

Simulating the Effective Reproduction Number R_{eff}

Epidemics can only begin when the index case is infectious enough for long enough to pass on the pathogen to another person. This condition can be modeled mathematically by stating $\frac{\beta}{\gamma} > 1$; β is the average number of secondary infections per unit time, and γ is the hazard rate of recovery from infection (this means the average duration of infection is equivalent to $\frac{1}{\gamma}$). This is also the same condition for R_0 , the average number of secondary cases caused by a single infected case in an otherwise susceptible population. We can relate R_0 to β and γ , as the mean number of secondary infections can be found by multiplying the number of infections per day by the number of the days people are infectious; this can be given by $\beta \times \frac{1}{\gamma}$. Therefore,

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

The effective reproduction number, R_{eff} , is the average number of secondary infections per infected case at a given point in the epidemic, and thus, it varies during the course of the epidemic. Unlike R_0 , R_{eff} takes into account existing immunity in the population and is proportional to the number of susceptible people. Thus, we can write R_{eff} as:

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

When the whole population is susceptible, the effective reproduction number is equal to R_0 . But as susceptibility declines over the course of the epidemic, the effective reproduction number declines as well. In this way, R_{eff} is responsive and dynamic. When R_{eff} drops to 1, each infected case is on average only able to replace themselves. Therefore, the epidemic slows, and begins to go into decline if R_{eff} falls below 1.

Now, we can model an epidemic to study the connection between R_{eff} and the epidemic curve. We will look at a closed, fully susceptible population in which a single infected person is introduced. We will choose to model our epidemic with an SIR model, selecting $\beta = 0.4 \text{ days}^{-1}$ and $\gamma = 0.1 \text{ days}^{-1}$, assuming an introduction of a single infected person in a totally susceptible population of 1 million for 100 days. This will give us $R_0 = \frac{0.4}{0.1} = 4$.

We can begin developing our SIR model by loading in our libraries, assigning our parameters, creating our model function, and obtaining our model output.

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

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 = 0.4, gamma = 0.1)
```

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

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

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

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

We can use them to generate our SIR model function.

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

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

    N = S + I + 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)))
  })
}
```

```
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")
```

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.

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

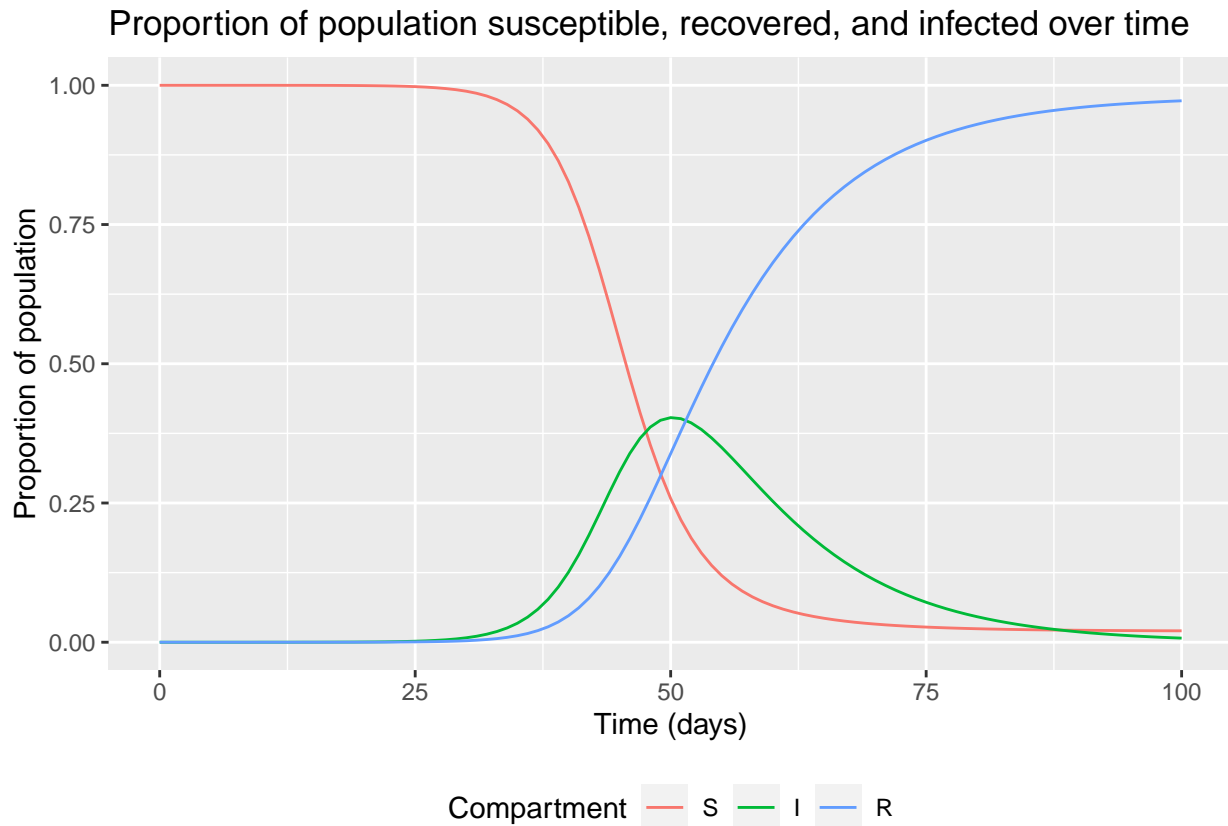
We calculated R_0 to be $R_0 = \frac{\beta}{\gamma} = \frac{0.4}{0.1} = 4$. Therefore, $R_{eff} = R_0 \times \frac{S}{N} = 4 \times \frac{S}{N}$. We can create a new column in our output to generate the effective reproduction number at each time step:

```
output$reff <- (parameters["beta"]/parameters["gamma"]) * (output$S / (output$S + output$I + output$R))
```

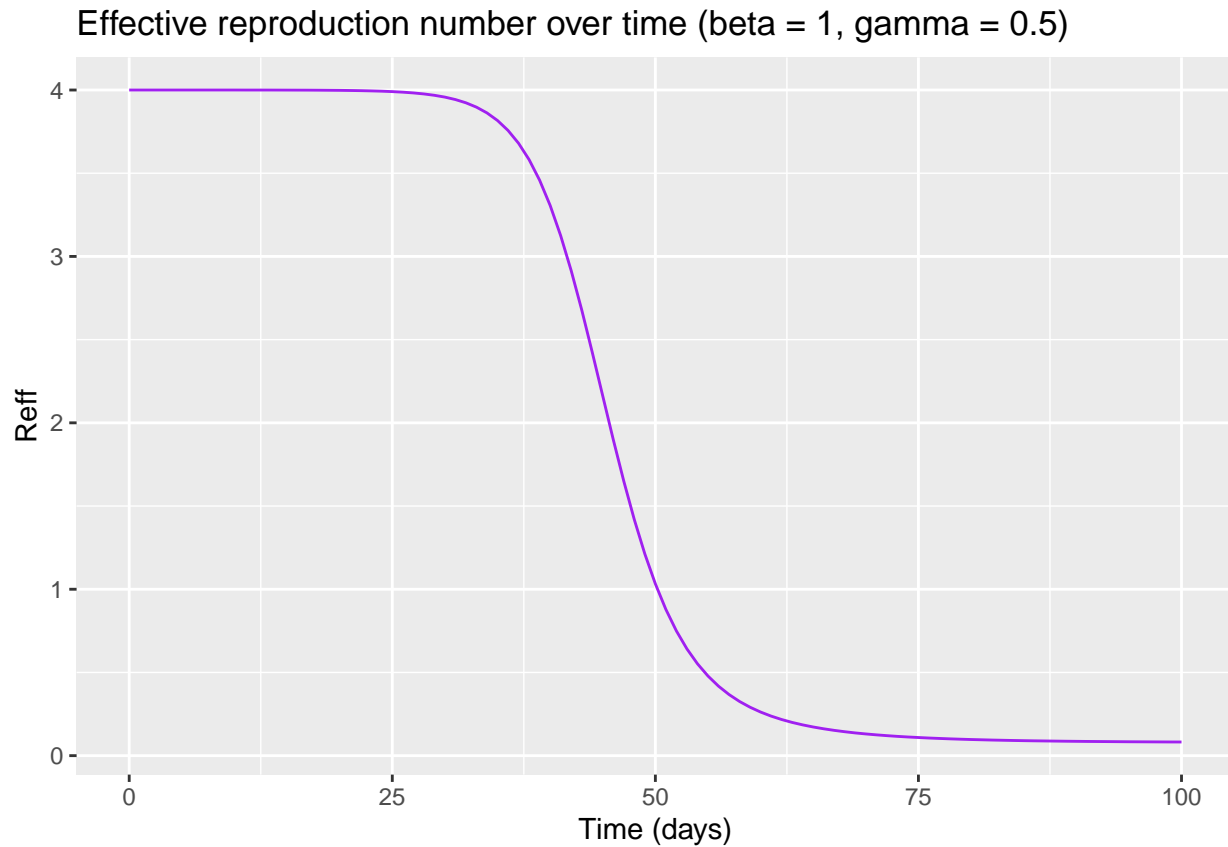
Now, we can plot both the proportion of the population who are susceptible, infectious, or recovered as well as R_{eff} over time.

```
ggplot(data = output_long,
       aes(x = time, y = proportion, group=variable, color=variable)) +
```

```
geom_line() +
  xlab("Time (days)") +
  ylab("Proportion of population") +
  labs(color = "Compartment", title = "Proportion of population susceptible, recovered, and infected over time",
  theme(legend.position = "bottom")
```



```
ggplot(data = output,
  aes(x = time, y = reff)) +
  geom_line(color="purple") +
  xlab("Time (days)") +
  ylab("Reff") +
  ggtitle("Effective reproduction number over time (beta = 1, gamma = 0.5)")
```



We see that R_{eff} is equal to R_0 at the start of the epidemic, where everyone is susceptible; every infected case causes 4 secondary infections on average. However, as the number of susceptible people begin to decrease, R_{eff} begins to decrease proportional to the number of susceptible persons. The peak of the epidemic is at about day 50, where approximately 40.3% of the population is infected. This is also where $R_{eff} = 1$, and where the epidemic comes to a standstill. As R_{eff} decreases below one, each infected case is unable to cause at least one more infected case to continue the epidemic. As a result, we see the proportion of infected persons in the population begin to decline and the proportion of recovered persons steadily increase to nearly 100%.