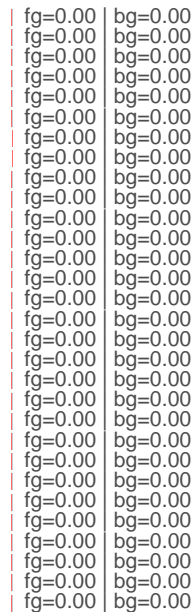


### **fraction genes in fg and bg**



fraction

n=1024/983 input genes with annotations