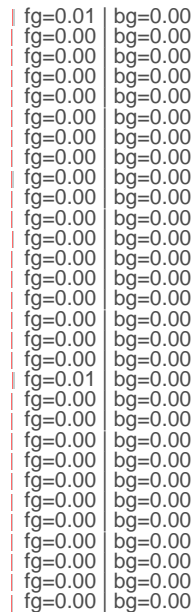


**fraction genes in fg and bg**



-log<sub>10</sub>(p)  
n=377/320 input genes with annotations