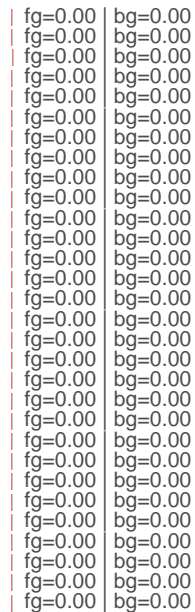


fraction genes in fg and bg



-log₁₀(p)
n=710/679 input genes with annotations