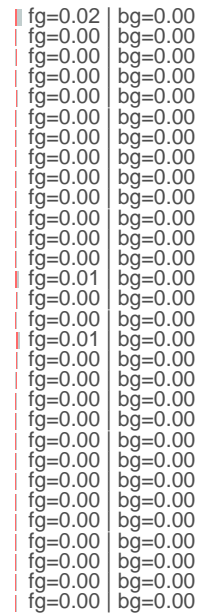


### **fraction genes in fg and bg**



fraction

n=439/468 input genes with annotations