Modeling Waning Immunity

We have seen how susceptibility in a population can change independently of a pandemic. For example, population turnover and vaccination. So far, our models have assumed that once an individuals recovers and gains immunity, they are permanently immune to re(infection). However, there are many diseases that only provide temporary immunity after recovery. Waning immunity can return those previously infected or vaccinated individuals back into the susceptible pool.

Model Structure

In order to model this, we can use a simple SIR model with no births or deaths (stable population size) and a totally susceptible population with the introduction of one infected individual. The infection and recovery rates are 0.4 and 0.2 days^{-1} respectively, and the average duration of immunity is 10 years. We will use a population size of 1,000,000.

σ (*sigma*) is defined as the waning rate of immunity. We can visualize this model structure as follows:

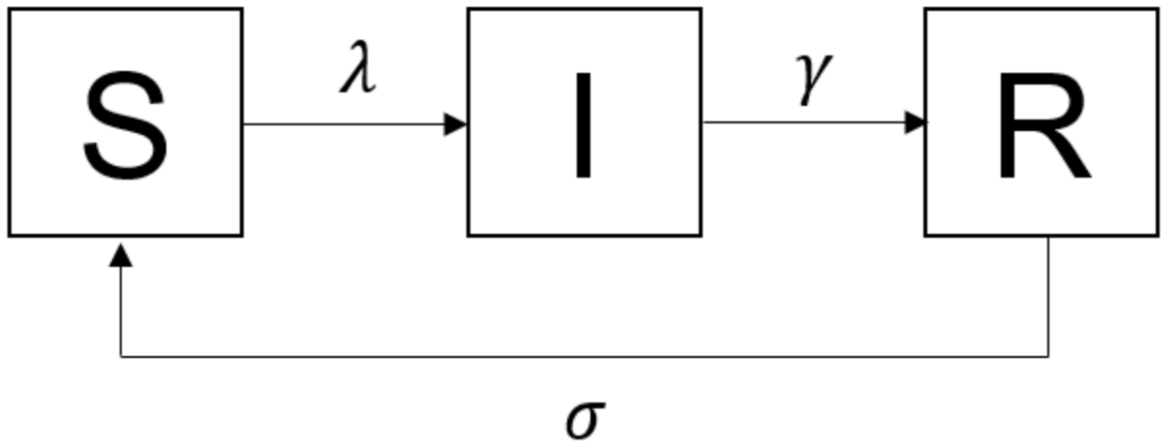


Figure 1: model

In this case, $\sigma = \frac{1}{10} = 0.1$ years^{-1}, because the average duration of immunity is 10 years.

The differential equations we can use that include σ, can be defined as:

$$\frac{dS}{dt} = -\lambda S + \sigma R \tag{1}$$

$$\frac{dI}{dt} = \lambda S - \gamma I \tag{2}$$

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

Where:

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

Developing the Model

We can now use the above information to generate our SIR model with the specified parameters.

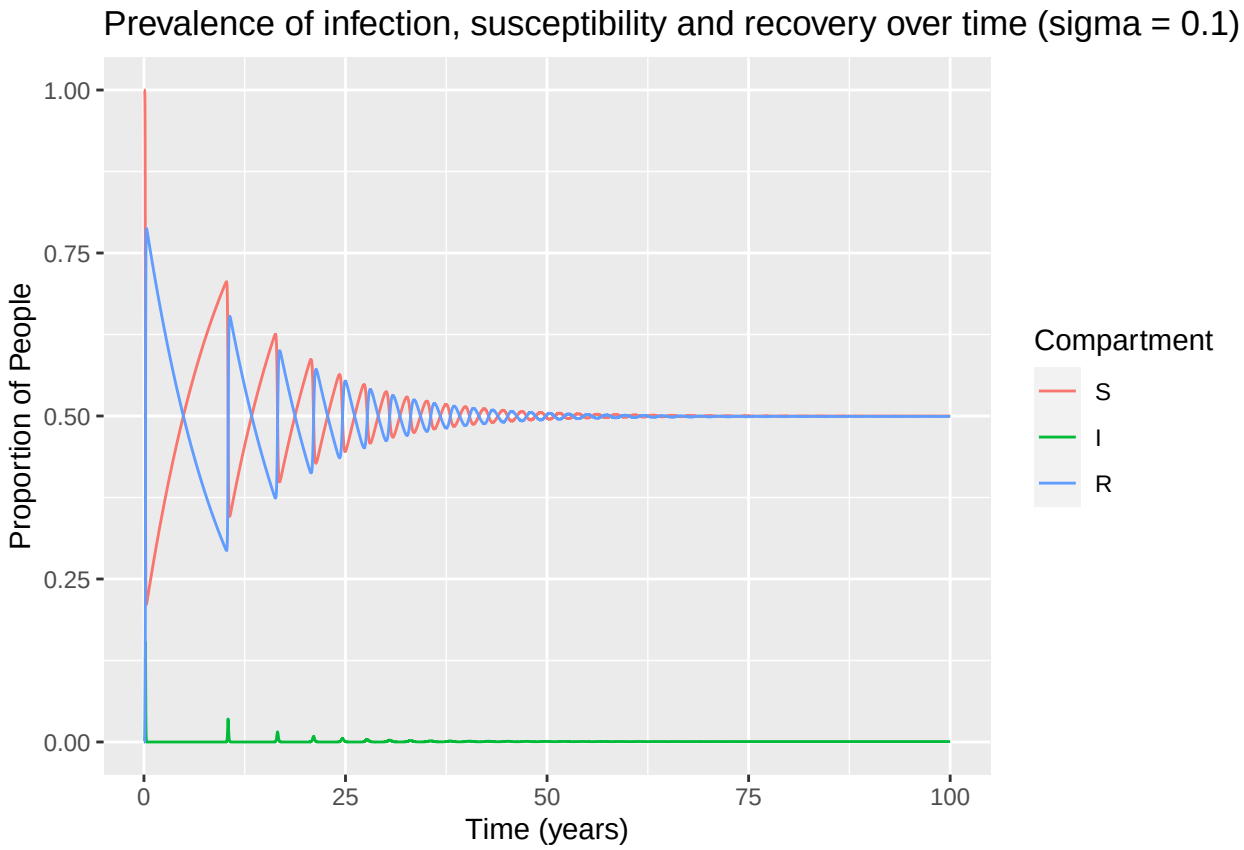
```
library(deSolve)
library(reshape2)
library(ggplot2)
```

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

times <- seq(from = 0, to = 100, by = 1/365)

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

parameters <- c(beta = 0.4 * 365, gamma = 0.2 * 365, sigma = 0.1)
```

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

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

      N = S + I + R

      lambda <- beta * I / N

      dS <- -lambda * S + sigma * R

      dI <- lambda * S - gamma * I

      dR <- gamma * I - sigma * R

      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(colour = "Compartment",title = "Prevalence of infection, susceptibility and recovery over time (s
```



Analysis of Model

We see that this plot is very similar to a model we developed previously that described the dynamics of an acute disease with a slow population turnover; we saw then and now spikes of epidemics alternating with long deep troughs with cycles of susceptibility and recovery until the infection dies out. The immunity of those recovered lasts for around 10 years; we see that small outbreaks happen about once every 10 years until the infection dies out. The rate of waning is still slower than population turnover (which is about 70 years), and because of this reason, the time between epidemics is shorter as the pool of susceptibles is replenished by those losing immunity.

Implications for a Vaccine Program

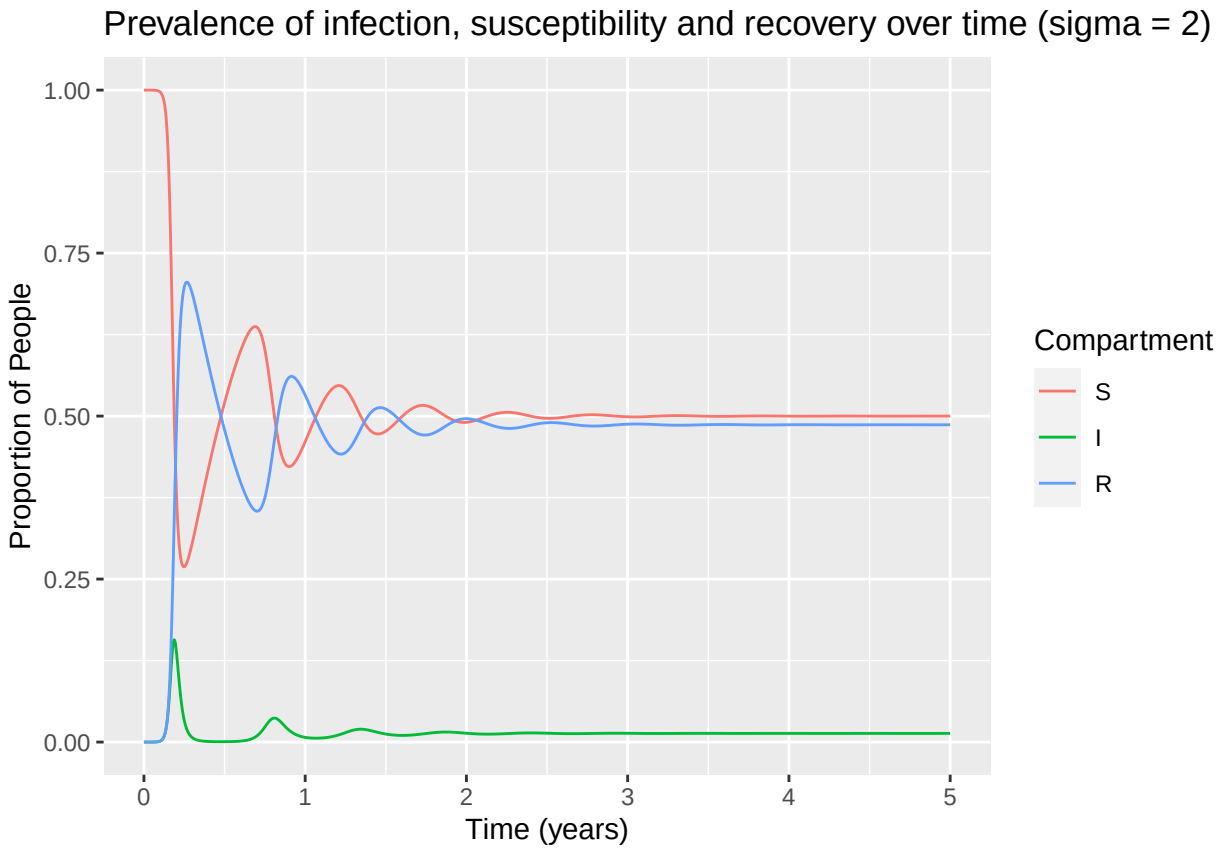
In this case, there would be many implications for a vaccination program against this disease. For example, a booster dose is recommended in the case of tetanus and diphtheria for adults every 10 years to protect against waning immunity. Such a dose could be administered within the 10 year waning period in order to ensure no resurgences of the disease in the population. However, it is important to remember this model makes many simplifying assumptions, and there are many other factors affecting susceptibility in a population.

Modifying the model

Now, we will model a scenario where the immunity period is much shorter, lasting only six months. We will use a time period of 5 years. In this case $\sigma = \frac{1}{0.5} = 2$.

```
parameters2 <- c(beta = 0.4 * 365, gamma = 0.2 * 365, sigma = 2)

times2 <- seq(from = 0, to = 5, by = 1/365)
```

```
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 (years)") +
  ylab("Proportion of People") +
  labs(colour = "Compartment",title = "Prevalence of infection, susceptibility and recovery over time (
```

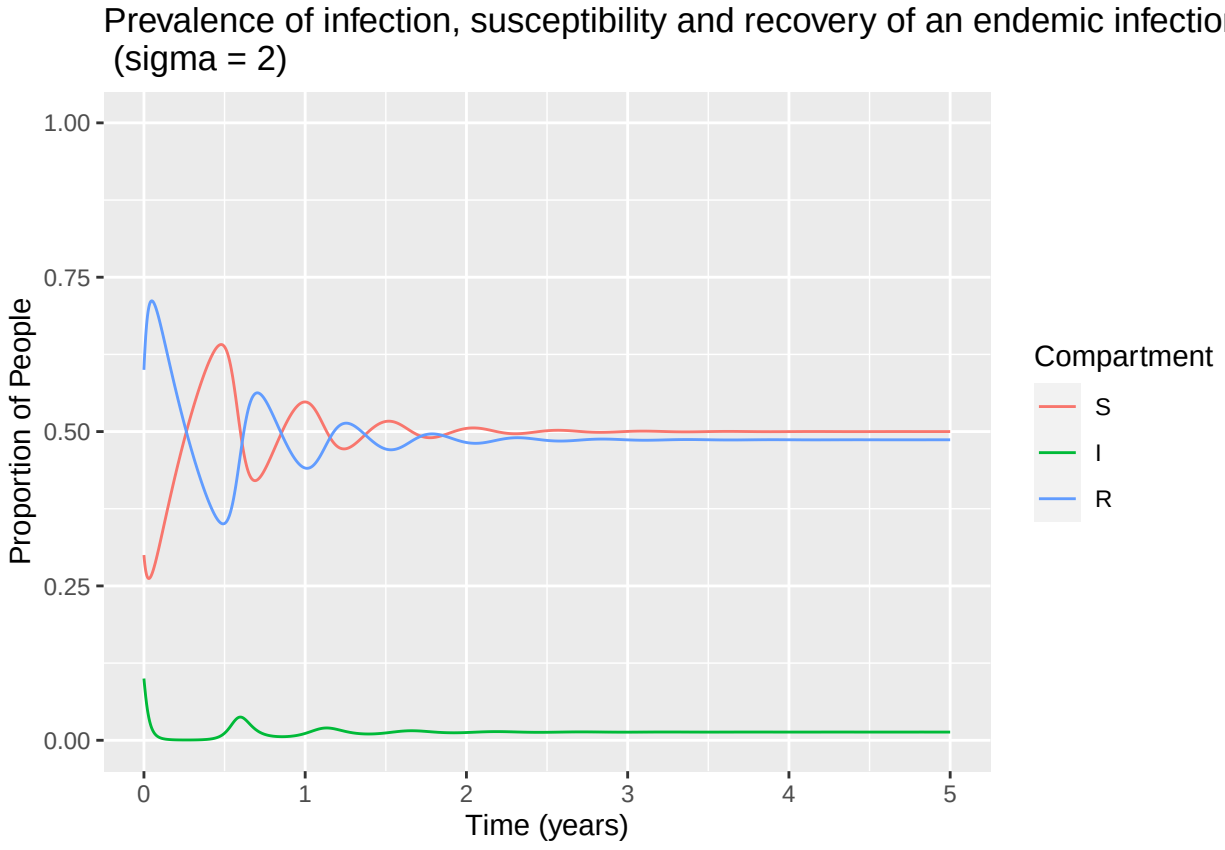


We see that this outcome reflects what we saw when we observed an acute disease in a population with fast turnover. The infection reaches an endemic equilibrium with the effective reproduction number at just over 1 (at the end of 5 years, about 13,000 individuals are infected), because just as in the previous population, the pool of susceptibles is continually replenished. Waning immunity acts in a similar way to the birth rate in SIR model dynamics and is connected to population turnover.

Lastly, we will now change the initial conditions to represent an endemic infection rather than the introduction of a single infected case into the population. We will assume an endemic prevalence of 10% and that 60% of the population are already immune at the first time step. We will use values of $\sigma = 2$ and total time 5 years like above.

```
N = 1000000
initial_number_susceptible2 <- 0.3 * N
initial_number_infected2 <- 0.1 * N
```

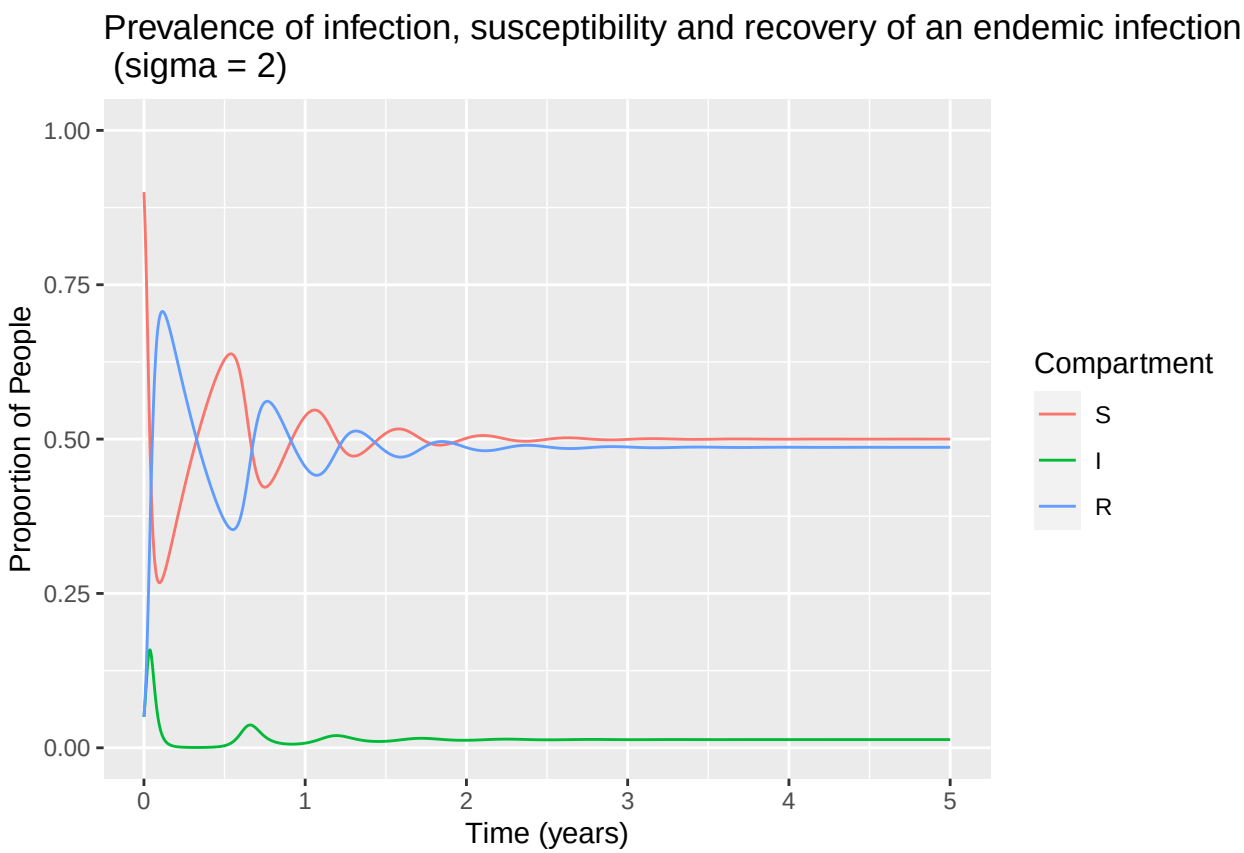
```r
initial_number_recovered2 <- 0.6 * N

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

output3 <- as.data.frame(ode(y = initial_state_values2,
                             times = times2,
                             func = SIR_model,
                             parms = parameters2))

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(colour = "Compartment",title = "Prevalence of infection, susceptibility and recovery of an endem
  ylim(c(0,1))
```



We see that the system stabilizes at the same values as in the previous example where we assumed introduction of a single infected case. Generally, when modeling an endemic infection that reaches an endemic equilibrium and has parameters that add to the susceptibles pool, the initial numbers in the compartments does not affect the endemic prevalence that is eventually reached, so long as there is at least one infected person. This stands in contrast to what we have observed before, when changing the initial proportion p of a population that was vaccinated could prevent an epidemic from occurring.

For example, if we assumed only 5% of the population was already immune, 5% were infected, and 90% were susceptible, we would still see the same endemic prevalence:

```
initial_number_susceptible3 <- 0.9 * N
initial_number_infected3 <- 0.05 * N
initial_number_recovered3 <- 0.05 * N

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

output4 <- as.data.frame(ode(y = initial_state_values3,
                             times = times2,
                             func = SIR_model,
                             parms = parameters2))

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(colour = "Compartment",title = "Prevalence of infection, susceptibility and recovery of an endem
  ylim(c(0,1))
```



The difference here is that there is a slightly larger peak of the epidemic in the beginning; however, even with these parameters, we see that it reaches the same endemic prevalence after 5 years.