Supplementary Material Item Descriptions

The supplementary material contains 4 subdirectories: **Code**, **Data**, **Graphs** and **Results**.

Code

core_functions.R: Contains all core functions of the EM algorithm of MCLUST-ME. (R file)

simulation_functions.R: Contains all functions required to run the simulations in the paper. (R file)

sim 1.R: Runs Simulation 1 in Section 7. (R file)

sim 2.R: Runs Simulation 2 in Section 7. (R file)

bic_simulation.R: Runs the BIC simulation in Section 8. (R file)

rnaseq_analysis.R: Performs cluster analysis in Section 9. (R file)

Data

rna_raw.RData: Raw RNA-seq data used in Section 9. (RData file)

rna_processed.RData: Processed RNA-seq data for Section 9. (RData file)

Graphs

Figure *.pdf, Figure *.png: Graphs used in the paper. (PDF and PNG files)

Results

res_sim1_0*.RData: Contains results from Simulation 1 with $p = 0.*$. (RData files)

res_sim2_0*.RData: Contains results from Simulation 2 with $p = 0.*$. (RData files)

bic1_multiseeds.RData: Contains results from Case 1 of BIC simulation. (RData file)

bic2_79.RData: Contains results from Case 2 of BIC simulation. (RData file)

bic3_51.RData: Contains results from Case 3 of BIC simulation. (RData file)

rna_*group.RData: Contains MCLUST-ME clustering result of RNA-seq data assuming $G = *$ groups. (RData files)

rna_cluster_res.RData: Contains MCLUST-ME clustering result of RNA-seq data with the optimal BIC value. (RData file)