

Lab 04

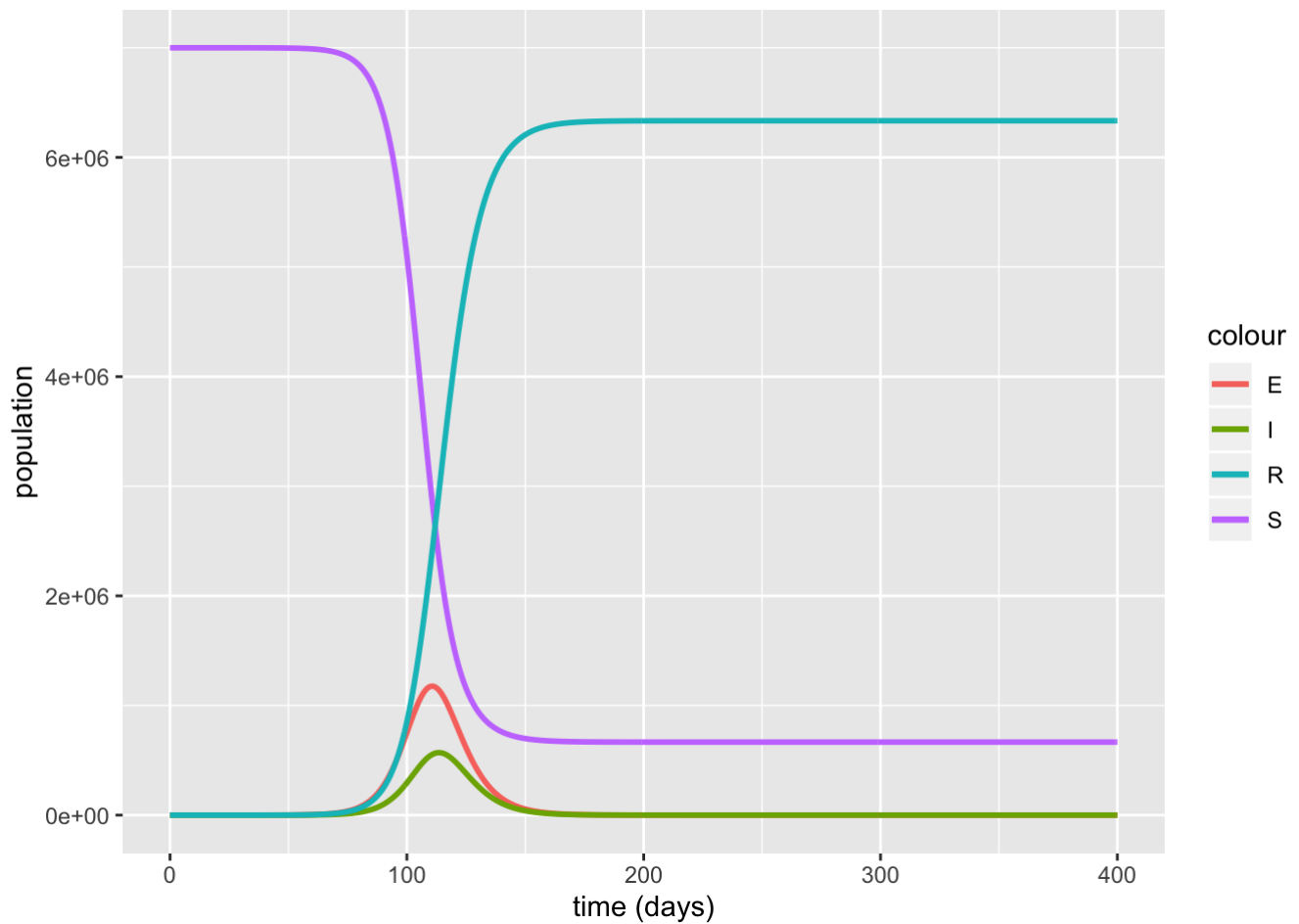
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1

Plot the results from the code that implements the model described above using the ggplot package instead of R's built-in plot function. Use this as an opportunity to acquaint yourself with the various parameters in this package.

```
library(deSolve)
library(ggplot2)
basicSIR <- function(time, state, parameters){
  with(as.list(c(state,parameters)),
    {
      dS <- -beta*S*I
      dE <- beta*S*I - alpha*E
      dI <- alpha*E - gamma*I
      dR <- gamma*I
      return(list(c(dS,dE,dI,dR)))
    })
}
time1 <- seq(from=0, to=400, by=1)
init_cond1 <- c(S=7000000-1, E=0, I=1, R=0)
parameters1 <- c(beta=0.0000001238, gamma=1/3, alpha=1/6)
# Ode
output1 <- ode(y=init_cond1, times=time1, func=basicSIR, parms=parameters1)
output1 <- as.data.frame(output1)
# Plot
ans1 <- ggplot(output1, aes(output1$time)) +
  geom_line(aes(y = output1$S, colour = "S"),lwd=1) +
  geom_line(aes(y = output1$E, colour = "E"),lwd=1) +
  geom_line(aes(y = output1$I, colour = "I"),lwd=1) +
  geom_line(aes(y = output1$R, colour = "R"),lwd=1) +
  xlab("time (days)") +
  ylab("population")
print(ans1)
```



2

Calculate the number of infected patients after 30 days

```
daysAfter <- output1$time[31]
infectedPatients <- output1$I[31]
ans2 <- paste0("The number of infected patients after ", daysAfter, " days is ", infectedPatients)
print(ans2)
```

```
## [1] "The number of infected patients after 30 days is 25.4823441279004"
```

3

How many people must be vaccinated to stop the infection?

```

# Vaccinated rate = delta
# Vaccinated people = V
vaccinatedSIR <- function(time, state, parameters){
  with(as.list(c(state,parameters)),
    {
      dS <- -beta*S*I - delta*S
      dE <- beta*S*I - alpha*E
      dI <- alpha*E - gamma*I
      dR <- gamma*I
      dV <- delta*S
      return(list(c(dS,dE,dI,dR,dV)))
    })
}

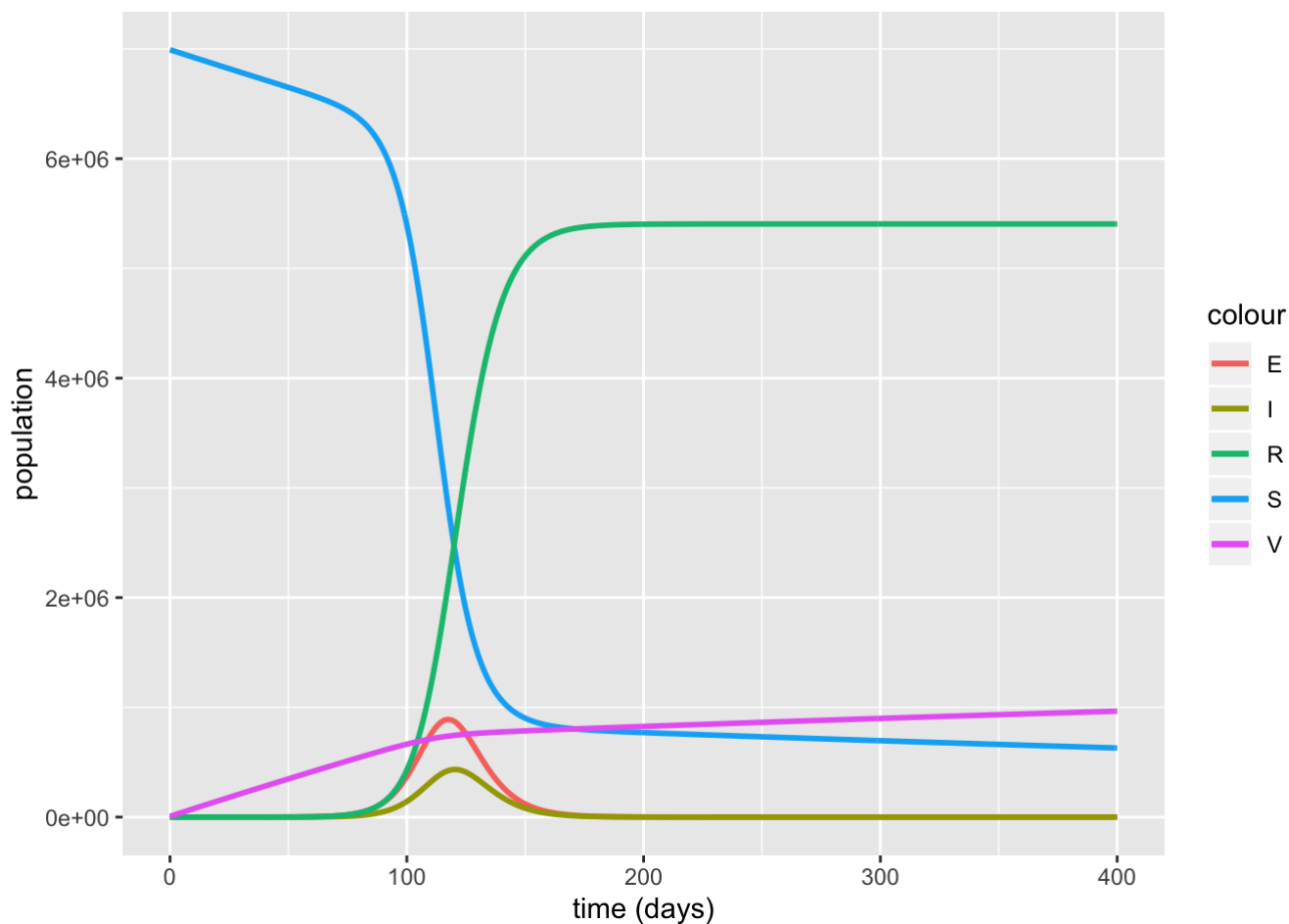
```

try delta = 1/1000

```

time3_1 <- seq(from=0, to=400, by=1)
init_cond3_1 <- c(S=7000000-1-7000, E=0, I=1, R=0, V=7000)
parameters3_1 <- c(beta=0.0000001238, gamma=1/3, alpha=1/6, delta=1/1000)
# Ode
output3_1 <- ode(y=init_cond3_1, times=time3_1, func=vaccinatedSIR, parms=parameters3_1)
output3_1 <- as.data.frame(output3_1)
# Plot
ans3_1 <- ggplot(output3_1, aes(output3_1$time)) +
  geom_line(aes(y = output3_1$S, colour = "S"),lwd=1) +
  geom_line(aes(y = output3_1$E, colour = "E"),lwd=1) +
  geom_line(aes(y = output3_1$I, colour = "I"),lwd=1) +
  geom_line(aes(y = output3_1$R, colour = "R"),lwd=1) +
  geom_line(aes(y = output3_1$V, colour = "V"),lwd=1) +
  xlab("time (days)") +
  ylab("population")
print(ans3_1)

```



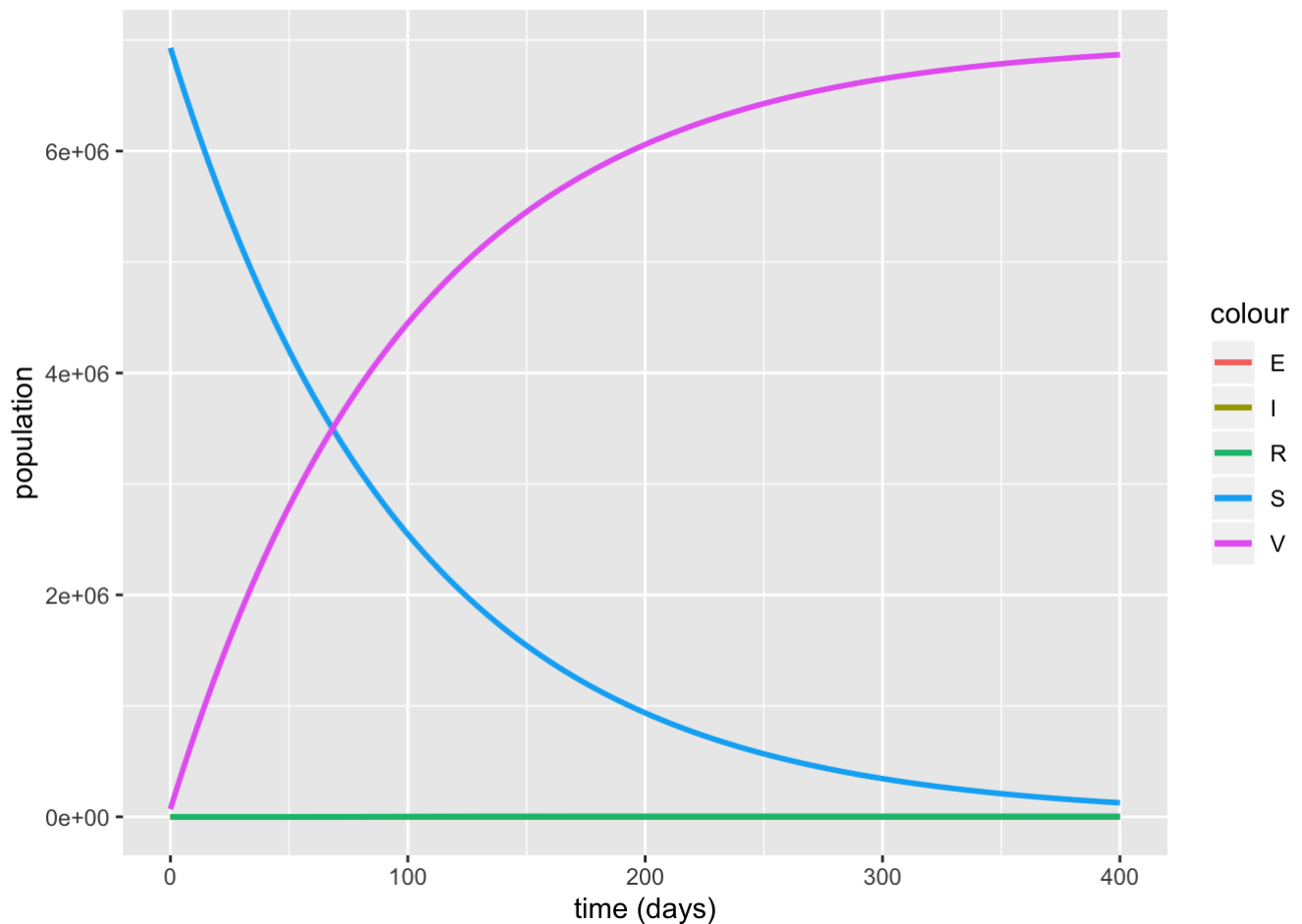
```
print(paste0("Maximum I: ", max(output3_1$I)))
```

```
## [1] "Maximum I: 433663.855608238"
```

There is still disease outbreak as we can see there is a peak of I around 120 days. Thus, we need to try bigger delta(vaccinated rate).

try delta = 1/100

```
time3_2 <- seq(from=0, to=400, by=1)
init_cond3_2 <- c(S=7000000-1-70000, E=0, I=1, R=0, V=70000)
parameters3_2 <- c(beta=0.0000001238, gamma=1/3, alpha=1/6, delta=1/100)
# Ode
output3_2 <- ode(y=init_cond3_2, times=time3_2, func=vaccinatedSIR, parms=parameters3_2)
output3_2 <- as.data.frame(output3_2)
# Plot
ans3_2 <- ggplot(output3_2, aes(output3_2$time)) +
  geom_line(aes(y = output3_2$S, colour = "S"), lwd=1) +
  geom_line(aes(y = output3_2$E, colour = "E"), lwd=1) +
  geom_line(aes(y = output3_2$I, colour = "I"), lwd=1) +
  geom_line(aes(y = output3_2$R, colour = "R"), lwd=1) +
  geom_line(aes(y = output3_2$V, colour = "V"), lwd=1) +
  xlab("time (days)") +
  ylab("population")
print(ans3_2)
```



```
print(paste0("Maximum I: ", max(output3_2$I)))
```

```
## [1] "Maximum I: 184.02599692293"
```

Although in the plot, there is no peak of line I in this scale of plot, there is actually disease outbreak (around 184 people). Thus, we need to try bigger delta(vaccinated rate).

try delta = 1/100 ~ 10/100

```
max_I <- c()
keep <- 0
for(i in 1:10){
  V_i <- 7000000*i/100
  time3_3 <- seq(from=0, to=400, by=1)
  init_cond3_3 <- c(S=7000000-1-V_i, E=0, I=1, R=0, V=V_i)
  parameters3_3 <- c(beta=0.0000001238, gamma=1/3, alpha=1/6, delta=i/100)
  output3_3 <- as.data.frame(ode(y=init_cond3_3, times=time3_3, func=vaccinatedSIR, p
arms=parameters3_3))
  max_I[i] <- max(output3_3$I)
  if(max_I[i]<=1 & keep==0){
    keep <- i # Under this circumstance, the maximum infected population would be 1
person.
  }
}
print(max_I)
```

```
## [1] 184.025997 8.738754 3.141047 1.873255 1.367819 1.105026
## [7] 1.000000 1.000000 1.000000 1.000000
```

```
ans3 <- paste0("At least ", keep, "% of the population must be vaccinated to stop the
infection. (i.e. ", 7000000*keep/100, ")")
print(ans3)
```

```
## [1] "At least 7% of the population must be vaccinated to stop the infection. (i.e.
490000)"
```

4

Think about how to modify this model to be more realistic (e.g. account for births and deaths)

```
# We can add birth, natural death and diseased death to our model.
# Birth rate = br
# Birth = B
# Death rate (natural) = drN
# Death (natural) = DN
# Death rate (disease) = drD
# Death (disease) = DD
```

5

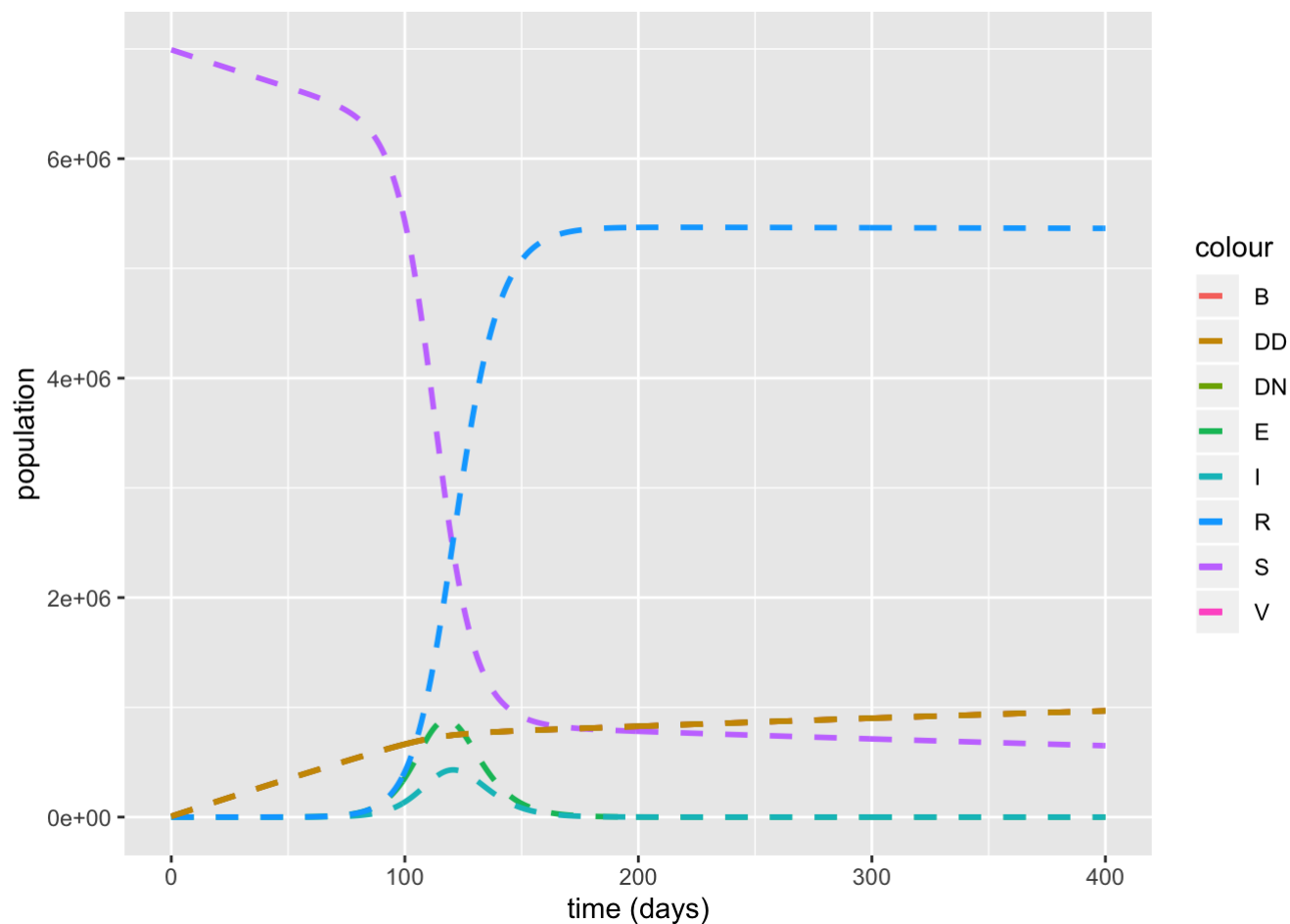
Alternate Assignment: Create your own model, implement it, plot the results and describe briefly the justification and assumptions of such model.

```

mySIR <- function(time, state, parameters){
  with(as.list(c(state,parameters)),
    {
      dS <- -beta*S*I - delta*S + br*(S+E+I+R+V)*(1-delta) - drN*S
      dE <- beta*S*I - alpha*E - drN*E
      dI <- alpha*E - gamma*I - drN*I - drD*I
      dR <- gamma*I - drN*R
      dV <- delta*S + br*(S+E+I+R+V)*delta - drN*V
      dB <- br*(S+E+I+R+V)
      dDN <- drN*S + drN*E + drN*I + drN*R + drN*V
      dDD <- drD*I
      return(list(c(dS,dE,dI,dR,dV,dB,dDN,dDD)))
    })
}

time5 <- seq(from=0, to=400, by=1)
init_cond5 <- c(S=7000000-1-7000, E=0, I=1, R=0, V=7000, B=0, DN=0, DD=0)
parameters5 <- c(beta=0.0000001238, gamma=1/3, alpha=1/6, delta=1/1000, br=0.00001, d
rN=0.00001, drD=0.001)
# Ode
output5 <- ode(y=init_cond5, times=time5, func=mySIR, parms=parameters5)
output5 <- as.data.frame(output5)
# Plot
ans5 <- ggplot(output5, aes(output5$time)) +
  geom_line(aes(y = output5$S, colour = "S"),lwd=1,linetype = "dashed") +
  geom_line(aes(y = output5$E, colour = "E"),lwd=1,linetype = "dashed") +
  geom_line(aes(y = output5$I, colour = "I"),lwd=1,linetype = "dashed") +
  geom_line(aes(y = output5$R, colour = "R"),lwd=1,linetype = "dashed") +
  geom_line(aes(y = output5$V, colour = "V"),lwd=1,linetype = "dashed") +
  geom_line(aes(y = output5$V, colour = "B"),lwd=1,linetype = "dashed") +
  geom_line(aes(y = output5$V, colour = "DN"),lwd=1,linetype = "dashed") +
  geom_line(aes(y = output5$V, colour = "DD"),lwd=1,linetype = "dashed") +
  xlab("time (days)") +
  ylab("population")
print(ans5)

```



```
# People in S, E, I, R, and V are all able to give birth.
# The birth of this population goes into either S(susceptible) or V(vaccinated).
# People in S, E, I, R, and V all might die naturally and become population DN.
# Infected population might die because of the disease.
# The rate of natural death is smaller than diseased death.
```