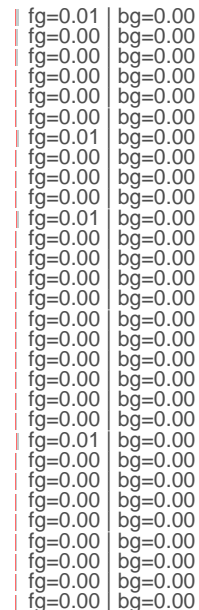


### **fraction genes in fg and bg**



fraction

n=332/274 input genes with annotations