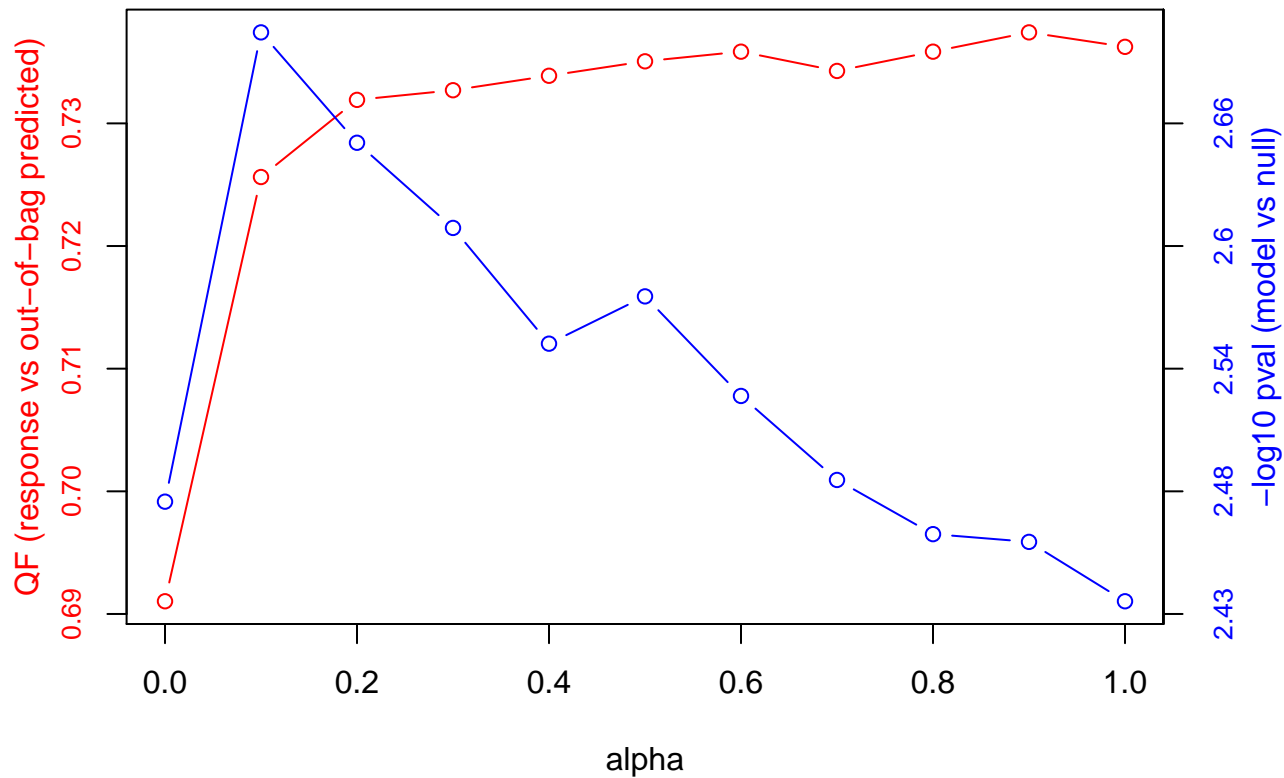
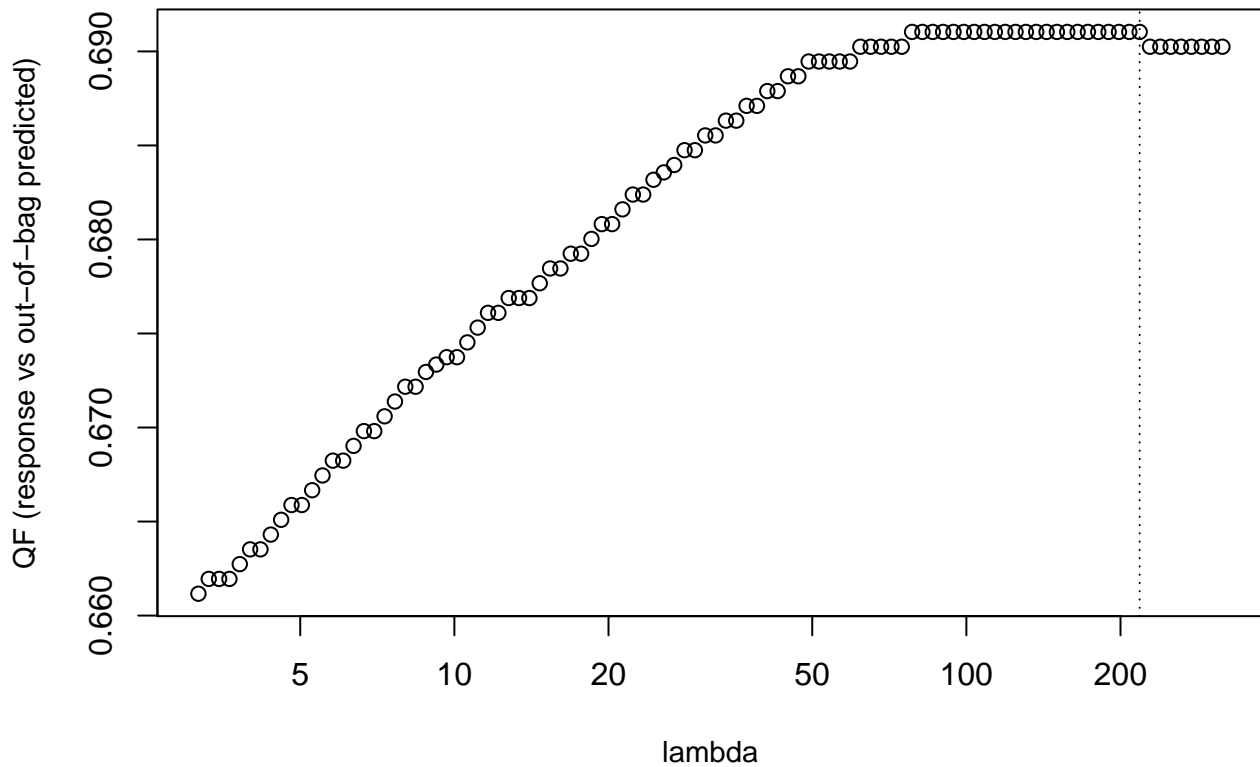


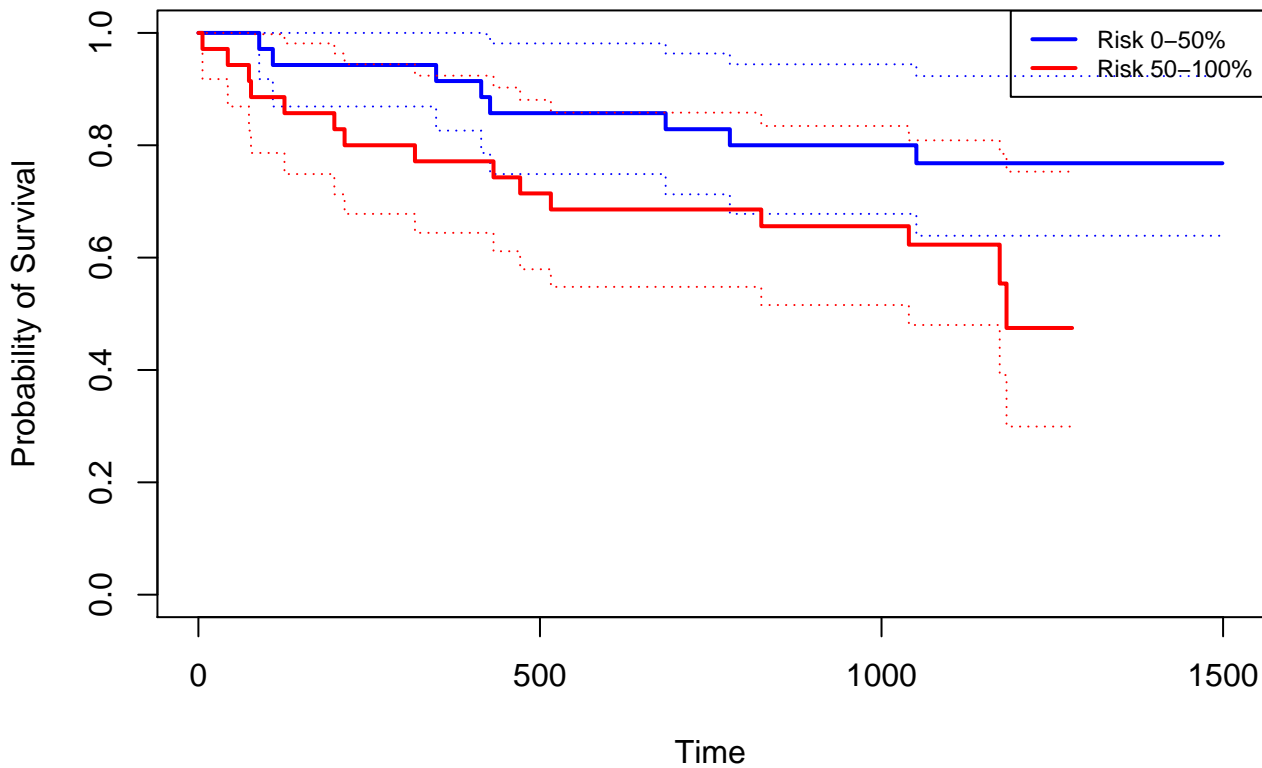
model performance vs alpha values



**alpha=0 ; QF=concordance index**



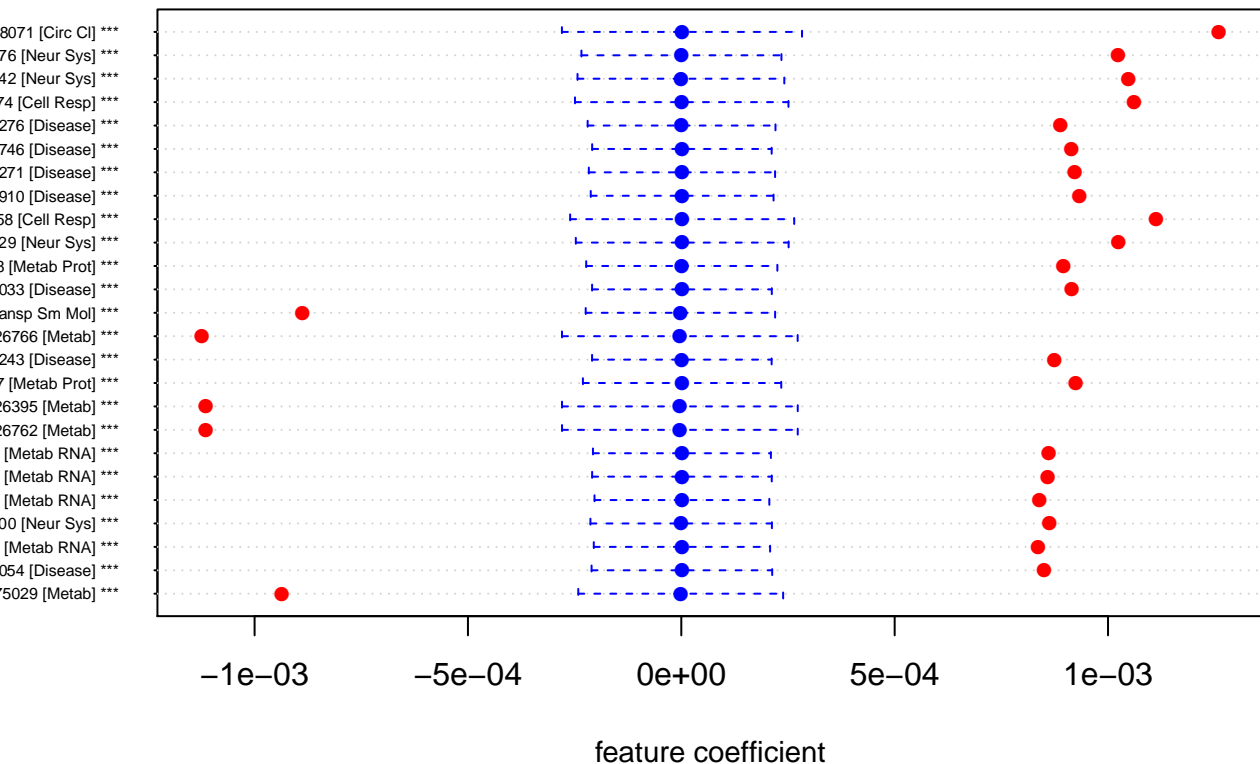
**alpha=0**



# Selected feature coefficients ranked by p-value for alpha=0

P-value significance codes: <0.001 (\*\*\*), <0.01 (\*\*), <0.05 (\*), <0.1 (.)

• model  
• null

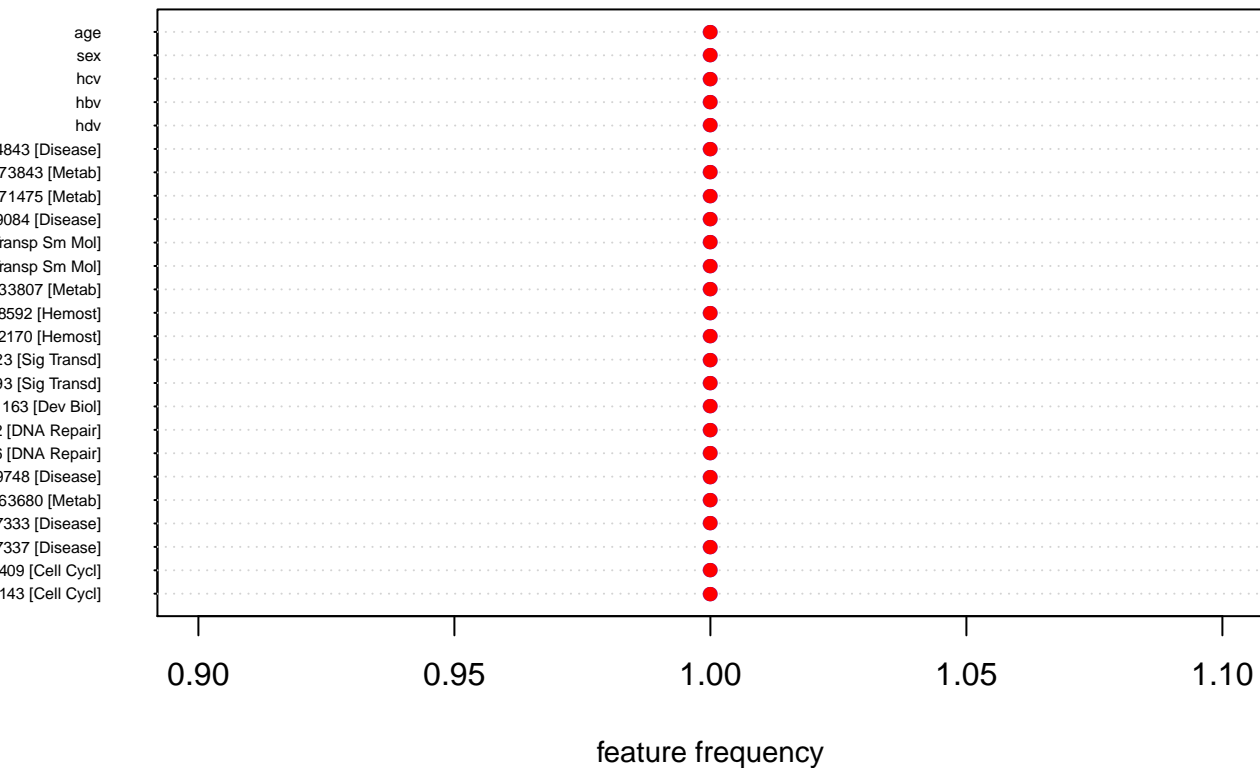


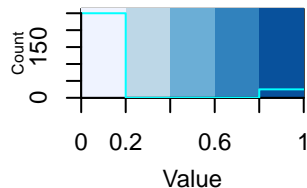


## Selected feature frequencies ranked by p-value for alpha=0

P-value significance codes: <0.001 (\*\*\*), <0.01 (\*\*), <0.05 (\*), <0.1 (.)

● model  
● null

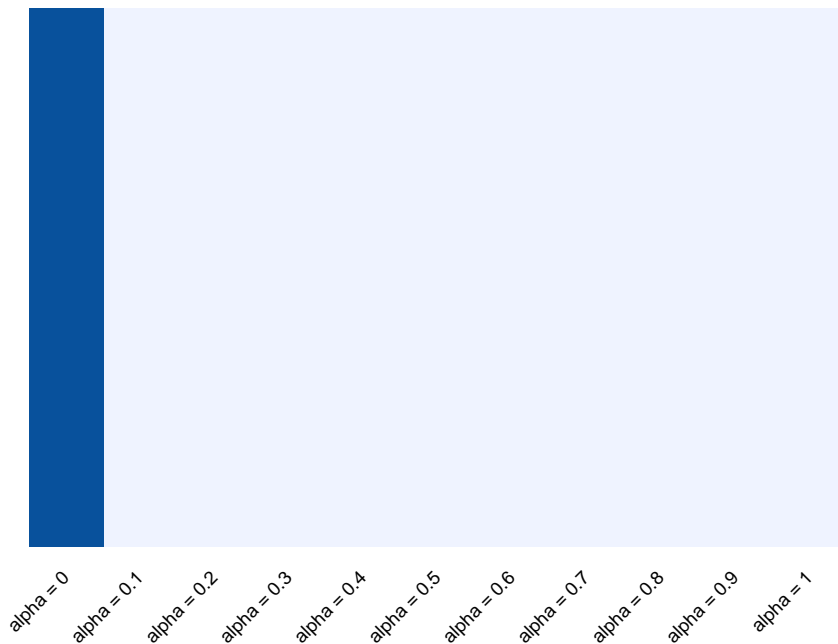




## Selected feature frequencies

Features ranked by p-value for  $\alpha=0$

P-value significance codes: <0.001 (\*\*\*), <0.01 (\*\*), <0.05 (\*), <0.1 (.)



age

sex

hcv

hbv

hdv

164843 [Disease]

73843 [Metab]

1971475 [Metab]

5619084 [Disease]

1369062 [Transp Sm M]

382556 [Transp Sm M]

9033807 [Metab]

418592 [Hemost]

392170 [Hemost]

198323 [Sig Transd]

198693 [Sig Transd]

211163 [Dev Biol]

112122 [DNA Repair]

112126 [DNA Repair]

4839748 [Disease]

163680 [Metab]

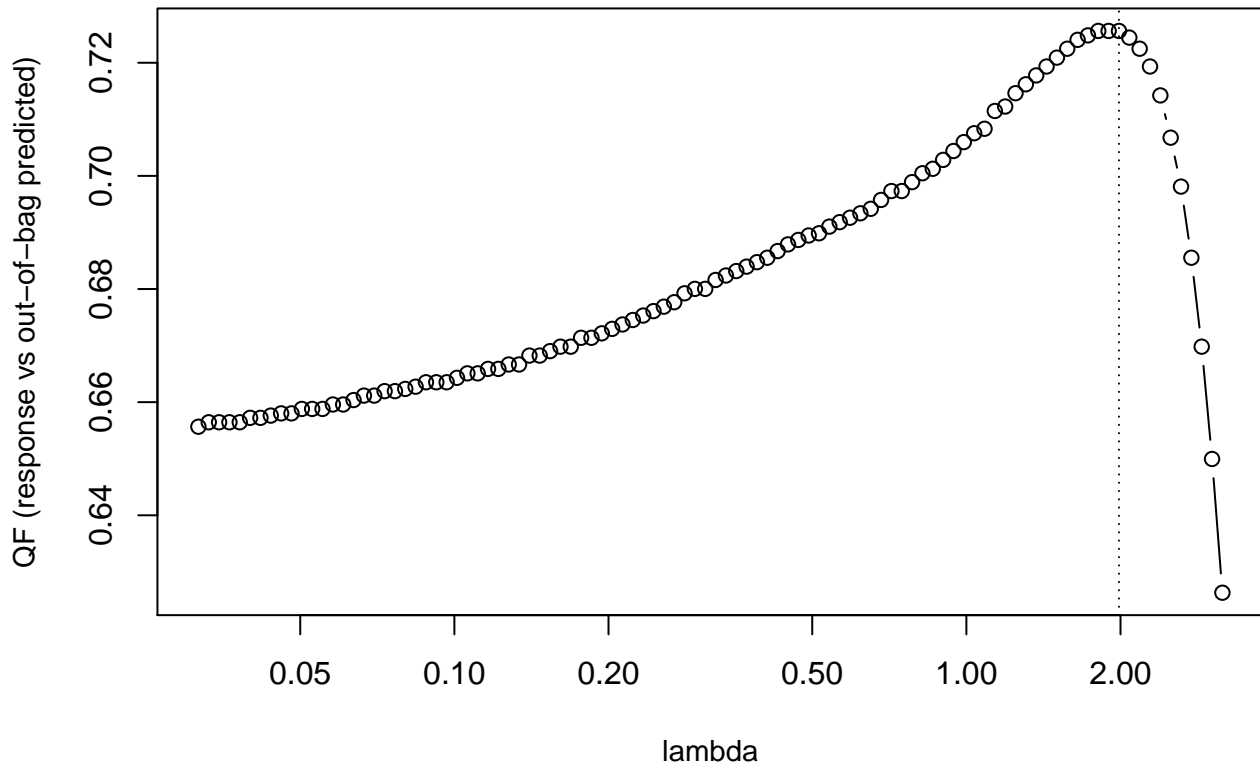
5467333 [Disease]

5467337 [Disease]

179409 [Cell Cycl]

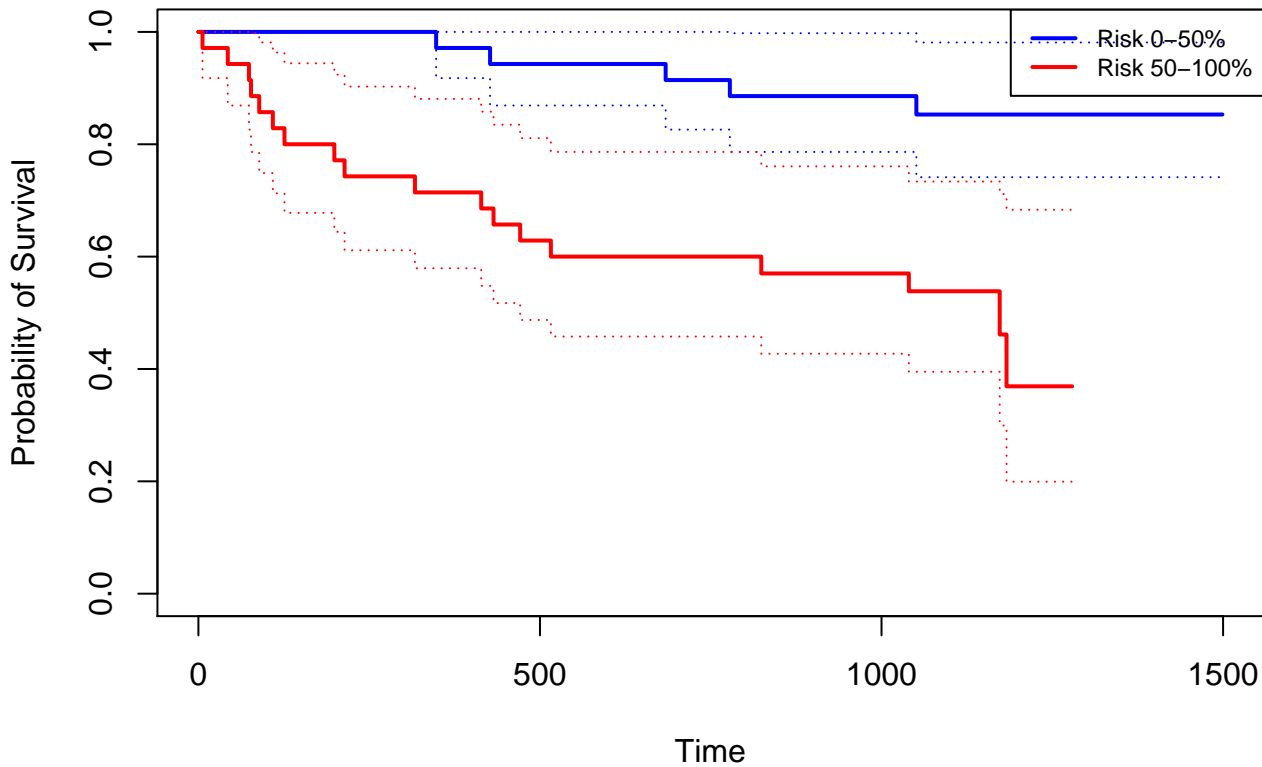
174143 [Cell Cycl]

**alpha=0.1 ; QF=concordance index**





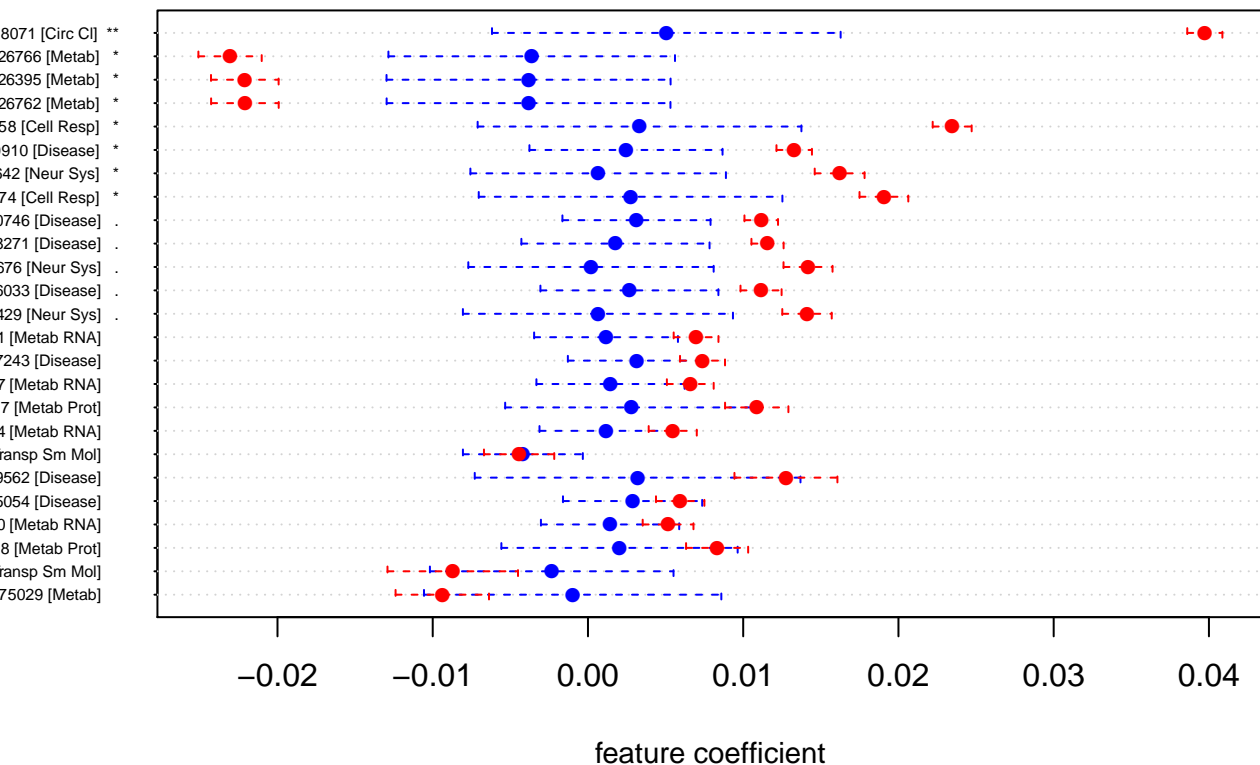
**alpha=0.1**

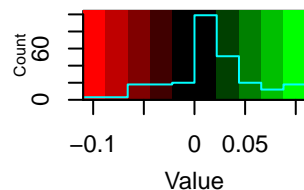


# Selected feature coefficients ranked by p-value for alpha=0.1

P-value significance codes: <0.001 (\*\*\*), <0.01 (\*\*), <0.05 (\*), <0.1 (.)

● model  
● null

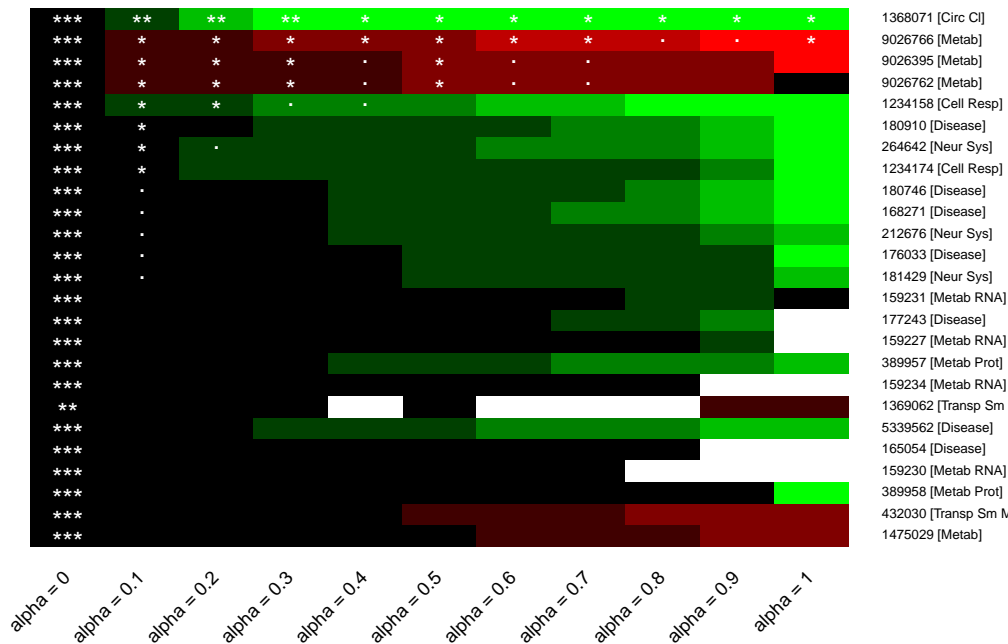




## Selected feature coefficients

### Features ranked by p-value for alpha=0.1

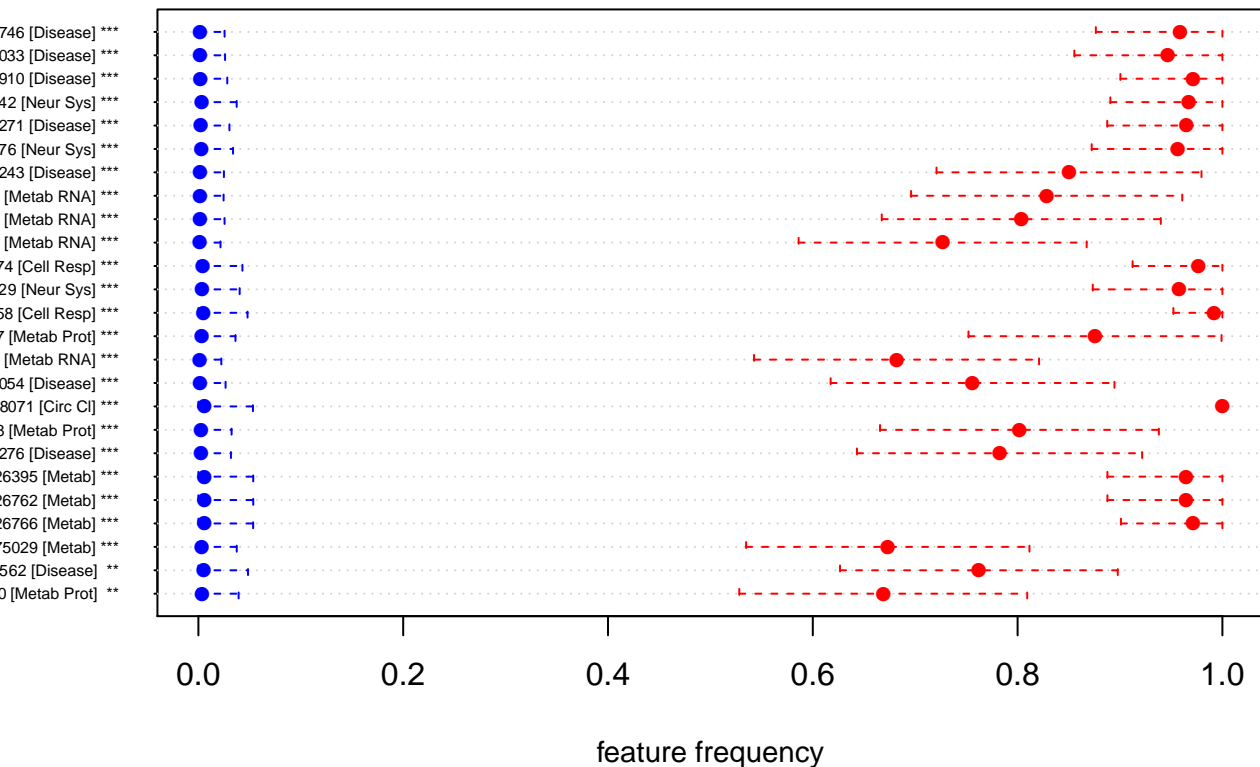
P-value significance codes: <0.001 (\*\*\*), <0.01 (\*\*), <0.05 (\*), <0.1 (.)



# Selected feature frequencies ranked by p-value for alpha=0.1

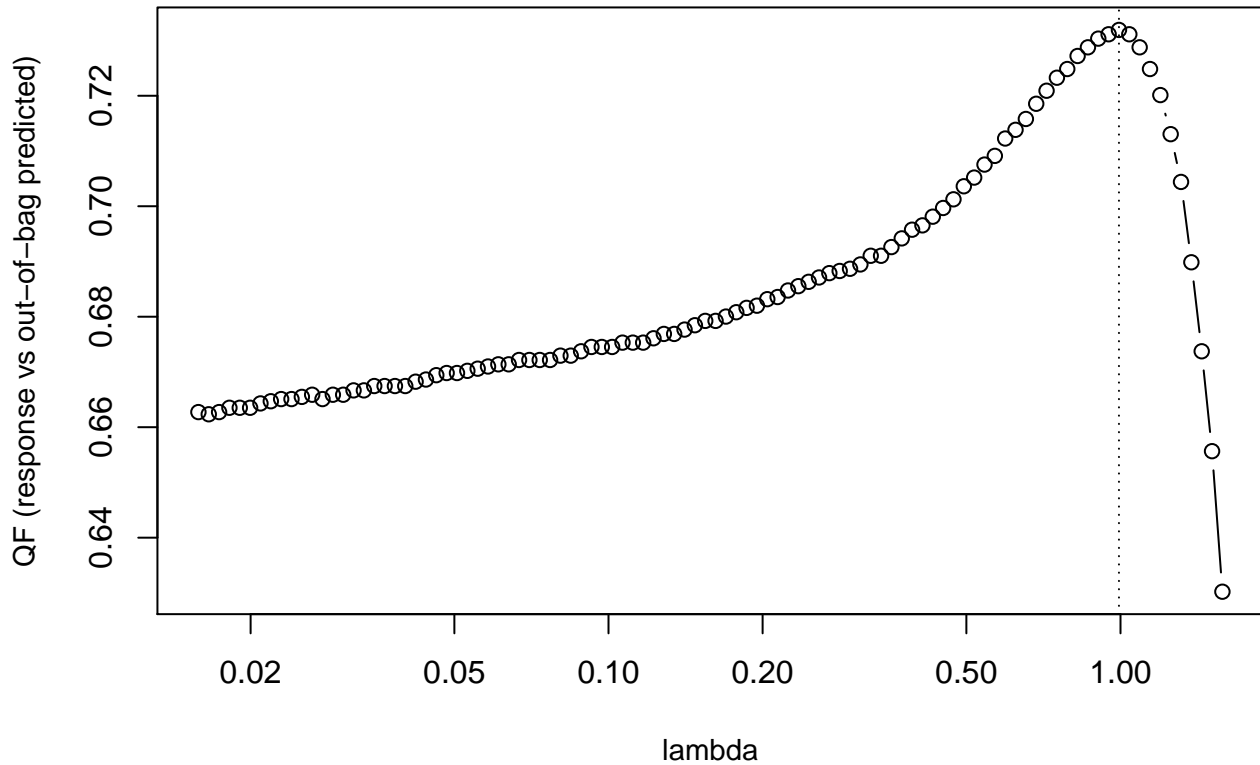
P-value significance codes: <0.001 (\*\*\*), <0.01 (\*\*), <0.05 (\*), <0.1 (.)

● model  
● null

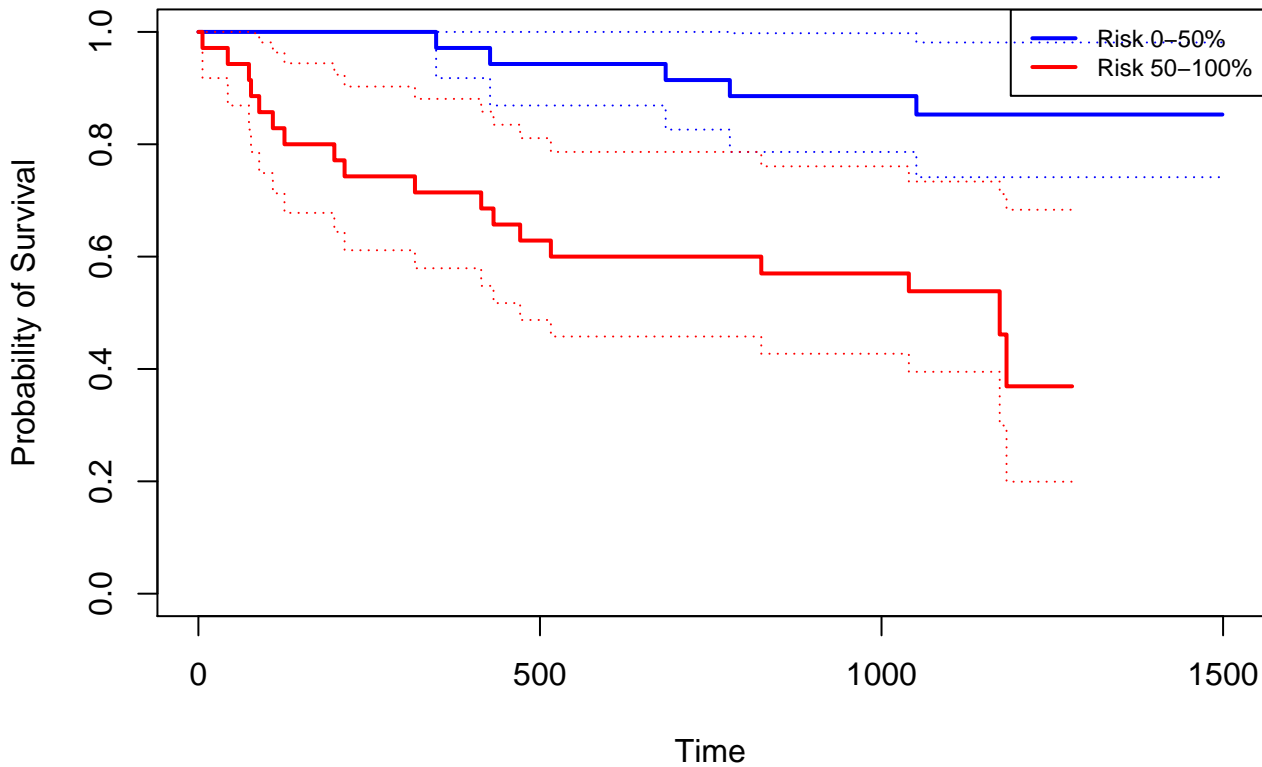




**alpha=0.2 ; QF=concordance index**



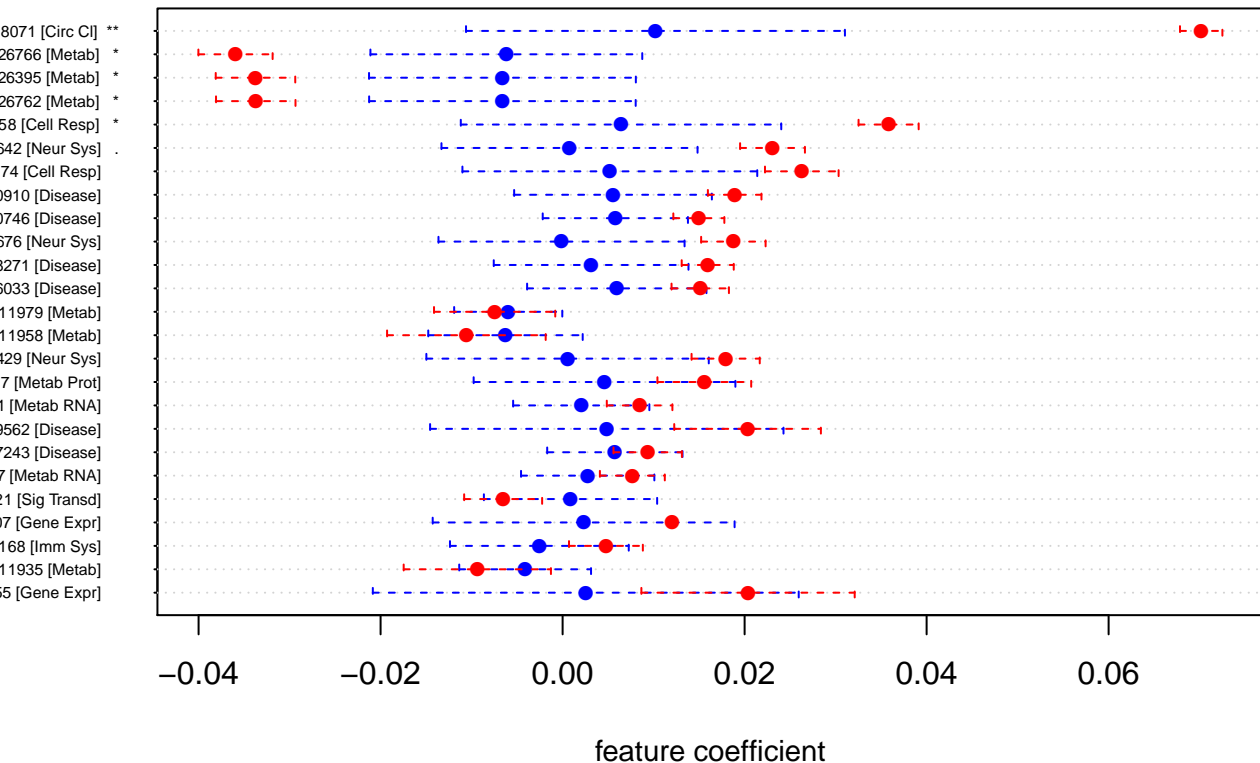
**alpha=0.2**



# Selected feature coefficients ranked by p-value for alpha=0.2

P-value significance codes: <0.001 (\*\*\*), <0.01 (\*\*), <0.05 (\*), <0.1 (.)

● model  
● null



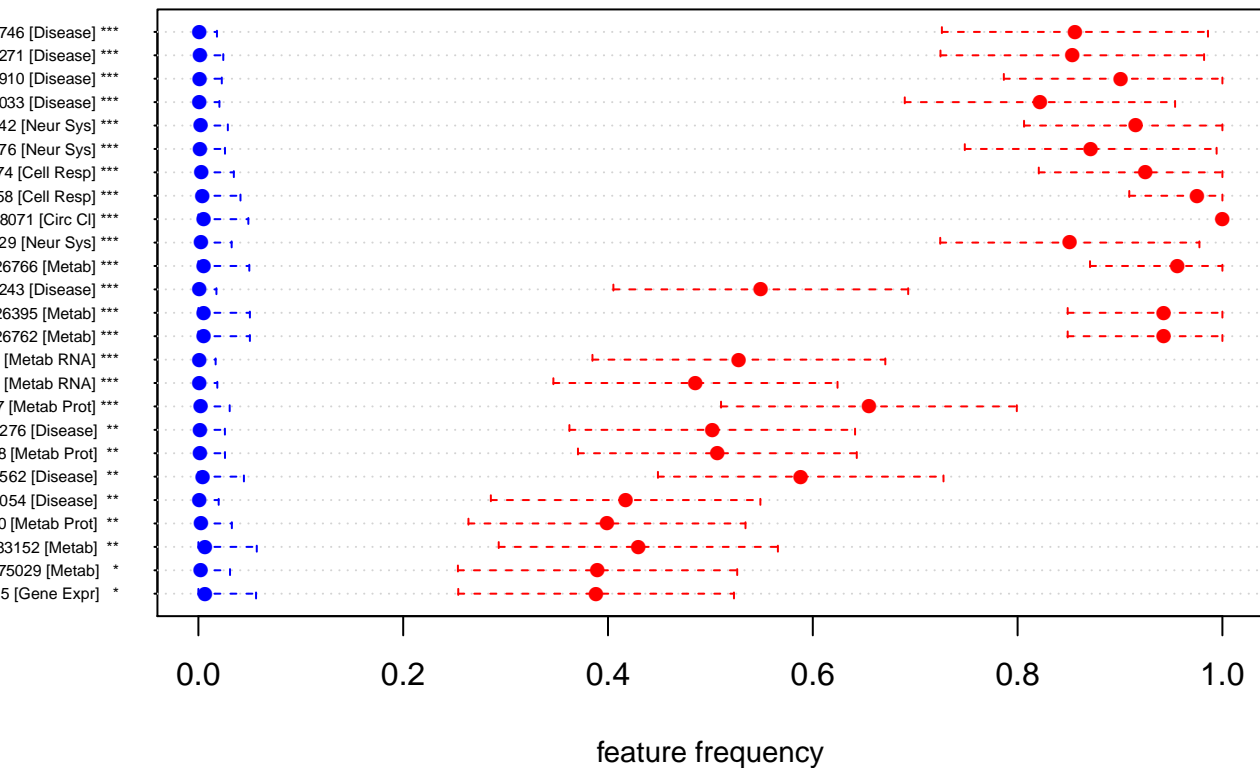


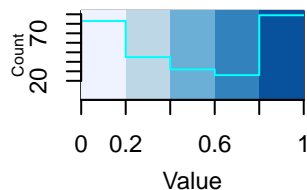


# Selected feature frequencies ranked by p-value for alpha=0.2

P-value significance codes: <0.001 (\*\*\*), <0.01 (\*\*), <0.05 (\*), <0.1 (.)

● model  
● null

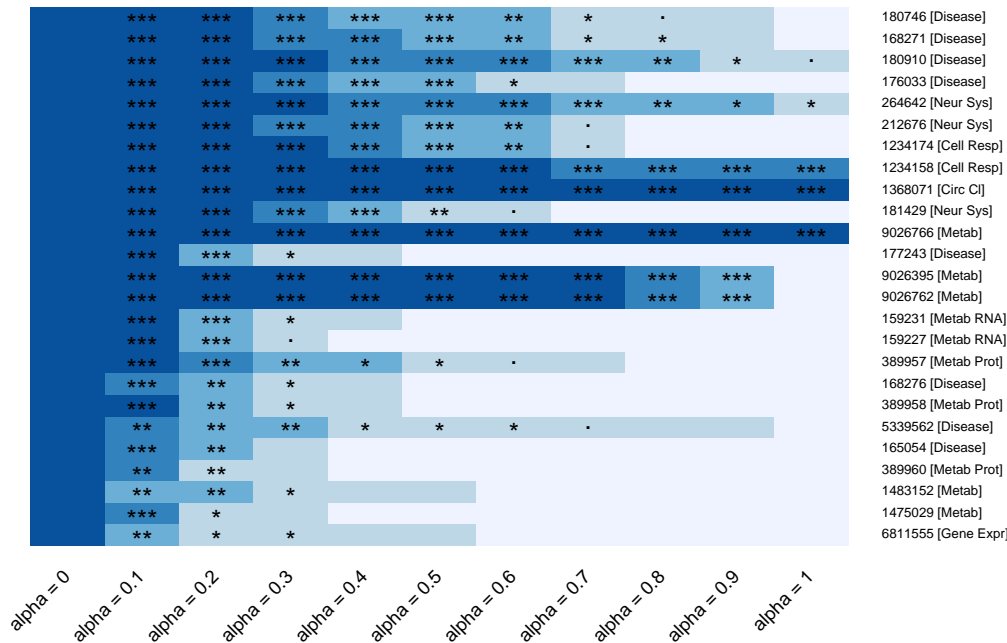




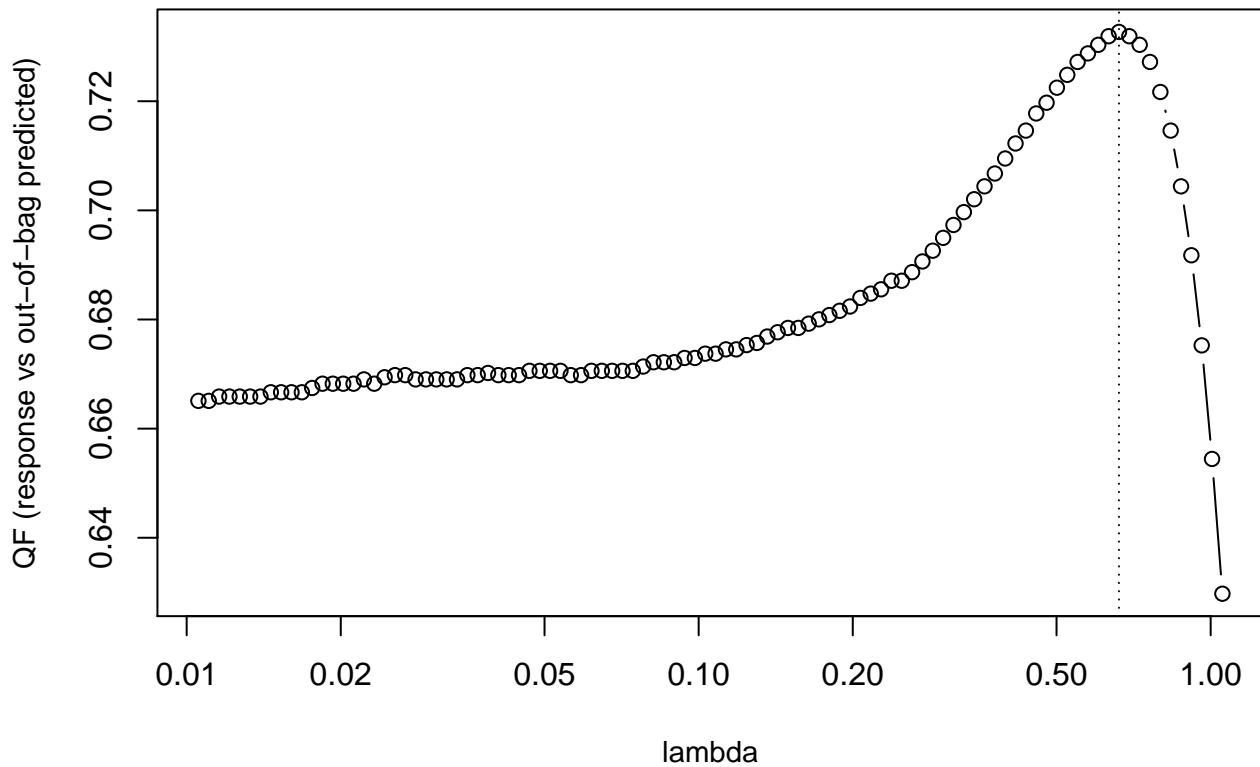
## Selected feature frequencies

### Features ranked by p-value for alpha=0.2

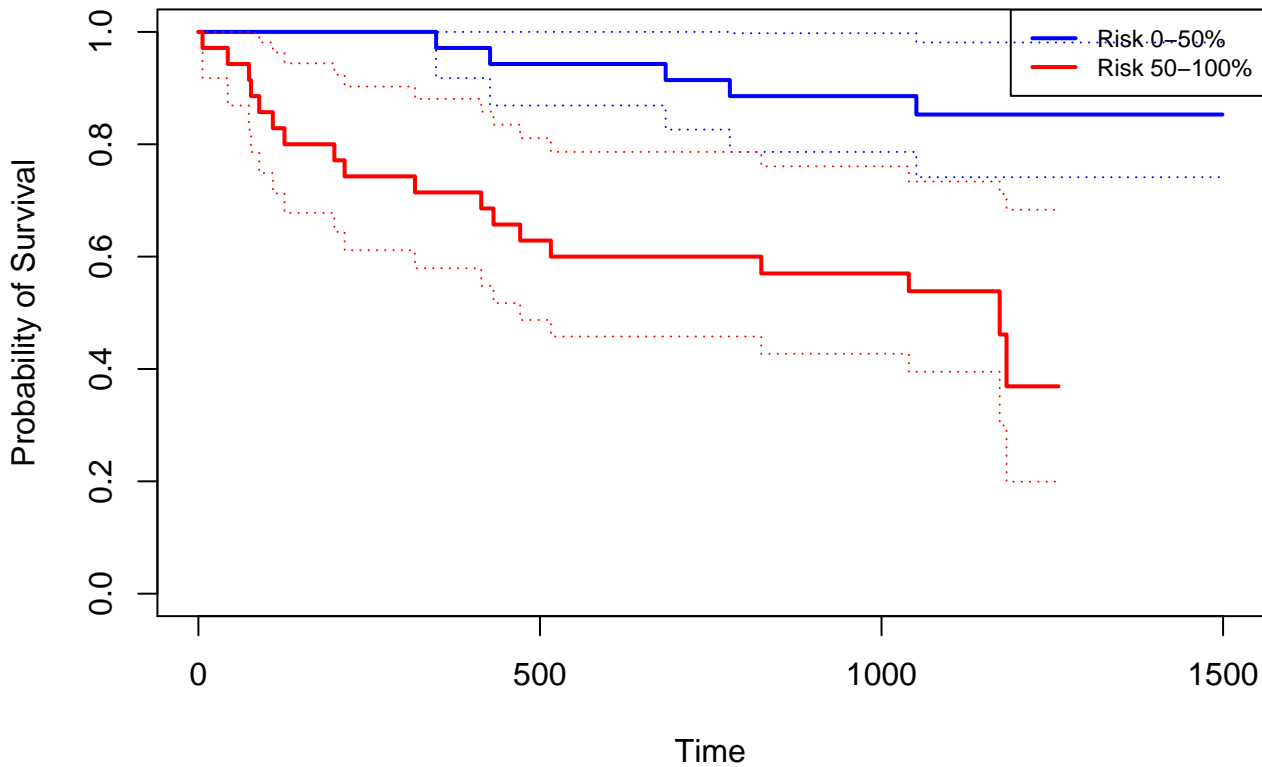
P-value significance codes: <0.001 (\*\*\*), <0.01 (\*\*), <0.05 (\*), <0.1 (.)



**alpha=0.3 ; QF=concordance index**



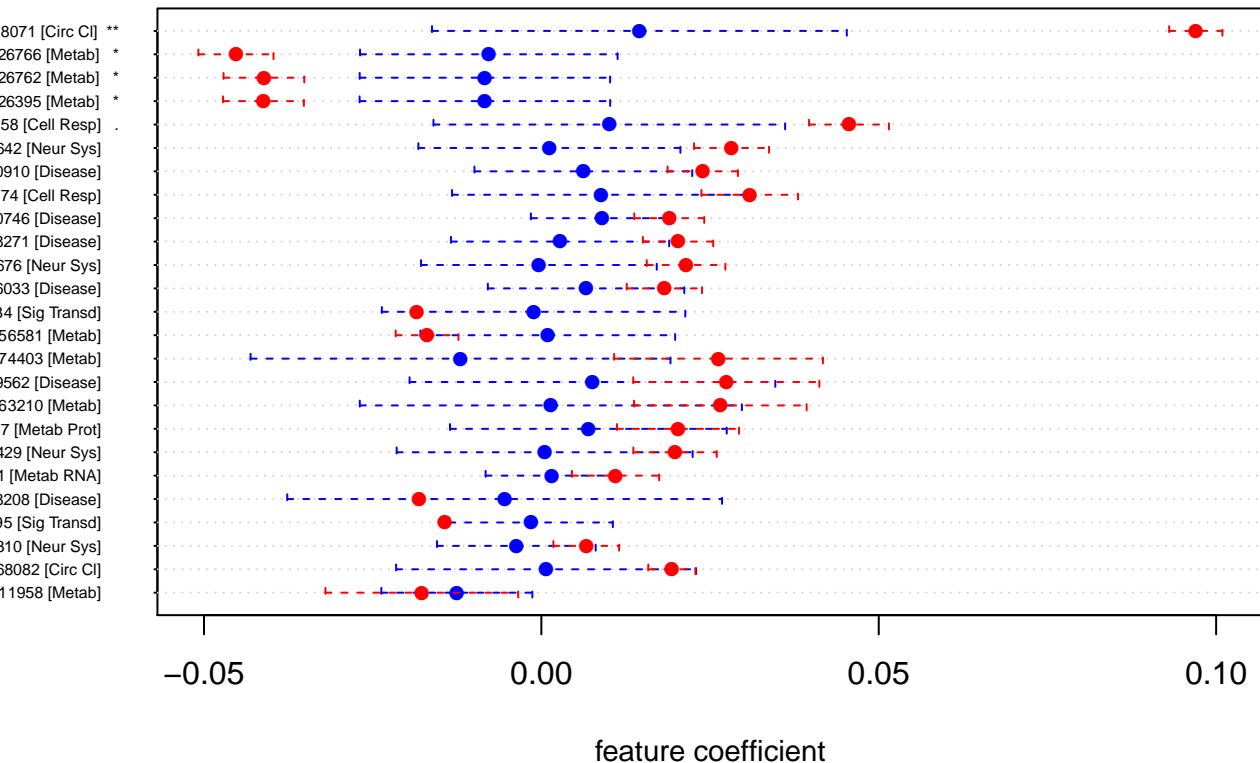
**alpha=0.3**

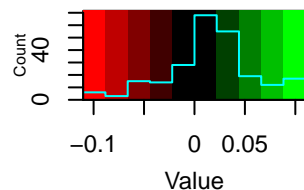


# Selected feature coefficients ranked by p-value for alpha=0.3

P-value significance codes: <0.001 (\*\*\*), <0.01 (\*\*), <0.05 (\*), <0.1 (.)

● model  
● null

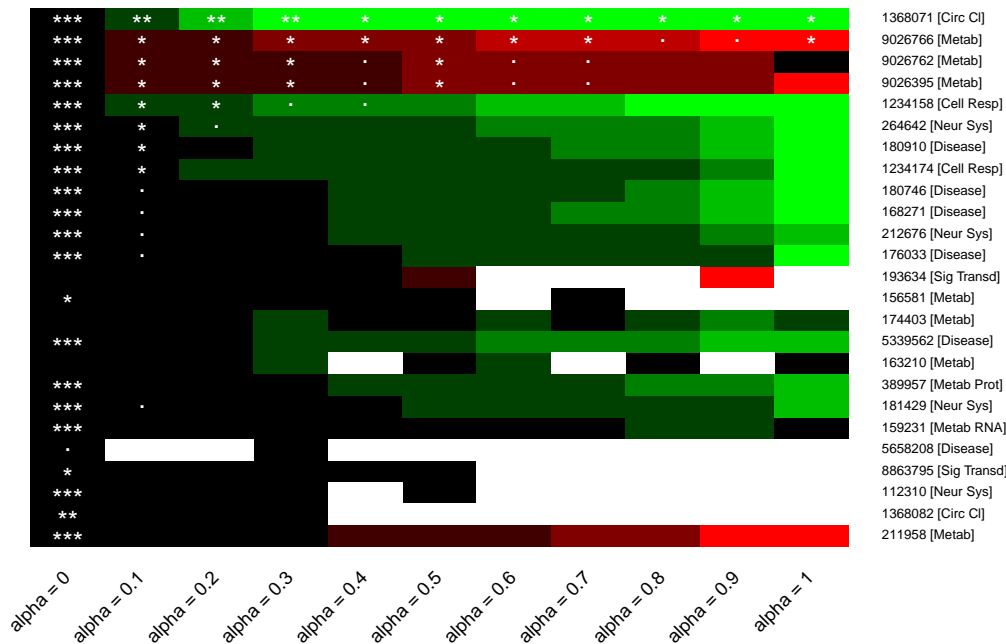




## Selected feature coefficients

### Features ranked by p-value for alpha=0.3

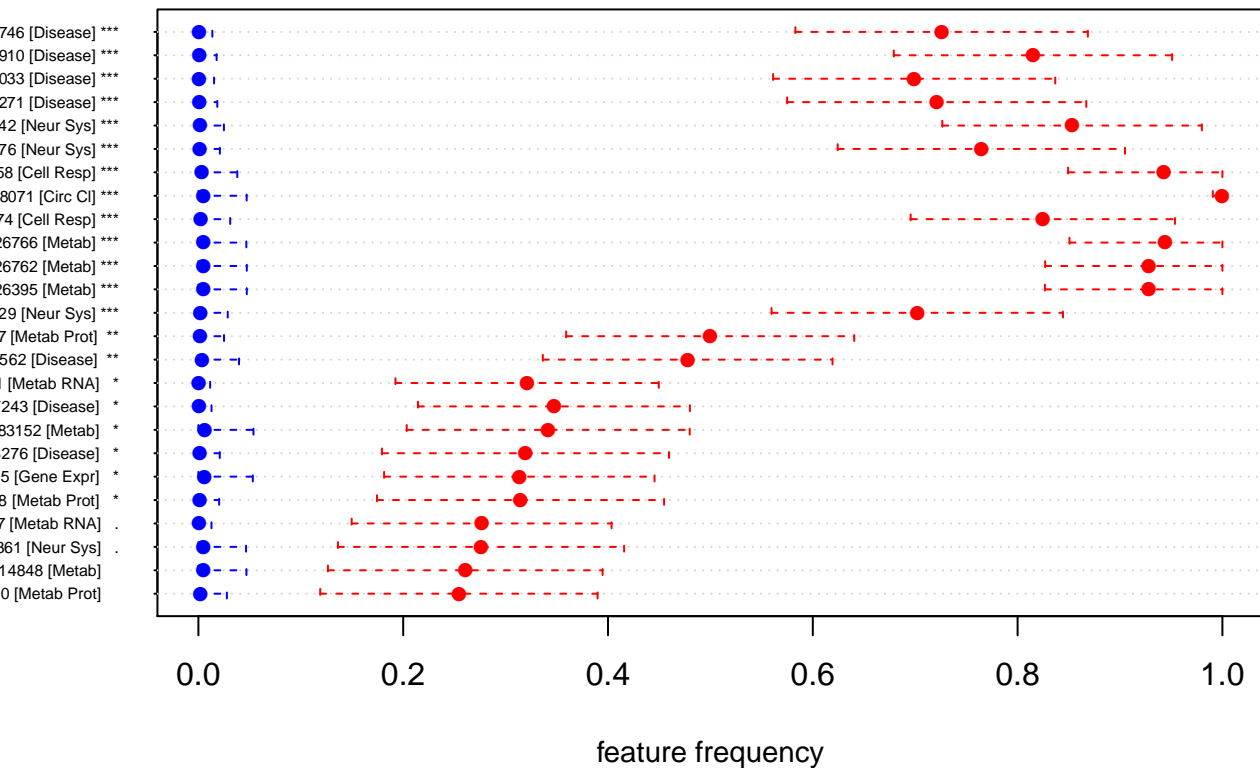
P-value significance codes: <0.001 (\*\*\*), <0.01 (\*\*), <0.05 (\*), <0.1 (.)



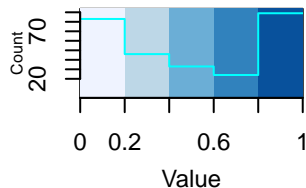
# Selected feature frequencies ranked by p-value for alpha=0.3

P-value significance codes: <0.001 (\*\*\*), <0.01 (\*\*), <0.05 (\*), <0.1 (.)

● model  
● null



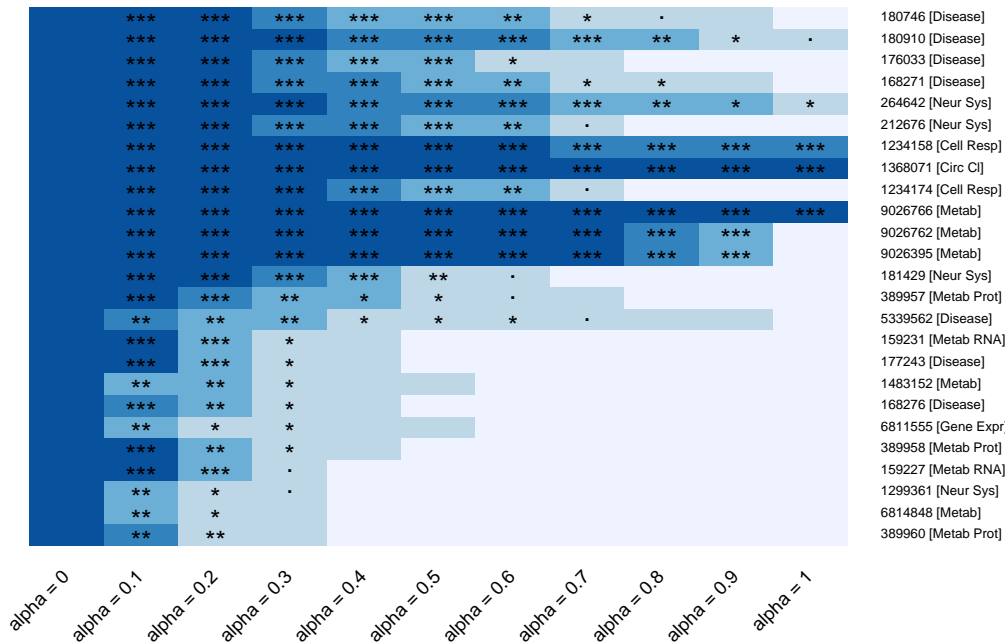




## Selected feature frequencies

### Features ranked by p-value for alpha=0.3

P-value significance codes: <0.001 (\*\*\*), <0.01 (\*\*), <0.05 (\*), <0.1 (.)



180746 [Disease]

180910 [Disease]

176033 [Disease]

168271 [Disease]

264642 [Neur Sys

212676 [Neur Sys

1234158 [Cell Res]

1368071 [Circ CI]

1234174 [Cell Res]

9026766 [Metab]

9026762 [Metab]

9026395 [Metab]

181429 [Neur Sys

389957 [Metab Pr

5339562 [Disease]

159231 [Metab R]

177243 [Disease]

1483152 [Metab]

168276 [Disease]

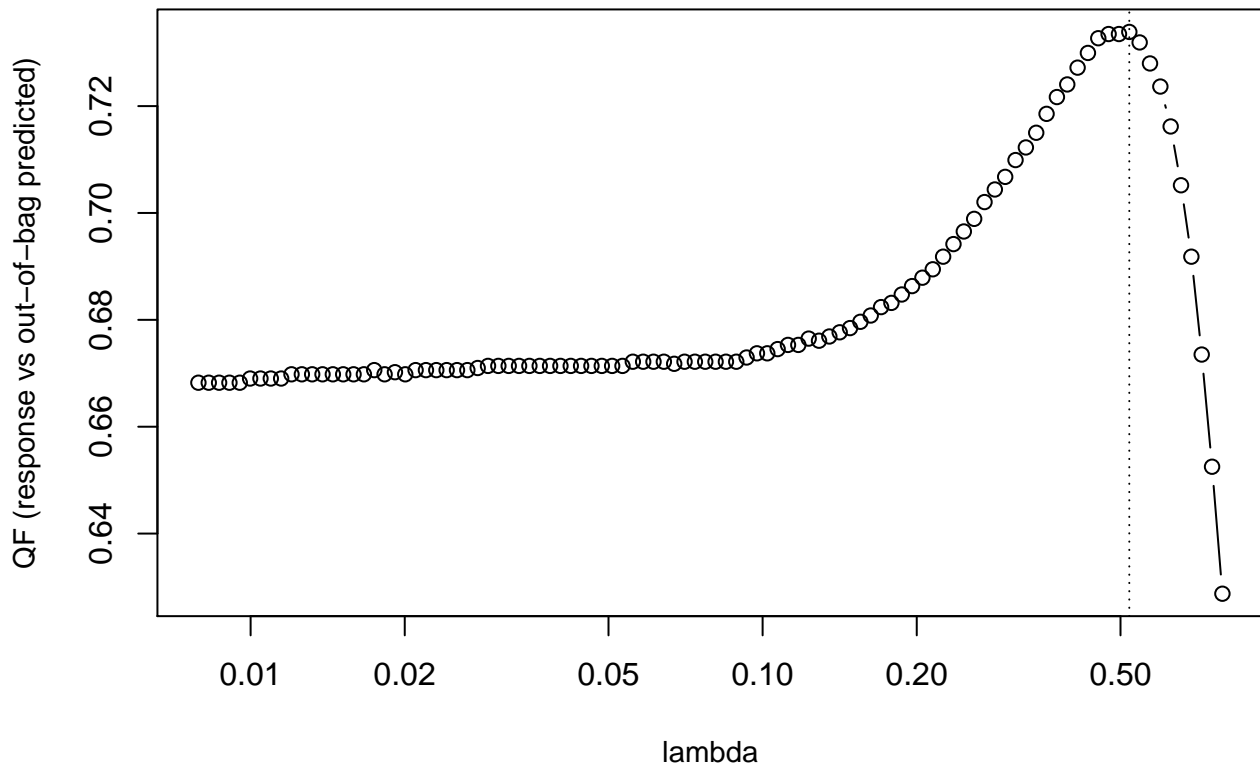
6811555 [Gene E

389958 [Metab P]

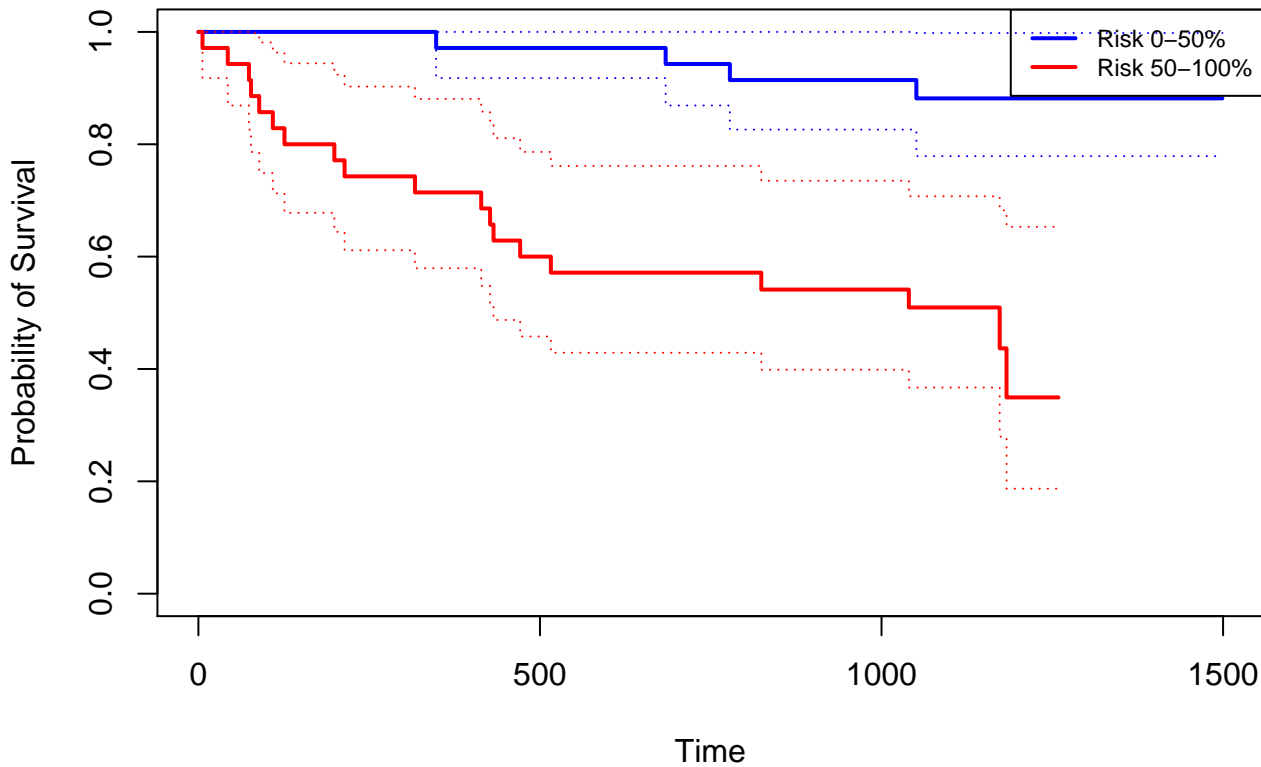
159227 [Metab R]

1299361 [Neur 3y]

**alpha=0.4 ; QF=concordance index**



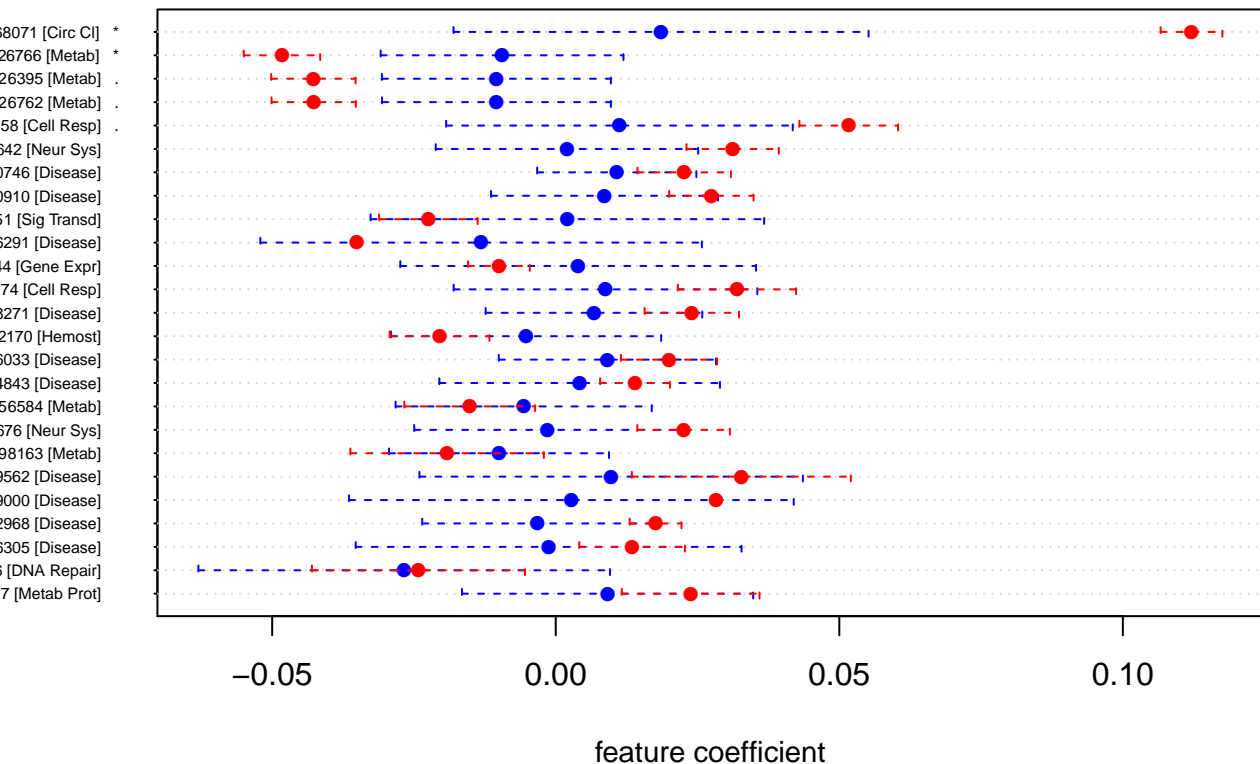
**alpha=0.4**

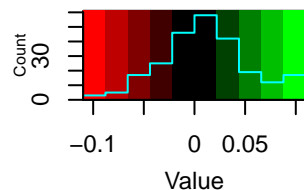


# Selected feature coefficients ranked by p-value for alpha=0.4

P-value significance codes: <0.001 (\*\*\*), <0.01 (\*\*), <0.05 (\*), <0.1 (.)

● model  
● null

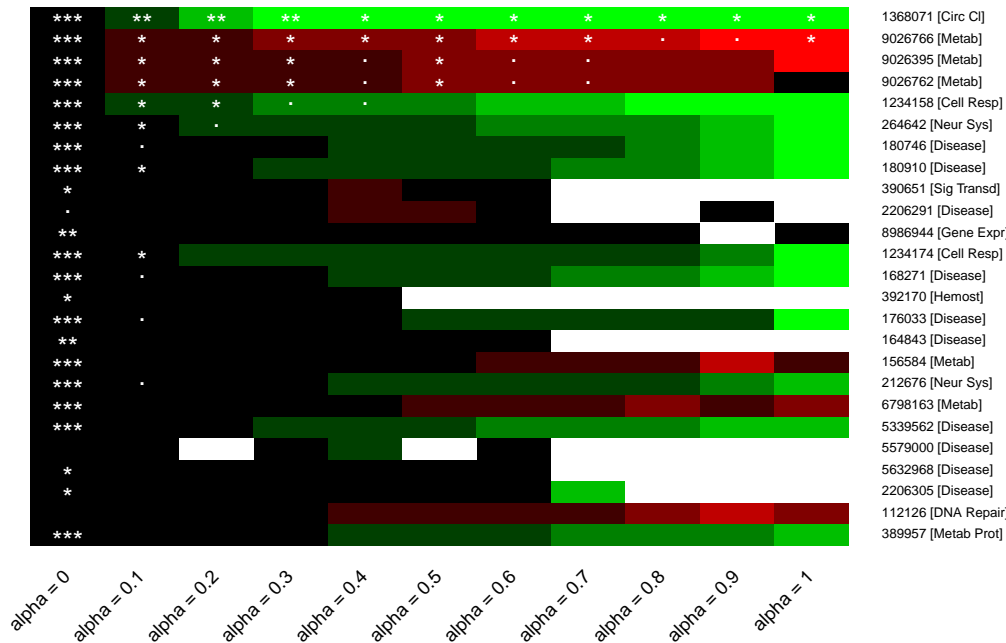




## Selected feature coefficients

### Features ranked by p-value for $\alpha=0.4$

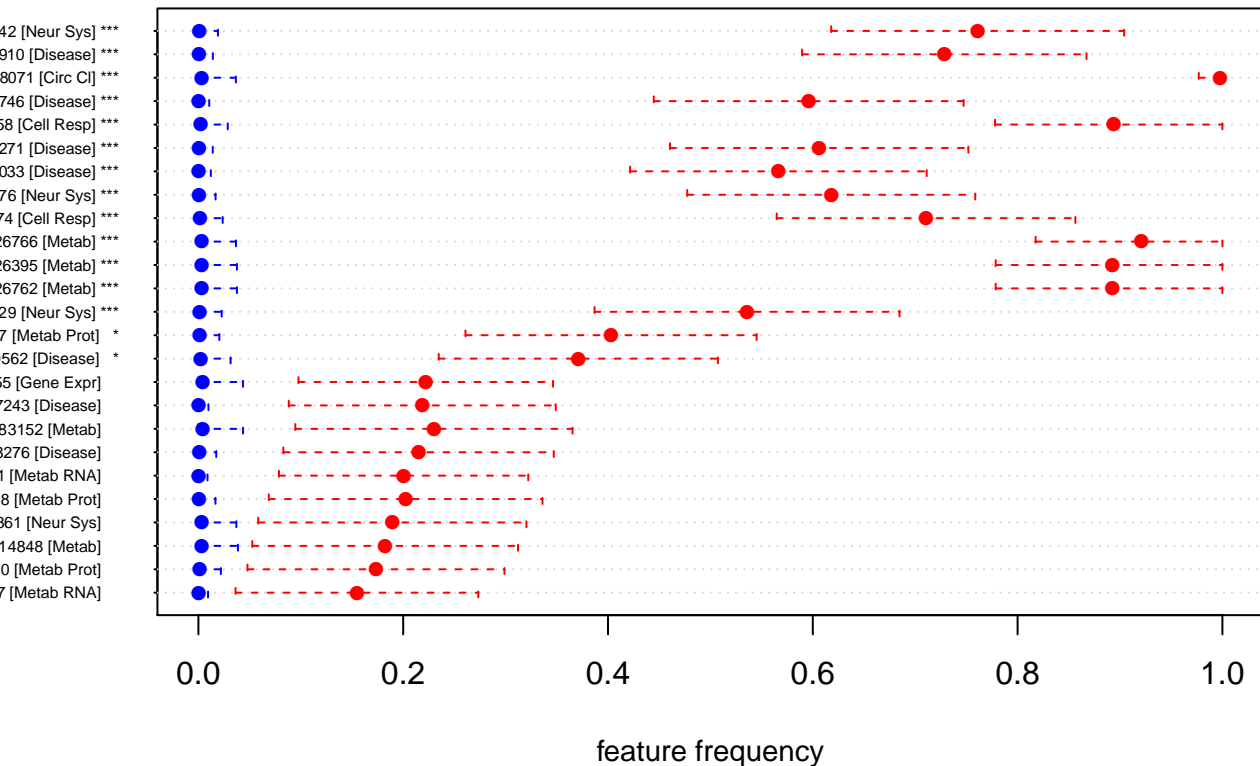
P-value significance codes: <0.001 (\*\*\*), <0.01 (\*\*), <0.05 (\*), <0.1 (.)



# Selected feature frequencies ranked by p-value for alpha=0.4

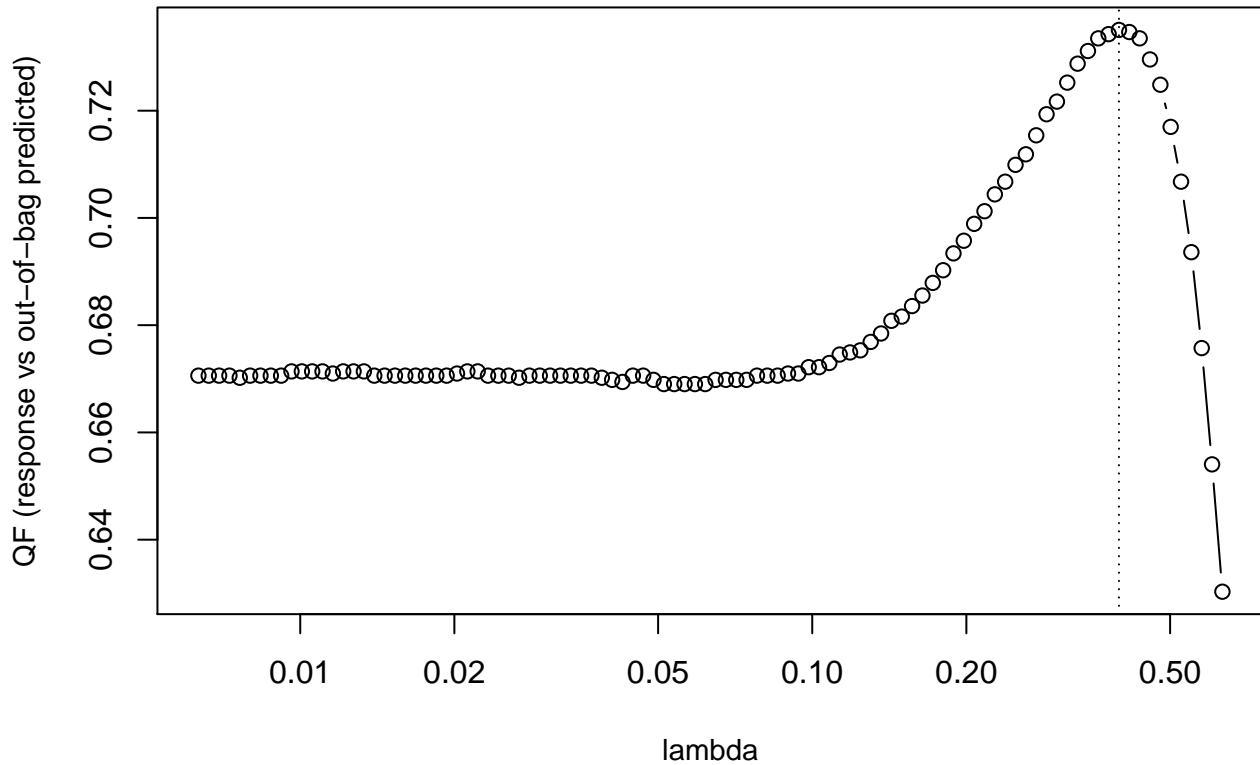
P-value significance codes: <0.001 (\*\*\*), <0.01 (\*\*), <0.05 (\*), <0.1 (.)

● model  
● null



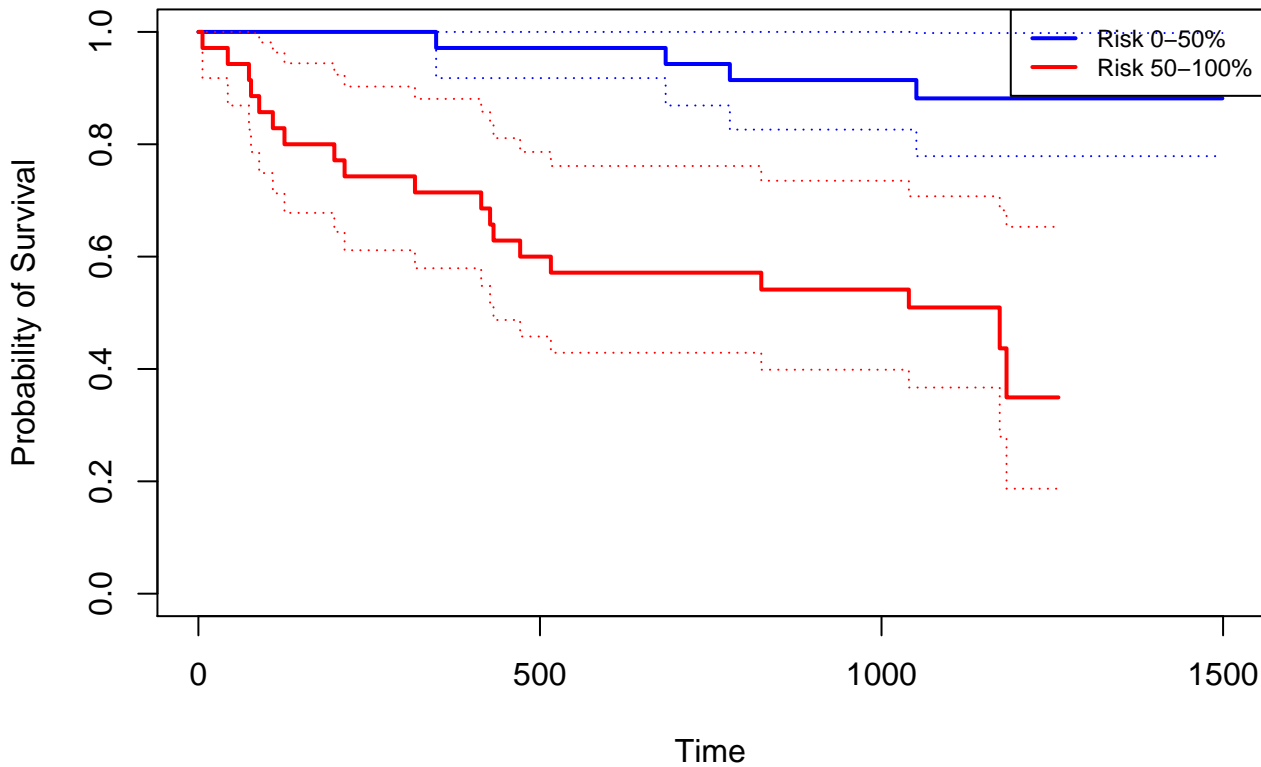


**alpha=0.5 ; QF=concordance index**





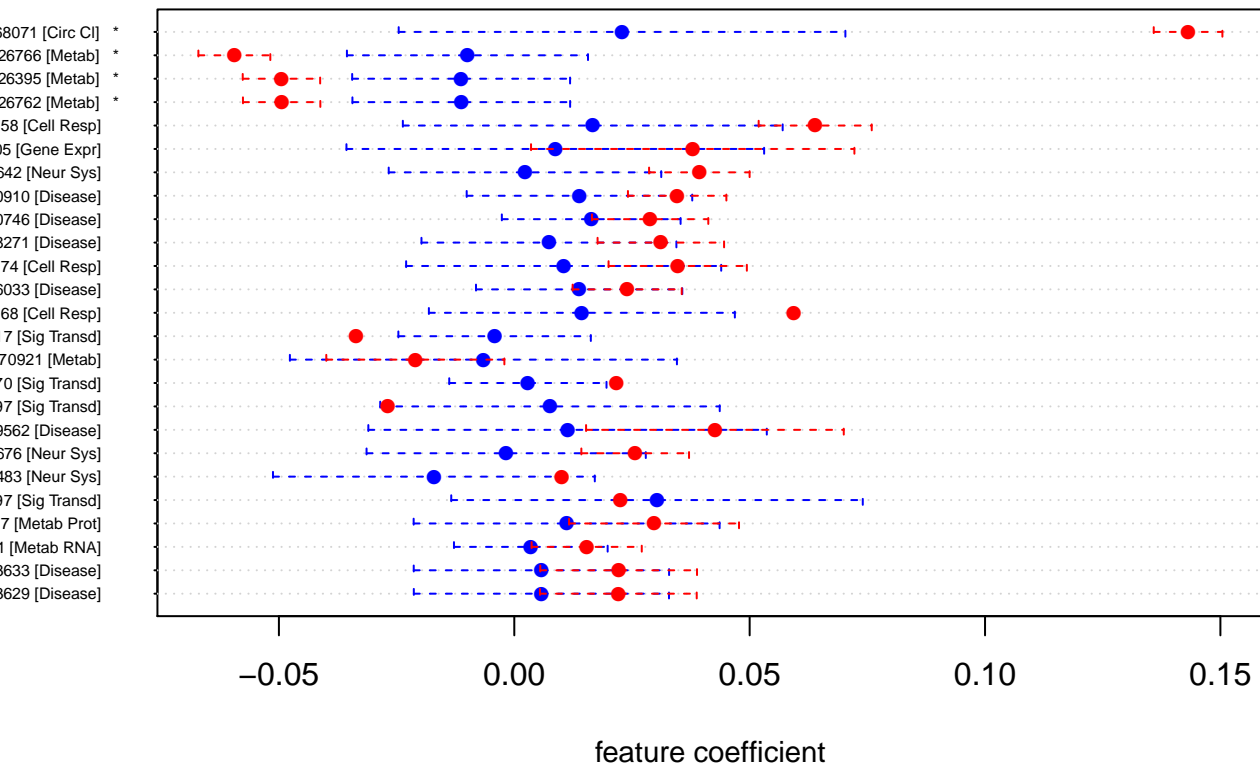
**alpha=0.5**

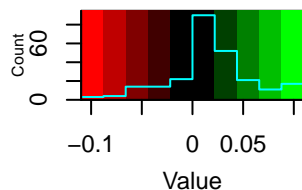


# Selected feature coefficients ranked by p-value for alpha=0.5

P-value significance codes: <0.001 (\*\*\*), <0.01 (\*\*), <0.05 (\*), <0.1 (.)

● model  
● null

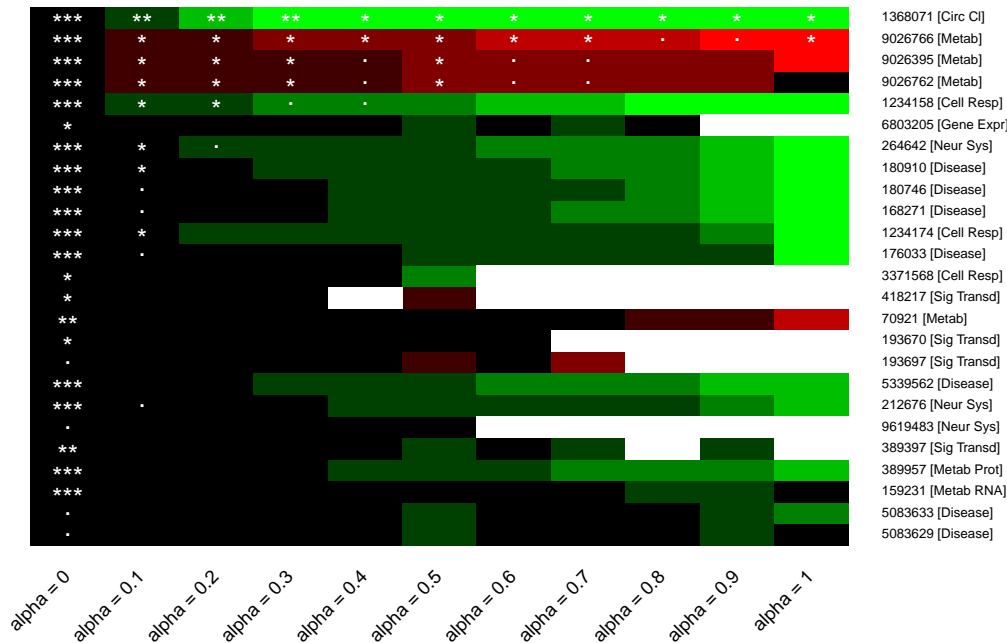




## Selected feature coefficients

Features ranked by p-value for  $\alpha=0.5$

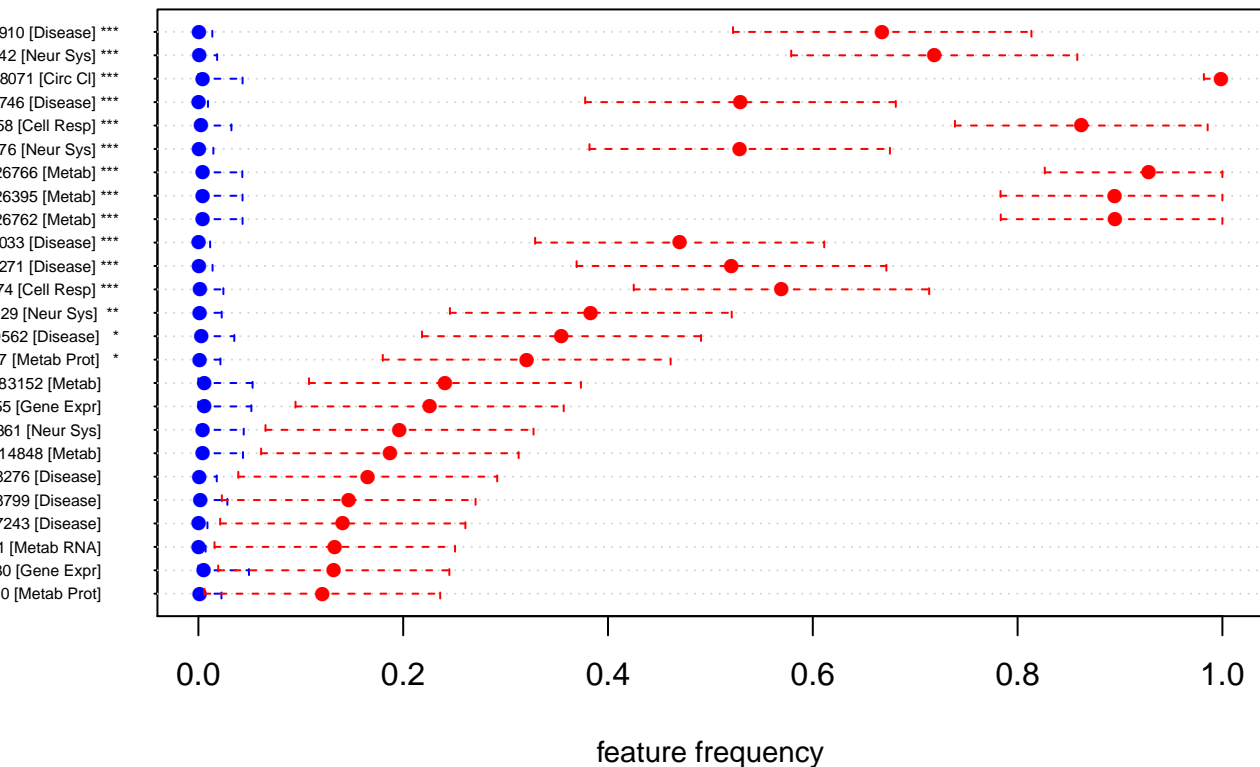
P-value significance codes: <0.001 (\*\*\*), <0.01 (\*\*), <0.05 (\*), <0.1 (.)



# Selected feature frequencies ranked by p-value for alpha=0.5

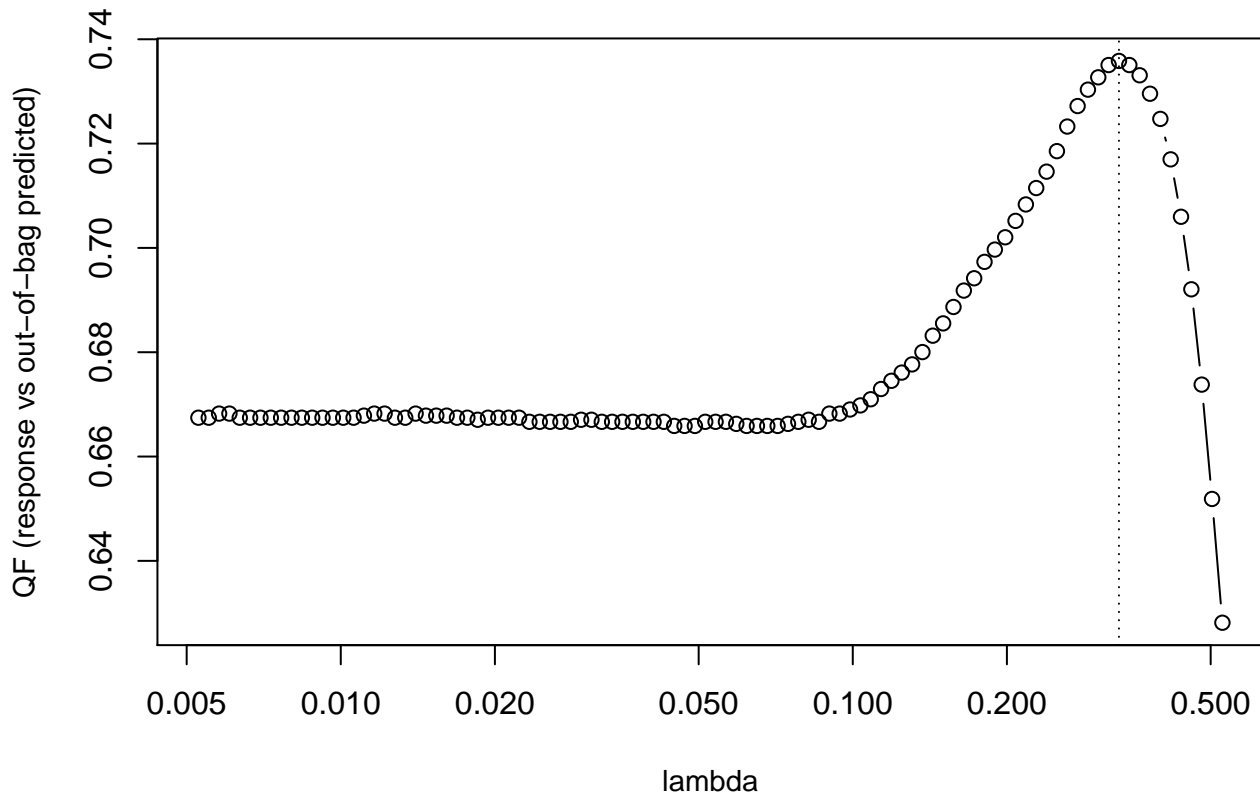
P-value significance codes: <0.001 (\*\*\*), <0.01 (\*\*), <0.05 (\*), <0.1 (.)

● model  
● null

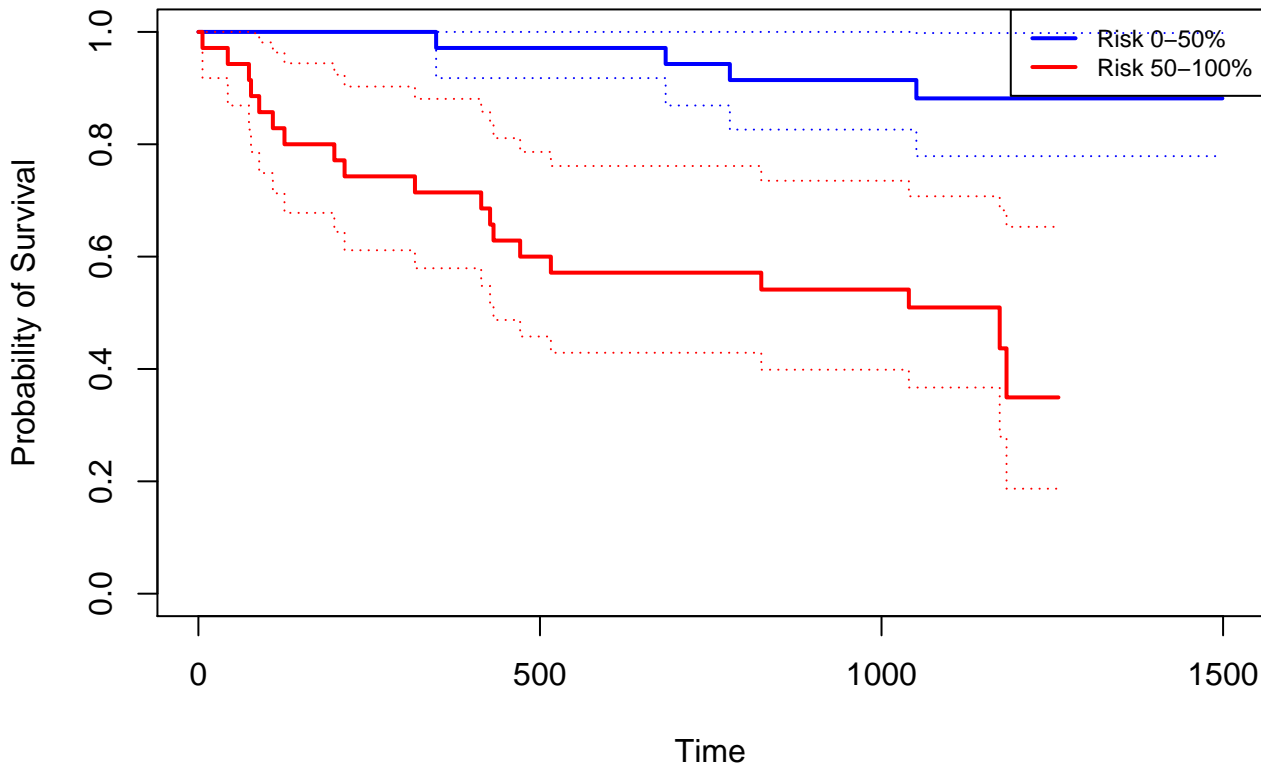




**alpha=0.6 ; QF=concordance index**



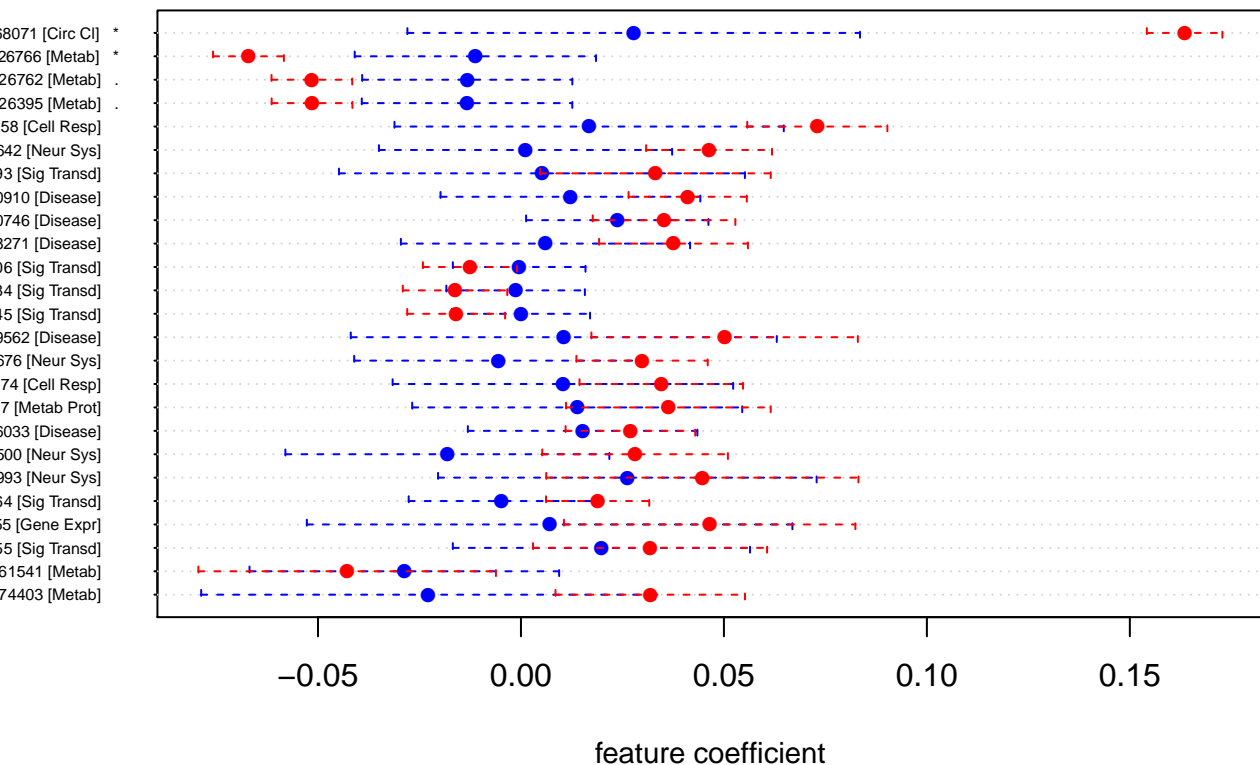
**alpha=0.6**



# Selected feature coefficients ranked by p-value for alpha=0.6

P-value significance codes: <0.001 (\*\*\*), <0.01 (\*\*), <0.05 (\*), <0.1 (.)

● model  
● null



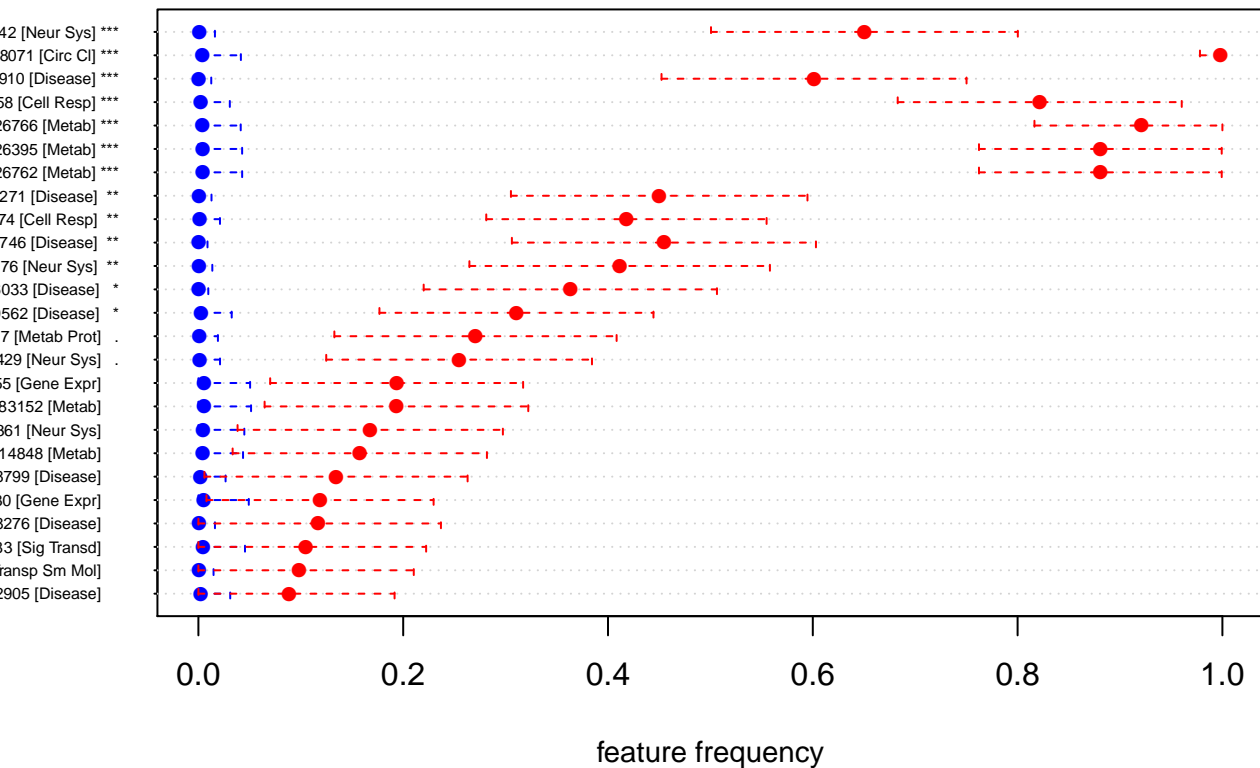




# Selected feature frequencies ranked by p-value for alpha=0.6

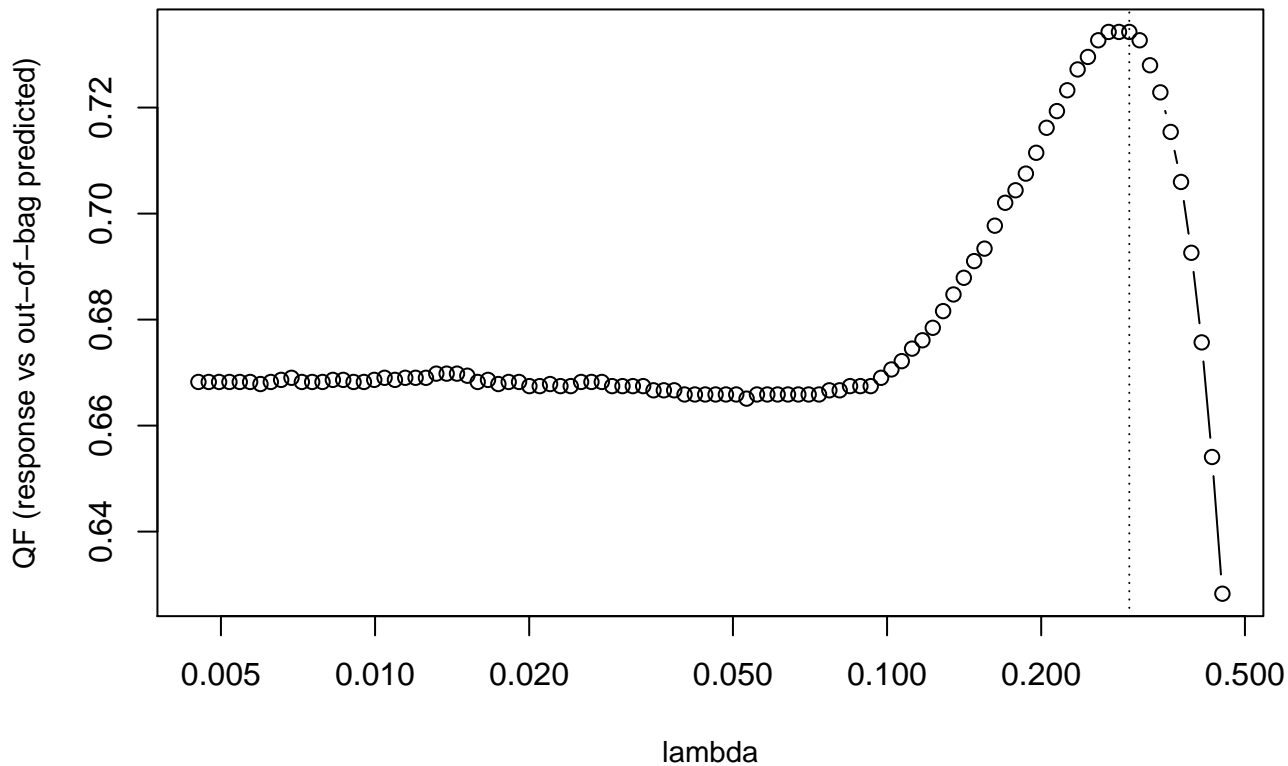
P-value significance codes: <0.001 (\*\*\*), <0.01 (\*\*), <0.05 (\*), <0.1 (.)

● model  
● null

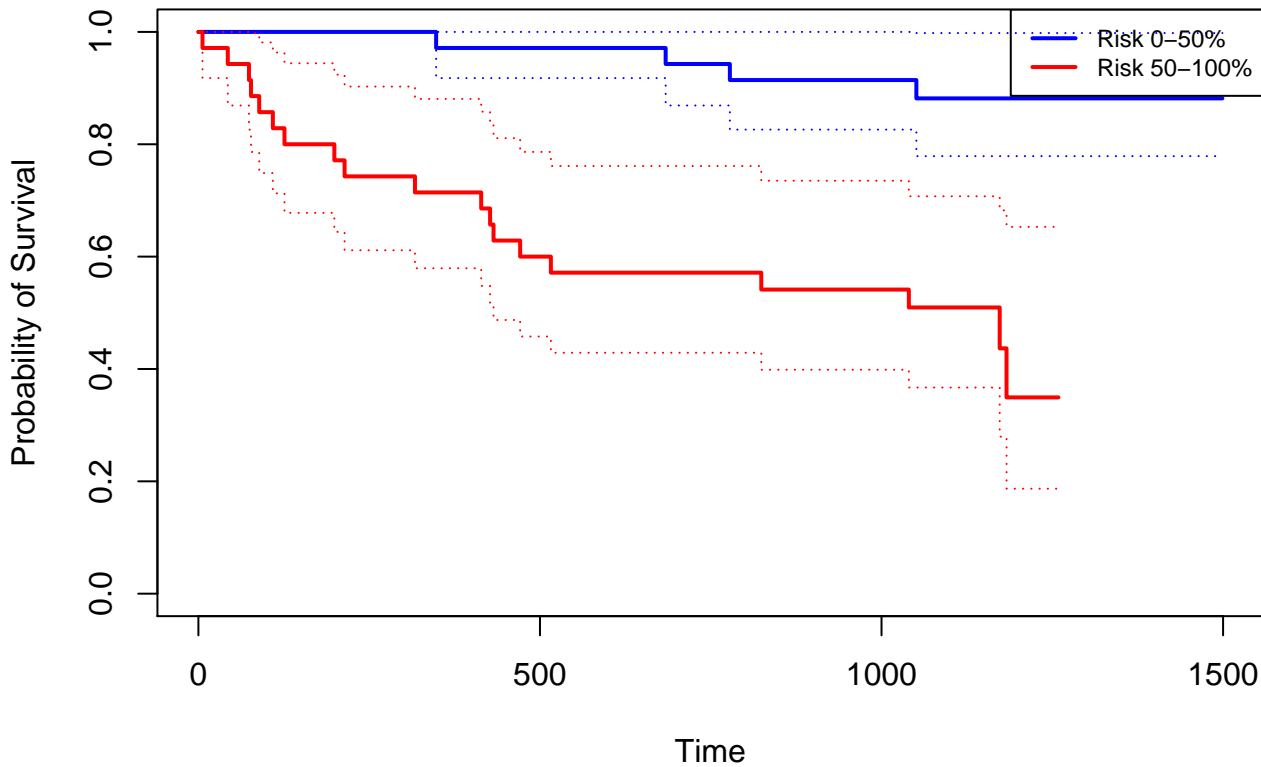




**alpha=0.7 ; QF=concordance index**



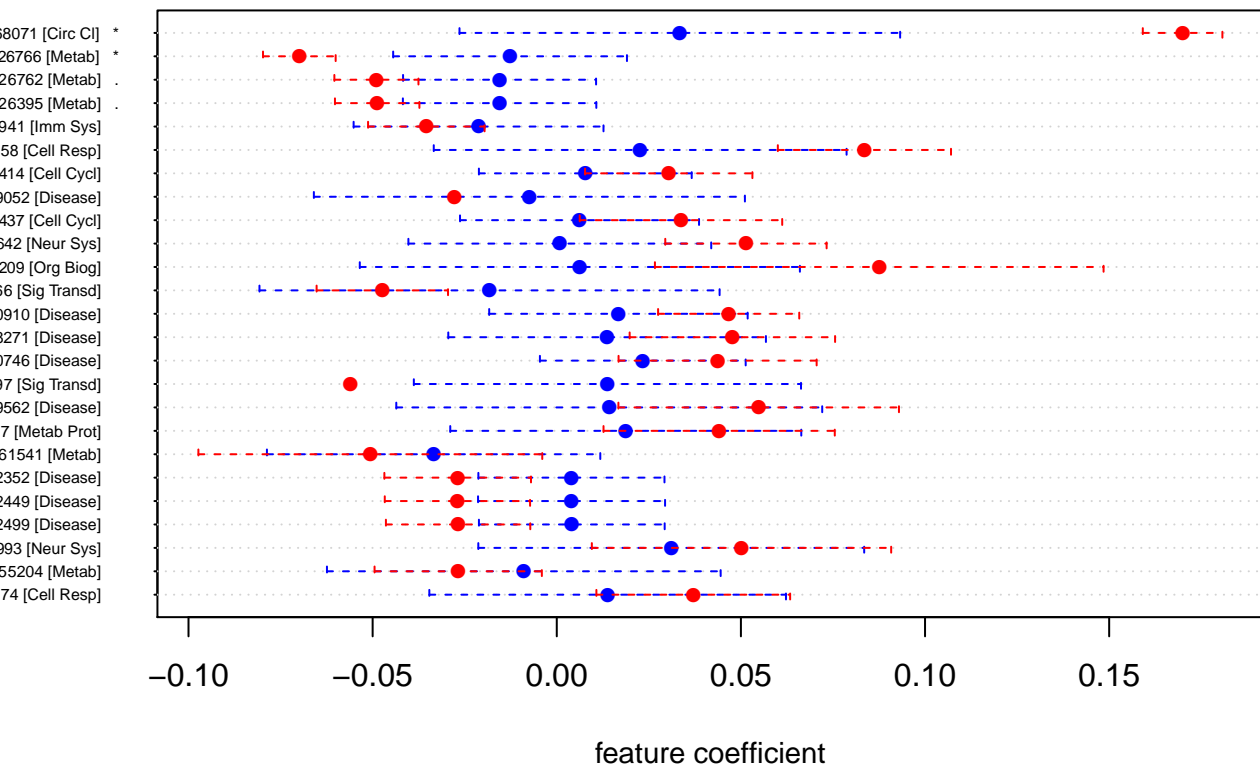
**alpha=0.7**



# Selected feature coefficients ranked by p-value for alpha=0.7

P-value significance codes: <0.001 (\*\*\*), <0.01 (\*\*), <0.05 (\*), <0.1 (.)

● model  
● null

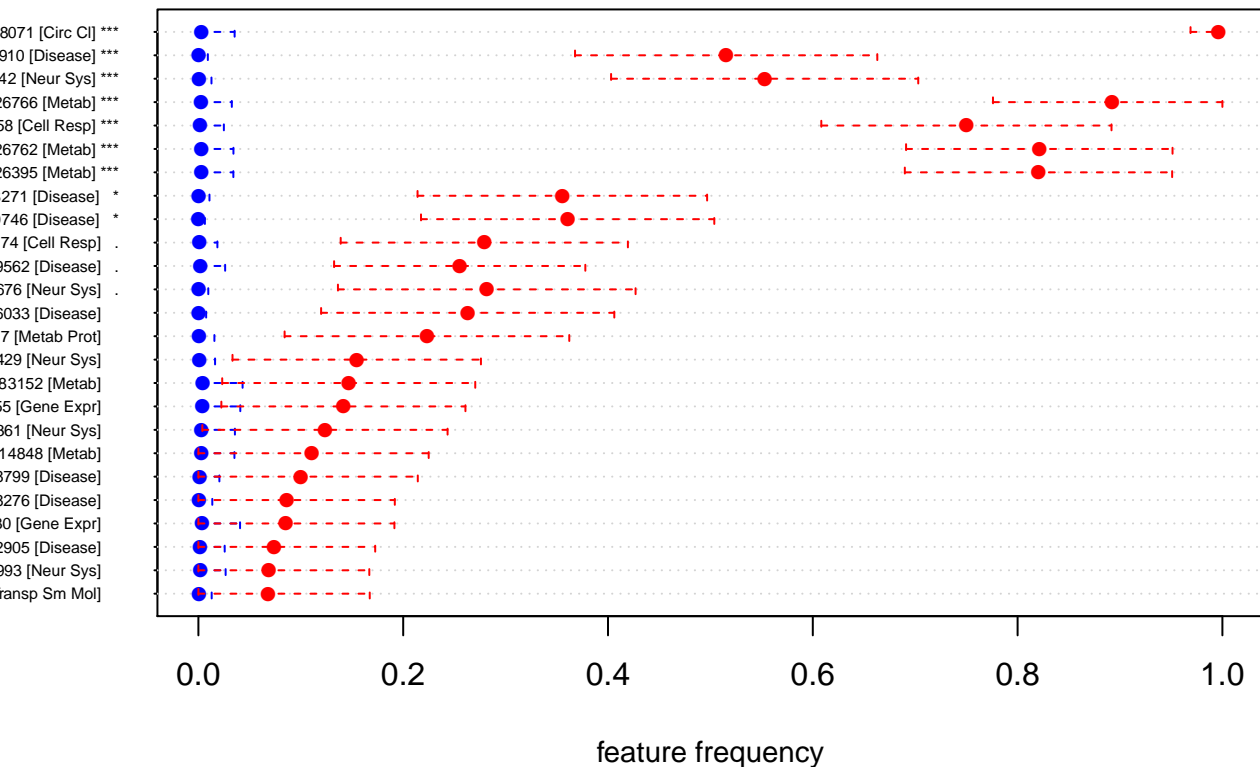




# Selected feature frequencies ranked by p-value for alpha=0.7

P-value significance codes: <0.001 (\*\*\*), <0.01 (\*\*), <0.05 (\*), <0.1 (.)

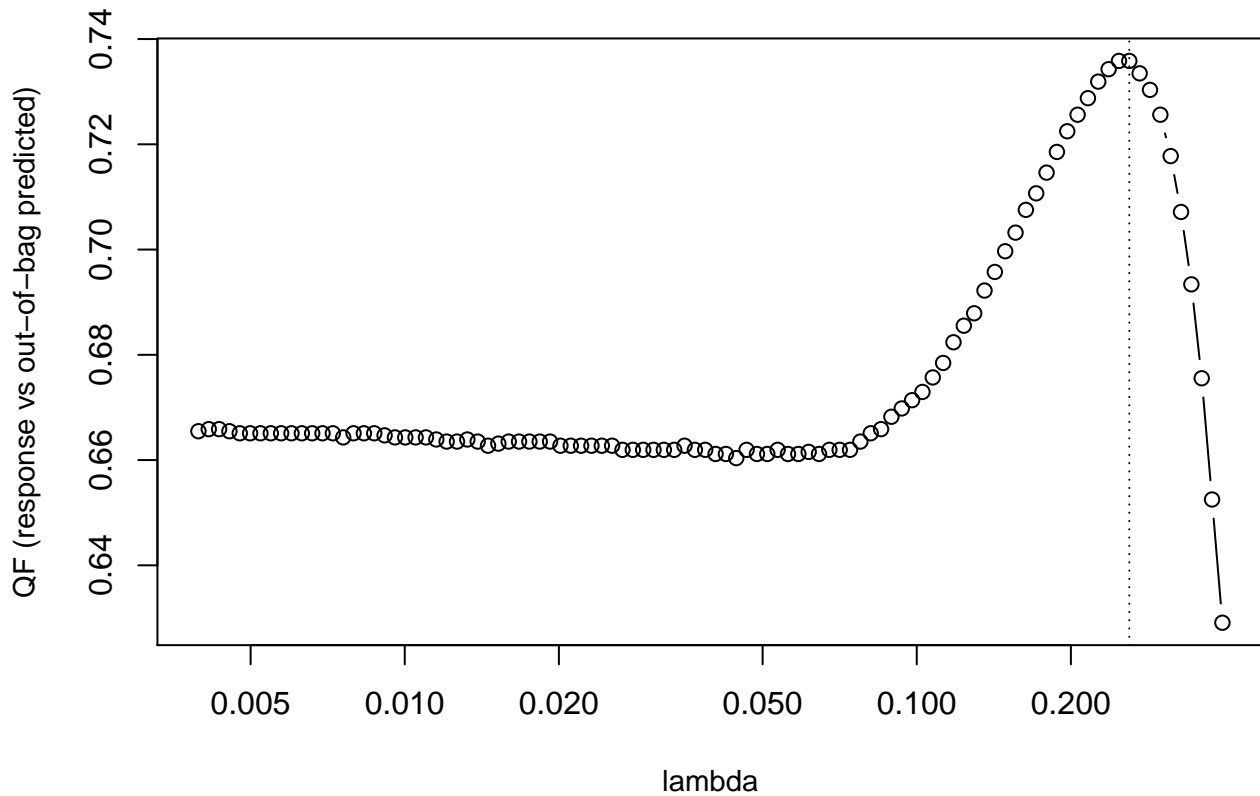
● model  
● null



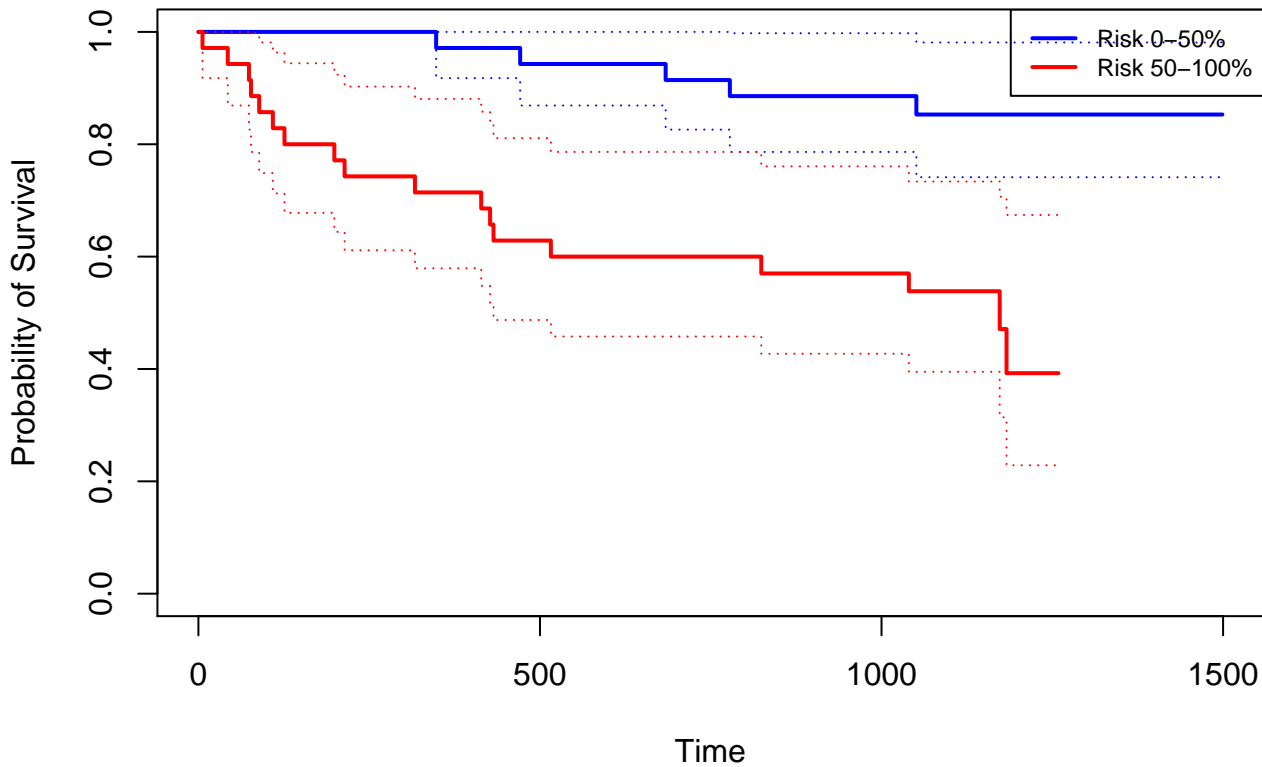




**alpha=0.8 ; QF=concordance index**



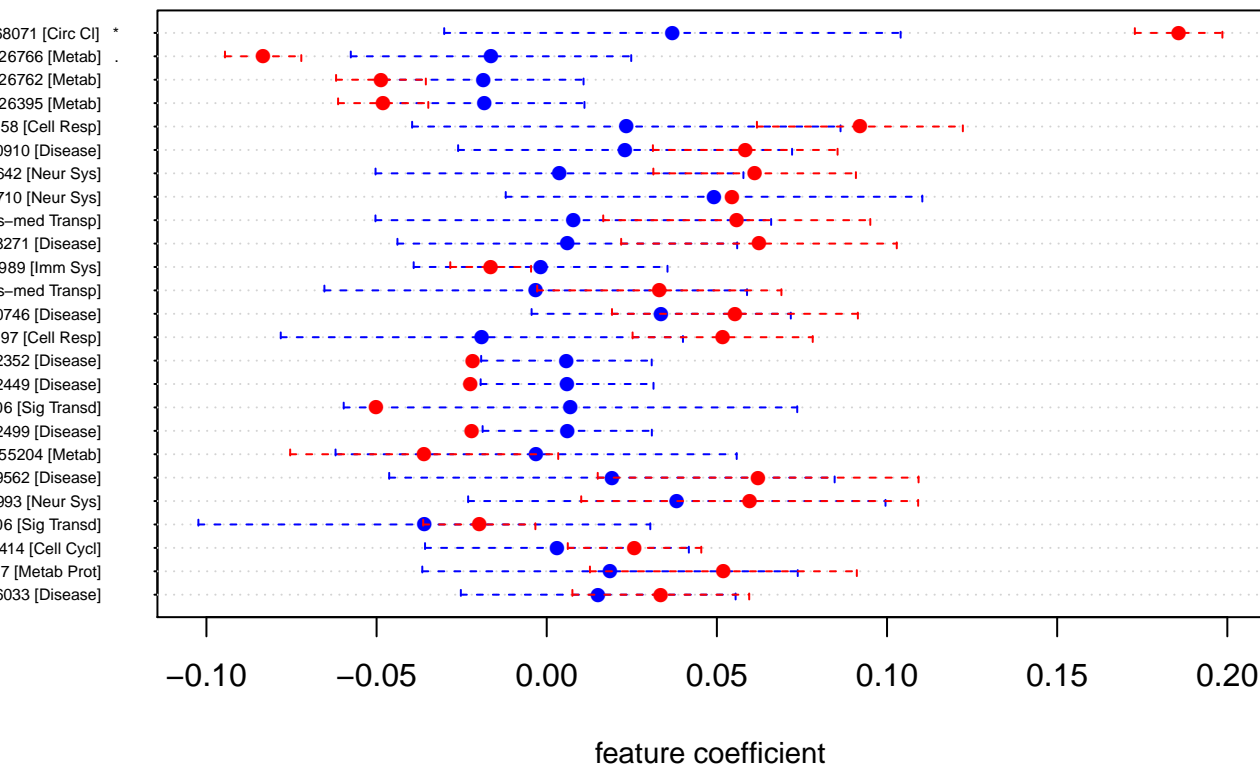
**alpha=0.8**

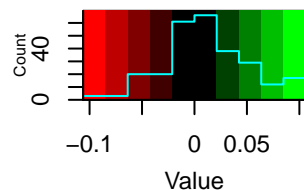


# Selected feature coefficients ranked by p-value for alpha=0.8

P-value significance codes: <0.001 (\*\*\*), <0.01 (\*\*), <0.05 (\*), <0.1 (.)

● model  
● null

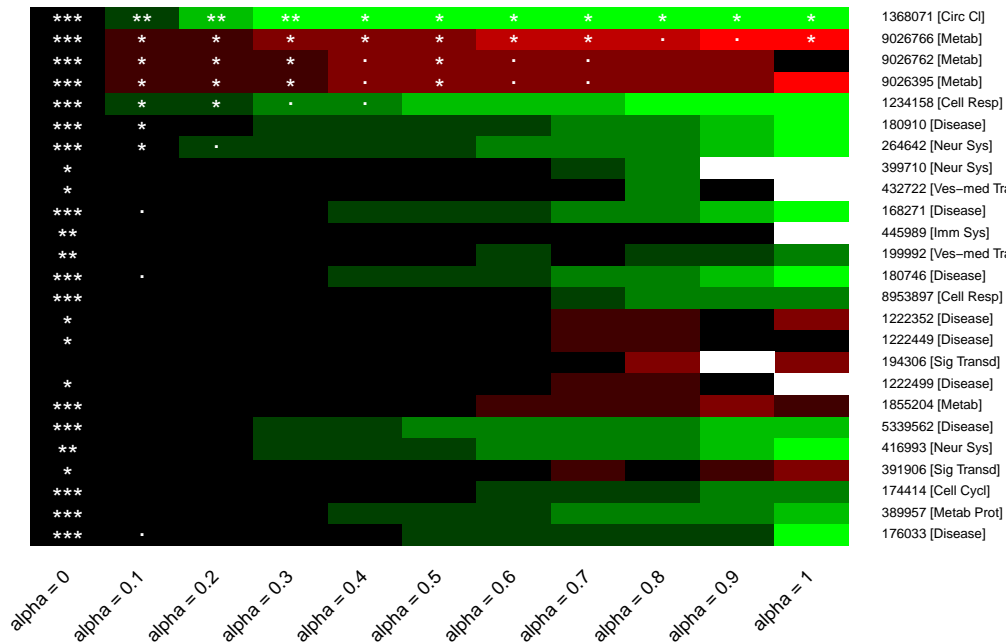




## Selected feature coefficients

### Features ranked by p-value for alpha=0.8

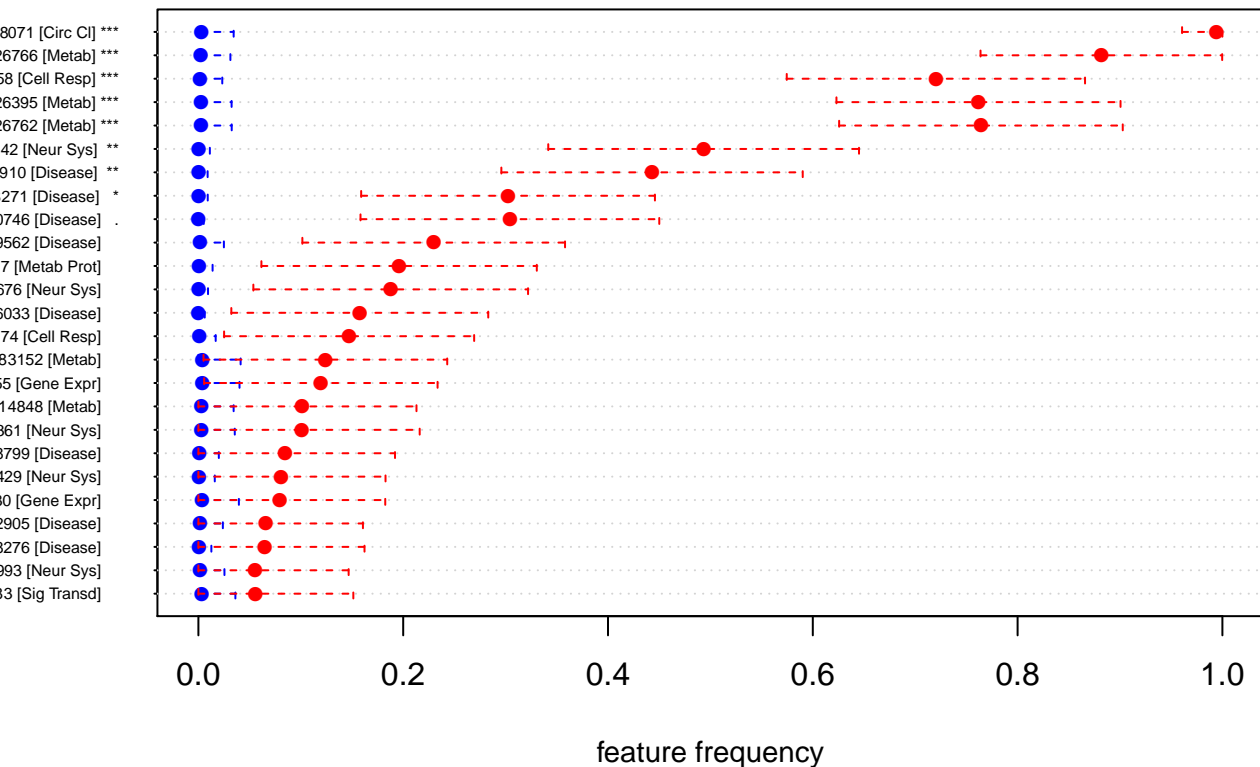
P-value significance codes: <0.001 (\*\*\*), <0.01 (\*\*), <0.05 (\*), <0.1 (.)



# Selected feature frequencies ranked by p-value for alpha=0.8

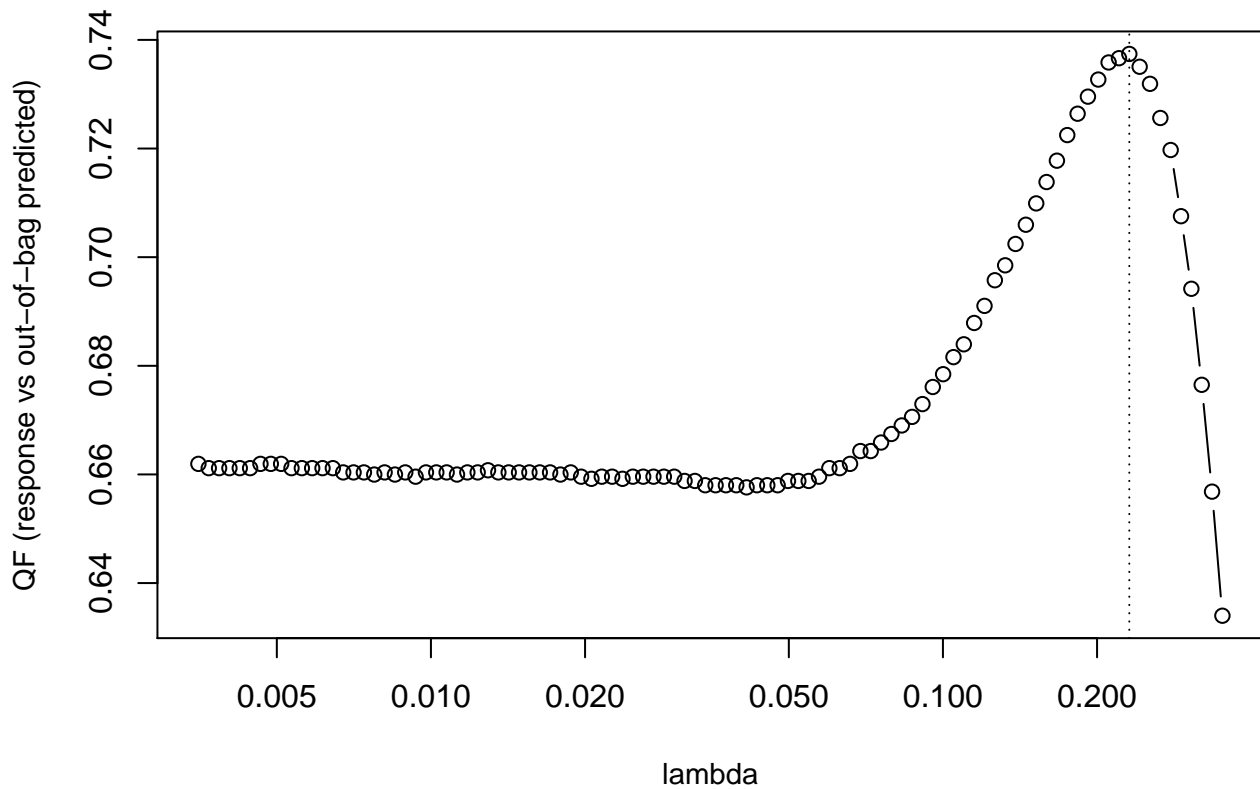
P-value significance codes: <0.001 (\*\*\*), <0.01 (\*\*), <0.05 (\*), <0.1 (.)

● model  
● null



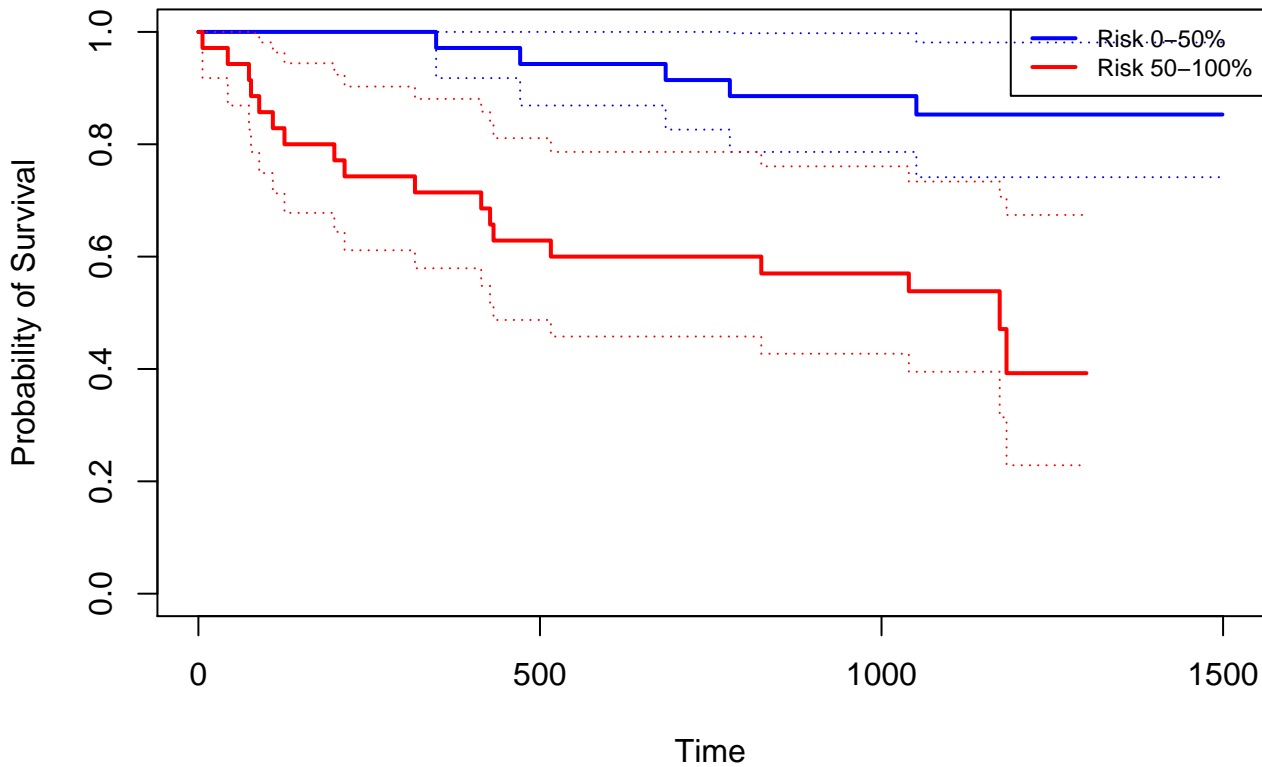


**alpha=0.9 ; QF=concordance index**





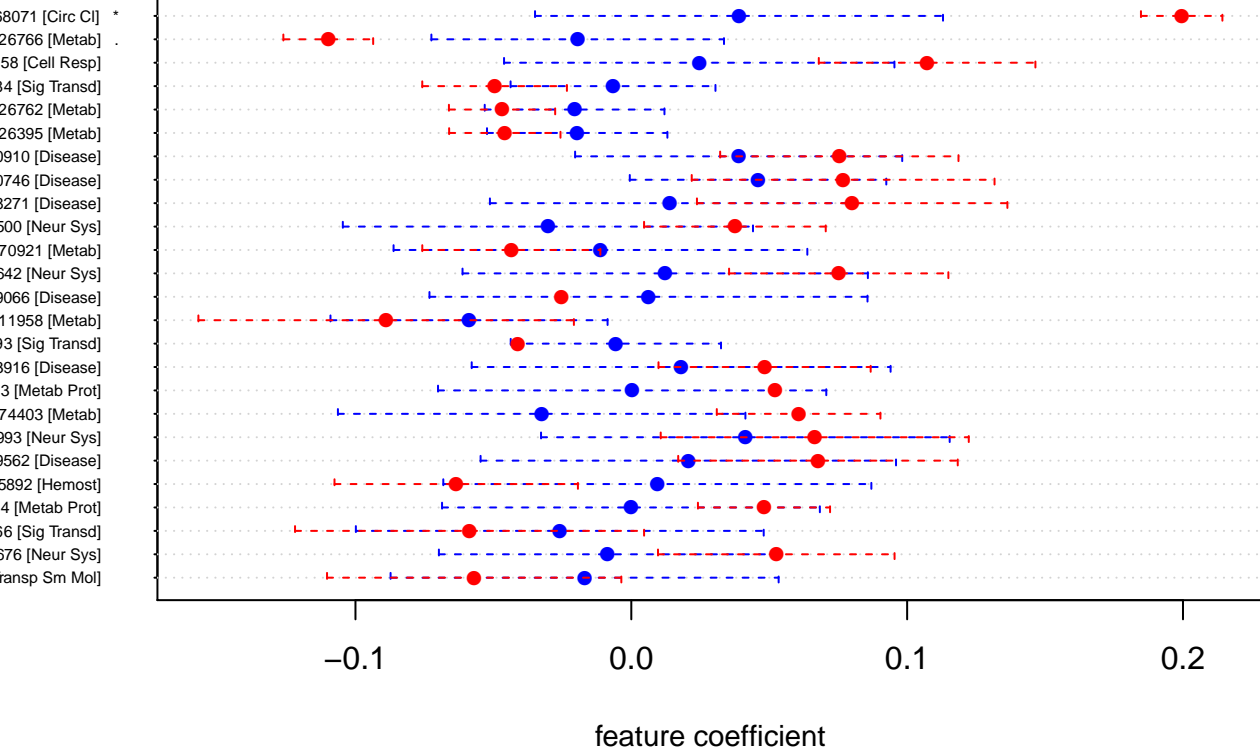
**alpha=0.9**

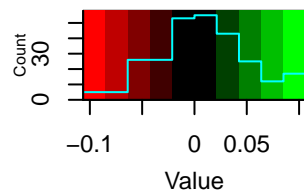


# Selected feature coefficients ranked by p-value for alpha=0.9

P-value significance codes: <0.001 (\*\*\*), <0.01 (\*\*), <0.05 (\*), <0.1 (.)

● model  
● null

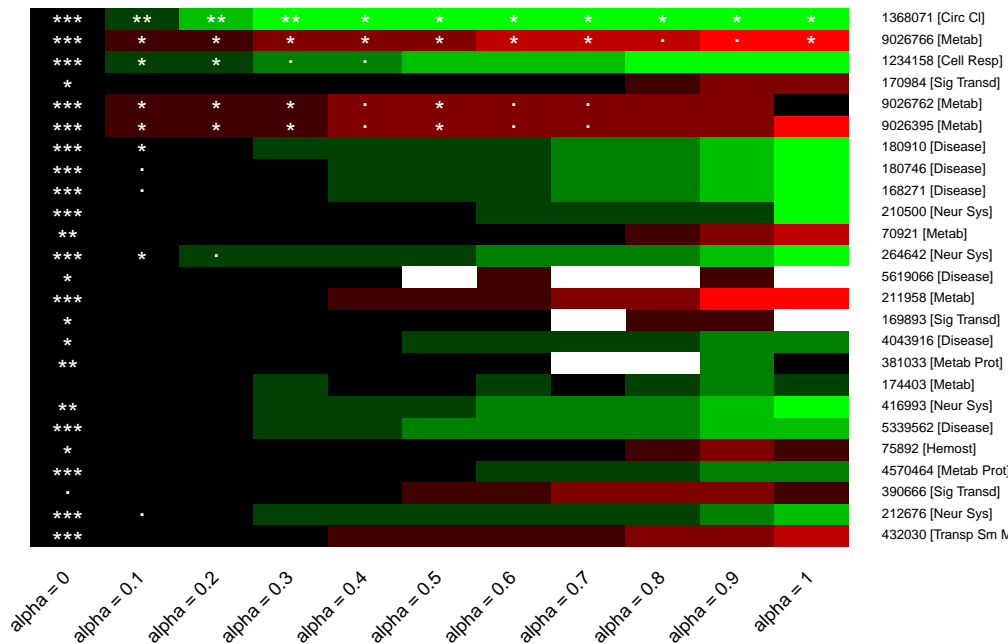




## Selected feature coefficients

### Features ranked by p-value for alpha=0.9

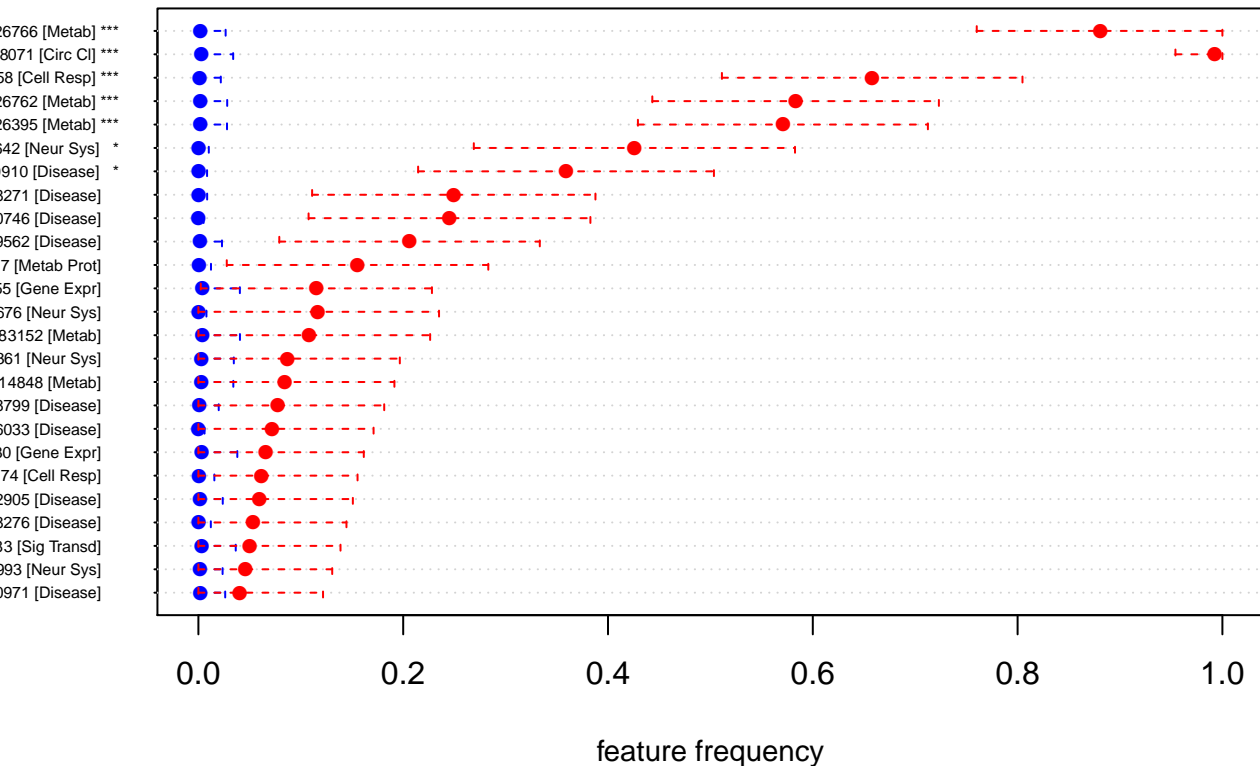
P-value significance codes: <0.001 (\*\*\*), <0.01 (\*\*), <0.05 (\*), <0.1 (.)



# Selected feature frequencies ranked by p-value for alpha=0.9

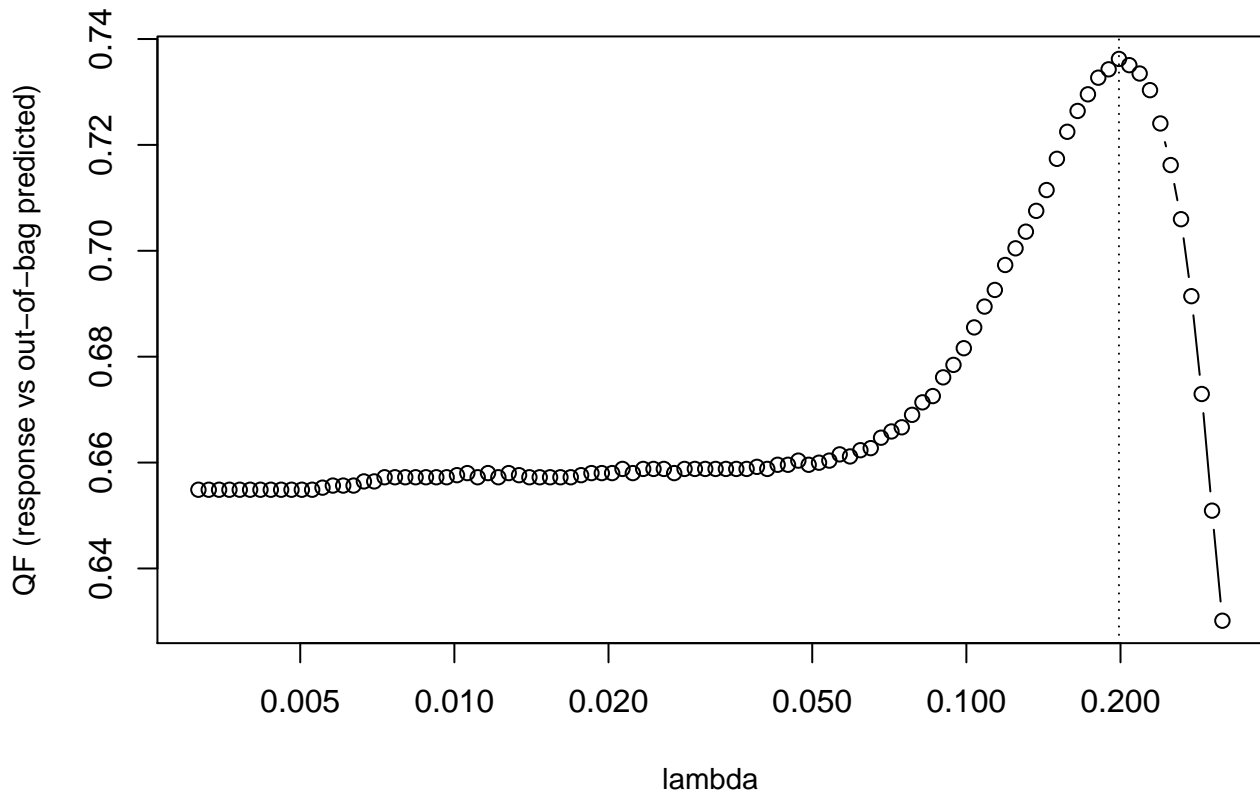
P-value significance codes: <0.001 (\*\*\*), <0.01 (\*\*), <0.05 (\*), <0.1 (.)

● model  
● null

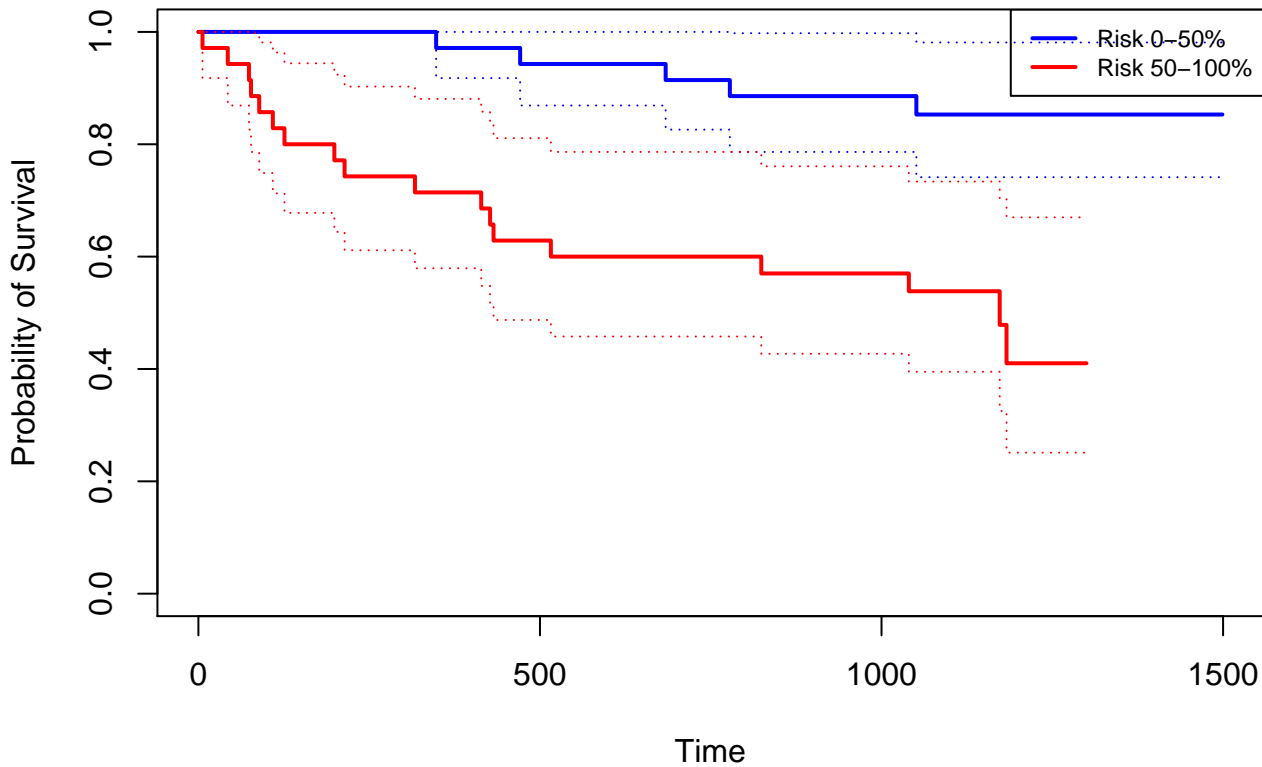




**alpha=1 ; QF=concordance index**



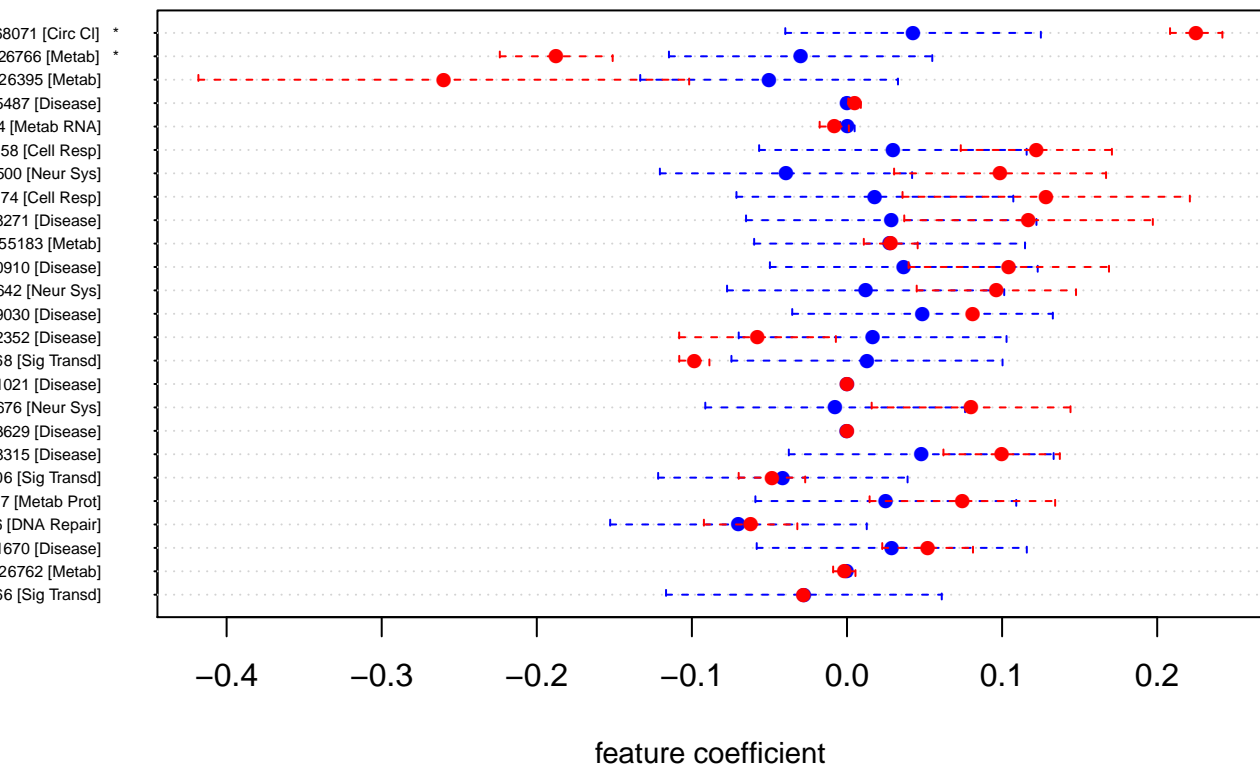
**alpha=1**



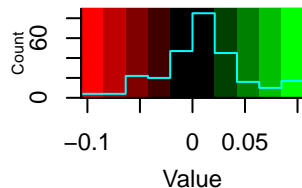
# Selected feature coefficients ranked by p-value for alpha=1

P-value significance codes: <0.001 (\*\*\*), <0.01 (\*\*), <0.05 (\*), <0.1 (.)

● model  
● null



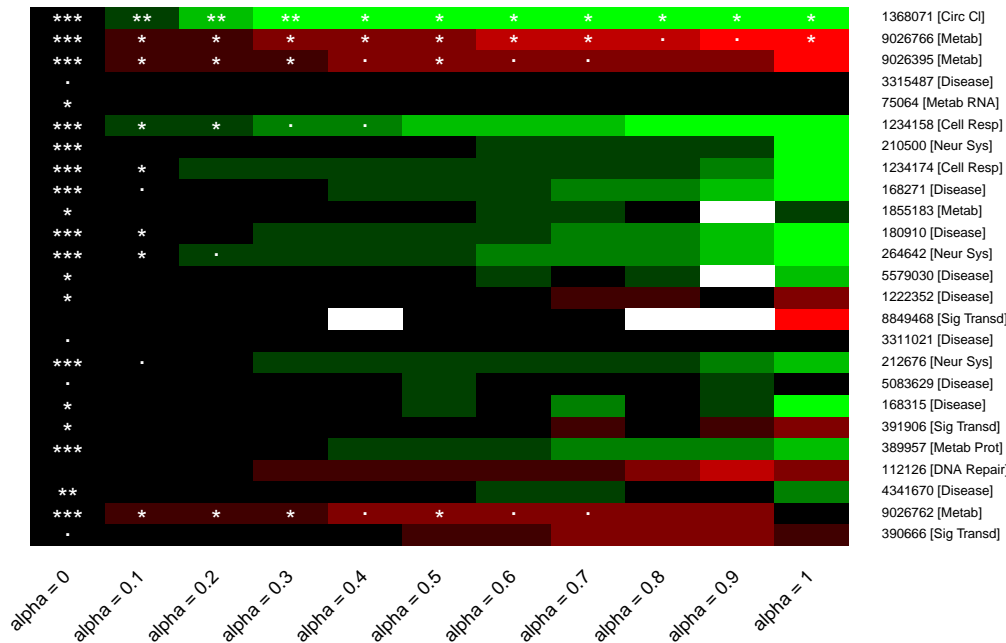




## Selected feature coefficients

### Features ranked by p-value for alpha=1

P-value significance codes: <0.001 (\*\*\*), <0.01 (\*\*), <0.05 (\*), <0.1 (.)



# Selected feature frequencies ranked by p-value for alpha=1

P-value significance codes: <0.001 (\*\*\*), <0.01 (\*\*), <0.05 (\*), <0.1 (.)

● model  
● null

