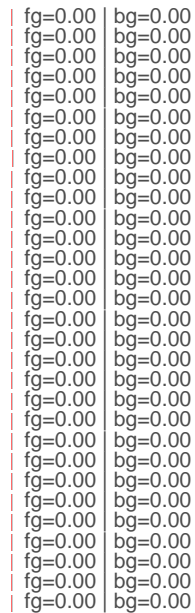


### **fraction genes in fg and bg**



fraction

n=1150/1300 input genes with annotations