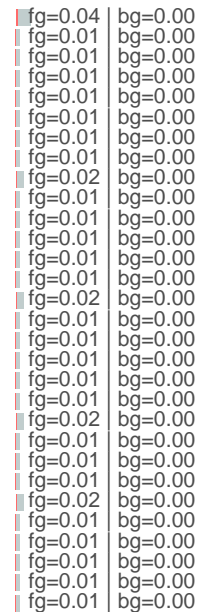


### **fraction genes in fg and bg**



-log<sub>10</sub>(p)  
n=83/70 input genes with annotations