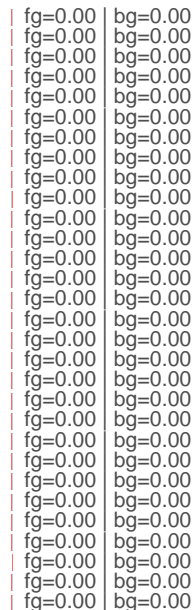


### **fraction genes in fg and bg**



fraction

n=699/679 input genes with annotations