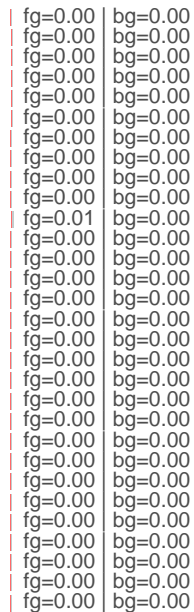


### **fraction genes in fg and bg**



fraction

n=580/483 input genes with annotations