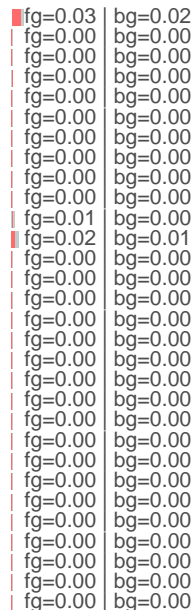


### **fraction genes in fg and bg**



fraction

n=489/512 input genes with annotations