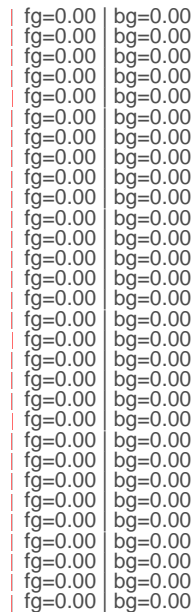


### **fraction genes in fg and bg**



fraction

n=799/796 input genes with annotations