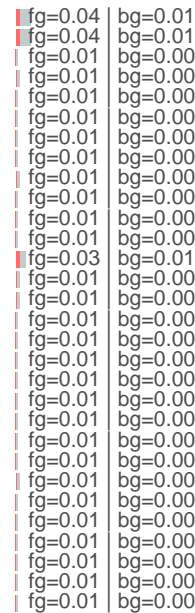


### **fraction genes in fg and bg**



fraction

n=137/135 input genes with annotations