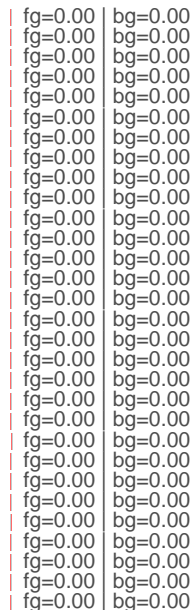


### **fraction genes in fg and bg**



fraction

n=459/437 input genes with annotations