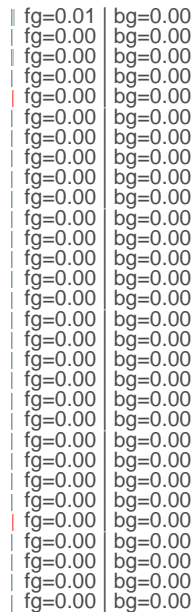


**fraction genes in fg and bg**



–log<sub>10</sub>(p)  
n=379/329 input genes with annotations