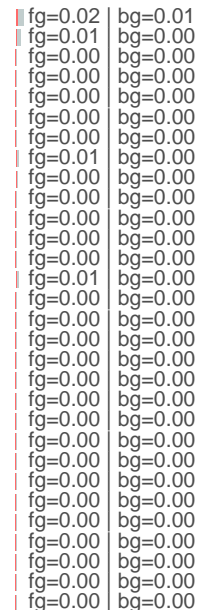


fraction genes in fg and bg



fraction

n=304/300 input genes with annotations