

Supplementary Materials for the manuscript “A censored beta mixture model for the estimation of the proportion of non-differentially expressed genes”

Anastasios Markitsis  
Department of Statistics  
The George Washington University

Yinglei Lai  
Department of Statistics and Biostatistics Center  
The George Washington University  
2140 Pennsylvania Avenue, N.W.  
Washington D.C., 20052, USA  
Tel: (202) 994-6664; Fax: (202) 994-6917; Email: ylai@gwu.edu

**Additional Figures.** The following figures give the comprehensive results for our simulation study. Gene expression data are simulated based on either an independence structure ( $\rho = 0$ , page 3), a weak dependence structure ( $\rho = 0.3$ , page 4), a relatively weak dependence structure ( $\rho = 0.5$ , page 5), a relatively strong dependence structure ( $\rho = 0.7$ , page 6) and a strong dependence structure ( $\rho = 0.9$ , page 7). In each page of figures, plots for root mean squared errors (RMSE), bias and standard deviation are presented to compare different estimation methods; plots for RMSE are also presented to compare different  $\lambda$  values for our method. The comparison plots for RMSE in log-scale are given in the first row of figures; the comparison plots for bias in cube root are given in the second row of figures; and the comparison plots for standard deviation in log-scale are given in the third row of figures. On the choice of  $\lambda$  for our method, the comparison plots for RMSE are given in the last row of figures. Different sample sizes are considered in our simulation study:  $n_1 = n_2 = 6$  (left panel), 18 (middle panel), and 30 (right panel).









