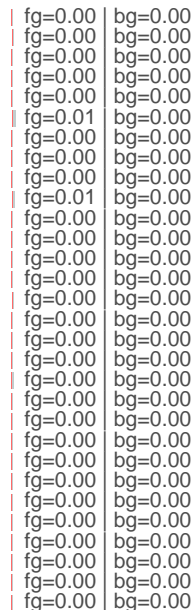


### **fraction genes in fg and bg**



fraction

n=314/294 input genes with annotations