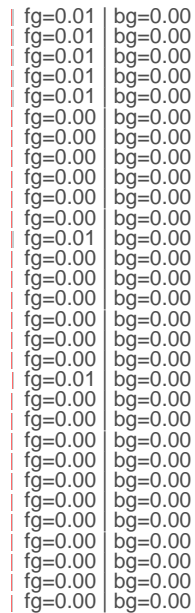


**fraction genes in fg and bg**



$-\log_{10}(p)$   
n=322/316 input genes with annotations