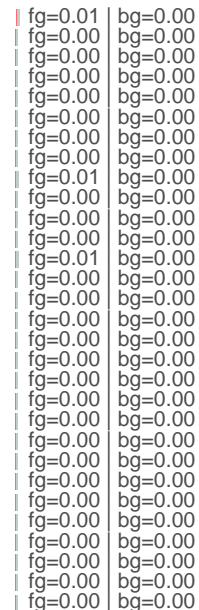


### **fraction genes in fg and bg**



fraction

n=252/198 input genes with annotations