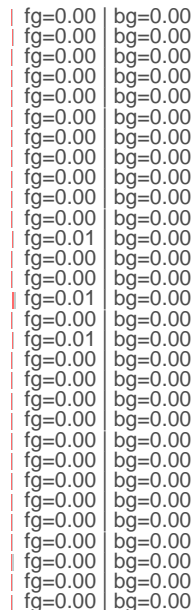


**fraction genes in fg and bg**



fraction

n=389/363 input genes with annotations