

## Simple Model for Vaccination

Vaccination can be a powerful way of controlling an epidemic. An epidemic can only continue if the infection is infectious enough for long enough, and there is an adequate pool of susceptibles to be infected. However, if more individuals in the population are vaccinated, the pool of susceptibles is reduced, decreasing the likelihood of the continuation of the epidemic. We will aim to represent vaccination in a simple way; we are assuming it has already happened before the model is run. We can change the initial condition to prepare the population so it has received a certain coverage of the vaccination. This is simplistic, but it will allow us to observe the fundamental effects of vaccination in infection dynamics.

We are starting with an infection rate  $\beta = 0.4 \text{ days}^{-1}$  and  $\gamma = 0.1 \text{ days}^{-1}$ . We will assume a proportion  $p$  of the population starts in the recovered compartment to represent those who have been vaccinated; we also assume the vaccine is perfectly effective, such that all those vaccinated have total immunity against the infection. We will model this scenario for a duration of 2 years, assume the vaccine coverage is 50%, and plot the prevalence in each compartment over time. We will use a population of 1,000,000.

We will begin developing our model.

```
library(deSolve)
library(reshape2)
library(ggplot2)

p <- 0.5
N <- 1000000
initial_number_susceptible <- (1-p) * (N - 1)
initial_number_infected <- 1
initial_number_recovered <- p * (N - 1)

initial_state_values <- c(S = initial_number_susceptible,
                          I = initial_number_infected,
                          R = initial_number_recovered)

times <- seq(from = 0, to = 2, by = 1/365)

parameters <- c(beta = 0.4 * 365, gamma = 0.1 * 365)
```

The differential equations we can use to describe the SIR model include:

$$\frac{dS}{dt} = -\lambda S \quad (1)$$

$$\frac{dI}{dt} = \lambda S - \gamma I \quad (2)$$

$$\frac{dR}{dt} = \gamma I \quad (3)$$

Where:

$$\lambda = \beta \frac{I}{N}$$

.

```

SIR_model <- function(time, state, parameters) {

  with(as.list(c(state, parameters)), {

    N = S + I + R

    lambda <- beta * I / N

    dS <- -lambda * S

    dI <- lambda * S - gamma * I

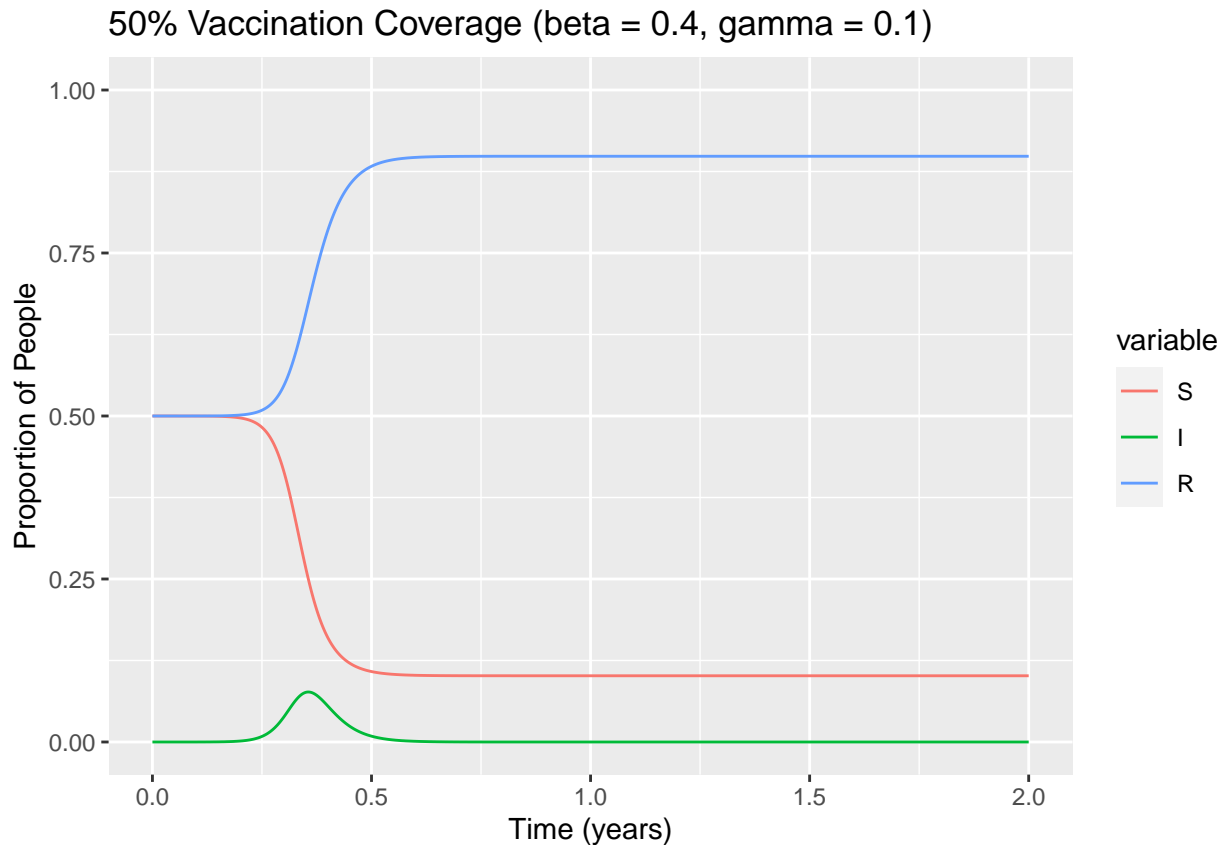
    dR <- gamma * I

    return(list(c(dS, dI, dR)))
  })
}

output1 <- as.data.frame(ode(y = initial_state_values,
                           times = times,
                           func = SIR_model,
                           parms = parameters))

output_long1 <- melt(as.data.frame(output1), id = "time")
output_long1$proportion <- output_long1$value/sum(initial_state_values)
ggplot(data = output_long1,
       aes(x = time, y = proportion, group=variable, color=variable)) +
  geom_line() +
  xlab("Time (years)") +
  ylab("Proportion of People") +
  labs(title = "50% Vaccination Coverage (beta = 0.4, gamma = 0.1)") +
  ylim(c(0,1))

```



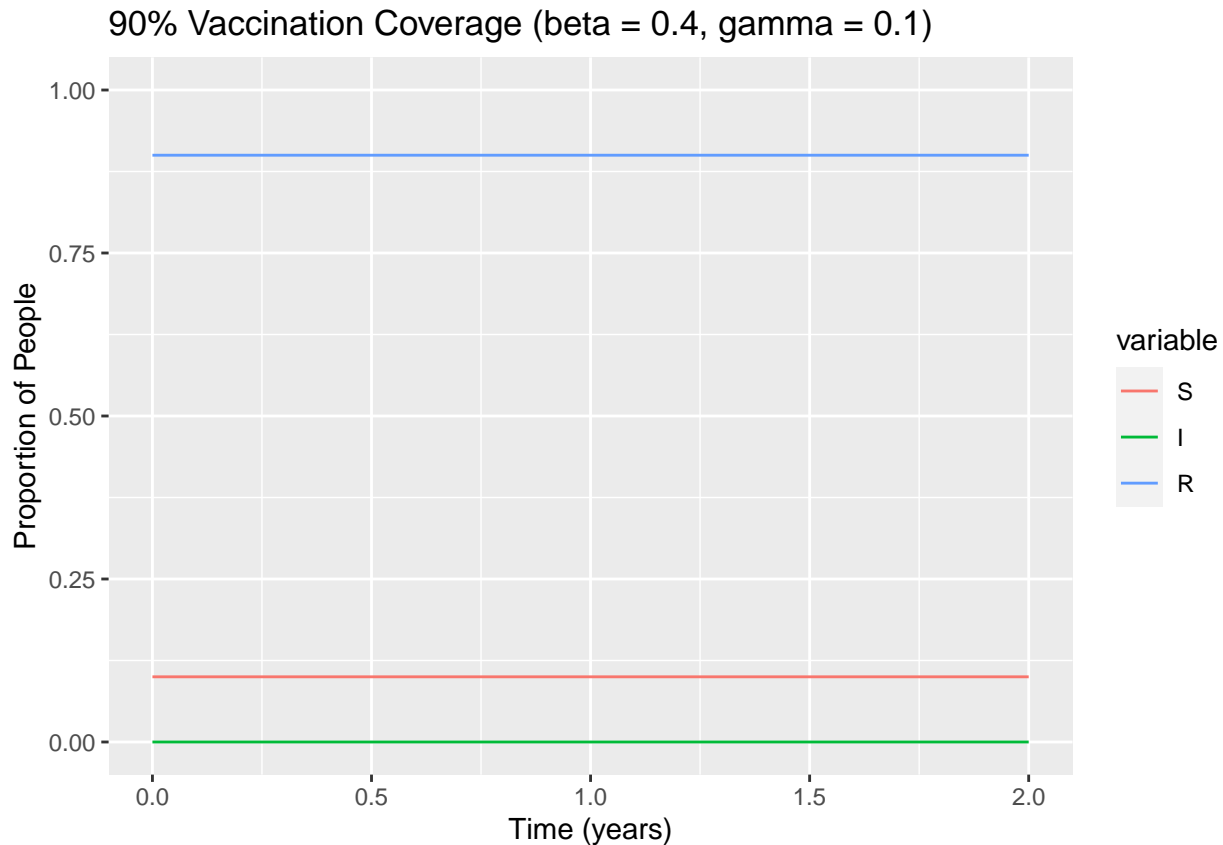
We see that the epidemic peaks at about 125 days after the introduction of an infectious person, and that only a small proportion of the population ends up infected. If we use a greater proportion of the population  $p = 0.9$ , we see no epidemic occurs:

```
p2 <- 0.9
initial_number_susceptible2 <- (1-p2) * (N - 1)
initial_number_infected2 <- 1
initial_number_recovered2 <- p2 * (N - 1)

initial_state_values2 <- c(S = initial_number_susceptible2,
                           I = initial_number_infected2,
                           R = initial_number_recovered2)

output2 <- as.data.frame(ode(y = initial_state_values2,
                           times = times,
                           func = SIR_model,
                           parms = parameters))

output_long2 <- melt(as.data.frame(output2), id = "time")
output_long2$proportion <- output_long2$value/sum(initial_state_values)
ggplot(data = output_long2,
       aes(x = time, y = proportion, group=variable, color=variable)) +
  geom_line() +
  xlab("Time (years)") +
  ylab("Proportion of People") +
  labs(title = "90% Vaccination Coverage ( $\beta = 0.4$ ,  $\gamma = 0.1$ )") +
  ylim(c(0,1))
```



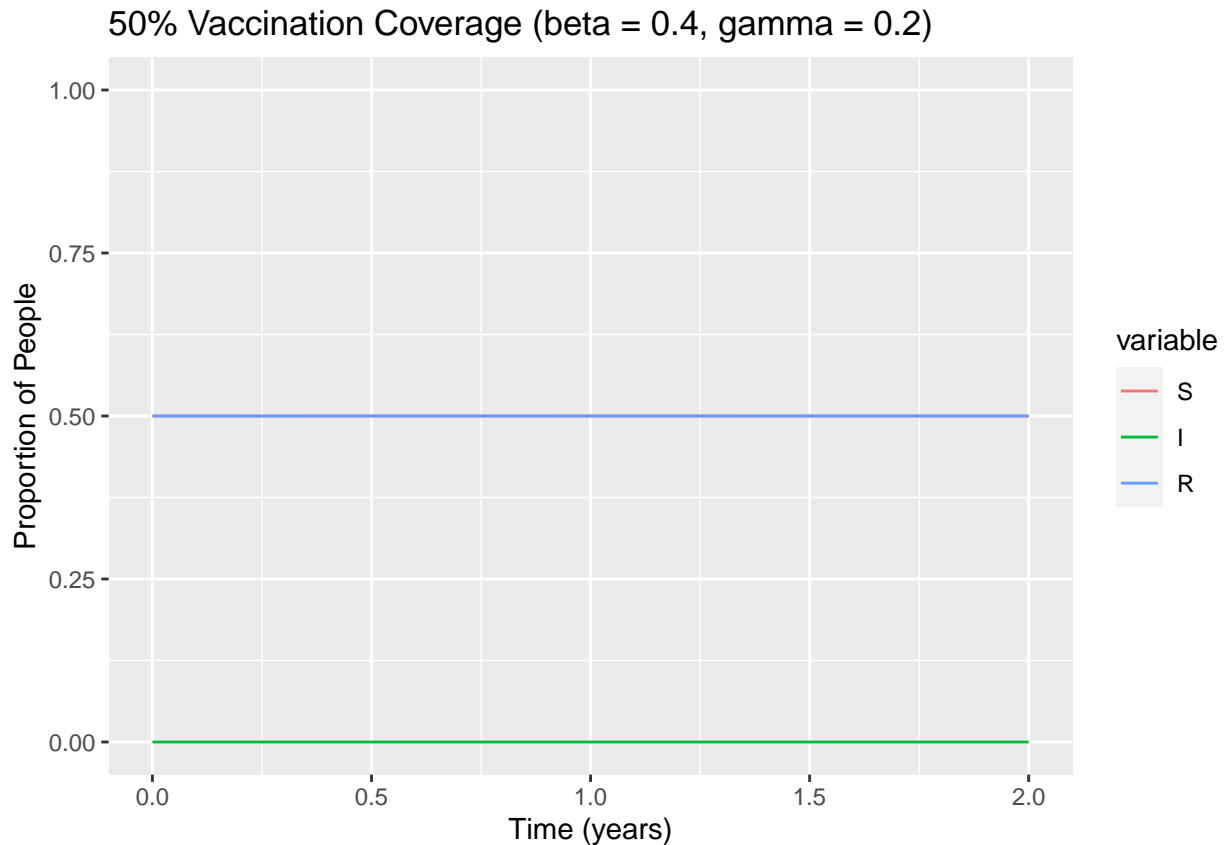
This suggests that once a certain population is immune, no epidemic can occur. This point is called the **critical vaccination threshold** or **herd immunity threshold**.

We can use our code to investigate how the herd immunity threshold changes if we are modeling a disease with a different recovery and infection rate. For example, what proportion of the population needs to be vaccinated in order to prevent an epidemic if  $\beta = 0.4 \text{ days}^{-1}$  and  $\gamma = 0.2 \text{ days}^{-1}$ ? We can use similar code above to model this scenario.

```
parameters3 <- c(beta = 0.4 * 365, gamma = 0.2 * 365)

output3 <- as.data.frame(ode(y = initial_state_values,
                             times = times,
                             func = SIR_model,
                             parms = parameters3))

output_long3 <- melt(as.data.frame(output3), id = "time")
output_long3$proportion <- output_long3$value/sum(initial_state_values)
ggplot(data = output_long3,
       aes(x = time, y = proportion, group=variable, color=variable)) +
  geom_line() +
  xlab("Time (years)") +
  ylab("Proportion of People") +
  labs(title = "50% Vaccination Coverage ( $\beta = 0.4$ ,  $\gamma = 0.2$ )") +
  ylim(c(0,1))
```



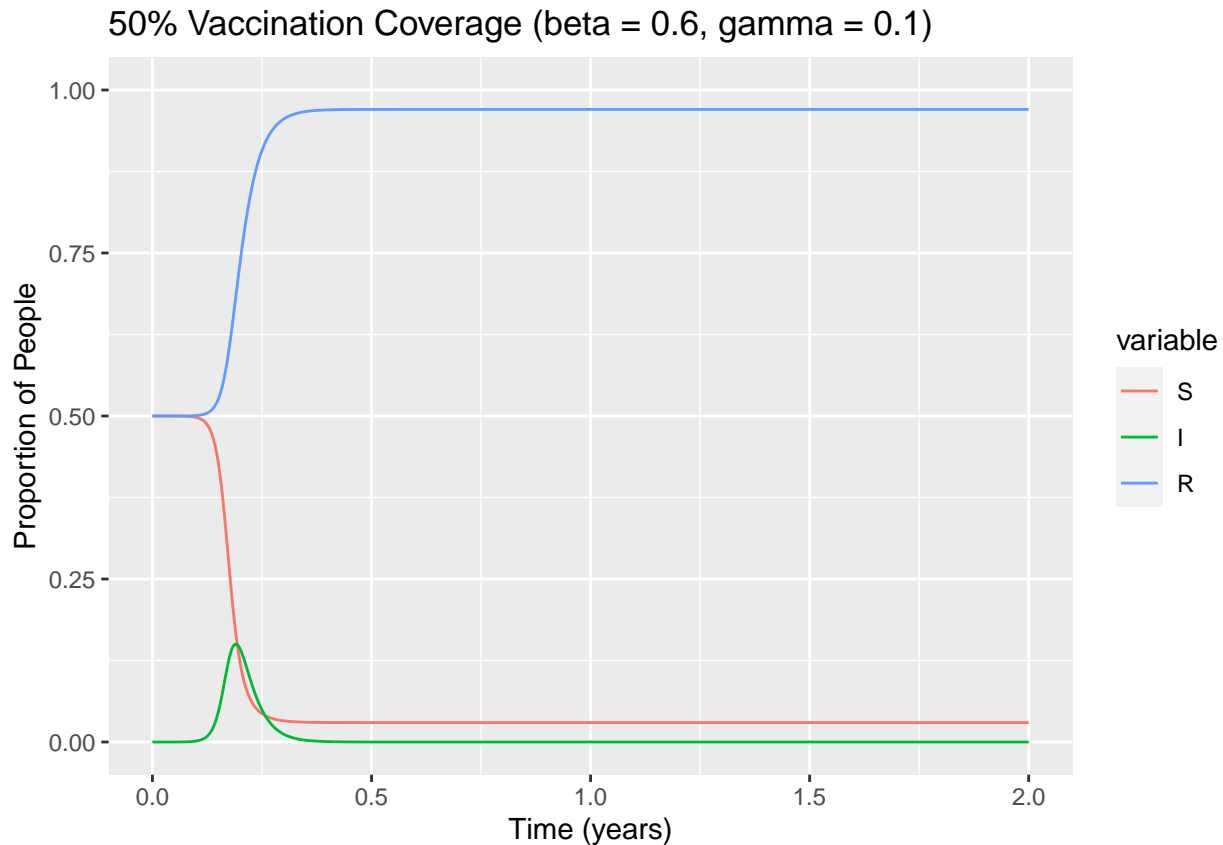
We see that when  $\beta = 0.4 \text{ days}^{-1}$  and  $\gamma = 0.2 \text{ days}^{-1}$  with a  $p$  of 0.5, no epidemic occurs.

What if  $\beta = 0.6 \text{ days}^{-1}$  and  $\gamma = 0.1 \text{ days}^{-1}$  with a  $p$  of 0.5?

```
parameters4 <- c(beta = 0.6 * 365, gamma = 0.1 * 365)

output4 <- as.data.frame(ode(y = initial_state_values,
                             times = times,
                             func = SIR_model,
                             parms = parameters4))

output_long4 <- melt(as.data.frame(output4), id = "time")
output_long4$proportion <- output_long4$value/sum(initial_state_values)
ggplot(data = output_long4,
       aes(x = time, y = proportion, group=variable, color=variable)) +
  geom_line() +
  xlab("Time (years)") +
  ylab("Proportion of People") +
  labs(title = "50% Vaccination Coverage (beta = 0.6, gamma = 0.1)") +
  ylim(c(0,1))
```



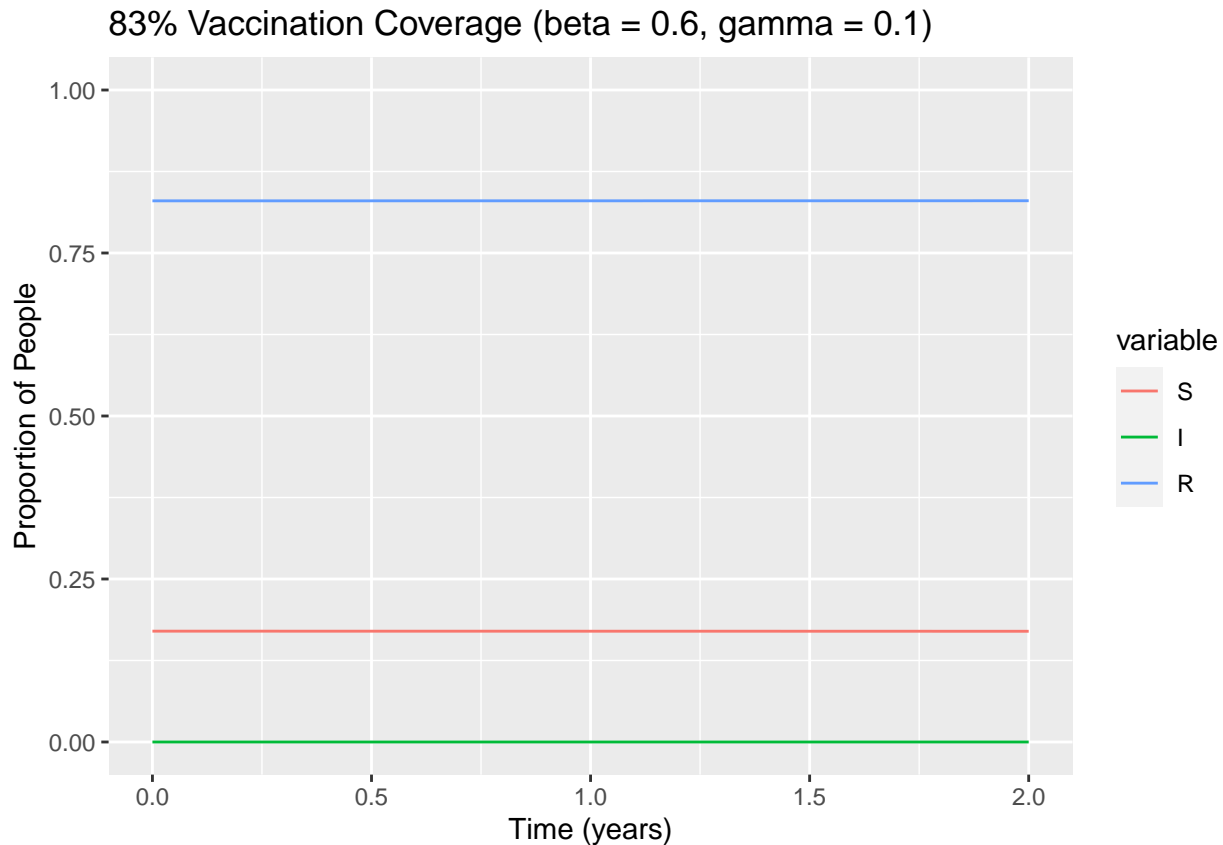
We see when  $\beta = 0.6 \text{ days}^{-1}$  and  $\gamma = 0.1 \text{ days}^{-1}$ , an epidemic, although small, does occur. This suggests that the proportion of the population that needs to be vaccinated varies with different infection-related parameters. We see that the required vaccination coverage in this case is about 83%:

```
p3 <- 0.83
initial_number_susceptible3 <- (1-p3) * (N - 1)
initial_number_infected3 <- 1
initial_number_recovered3 <- p3 * (N - 1)

initial_state_values3 <- c(S = initial_number_susceptible3,
                          I = initial_number_infected3,
                          R = initial_number_recovered3)

output83 <- as.data.frame(ode(y = initial_state_values3,
                             times = times,
                             func = SIR_model,
                             parms = parameters4))

output_long83 <- melt(as.data.frame(output83), id = "time")
output_long83$proportion <- output_long83$value/sum(initial_state_values)
ggplot(data = output_long83,
       aes(x = time, y = proportion, group=variable, color=variable)) +
  geom_line() +
  xlab("Time (years)") +
  ylab("Proportion of People") +
  labs(title = "83% Vaccination Coverage (beta = 0.6, gamma = 0.1)") +
  ylim(c(0,1))
```

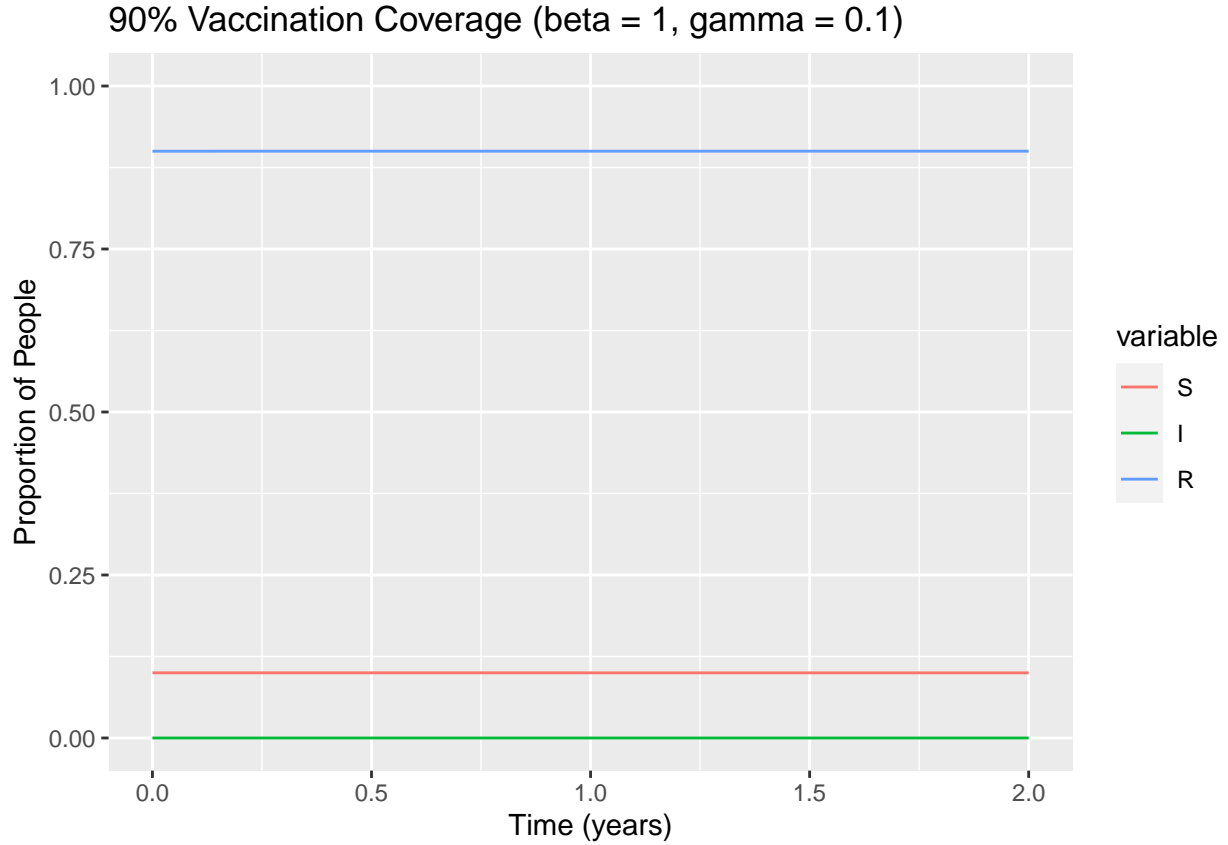


When  $\beta$  is large and  $\gamma$  is small, the disease has a larger force of infection  $\lambda$  and is infectious for a long period of time (infectious period is  $\frac{1}{\gamma}$ ). When the opposite is true, the disease cannot infect as much of the population as rapidly. Therefore, a large value of  $\beta$  and a small value of  $\gamma$  can be counteracted if the population proportion  $p$  that is immune to the disease is high. For example, if we attempt  $\beta = 1 \text{ days}^{-1}$  and  $\gamma = 0.1 \text{ days}^{-1}$  with a proportion  $p = 0.9$ :

```
parameters5 <- c(beta = 1 * 365, gamma = 0.1 * 365)

output5 <- as.data.frame(ode(y = initial_state_values2,
                             times = times,
                             func = SIR_model,
                             parms = parameters5))

output_long5 <- melt(as.data.frame(output5), id = "time")
output_long5$proportion <- output_long5$value/sum(initial_state_values)
ggplot(data = output_long5,
       aes(x = time, y = proportion, group=variable, color=variable)) +
  geom_line() +
  xlab("Time (years)") +
  ylab("Proportion of People") +
  labs(title = "90% Vaccination Coverage (beta = 1, gamma = 0.1)") +
  ylim(c(0,1))
```



We see no epidemic occurs. The pool of susceptibles is too low for the disease to survive and reproduce within the population.

The effective reproduction number,  $R_{eff}$ , is the average number of secondary infections per infected case at a given point in the epidemic.  $R_{eff}$  takes into account existing immunity in the population and is proportional to the number of susceptible people. We can write  $R_{eff}$  as:

$$R_{eff} = R_0 \times \frac{S}{N}$$

Where  $R_0$  equals:

$$R_0 = \frac{\beta}{\gamma}$$

Vaccination changes the effective reproductive number because  $R_{eff}$  takes into account existing immunity. In modeling, herd immunity occurs when  $R_{eff} < 1$ . We can derive a formula to calculate the critical vaccination threshold from the formula of  $R_{eff}$ .

$$R_{eff} = R_0 \times \frac{S}{N}$$

$$1 = R_0 \times (1 - p)$$

$$\frac{1}{R_0} = (1 - p)$$

$$p_c = 1 - \frac{1}{R_0}$$



Where  $R_0 = \frac{\beta}{\gamma}$ .  $p_c$  is the critical vaccination threshold. If we knew  $R_0$  for a particular disease, we could estimate what proportion of the population would need to be vaccinated to raise herd immunity.