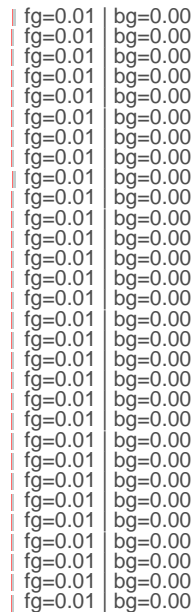


### **fraction genes in fg and bg**



$-\log_{10}(p)$   
n=169/150 input genes with annotations