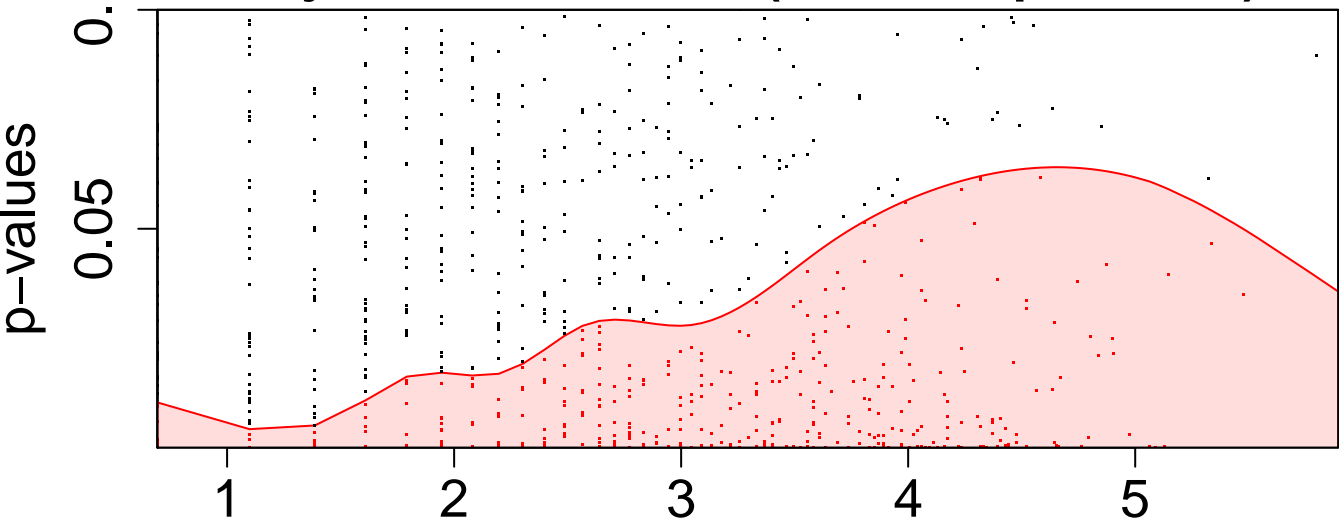
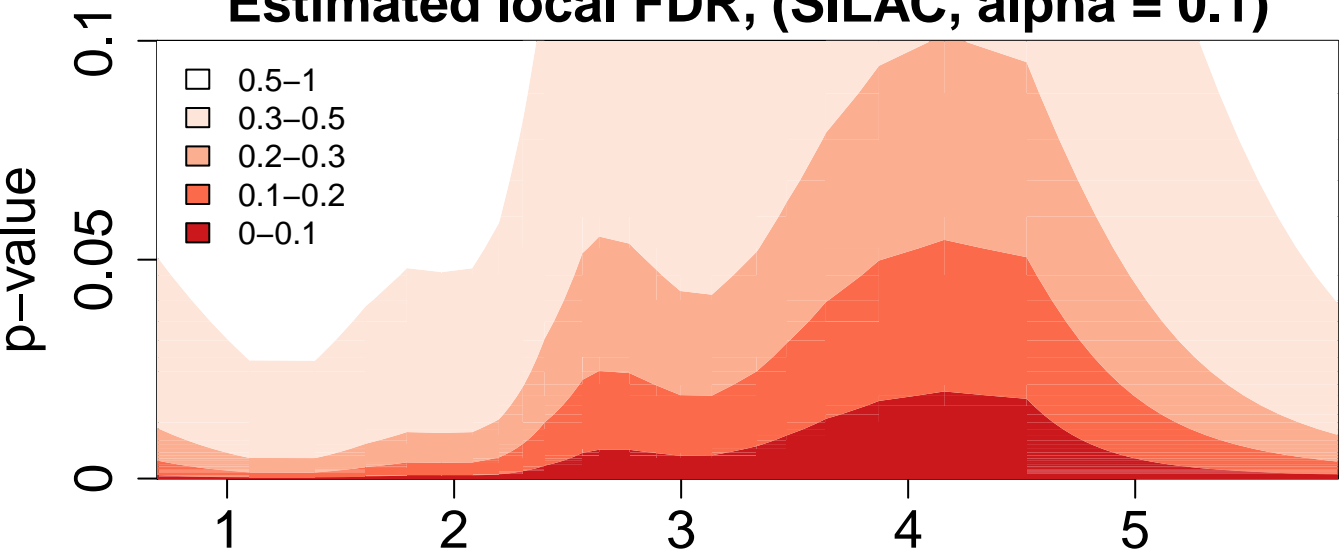


Rejection threshold, (SILAC, $\alpha = 0.1$)



$x = \log(\text{number of peptides})$

Estimated local FDR, (SILAC, $\alpha = 0.1$)



$x = \log(\text{number of peptides})$