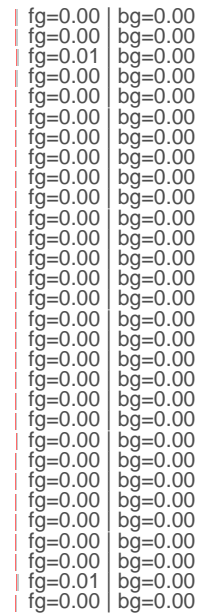


### **fraction genes in fg and bg**



fraction

n=321/303 input genes with annotations