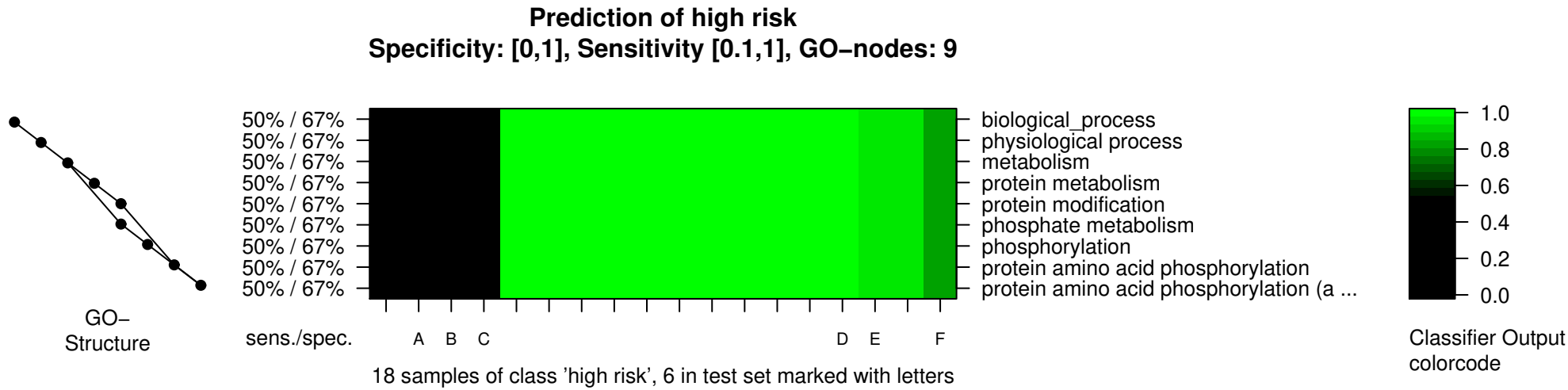
Prediction of high risk
Specificity: [0,1], Sensitivity [0.1,1], GO−nodes: 9
GO−
Structure
50% / 67%
50% / 67%
50% / 67%
50% / 67%
50% / 67%
50% / 67%
50% / 67%
50% / 67%
50% / 67%
sens./spec.
A
B
C
D
E
F
biological_process
physiological process
metabolism
protein metabolism
protein modification
phosphate metabolism
phosphorylation
protein amino acid phosphorylation
protein amino acid phosphorylation (a ...
18 samples of class 'high risk', 6 in test set marked with letters
1.0
0.8
0.6
0.4
0.2
0.0
Classifier Output
colorcode