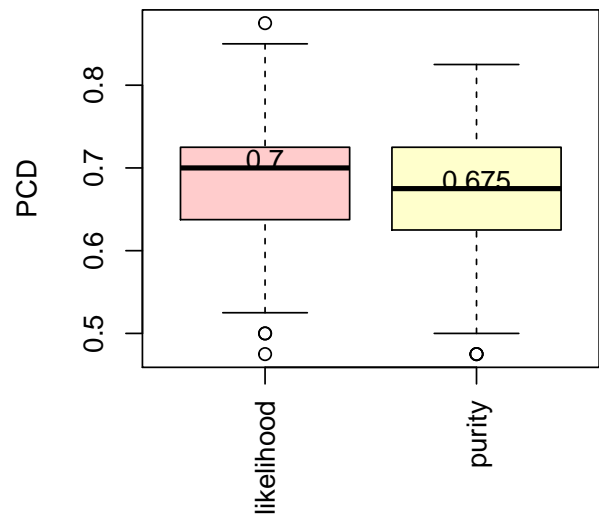
**PCD:  $p = 3$ ,  $\delta = 0$**



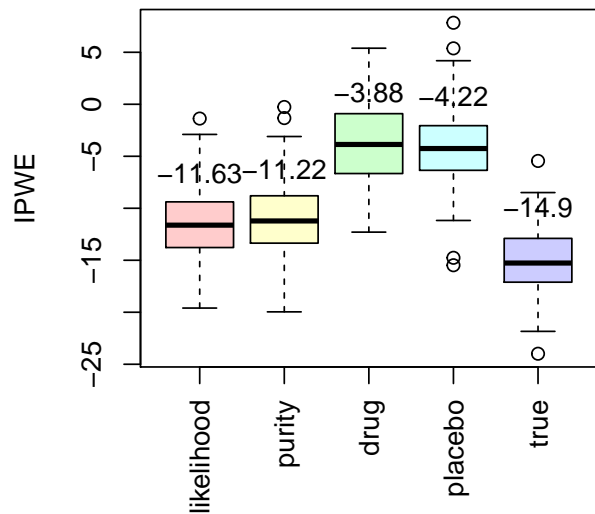
**IPWE:  $p = 3$ ,  $\delta = 0.1$**



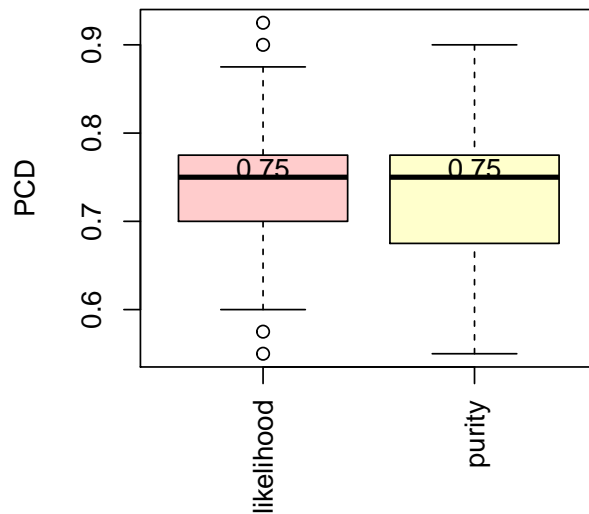
**PCD:  $p = 3$ ,  $\delta = 0.1$**



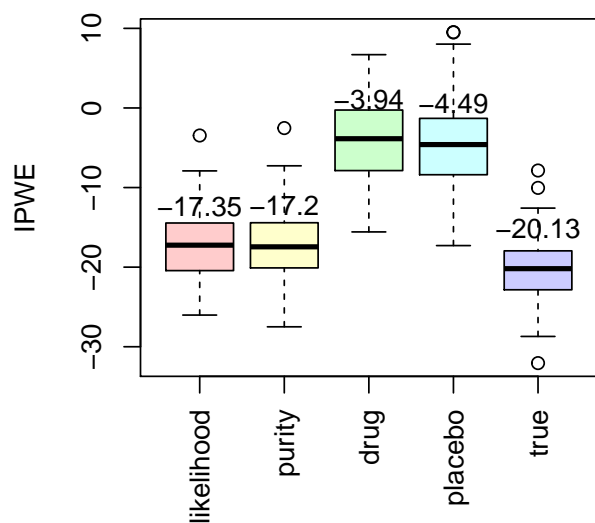
**IPWE:  $p = 3$ ,  $\delta = 0.5$**



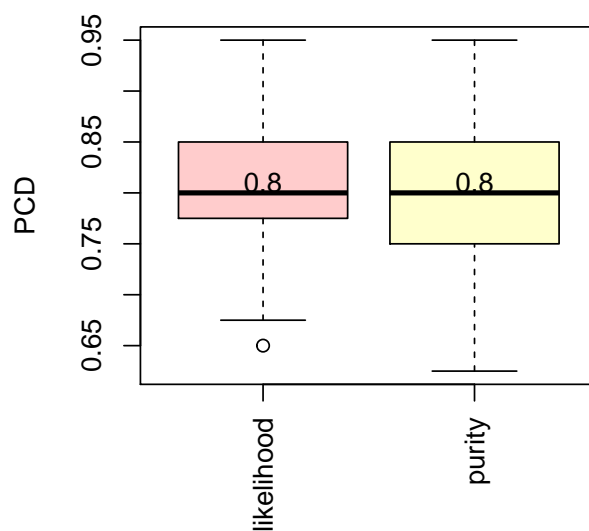
**PCD:  $p = 3$ ,  $\delta = 0.5$**



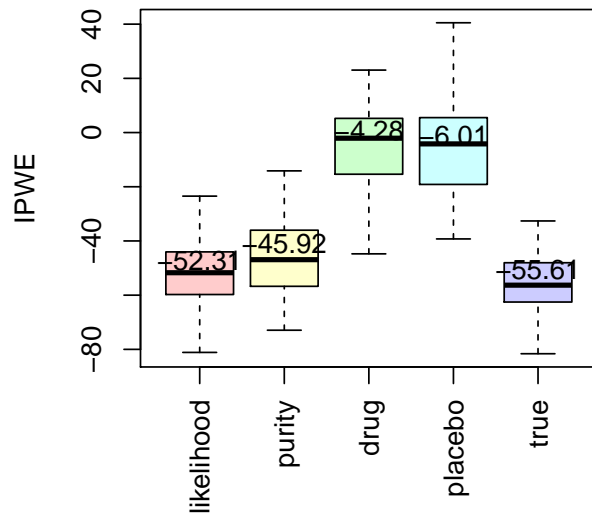
**IPWE:  $p = 3$ ,  $\delta = 1$**



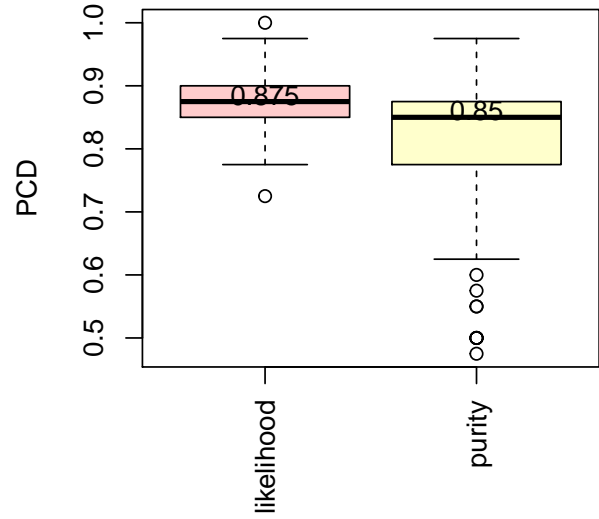
**PCD:  $p = 3$ ,  $\delta = 1$**



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

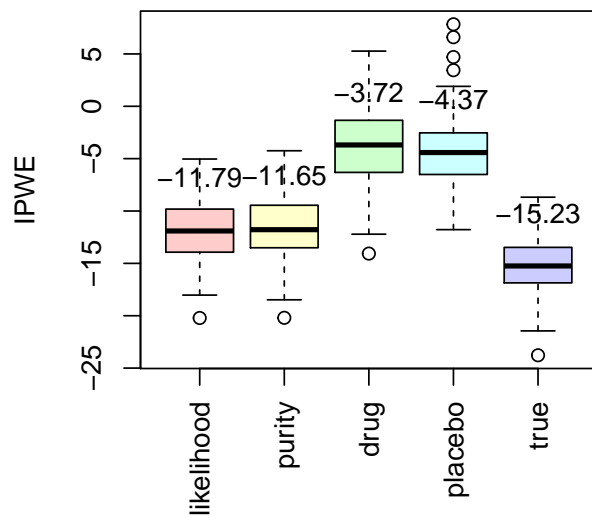


**PCD:  $p = 3$ ,  $\delta = 3$**

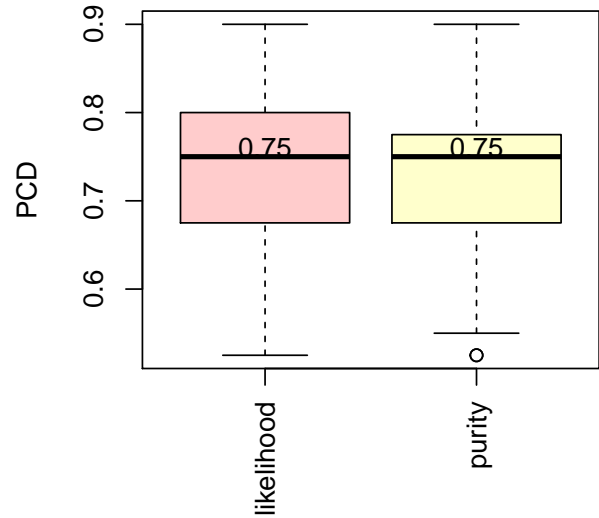


When dimension  $p = 10$

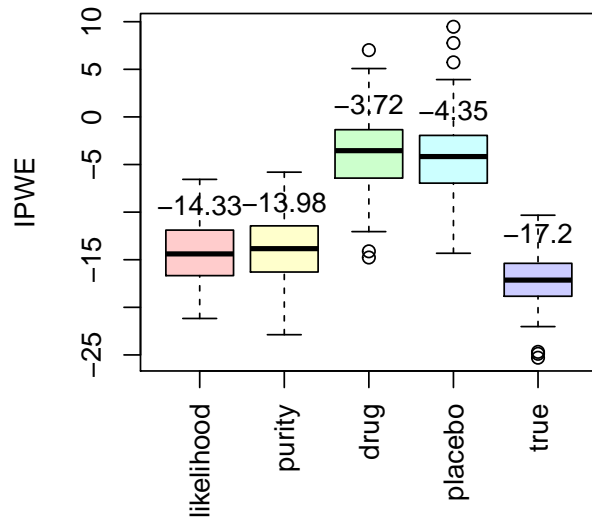
**IPWE:  $p = 10$ ,  $\delta = 0$**



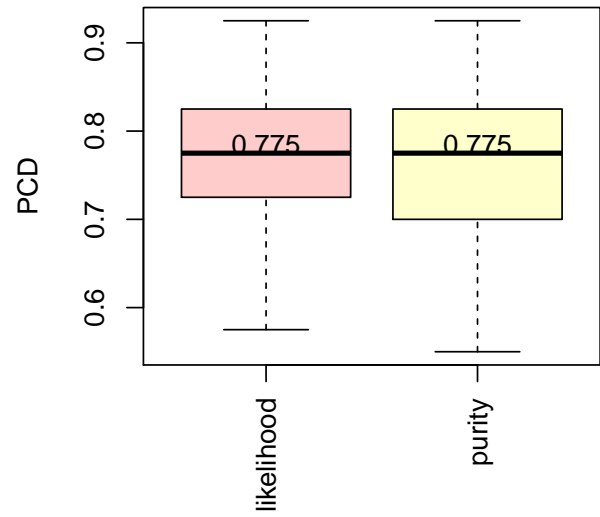
**PCD:  $p = 10$ ,  $\delta = 0$**



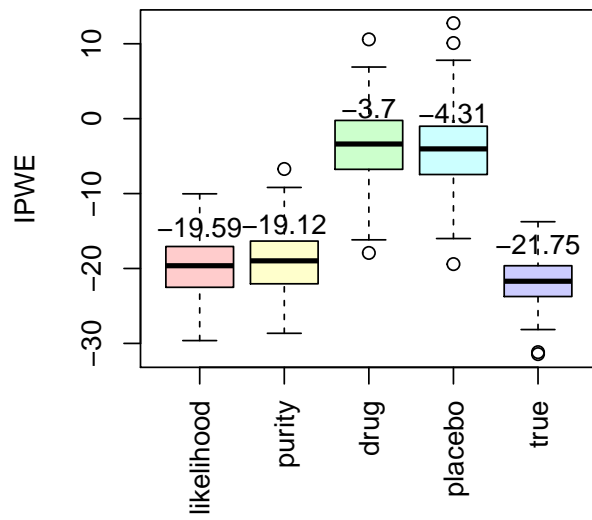
**IPWE:  $p = 10$ ,  $\delta = 0.1$**



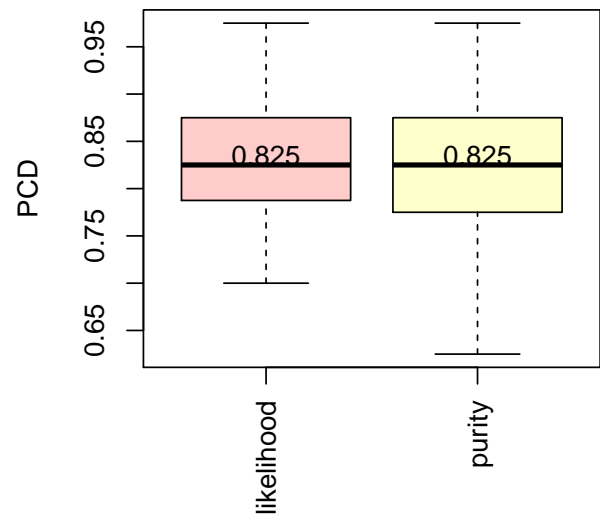
**PCD:  $p = 10$ ,  $\delta = 0.1$**



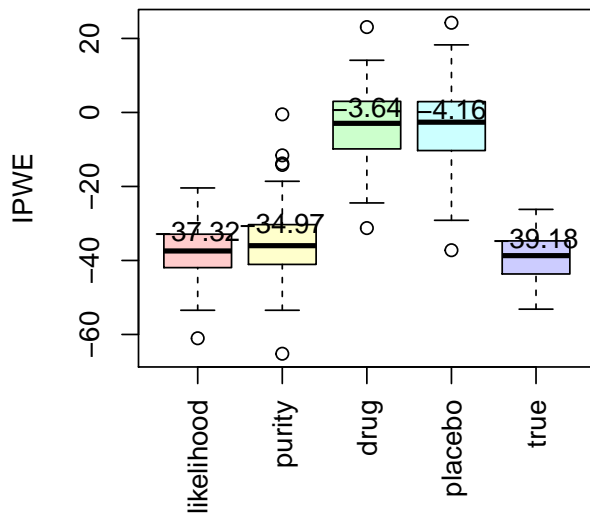
**IPWE:  $p = 10$ ,  $\delta = 0.5$**



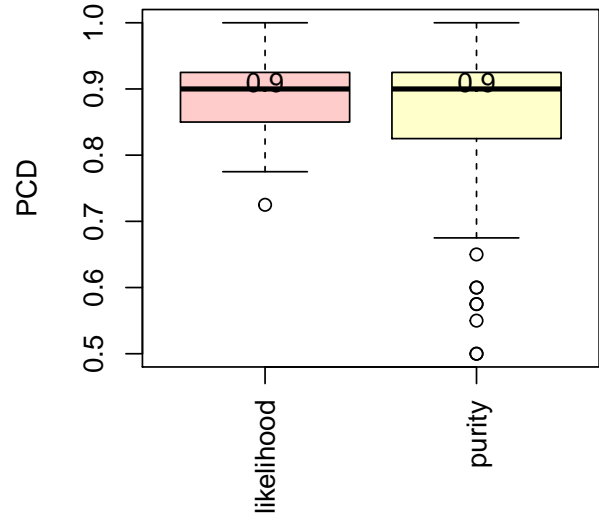
**PCD:  $p = 10$ ,  $\delta = 0.5$**



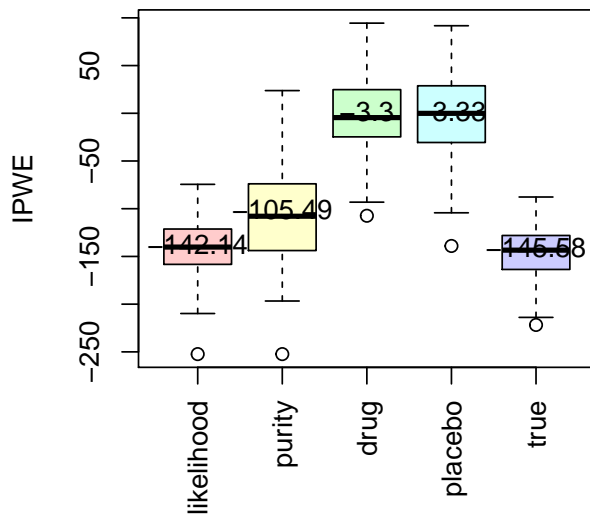
**IPWE:  $p = 10$ ,  $\delta = 1$**



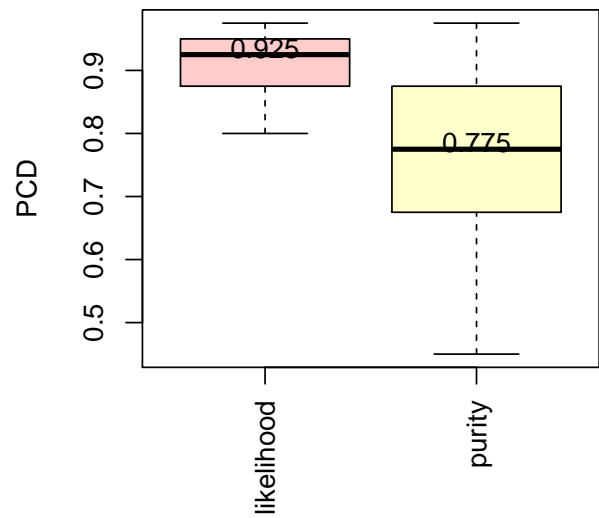
**PCD:  $p = 10$ ,  $\delta = 1$**



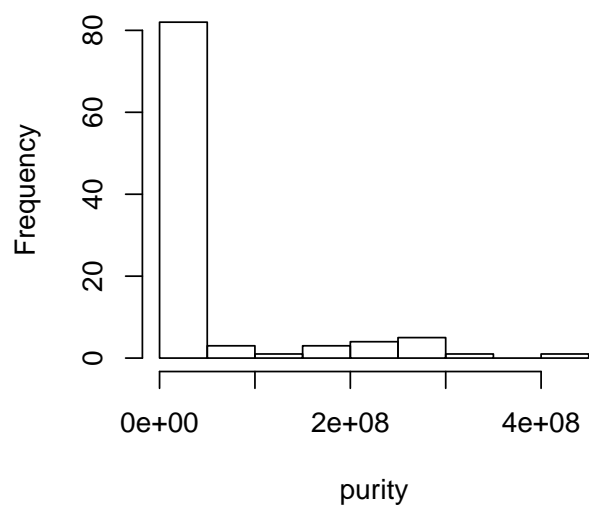
**IPWE:  $p = 10$ ,  $\delta = 3$**



**PCD:  $p = 10$ ,  $\delta = 3$**



**Histogram of purity**



**Histogram of likelihood**

