# SIR Dynamics with Varying Parameters

Now, we will try to model, intuitively, the roles of $\beta$ and $\gamma$ in starting an epidemic.

Imagine there is a disease where every person infects 1 person on average every 2 days, and is infectious for 4 days. What are the values for $\beta$ and $\gamma$? We know that $\beta$ is our force of infection rate (we can model $\lambda$, the force of infection, as a function of the infection rate $\beta$, and the proportion of the population that is infectious, $\frac{I}{N}$), and thus in this case, $\beta$ would equal 1 person/2 days = 0.5 days$^{-1}$. $\gamma$ is the recovery rate, and can be derived from 1 / infectious period, and thus 1 / 4 days = 0.25 days$^{-1}$. We can use these values to model the epidemic. In this example, we will model using the proportion of the population in each compartment rather than the actual numbers - this can be more informative, especially if the population size changes over time.

We will model the epidemic with $\beta = 0.5$ days$^{-1}$ and $\gamma = 0.25$ days$^{-1}$, assuming an introduction of a single infected person in a totally susceptible population of 1 million for 100 days.

We will begin by loading in the required libraries.

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

We will now fill in the state values and other variables - including rates - for our model.

```r
initial_number_susceptible <- 1000000 - 1
initial_number_infected <- 1
initial_number_recovered <- 0

times <- seq(from = 0, to = 100, by = 1)

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

parameters <- c(beta = 0.5, gamma = 0.25)
```

Now, we can create our actual SIR model, using the same descriptive differential equations:

$$\frac{dS}{dt} = -\beta\left(\frac{I}{N}\right)S \tag{1}$$

$$\frac{dI}{dt} = \beta\left(\frac{I}{N}\right)S - \gamma I \tag{2}$$

$$\frac{dR}{dt} = \gamma I \tag{3}$$

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

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

      N = S + I + R

```

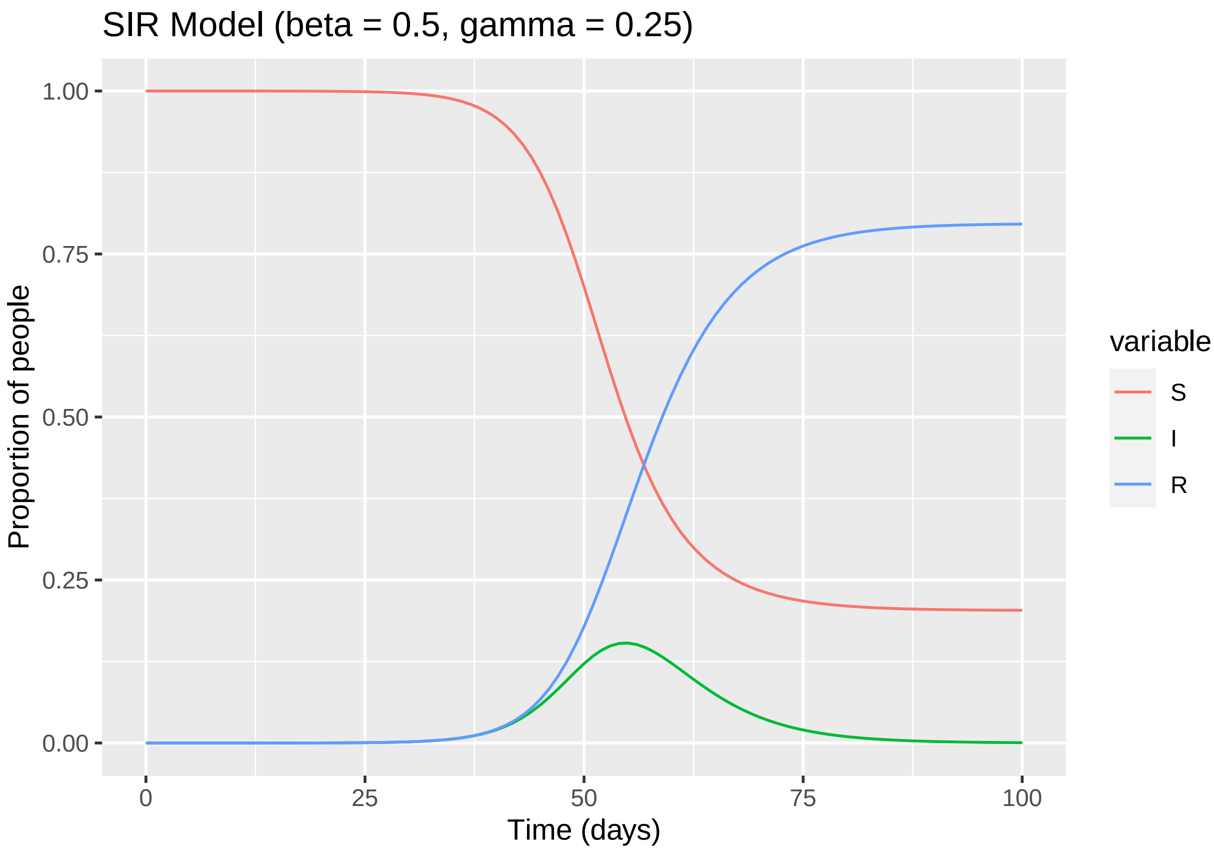
```r
    lambda <- beta * I / N

    # people move out of (-) the S compartment at rate lambda (force of infection)
    dS <- (-1) * lambda * S

    # people move into (+) the I compartment from S at a rate lambda
    # and move out of (-) the I compartment at rate gamma (recovery)
    dI <- (lambda * S) - (gamma) * (I)

    # people move into (+) the R compartment from I at a rate gamma
    dR <- (gamma) * (I)

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

We can create a new column in output_long for the proportion of the population in each compartment at each time step, or day in this case.

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

output_long <- melt(as.data.frame(output), id = "time")

output_long$proportion <- output_long$value/sum(initial_state_values)
```

And now, we can plot the output.

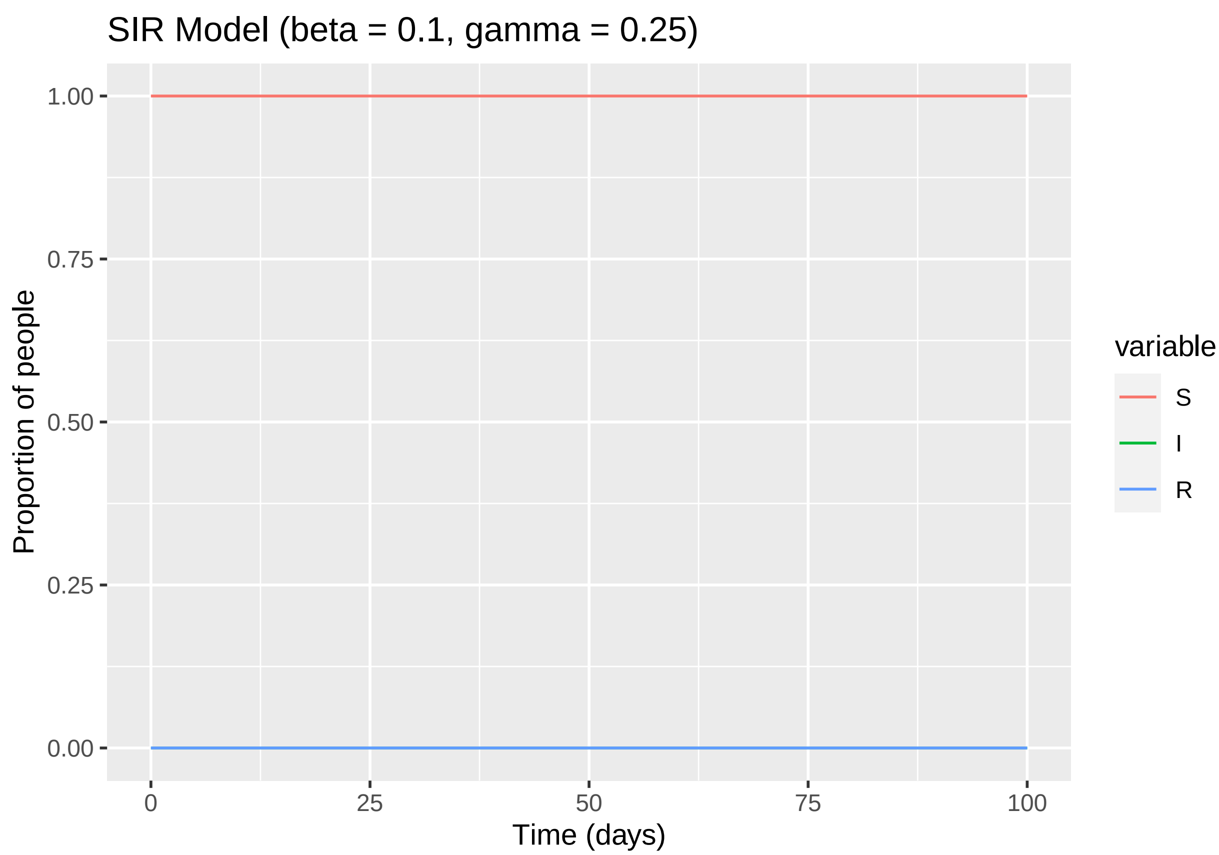
```r
ggplot(data = output_long,
       aes(x = time, y = proportion, group=variable, color=variable)) +
  geom_line() +
  xlab("Time (days)") +
  ylab("Proportion of people") +
  ggtitle("SIR Model (beta = 0.5, gamma = 0.25)")
```




In this model, we can observe a few interesting things. Most of the population remains susceptible. 99% of the population remains susceptible by day 35, and soon after, more people become ill; the peak of the epidemic is at day 55, where roughly 15.3% of the population is infected. At the end of the 100 day period, there are nearly no infected individuals left, 20.3% of the population remains susceptible and 79.5% of the population is recovered.

Now, let us imagine an infection control measure is introduced. For example, infected people are isolated so that they cannot spread the infection. As a result, our force of infection rate $\beta$ drops to 0.1. We can model a new scenario using this parameters.

```
parameters1 <- c(beta = 0.1, gamma = 0.25)

output1 <- as.data.frame(ode(y = initial_state_values,
                            times = times,
                            func = SIR_model,
                            parms = parameters1))

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 (days)") +
  ylab("Proportion of people") +
  ggtitle("SIR Model (beta = 0.1, gamma = 0.25)")
```



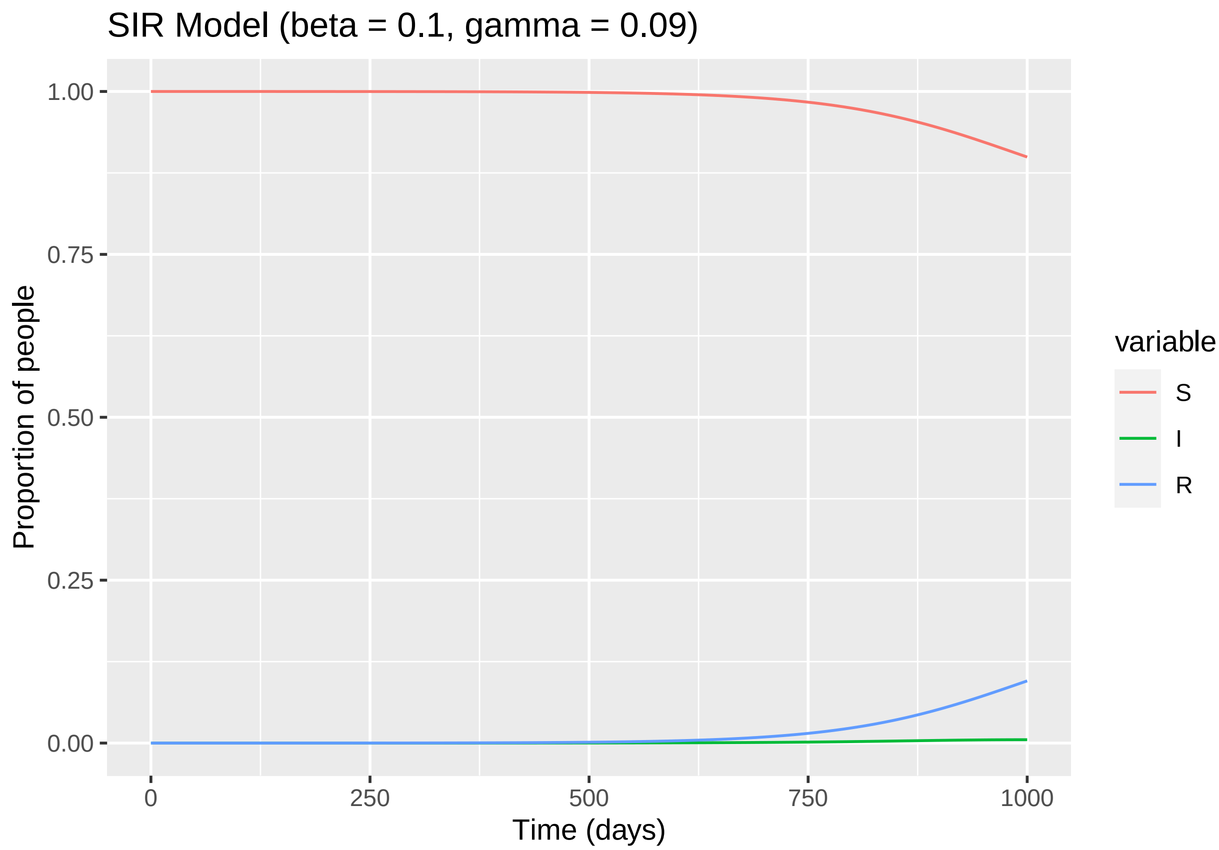

We see here that no epidemic takes place with parameters of $\beta = 0.1$ and $\gamma = 0.25$. The first infectious case does not lead to an epidemic. We then ask, assuming $\beta = 0.1$, what value of $\gamma$ do you need in order to see an epidemic? And what could give rise to this change in $\gamma$?

$\gamma$ may change in a real life scenario due to changes in social behavior, quarantining policy, and public cooperation. $\gamma$ may also change depending on strain evolution of the infectious agent.

To see what conditions are needed to start an epidemic, we can experiment with different values of $\gamma$ while holding $\beta = 0.1$ constant. We can first try the value of $\gamma = 0.09$ and run our model for 1,000 days to observe if an epidemic occurs.

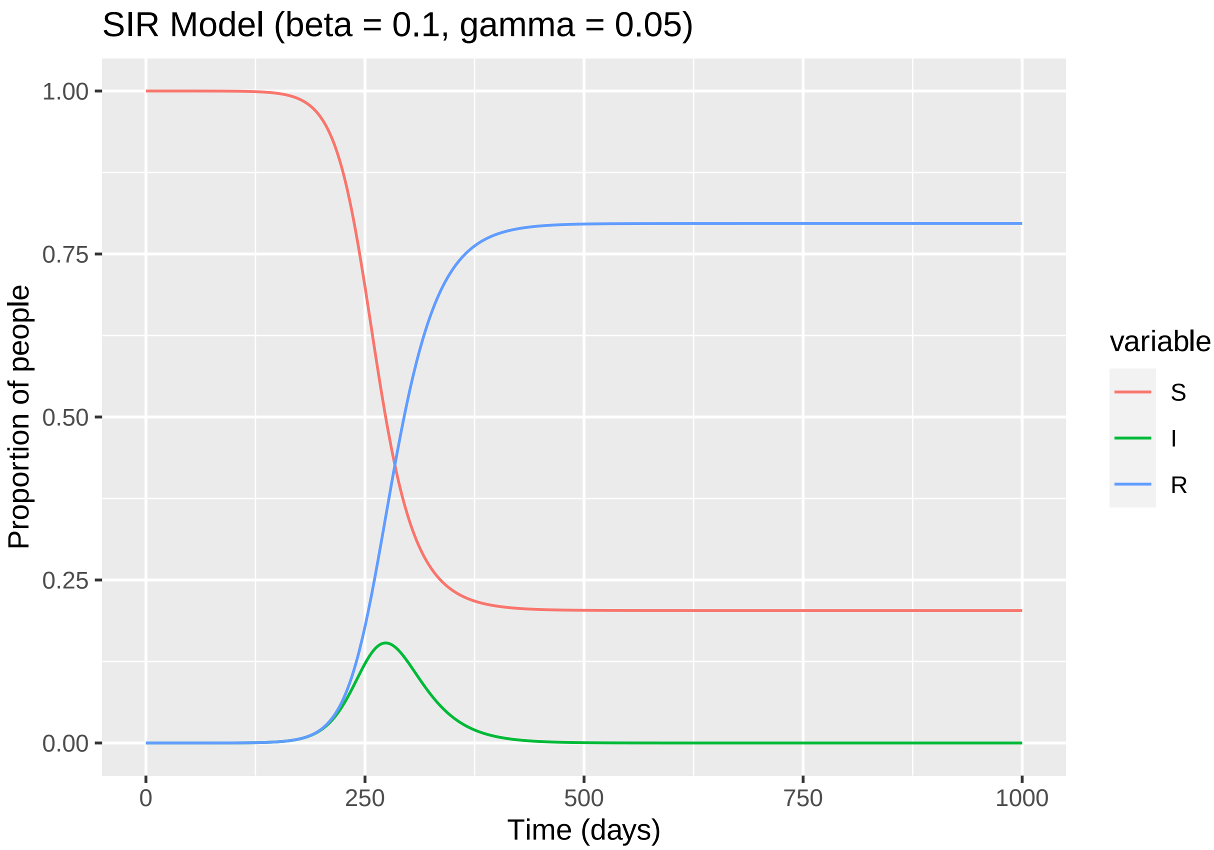
```
parameters2 <- c(beta = 0.1, gamma = 0.09)

times2 <- seq(from = 0, to = 1000, by = 1)

output2 <- as.data.frame(ode(y = initial_state_values,
                            times = times2,
                            func = SIR_model,
                            parms = parameters2))

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 (days)") +
  ylab("Proportion of people") +
```

```r
  ggtitle("SIR Model (beta = 0.1, gamma = 0.09)")
```




We see a very small epidemic occur towards the end of 1,000 days using a value of $\gamma = 0.09$. If we decrease $\gamma$ to 0.05:

```r
parameters3 <- c(beta = 0.1, gamma = 0.05)

output3 <- as.data.frame(ode(y = initial_state_values,
                             times = times2,
                             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 (days)") +
  ylab("Proportion of people") +
  ggtitle("SIR Model (beta = 0.1, gamma = 0.05)")
```




We see an epidemic of greater scale now, with most of the population contracting the disease.

This suggests a strong link between $\gamma$, $\beta$, and the severity of an epidemic. We can hypothesize that for an epidemic to occur, the ratio $\frac{\beta}{\gamma}$ must be greater than 1 - infectious people have to be infectious enough ($\beta$ must be high enough) for long enough ($\gamma$ has to be low enough) to pass on the pathogen. As a result $\beta$ must be greater than $\gamma$. A low infection rate can still lead to an epidemic as long as persons in the population are infectious for long enough to spread the disease.