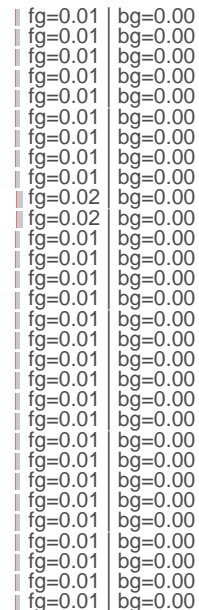


### **fraction genes in fg and bg**



fraction

n=165/219 input genes with annotations