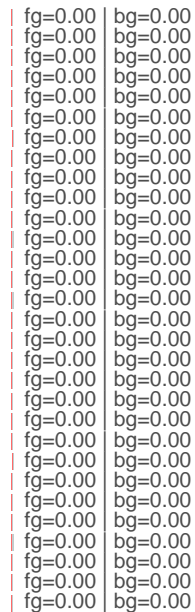


### **fraction genes in fg and bg**



fraction

n=430/385 input genes with annotations