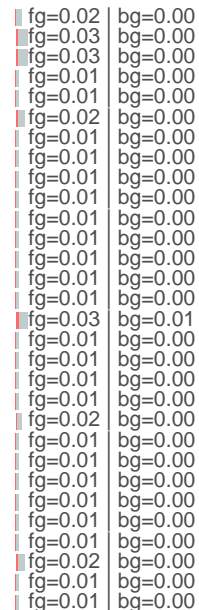


### **fraction genes in fg and bg**



fraction

n=101/99 input genes with annotations