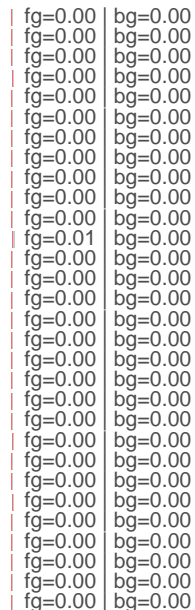


### **fraction genes in fg and bg**



fraction

n=573/542 input genes with annotations