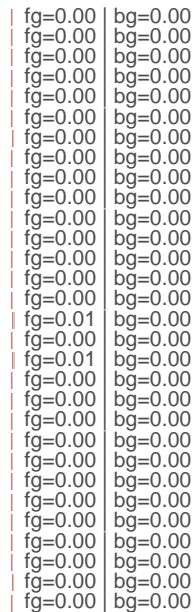


### **fraction genes in fg and bg**



fraction

n=360/312 input genes with annotations