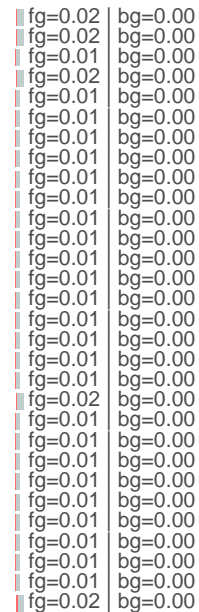


**fraction genes in fg and bg**



fraction

n=80/66 input genes with annotations