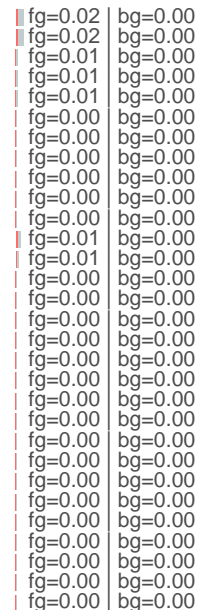


### **fraction genes in fg and bg**



fraction

n=271/286 input genes with annotations