#Retrieve gene official symbol from entrez\_gene\_id

#Execute command line by line otherwise it will not work

#First we have to use bioconductor as bioclite

#First install the packages

source("https://bioconductor.org/biocLite.R")

biocLite("org.Hs.eg.db")

library(org.Hs.eg.db)

biocLite("annotate")

library(annotate)

# then set a vector

gene\_id <- c("7157" , "1956" , "7124" , "348" , "7422" , "3569" , "4524" , "7040" , "2064" , "2099" , "1636" , "3586" , "351" , "3091")

#Now we can extract two way by passing a vector

# First through lookup

lookUp(gene\_id, 'org.Hs.eg', 'SYMBOL')

#Second

getSYMBOL(gene\_id, data = "org.Hs.eg")