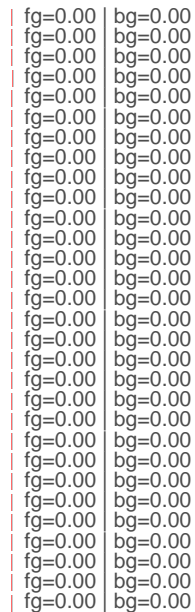


**fraction genes in fg and bg**



fraction

n=693/674 input genes with annotations