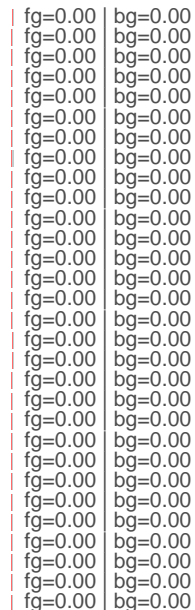


### **fraction genes in fg and bg**



fraction

n=385/350 input genes with annotations