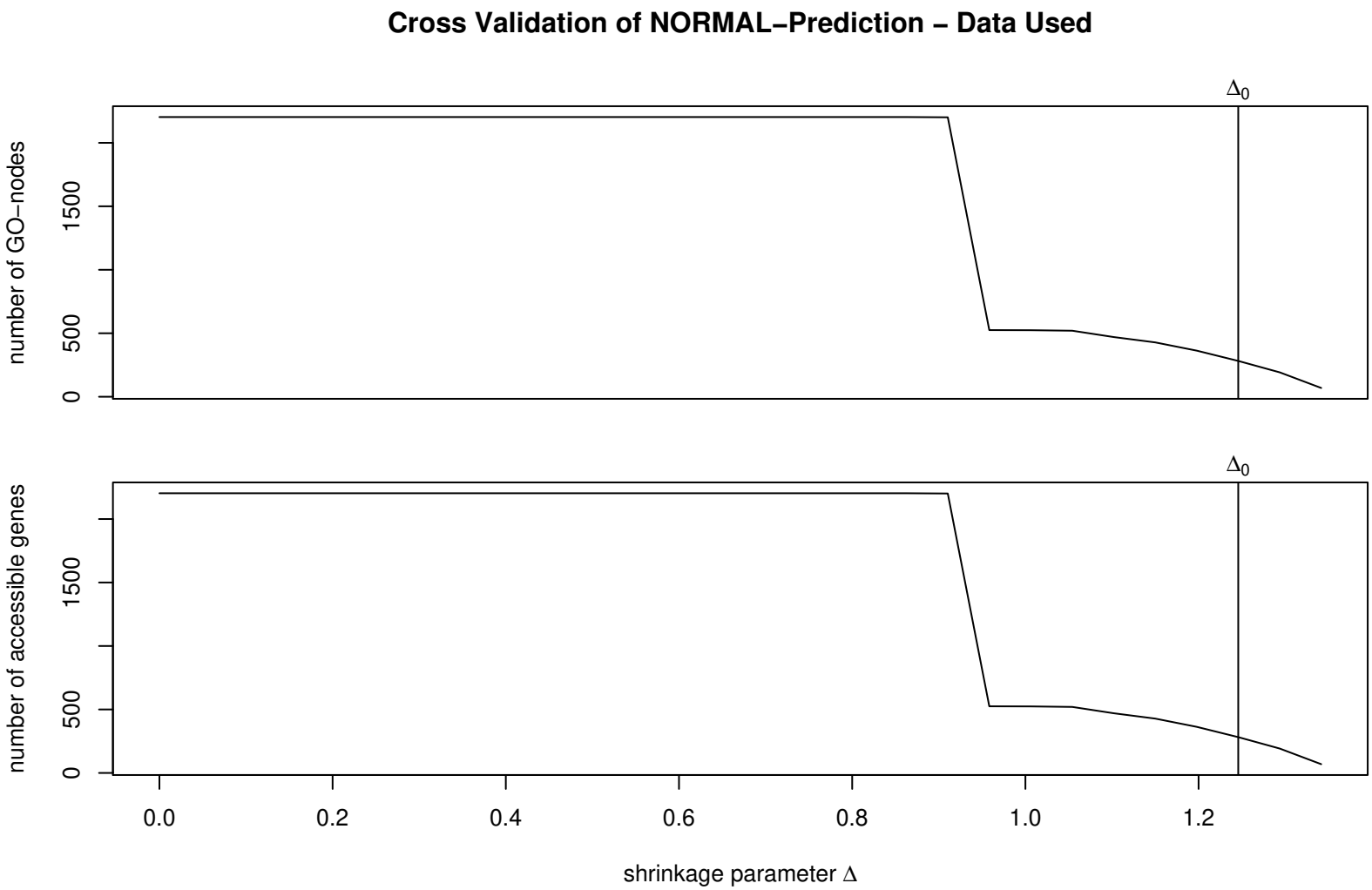
Cross Validation of NORMAL−Prediction − Data Used
number of GO−nodes
0
500
1500
Δ_0
number of accessible genes
0
500
1500
Δ_0
0.0
0.2
0.4
0.6
0.8
1.0
1.2
shrinkage parameter Δ