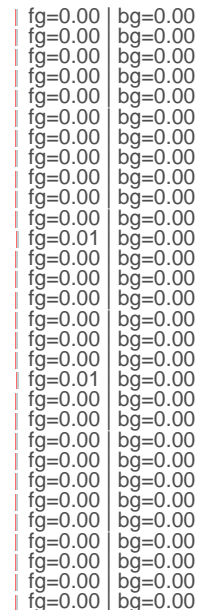


### **fraction genes in fg and bg**



fraction

n=229/181 input genes with annotations