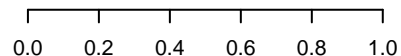
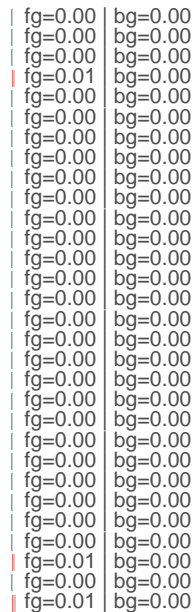


### **fraction genes in fg and bg**



fraction

n=268/228 input genes with annotations