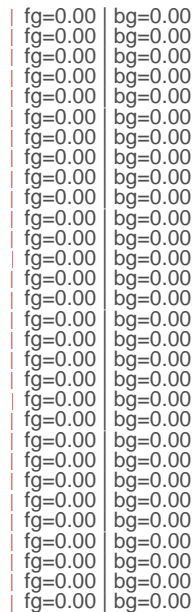


### **fraction genes in fg and bg**



fraction

n=797/854 input genes with annotations