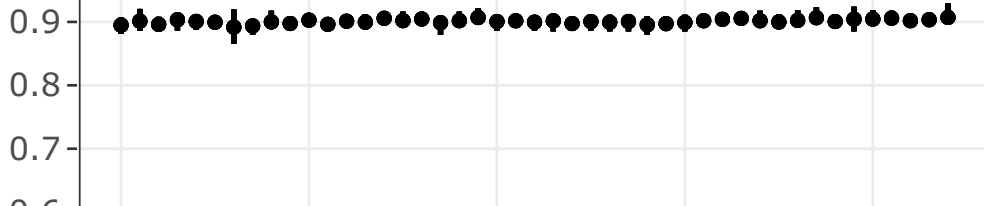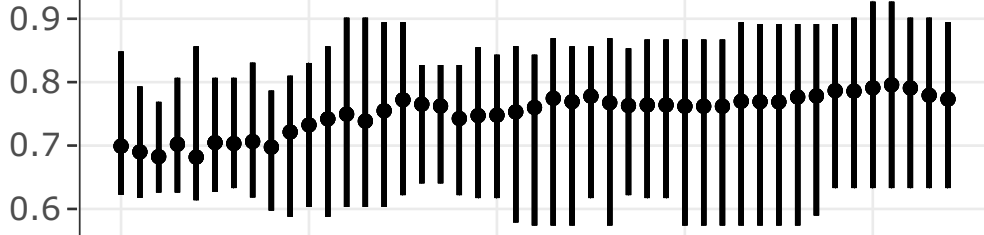Gene Optimziation for Two-Step Classi

Sequence: 1, Workflow: smote_rf, Measure: f_meas

Sequence: 2, Workflow: hybrid_svm, Measure: f_meas

F1-Score

Genes Added