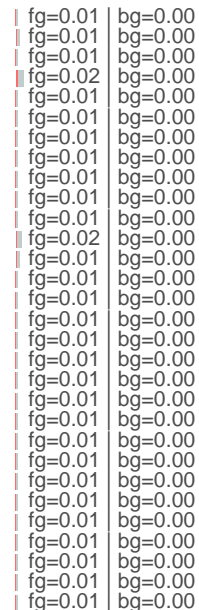


### **fraction genes in fg and bg**



fraction

n=149/148 input genes with annotations