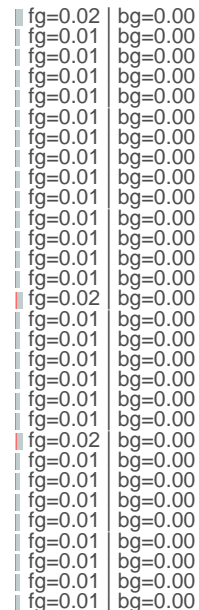


### **fraction genes in fg and bg**



fraction

n=87/120 input genes with annotations