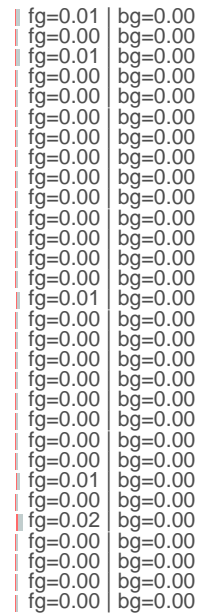


### **fraction genes in fg and bg**



fraction

n=172/163 input genes with annotations