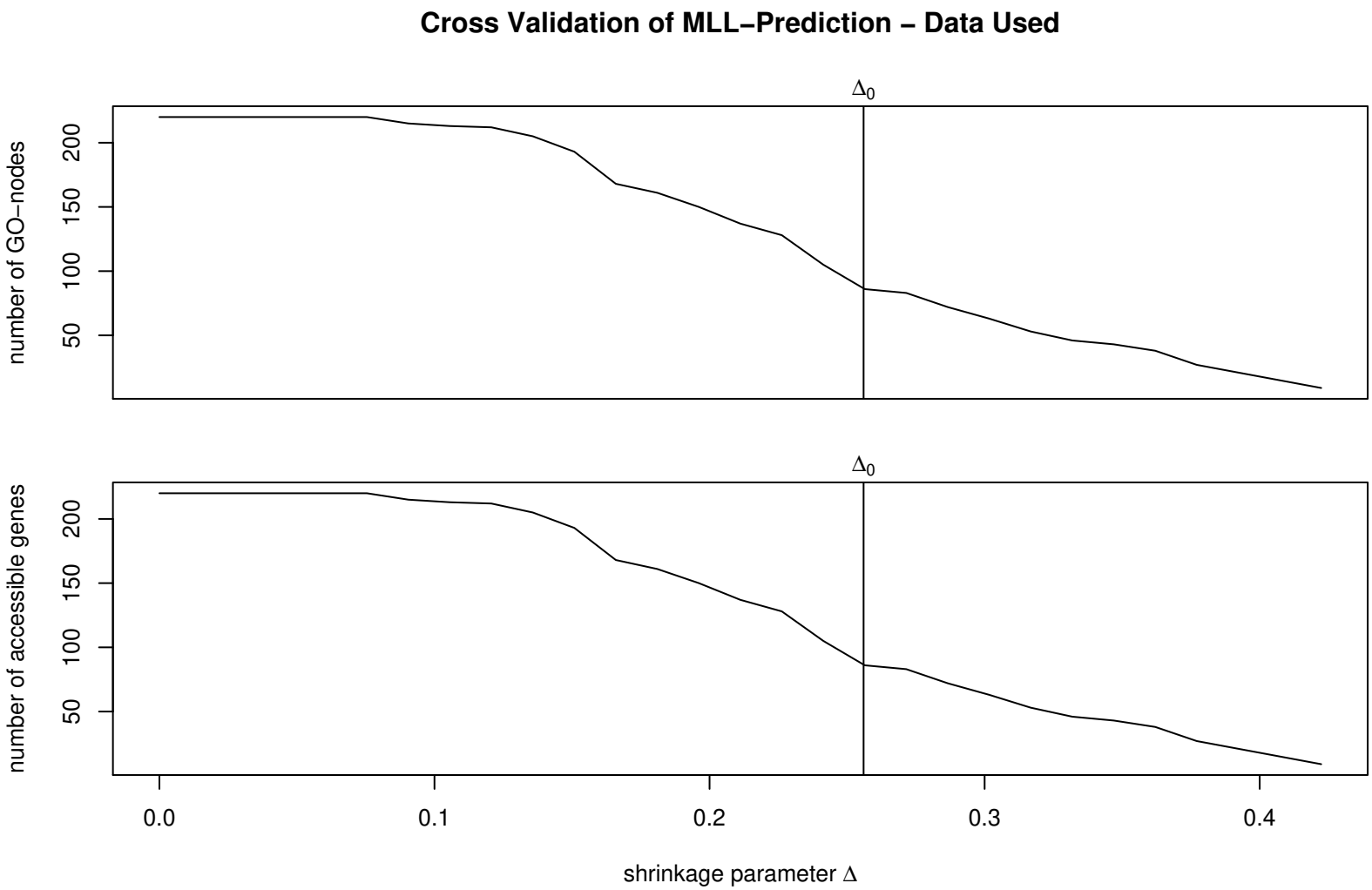
Cross Validation of MLL−Prediction − Data Used
Δ_0
number of GO−nodes
50
100
150
200
Δ_0
number of accessible genes
50
100
150
200
0.0
0.1
0.2
0.3
0.4
shrinkage parameter Δ