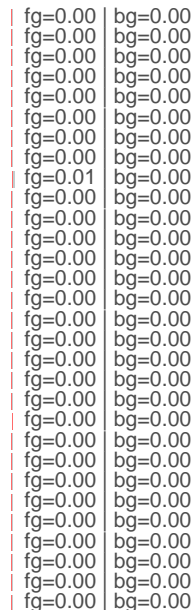


### **fraction genes in fg and bg**



fraction

n=574/530 input genes with annotations