Infectious Disease Modeling with R

Compartmental Models: SI, SIS, SIR, SEIR

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Outline

Introduction

- In the field of epidemiology, **mathematical models** are crucial tools for understanding and predicting the spread of infectious diseases.
- **Compartmental models** are the most fundamental approaches, which divide a population into different groups based on their infection status.
  - The **SI, SIS, SIR, and SEIR models** are foundational examples of this approach, each offering a different level of complexity and representing different disease dynamics.
- Mathematical models allow us to simulate outbreaks, predict their course, and evaluate the potential impact of public health interventions like vaccination or social distancing.
- These models simplify complex biological systems into a set of mathematical equations, capturing the key mechanisms of disease spread.
- For this presentation, **R programming language** is applied to explore several classic compartmental models.

The SI (Susceptible-Infectious) Model

The SI model is the simplest compartmental model, suitable for diseases that confer no immunity upon recovery. Individuals move from being susceptible to infectious.

- **Susceptible (S):** Individuals at risk of infection.
- **Infectious (I):** Individuals who are infected and can transmit the disease.

The governing differential equations are:

$$\frac{dS}{dt} = -\beta \frac{SI}{N}$$
$$\frac{dI}{dt} = \beta \frac{SI}{N}$$

where β is the transmission rate and N is the total population.

R Code for SI Model

```r
#Project: Infectious Diseases Modeling ----
#Title: SI (Susceptible-Infectious) Model Simulation in R
#Author: Tesfahun Taddege (Epidemiologist) ----
# SI Model Simulation
library(deSolve)
# Population and initial conditions
population <- 1000
initial_infected_si <- 1
initial_susceptible_si <- population - initial_infected_si
# SI Model Equations
si_model <- function(time, state, parameters) {
with(as.list(c(state, parameters)), {
  dS <- -beta * S * I / population
  dI <-  beta * S * I / population
  return(list(c(dS, dI)))
})
}
# Parameters
si_parameters <- c(beta = 0.5)
si_initial_state <- c(S = initial_susceptible_si, I = initial_infected_si)
times <- seq(0, 50, by = 1)
```

R Code for SI Model . . .

```r

# Solve
si_output <- as.data.frame(ode(y = si_initial_state, times = times, func = si_model,
    parms = si_parameters))

# Plot
png("si_plot.png", width=800, height=600)
plot(si_output$time, si_output$S, type="l", col="blue", ylim=c(0,population), xlab="
    Time", ylab="Number of Individuals", main="SI Model")
lines(si_output$time, si_output$I, type="l", col="red")
legend("right", legend=c("Susceptible", "Infectious"), col=c("blue", "red"), lty=1)
dev.off()
```

Listing 1: R code for simulating the SI model.

SI Model Simulation Results

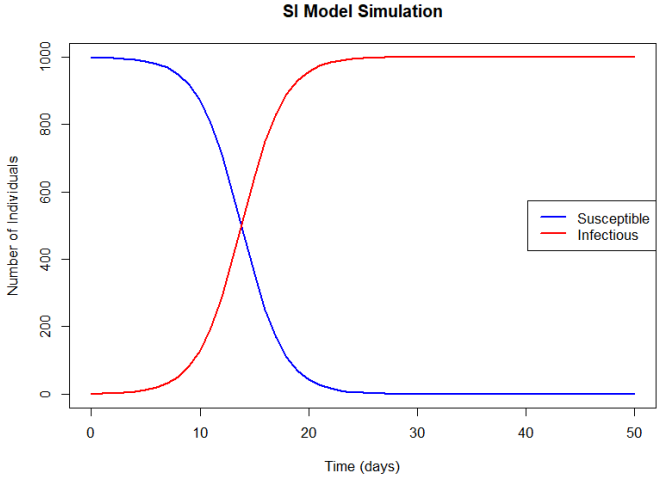

Figure 1: In the SI model, the entire population eventually becomes infectious as there is no recovery.

The SIS (Susceptible-Infectious-Susceptible) Model

The SIS model is used for diseases where recovery does not confer immunity, and individuals become susceptible again (e.g., the common cold).

- **Susceptible (S):** At risk of infection.
- **Infectious (I):** Infected and can transmit. After recovery, they return to the Susceptible group.

The differential equations are:

$$\frac{dS}{dt} = -\beta \frac{SI}{N} + \gamma I$$
$$\frac{dI}{dt} = \beta \frac{SI}{N} - \gamma I$$

where γ is the recovery rate.

R Code for SIS Model

```r
# Project: Infectious Diseases Modeling
# Title: SIS (Susceptible-Infectious-Susceptible) Model Simulation in R
#Author: Tesfahun Taddege (Epidemiologist) ----
#Date: Jan 23, 2023 ----
#Email: ttaddege@gmail.com---
# SIS Model Simulation
library(deSolve)

# Population and initial conditions
population <- 1000
initial_infected_sis <- 1
initial_susceptible_sis <- population - initial_infected_sis

# SIS Model Equations
sis_model <- function(time, state, parameters) {
  with(as.list(c(state, parameters)), {
    dS <- -beta * S * I / population + gamma * I
    dI <-  beta * S * I / population - gamma * I
    return(list(c(dS, dI)))
  })
}
```

R Code for SIS Model . . .

```r
# Parameters
sis_parameters <- c(beta = 0.5, gamma = 0.1)
sis_initial_state <- c(S = initial_susceptible_sis, I = initial_infected_sis)
times <- seq(0, 150, by = 1)
# Solve
sis_output <- as.data.frame(ode(y = sis_initial_state, times = times, func = sis_
    model, parms = sis_parameters))
# Plot
png("sis_plot.png", width=800, height=600)
plot(sis_output$time, sis_output$S, type="l", col="blue", ylim=c(0,population), xlab
    ="Time", ylab="Number of Individuals", main="SIS Model")
lines(sis_output$time, sis_output$I, type="l", col="red")
legend("right", legend=c("Susceptible", "Infectious"), col=c("blue", "red"), lty=1)
dev.off()
```

Listing 2: R code for simulating the SIS model.

SIS Model Simulation Results

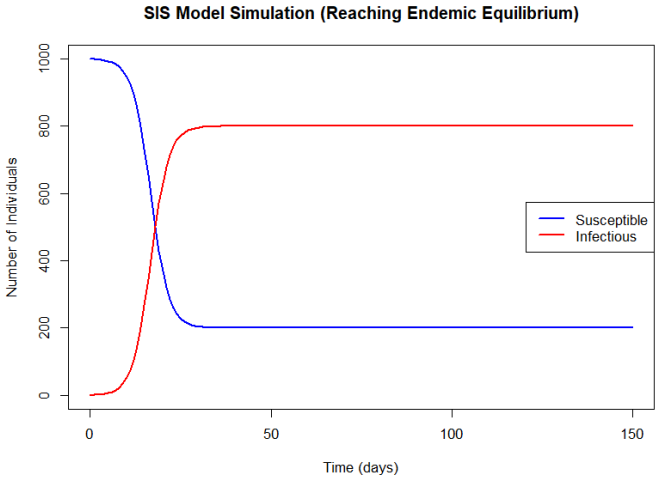

Figure 2: The SIS model often reaches an endemic equilibrium where the disease persists in the population.

The SIR (Susceptible-Infectious-Recovered) Model

The SIR model is a cornerstone of epidemiology, used for diseases where recovery confers long-term immunity (e.g., measles, mumps).

- **Susceptible (S):** Individuals at risk.
- **Infectious (I):** Infected and can transmit.
- **Recovered (R):** Have recovered and are now immune.

The differential equations are:

$$\frac{dS}{dt} = -\beta \frac{SI}{N}$$
$$\frac{dI}{dt} = \beta \frac{SI}{N} - \gamma I$$
$$\frac{dR}{dt} = \gamma I$$

R Code for SIR Model (Measles Example)

```r
# SIR Model Simulation
library(deSolve)

# Population data for a larger scale outbreak
population_sir <- 100000
initial_infected_sir <- 10
initial_recovered_sir <- 0
initial_susceptible_sir <- population_sir - initial_infected_sir

# SIR Model Equations
sir_model <- function(time, state, parameters) {
  with(as.list(c(state, parameters)), {
    N <- S + I + R
    dS <- -beta * S * I / N
    dI <-  beta * S * I / N - gamma * I
    dR <-  gamma * I
    return(list(c(dS, dI, dR)))
  })
}
```

R Code for SIR Model (Measles Example)...

```r

# Measles Parameters (High R0)
R0 <- 15
gamma_sir <- 1/8 # Infectious period of ~8 days
beta_sir <- R0 * gamma_sir
sir_parameters <- c(beta = beta_sir, gamma = gamma_sir)

# Initial State and Time
sir_initial_state <- c(S=initial_susceptible_sir, I=initial_infected_sir, R=initial_recovered_sir)
times_sir <- seq(0, 100, by = 1)

# Solve
sir_output <- as.data.frame(ode(y = sir_initial_state, times = times_sir, func = sir_model, parms = sir_parameters))
```

R Code for SIR Model (Measles Example)...

```r
# Plot
png("sir_plot.png", width=800, height=600)
plot(sir_output$time, sir_output$S, type="l", col="blue", ylim=c(0,population_sir),
     xlab="Time (days)", ylab="Number of Individuals", main="SIR Model for Measles")
lines(sir_output$time, sir_output$I, type="l", col="red")
lines(sir_output$time, sir_output$R, type="l", col="green")
legend("topright", legend=c("Susceptible", "Infectious", "Recovered"), col=c("blue",
       "red", "green"), lty=1)
dev.off()
```

SIR Model Simulation Results

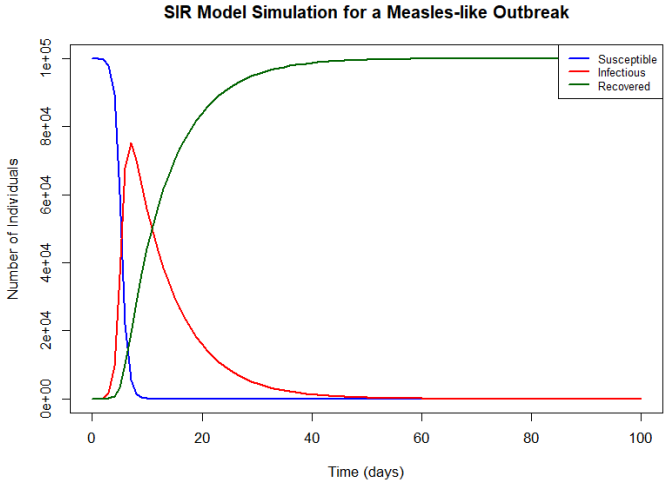

Figure 3: The classic epidemic curve: Susceptibles decline, Infectious peak, and Recovered rise, leading to herd immunity.

The SEIR (Susceptible-Exposed-Infectious-Recovered) Model

The SEIR model adds an "Exposed" compartment for individuals who have been infected but are not yet infectious (latent period). This is common for many diseases like influenza and COVID-19.

- **Exposed (E):** Infected but not yet able to transmit the virus.

The differential equations become:

$$\frac{dS}{dt} = -\beta \frac{SI}{N}$$
$$\frac{dE}{dt} = \beta \frac{SI}{N} - \sigma E$$
$$\frac{dI}{dt} = \sigma E - \gamma I$$
$$\frac{dR}{dt} = \gamma I$$

where σ is the rate of progression from exposed to infectious (1/latent period).

R Code for SEIR Model . . .

```r
# SEIR Model Simulation
library(deSolve)
# Population and initial conditions
population_seir <- 100000
initial_exposed_seir <- 1
initial_infected_seir <- 0
initial_recovered_seir <- 0
initial_susceptible_seir <- population_seir - initial_exposed_seir
# SEIR Model Equations
seir_model <- function(time, state, parameters) {
  with(as.list(c(state, parameters)), {
    N <- S + E + I + R
    dS <- -beta * S * I / N
    dE <-  beta * S * I / N - sigma * E
    dI <-  sigma * E - gamma * I
    dR <-  gamma * I
    return(list(c(dS, dE, dI, dR)))
  })
}
```

R Code for SEIR Model

```r
# Parameters with latent period
gamma_seir <- 1/7  # Infectious period of 7 days
sigma_seir <- 1/5  # Latent period of 5 days
R0_seir <- 2.5
beta_seir <- R0_seir * gamma_seir
seir_parameters <- c(beta=beta_seir, gamma=gamma_seir, sigma=sigma_seir)

# Initial State and Time
seir_initial_state <- c(S=initial_susceptible_seir, E=initial_exposed_seir, I=
    initial_infected_seir, R=initial_recovered_seir)
times_seir <- seq(0, 200, by = 1)

# Solve
seir_output <- as.data.frame(ode(y = seir_initial_state, times = times_seir, func =
    seir_model, parms = seir_parameters))
```

R Code for SEIR Model . . .

```r
# Plot
png("seir_plot.png", width=800, height=600)
plot(seir_output$time, seir_output$S, type="l", col="blue", ylim=c(0,population_seir), xlab="Time (days)", ylab="Number of Individuals", main="SEIR Model")
lines(seir_output$time, seir_output$E, type="l", col="orange")
lines(seir_output$time, seir_output$I, type="l", col="red")
lines(seir_output$time, seir_output$R, type="l", col="green")
legend("topright", legend=c("S", "E", "I", "R"), col=c("blue", "orange", "red", "green"), lty=1)
dev.off()
```

Listing 3: R code for simulating the SEIR model.

SEIR Model Simulation Results

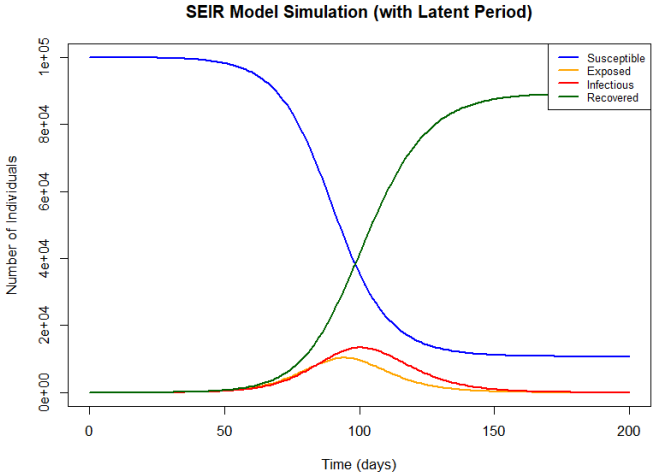

Figure 4: The Exposed compartment introduces a delay, shifting the infectious peak to the right compared to an SIR model.

Expanding the Models

The basic models can be extended to capture more complex realities:

- **Models with Vital Dynamics:** Incorporate birth (μN) and death ($\mu S, \mu I, \ldots$) rates, crucial for modeling endemic diseases over long time scales.

$$\frac{dS}{dt} = \mu N - \beta \frac{SI}{N} - \mu S$$

- **SEIS Model:** For diseases with a latent period but no lasting immunity (Exposed $\rightarrow$ Infectious $\rightarrow$ Susceptible).
- **MSIR Model:** Accounts for maternal immunity (Maternally immune $\rightarrow$ Susceptible $\rightarrow \ldots$).
- **Age-Structured Models:** Divides the population into age groups, each with its own parameters, to account for different contact patterns and disease severity by age.
- **Spatial Models:** Model the geographic spread of a disease across a landscape using metapopulation models or network models.
- **Stochastic Models:** Instead of deterministic differential equations, use random processes (e.g., Gillespie algorithm) to model chance events, which are important in small populations or at the start of an outbreak.

Thank You !!!

- **For More Information, Please Contact:**

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