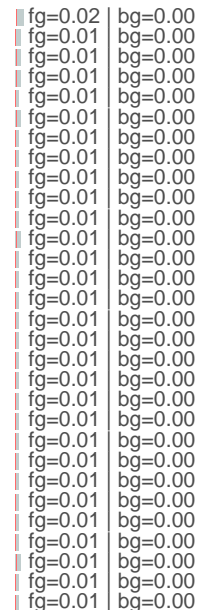


### **fraction genes in fg and bg**



–log<sub>10</sub>(p)  
n=116/85 input genes with annotations

fraction