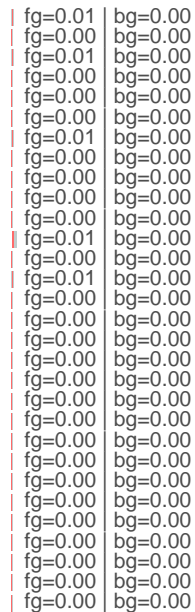


### **fraction genes in fg and bg**



fraction

n=380/346 input genes with annotations