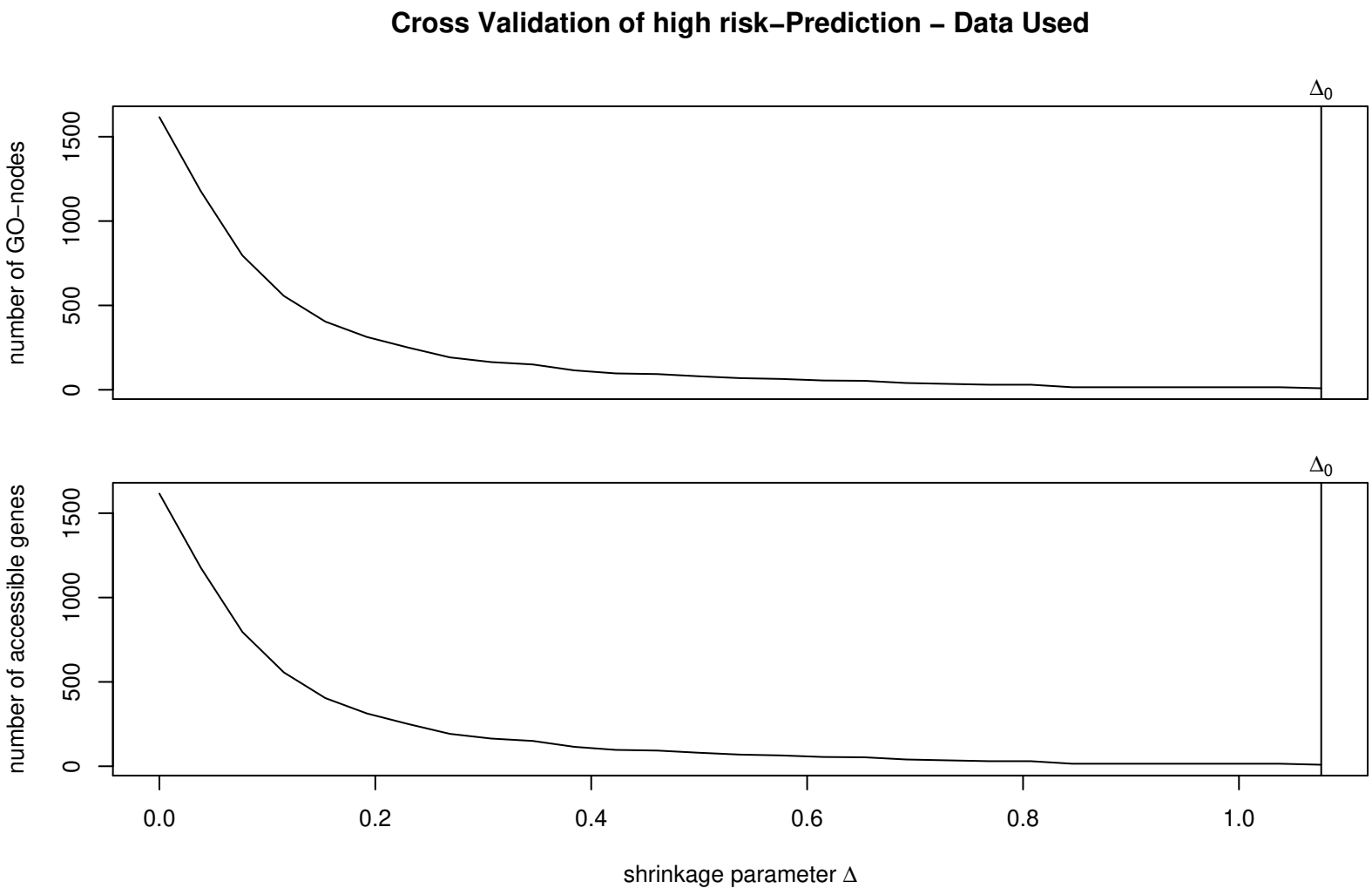
Cross Validation of high risk−Prediction − Data Used
number of GO−nodes
number of accessible genes
0
500
1000
1500
Δ_0
0.0
0.2
0.4
0.6
0.8
1.0
shrinkage parameter Δ