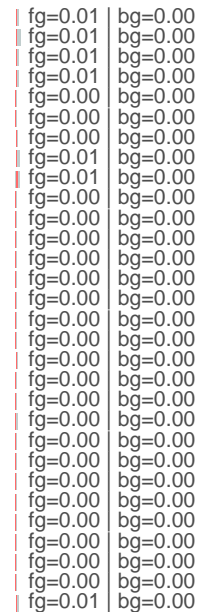


### **fraction genes in fg and bg**



fraction

n=319/314 input genes with annotations