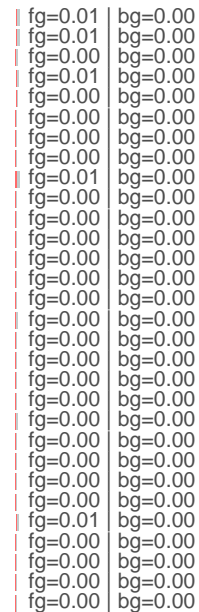


### **fraction genes in fg and bg**



fraction

n=324/290 input genes with annotations