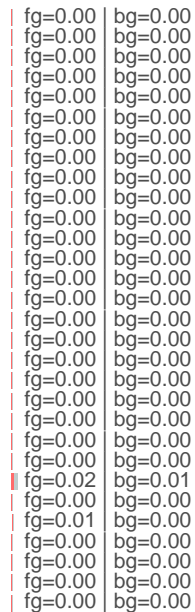


### **fraction genes in fg and bg**



fraction

n=307/259 input genes with annotations