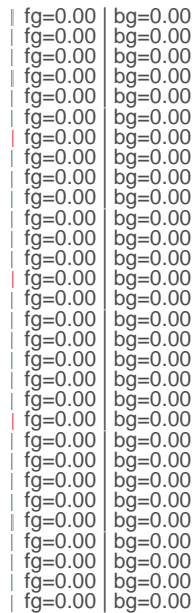


### **fraction genes in fg and bg**



fraction

n=361/348 input genes with annotations