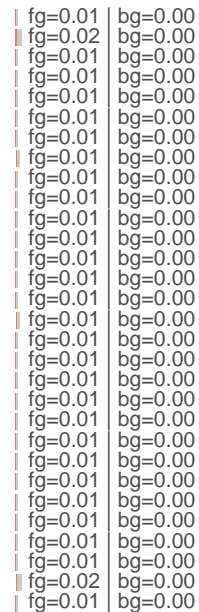


### **fraction genes in fg and bg**



fraction

n=160/125 input genes with annotations