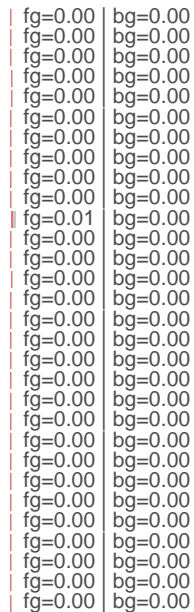


### **fraction genes in fg and bg**



fraction

n=344/314 input genes with annotations