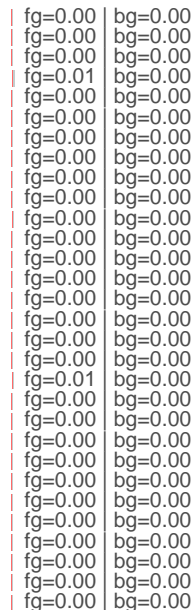


**fraction genes in fg and bg**



fraction

n=550/489 input genes with annotations