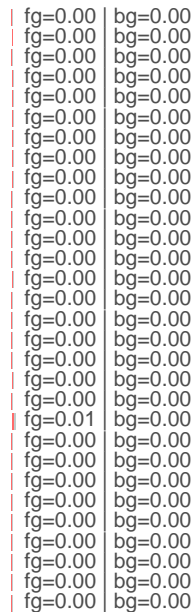


### **fraction genes in fg and bg**



fraction

n=552/570 input genes with annotations