

SIR Model with Constant Force of Infection

We will create a simplified SIR model. An SIR model is defined as an epidemiological model that computes the theoretic number of people infected with a contagious illness in a closed population over time.

The differential equations that describe this system include:

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

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

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

The SIR model is a cornerstone of infectious disease modeling. We can use the SIR model to describe a disease that can be split into 3 states: susceptible (S), infected (I), or recovered (R). We must also assume that all those infected are infectious (able to transmit the disease to another), and that all who have recovered are immune to catching the disease again. This model is similar to the model we used before, but the addition of the susceptible compartment (S) is what differs the SIR model from the previous, simpler models. Depending on how many people in the population are infectious, susceptible people experience a force of infection λ ($lambda$), which is the transition rate at which they become infected.

Now, we will attempt to simulate the outbreak of a new infectious disease that our simulated population of 10^6 have never encountered before. This means we assume: a single case starts this outbreak, everyone in the population is susceptible to the disease, and no one has recovered or is immune. This could parallel a scenario where an infected person introduce a new disease into an isolated population, such as an island, or when infections transmit from an animal population to humans, such as COVID-19. We can therefore define for our model: $S = 10^6 - 1 = 999999$, $I = 1$ and $R = 0$.

We will create a model in R to describe this situation using a constant force of infection λ ($lambda$) = 0.2 days⁻¹. We will run the model to simulate 60 days.

We will begin by loading in the required packages.

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

Now, we need to define our model inputs. We will use values of λ ($lambda$) = 0.2 days⁻¹ and γ ($gamma$) = 0.1 days⁻¹.

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

force_of_infection <- 0.2
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(lambda = force_of_infection, gamma = recovery_rate)
```

After doing so, we can create an SIR model function using the differential equations that describe the system.

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

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

    dS <- (-1) * (lambda) * S
    dI <- (lambda) * (S) - (gamma) * (I)
    dR <- (gamma) * (I)

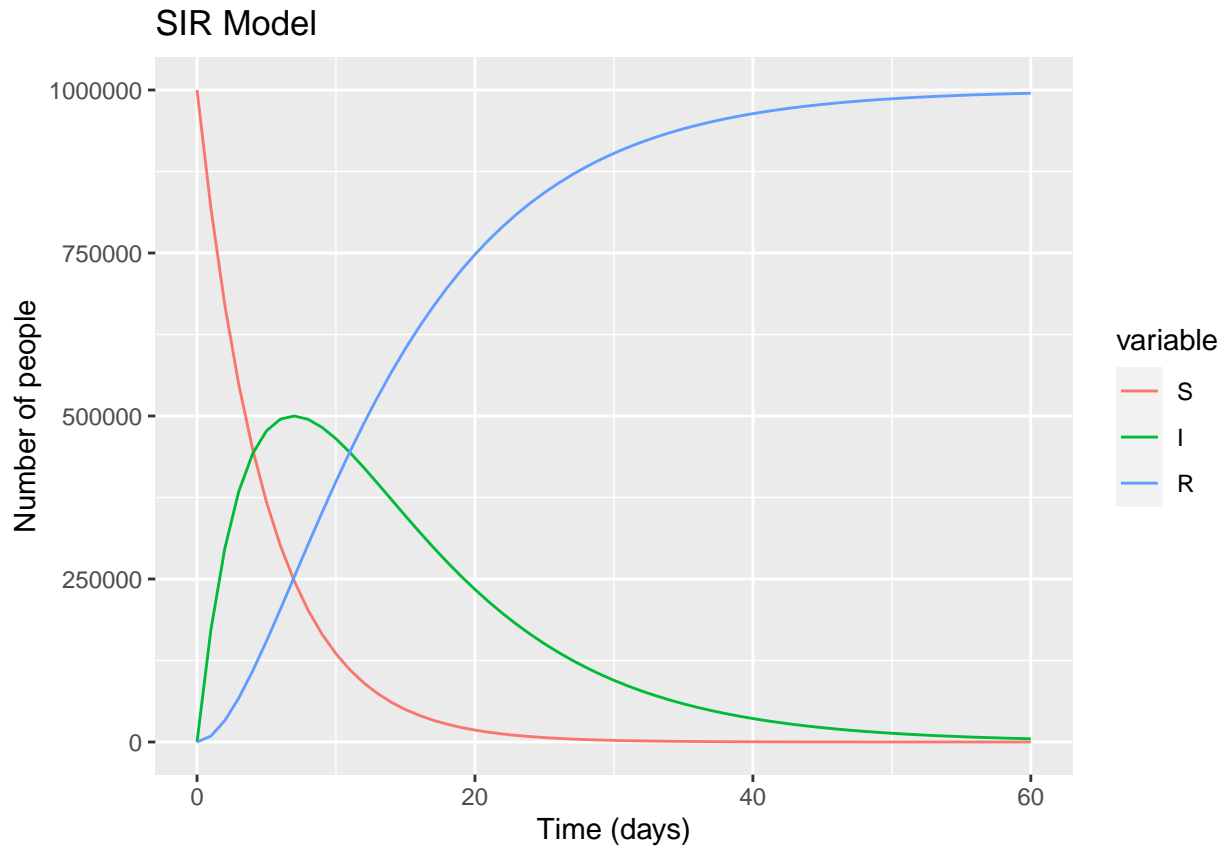
    return(list(c(dS, dI, dR)))
  })
}
```

We can finally run the model and obtain an output, as well as plot the model.

```
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 turn this dataset into a long format,
                                                    # so that the number in each compartment at each 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")
```



Over the 2 month period, we see that eventually nearly everyone in the population recovers, with the exception of about 5,000 individuals that are still infected. We can see at the peak of epidemic, there are 500,000 people in the population infected - this occurs at only about the 7th day. People in the population get infected at a much faster rate during this first week. After the first week, the number infected begins to decrease, while the amount recovered increases steadily and eventually levels.