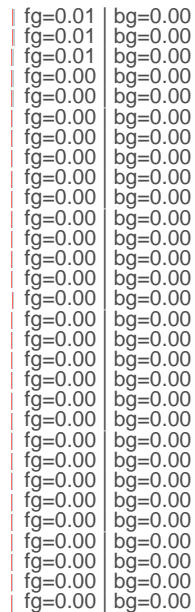


### **fraction genes in fg and bg**



fraction

n=387/375 input genes with annotations