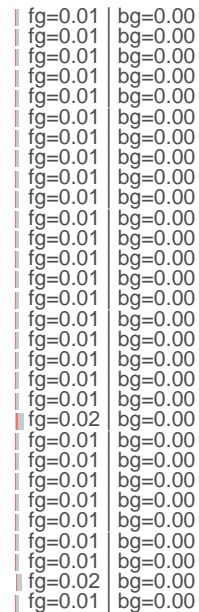


### **fraction genes in fg and bg**



–log<sub>10</sub>(p)  
n=115/95 input genes with annotations