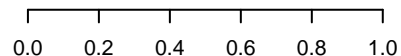
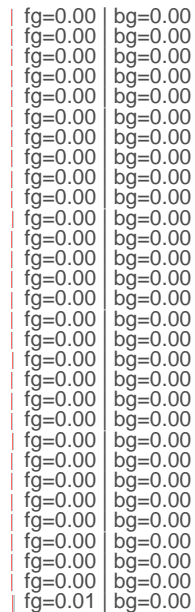


fraction genes in fg and bg



fraction

n=340/322 input genes with annotations