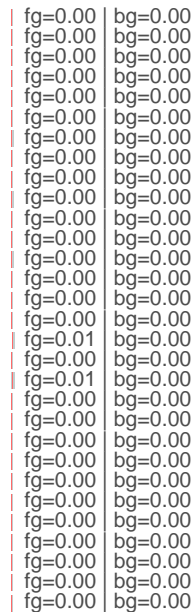


**fraction genes in fg and bg**



fraction

n=361/340 input genes with annotations