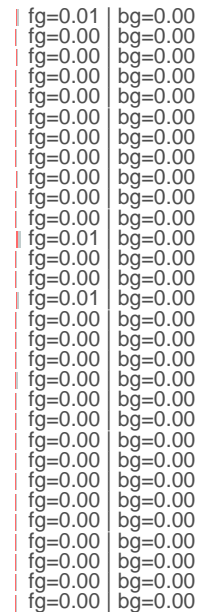


fraction genes in fg and bg



–log₁₀(p)
n=360/366 input genes with annotations