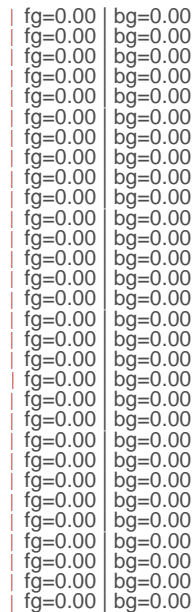


fraction genes in fg and bg



-log₁₀(p)
n=386/337 input genes with annotations