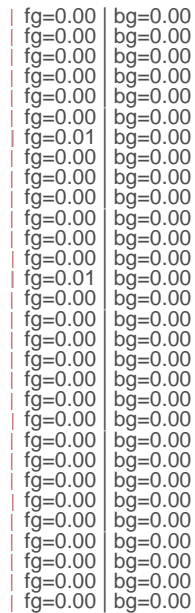


### **fraction genes in fg and bg**



fraction

n=394/346 input genes with annotations