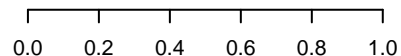
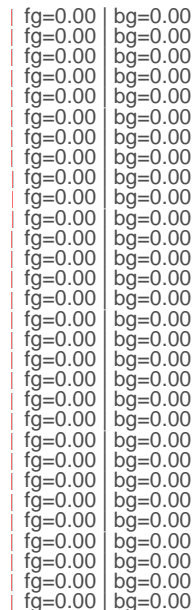


### **fraction genes in fg and bg**



fraction

n=1251/1433 input genes with annotations