

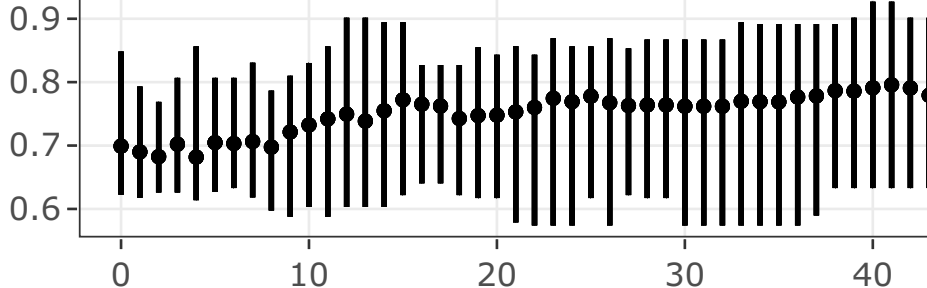
# Gene Optimziation for Two-Step Classi

Sequence: 1, Workflow: smote\_rf, Measure: f\_meas



Sequence: 2, Workflow: hybrid\_svm, Measure: f\_meas

F1-Score



Genes Added