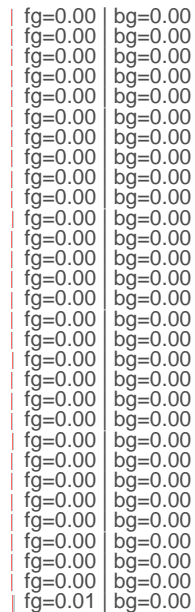


### **fraction genes in fg and bg**



fraction

n=340/322 input genes with annotations