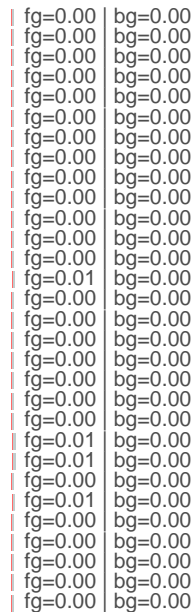


### **fraction genes in fg and bg**



fraction

n=216/190 input genes with annotations