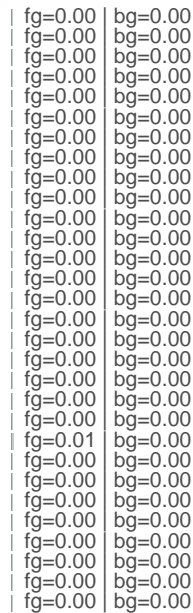


### **fraction genes in fg and bg**



fraction

n=261/238 input genes with annotations