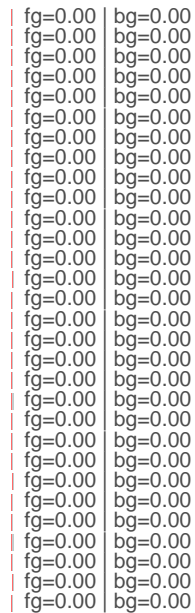


**fraction genes in fg and bg**



fraction

n=392/318 input genes with annotations