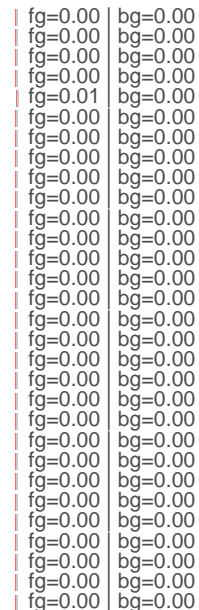


### **fraction genes in fg and bg**



fraction

n=200/178 input genes with annotations