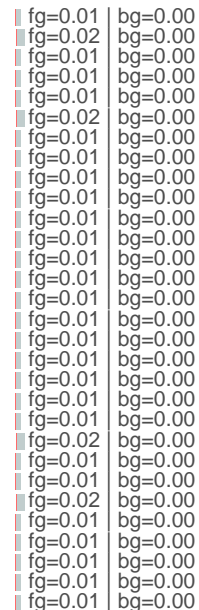


### **fraction genes in fg and bg**



-log10(p)  
n=78/73 input genes with annotations