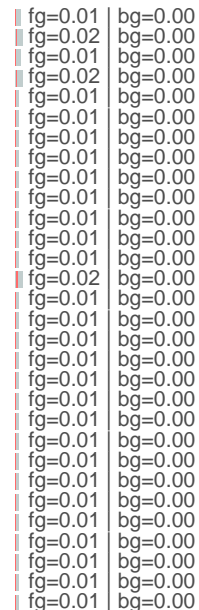


### **fraction genes in fg and bg**



fraction

n=132/91 input genes with annotations