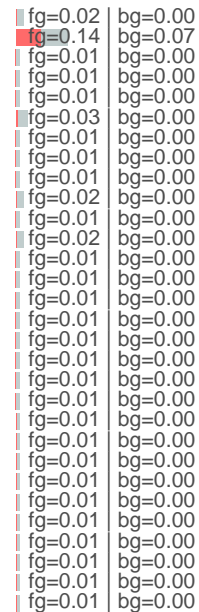


### **fraction genes in fg and bg**



fraction

n=66/70 input genes with annotations