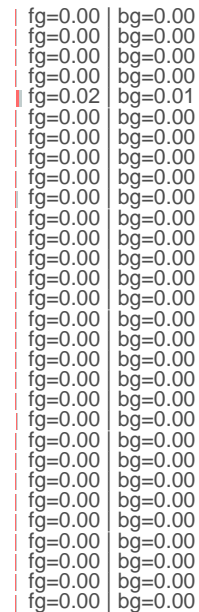


### **fraction genes in fg and bg**



fraction

n=381/310 input genes with annotations