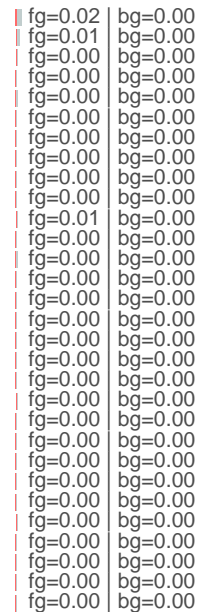


### **fraction genes in fg and bg**



fraction

n=390/387 input genes with annotations