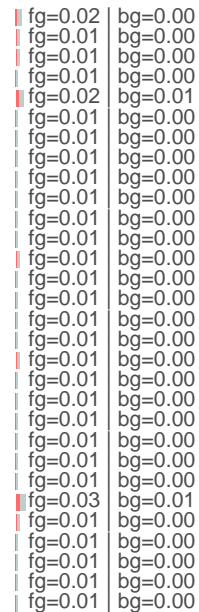


### **fraction genes in fg and bg**



fraction

n=138/133 input genes with annotations