SIR Model with a Dynamic Force of Infection

In the previous model, we had expressed before that the force of infection λ (lambda) stayed constant. However, due to changes in the infected proportion of a population, the force of infection can change over time. At the beginning of the epidemic, there are not many infectious people, so the force of infection may not be very strong. However, as more people begin to get infected in the population, the force of infection can increase as people move from the susceptible to infectious compartmentments. We can continue using our simple SIR model, except now we can model λ as a function of the infection rate β, and the proportion of the population that is infectious, I/N.

Some of the relevant variables we are using include:

- C: average number of contacts a susceptible person makes each day
- I/N: Proportion of contacts that are made with an infectious person
- p: Per contact with an infectious person, this is the probability of a susceptible person becoming infected
- We can estimate the infection rate, β, to be pxc

And some of the assumptions we are making include:

- a homogeneous population - everyone in the same compartment is subject to the same hazards
- a well-mixed population - all susceptible people have the same risk as getting infected, dependent on the number of infected people
- a closed population - there are no births or deaths, so the population size stays constant

Therefore $\lambda = \beta \frac{I}{N}$. The differential equations that can describe this system include:

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

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

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

We will begin, as usual, by loading in the required libraries.

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

We will define our model inputs. We will use the same initial conditions as the last model ($S = 999999$, $I = 1$ and $R = 0$), simulation period (60 days) and γ (0.1 days^{-1}) with a daily infection rate β equals 1.

```r
initial_number_susceptible <- 999999
initial_number_infected <- 1 # we begin with one infection in the population
initial_number_recovered <- 0

daily_infection_rate <- 1
recovery_rate <- 0.1

follow_up_duration <- 60
```

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

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

parameters <- c(beta = daily_infection_rate, gamma = recovery_rate)
```

Now, we can create our modified SIR model.

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

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

      N = S + I + R

      # people move out of (-) the S compartment at rate lambda (force of infection)
      dS <- (-1) * (beta) * (I / N) * 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 <- ((beta) * (I / N) * 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 generate our model's output and plot our findings using the ode() function in deSolve.

```
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")

ggplot(data = output_long,
       aes(x = time, y = value, group=variable, color=variable)) +
  geom_line() +
  xlab("Time (days)") +
  ylab("Number of people") +
  ggtitle("SIR Model With Varying Rate of Infection")
```

SIR Model With Varying Rate of Infection
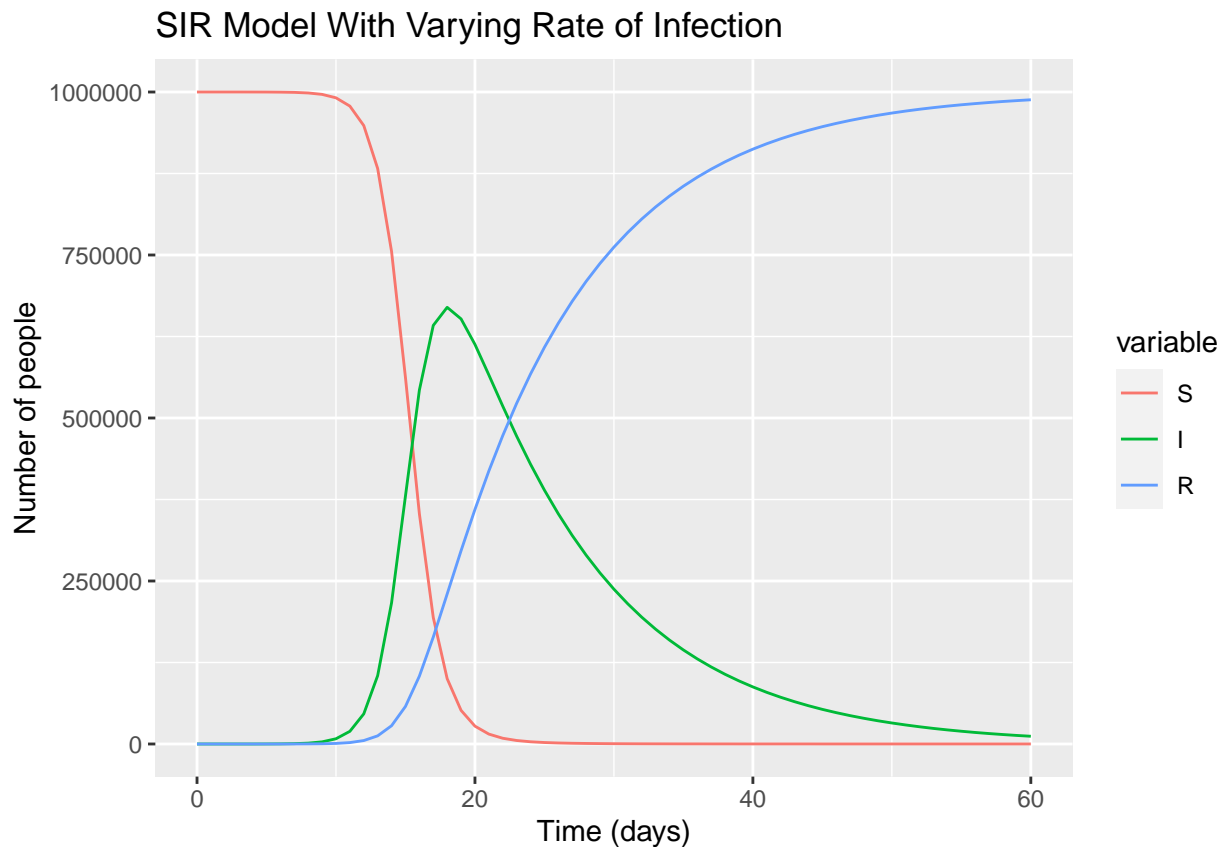
At the beginning of the epidemic, when the number of infected persons are low, the force of infection is small, and thus the number of susceptible individuals stays high and the number of infected individuals low for the first 10 days. However, after the 10 day period, the number of infected individuals begins to increase rapidly, and thus the force of infection increases. As a result, the number of susceptible individuals moving into the infected compartment increases rapidly. The epidemic reaches its peak at about day 18. After, the number of infected persons steadily declines. At the end of the 60 day period, nearly all individuals in the cohort have recovered - nearly all were infected at some point.

Now, let's try to see how the pattern of the epidemic changes with different values of β or γ.

Let's start with a higher level of $\beta = 2$ and rerun the model, with γ held constant at 0.1.

```
daily_infection_rateb2 <- 2
parametersb2 <- c(beta = daily_infection_rateb2, gamma = recovery_rate)

outputb2 <- as.data.frame(ode(y = initial_state_values,
                              times = times,
                              func = SIR_model,
                              parms = parametersb2))

output_longb2 <- melt(as.data.frame(outputb2), id = "time")

ggplot(data = output_longb2,
       aes(x = time, y = value, group=variable, color=variable)) +
  geom_line() +
  xlab("Time (days)") +
  ylab("Number of people") +
  ggtitle("SIR Model With Varying Rate of Infection (beta = 2, gamma = 0.1)")
```

SIR Model With Varying Rate of Infection (beta = 2, gamma = 0.1)
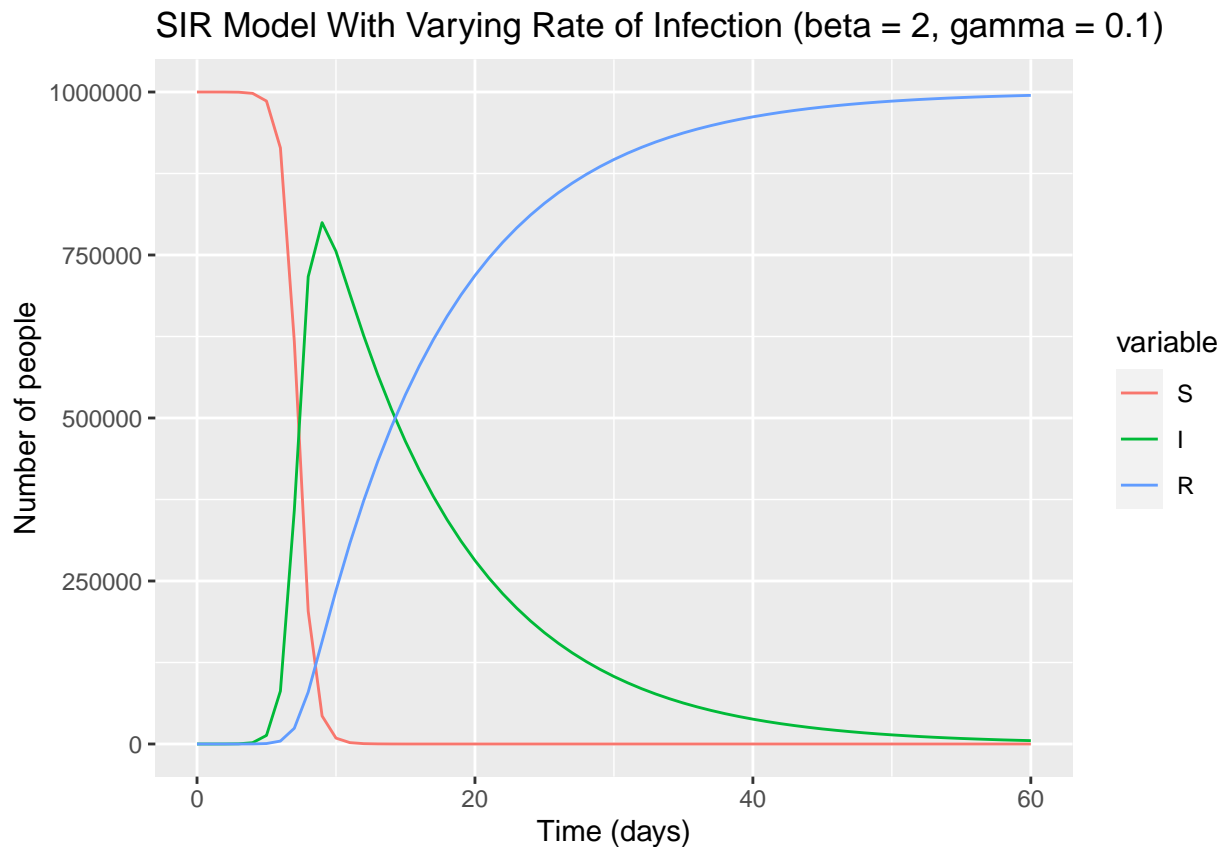
In this case, we see a much sharper and quicker increase of infected persons, with a peak that is higher than previous (almost 800,000 individuals).

If we try a smaller beta of $\beta = 0.5$:

```r
daily_infection_rateb5 <- 0.5
parametersb5 <- c(beta = daily_infection_rateb5, gamma = recovery_rate)

outputb5 <- as.data.frame(ode(y = initial_state_values,
                              times = times,
                              func = SIR_model,
                              parms = parametersb5))

output_longb5 <- melt(as.data.frame(outputb5), id = "time")

ggplot(data = output_longb5,
       aes(x = time, y = value, group=variable, color=variable)) +
  geom_line() +
  xlab("Time (days)") +
  ylab("Number of people") +
  ggtitle("SIR Model With Varying Rate of Infection (beta = 0.5, gamma = 0.1)")
```

SIR Model With Varying Rate of Infection (beta = 0.5, gamma = 0.1)
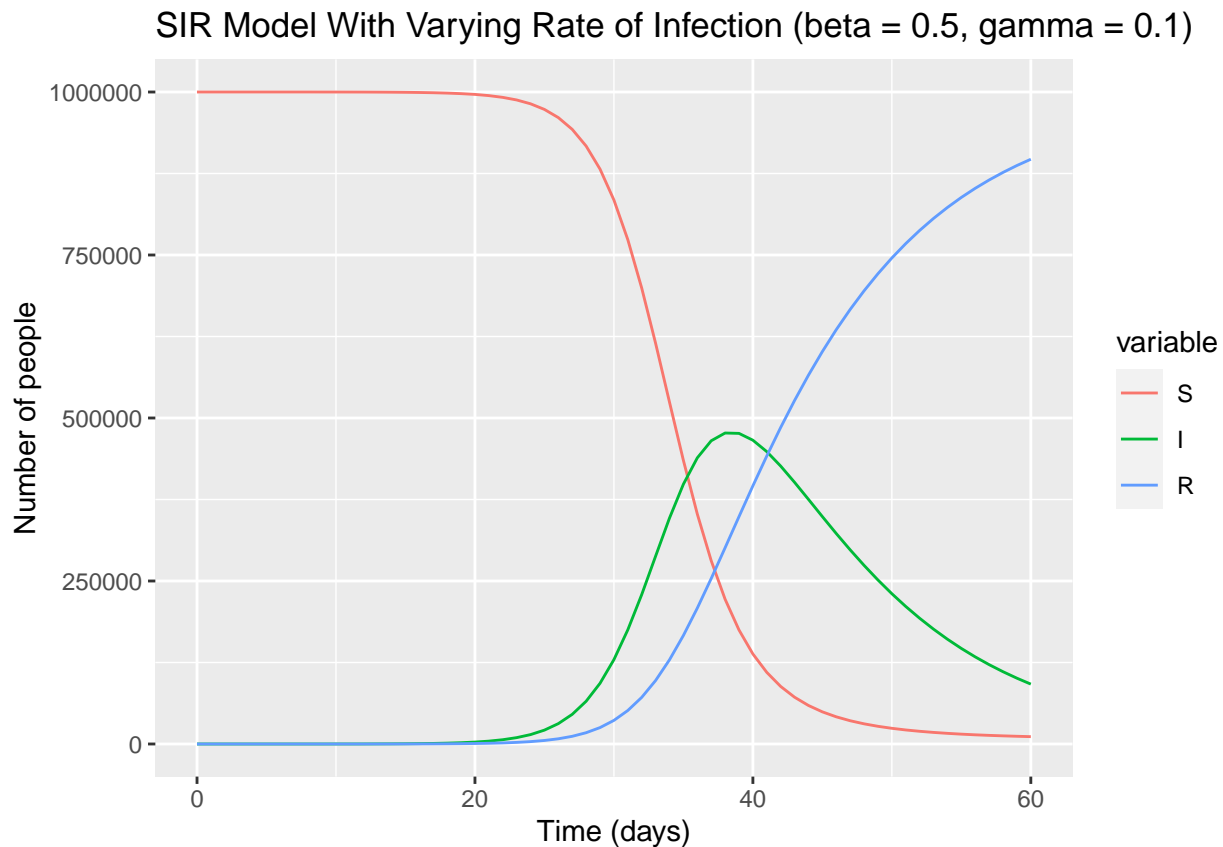
We see a very different epidemic here. Less than half the population is infected at the peak of the outbreak, with the infection not penetrating nearly all of the population till about day 20. However, it is interesting to note that unlike the previous models, not nearly all has recovered after 60 days, possibly because the bulk of the outbreak begins later. As with the previous two models, nearly all of the population is infected at some point.

Now, let's try changing the γ rates. We'll start with a higher level of $\gamma = 0.5$, with β held constant at 1.

```
recovery_ratel5 <- 0.5
parametersl5 <- c(beta = daily_infection_rate, gamma = recovery_ratel5)

outputl5 <- as.data.frame(ode(y = initial_state_values,
                              times = times,
                              func = SIR_model,
                              parms = parametersl5))

output_longl5 <- melt(as.data.frame(outputl5), id = "time")

ggplot(data = output_longl5,
       aes(x = time, y = value, group=variable, color=variable)) +
  geom_line() +
  xlab("Time (days)") +
  ylab("Number of people") +
  ggtitle("SIR Model With Varying Rate of Infection (gamma = 0.5, beta = 1)")
```

SIR Model With Varying Rate of Infection (gamma = 0.5, beta = 1)
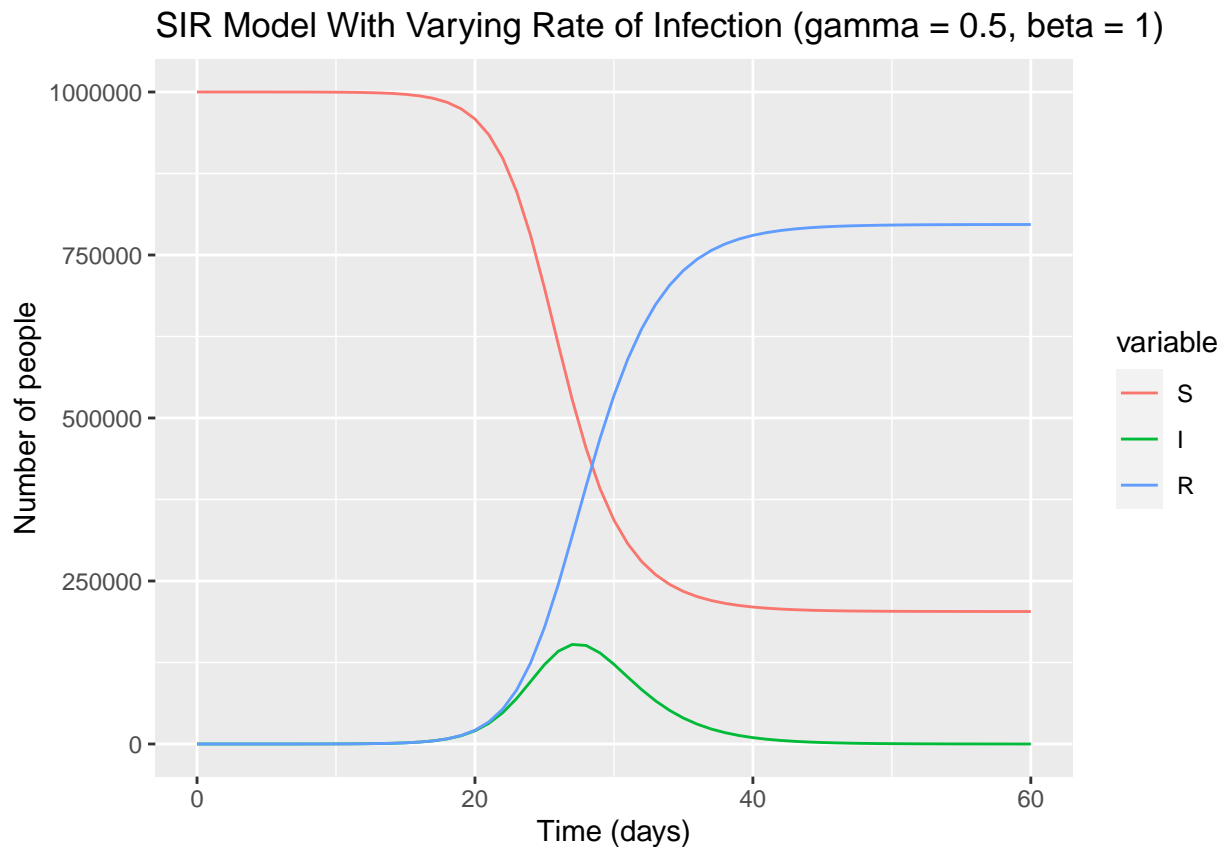
In this outbreak, we see some similarities to the previous models. For example, the infection does not penetrate the vast majority of the population until about day 20. However, we see that the peak of the infection is much smaller (only about 140,000 individuals are infected at the peak of the epidemic). In addition, we also see a significant proportion of the population (about a quarter) does not contract the infection at all. In essence, we see that there is a lower and later peak of infected persons and an earlier rise in the recovered curve.

Now, if we decrease gamma to $\gamma = 0.01$:

```
recovery_ratel1 <- 0.01
parametersl1 <- c(beta = daily_infection_rate, gamma = recovery_ratel1)

outputl1 <- as.data.frame(ode(y = initial_state_values,
                              times = times,
                              func = SIR_model,
                              parms = parametersl1))

output_longl1 <- melt(as.data.frame(outputl1), id = "time")

ggplot(data = output_longl1,
       aes(x = time, y = value, group=variable, color=variable)) +
  geom_line() +
  xlab("Time (days)") +
  ylab("Number of people") +
  ggtitle("SIR Model With Varying Rate of Infection (gamma = 0.01, beta = 1)")
```

SIR Model With Varying Rate of Infection (gamma = 0.01, beta = 1)
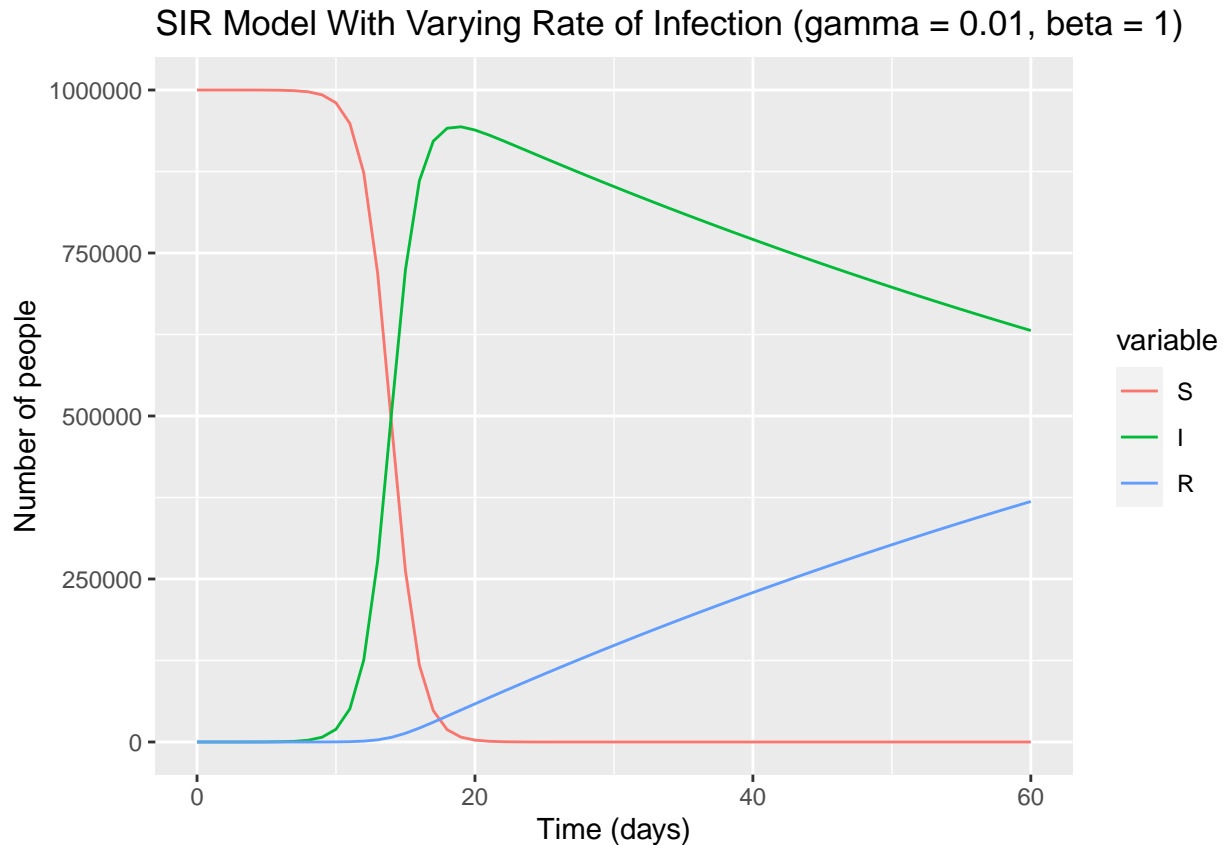
We see here that nearly all of the population is infected by day 20, and that nearly all are infected at some point. This makes sense, as the recovery rate in this model is very minimal, which makes it harder to recover and easier for the infection to spread.

When β is increased, the infection spreads to more people more quickly. If γ is increased, the infection spreads slower and spreads to a smaller amount of people - if $\gamma = 1$, then no epidemic ever occurs When β is decreased, the infection takes more time to spread, and does not make a distinguishable impact on the population till later. When γ is decreased substantially, nearly all of the population is infected, due to a higher force of infection and low recovery rate. If persons in the population stay infected for a long time before recovering, (γ is low) the epidemic flattens out; but if the recovery happens quickly (γ is high) then there is a small peak of the infection and the epidemic dies out rapidly. Both β and γ values can have substantial impacts on the course of an epidemic.'