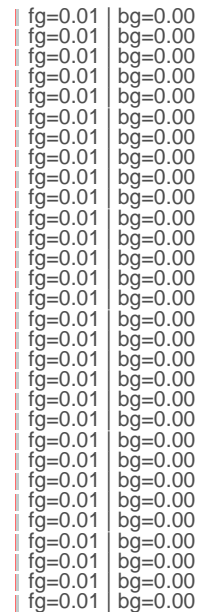


### **fraction genes in fg and bg**



fraction

n=106/90 input genes with annotations