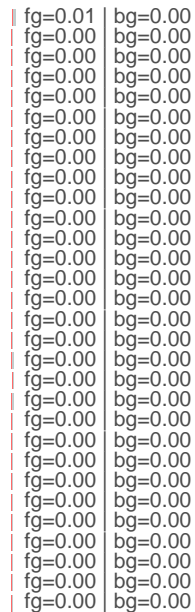


### **fraction genes in fg and bg**



fraction

n=385/354 input genes with annotations