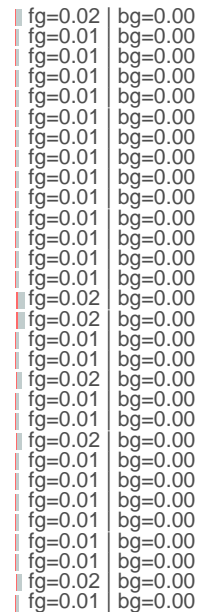


### **fraction genes in fg and bg**



fraction

n=102/96 input genes with annotations