Lecture 7: SIR Models

Radu Balan

Department of Mathematics, NWC
University of Maryland, College Park, MD

Version: February 16, 2024
In this lecture we continue discussing epidemiological models. There are two main types of epidemic models:

- deterministic (or, compartmental) model
- stochastic (e.g., agent based) model

We focus on three deterministic models:

1. **SI (Susceptible-Infected) Model**
2. **SIR (Susceptible-Infected-Removed) Model**
3. **SEIR (Susceptile-Exposed-Infected-Removed) Model**

Today we discuss the SIR model.
The SIR Model with No vitals

Assume a system with three compartments: ‘Susceptible’ (S), ‘Infected’ (I) and ‘Removed’ or ‘Recovered’ (R). At time $t_0 = 0$ the system has a total of $N$ individuals (initial total population). Most of them are susceptible $S(0)$, but some are infected, $I(0)$ and possibly some are in the recovered state, $R(0)$. Our intention is to model the time evolution of these populations. We start with SI model:

$$\begin{align*}
\frac{dS}{dt} &= -\beta S \frac{I}{N}, \quad S(0) \\
\frac{dI}{dt} &= \beta S \frac{I}{N}, \quad I(0)
\end{align*}$$

where $\beta \geq 0$ is a parameter. We append a new term to model transition from $I \mapsto R$, assuming a constant rate of transition $\alpha$:

$$\begin{align*}
\frac{dS}{dt} &= -\beta S \frac{I}{N}, \quad S(0) \\
\frac{dI}{dt} &= \beta S \frac{I}{N} - \alpha I, \quad I(0) \\
\frac{dR}{dt} &= \alpha I, \quad R(0)
\end{align*}$$
The SIR Model

Deterministic simulations

Simulation of the SIR model:

$$\beta = 2 \ , \ \alpha = 1 \ , \ S(0) = 2000 \ , \ I(0) = 23 \ , \ R(0) = 0$$

Results were obtained with an Euler scheme with step size $h = 0.01$. Note: The infected population $I(t)$ first increases and then decreases eventually to 0. The susceptible population decreases, but converges to some limiting value $S(\infty) > 0$. The removed population is monotone increasing and converges to some value $R(\infty) < N$. Some of the susceptible population who do not get infected are protected by the recovered population surrounding them. This is known as herd immunity.
The SIR Model

Deterministic simulations (2)

Initial conditions: \( S(0) = 2000, \ I(0) = 23, \ R(0) = 0. \)

\[ \beta = 1 \quad \alpha = 1. \]

\[ \beta = 5 \quad \alpha = 1. \]
The SIR Model: The normalized form

For reasons of normalizations, we prefer to compute \textit{fractions} of susceptible population, infected population, and of removed population:

\[ s(t) = \frac{S(t)}{N}, \quad i(t) = \frac{I(t)}{N}, \quad r(t) = \frac{R(t)}{N} \]

In which case the model becomes:

\[
\begin{align*}
\frac{ds}{dt} &= -\beta si, \quad s(0) = \frac{S(0)}{N} \\
\frac{di}{dt} &= \beta si - \alpha i, \quad i(0) = \frac{I(0)}{N} \\
\frac{dr}{dt} &= \alpha i, \quad r(0) = \frac{R(0)}{N}
\end{align*}
\]

(SIR Model)

Note \( s(t) + i(t) + r(t) = 1 \) for all \( t \) (conservation of total population). The bad news: there is no closed form solution. The good news: some relationships can be expressed in closed form.
The SIR Model: Numerical solution vs. Agent Based Modeling

Similar to the SI model, one way of implementing an agent based simulation is to pretend the nonlinear term is linear in $s \tilde{\beta}(t) = \beta i(t)$. Thus the rate matrix is given by

$$
\frac{d}{dt} \begin{bmatrix} s \\ i \\ r \end{bmatrix} = A \begin{bmatrix} s \\ i \\ r \end{bmatrix}, \quad A = \begin{bmatrix} -\beta i & 0 & 0 \\ \beta i & -\alpha & 0 \\ 0 & \alpha & 0 \end{bmatrix}
$$

and for a discretization step $T_0$, at time step $p > 0$, the transition matrix to transition from time $(p-1)T_0$ to $pT_0$ with $i_{p-1} = i((p-1)T_0)$ is given by

$$
\Pi(p) = \begin{bmatrix}
\frac{\beta i_{p-1}}{\alpha-\beta i_{p-1}} e^{-\beta T_0 i_{p-1}} & \frac{\beta i_{p-1}}{\alpha-\beta i_{p-1}} e^{-\alpha T_0} & 0 & 0 \\
1 - \frac{\alpha}{\alpha-\beta i_{p-1}} e^{-\beta T_0 i_{p-1}} + \frac{\beta i_{p-1}}{\alpha-\beta i_{p-1}} e^{-\alpha T_0} & 1 - e^{-\alpha T_0} & 1
\end{bmatrix}, \ p = 1, 2, ...
$$
The SIR Model: Numerical solution vs. Agent Based Modeling (2)

At every time step, the transition matrix can be approximated by the first order term in $e^{tA} \approx I + tA$:

$$
\Pi_E^{(p)} = \begin{bmatrix}
1 - \beta T_0 i_{p-1} & 0 & 0 \\
\beta T_0 i_{p-1} & 1 - \alpha T_0 & 0 \\
0 & \alpha T_0 & 1
\end{bmatrix}
$$

This matrix has a direct interpretation, and allows for a more flexible implementation. For instance, for the transition $S \rightarrow I$ at time step $p$ (i.e., from time $(p - 1)T_0$ to time $pT_0$):

1. If $\text{State}(\text{Agent } k \text{ at time } (p - 1)T_0) = \text{Susceptible}$ then:
   1. Draw a random variable $u$ distributed uniformly over the set of all agents, $u \sim U\{1, 2, ..., M\}$.
   2. If $\text{State}(\text{Agent } u \text{ at time } (p - 1)T_0) = \text{Infected}$ then:
      1. Draw a random number $z \sim U[0, 1]$ uniformly distributed in $[0, 1]$.
      2. If $z \in [1 - \beta T_0, 1]$ then $\text{State}(\text{Agent } k \text{ at time } pT_0) = \text{Infected}$.
      3. Otherwise $\text{State}(\text{Agent } k \text{ at time } pT_0) = \text{Susceptible}$
   3. Otherwise $\text{State}(\text{Agent } k \text{ at time } pT_0) = \text{Susceptible}$.
The SIR Model: Numerical Solution vs. Agent Based Modeling (3)

Figure: Results over 1000 simulations for $T_0 = 0.01$, with parameters $\beta = 2$ and $\alpha = 1$. The shaded area has semiwidth of one std of simulations. Top row utilizes the exponential matrix; the bottom row utilizes the linearized approximation for the transition matrix. The Euler scheme has a stepsize $h = 0.001$. 
The SIR Model: Numerical Solution vs. Agent Based Modeling (4)

Figure: Results over 1000 simulations for $T_0 = 0.001$, with parameters $\beta = 2$ and $\alpha = 1$. The shaded area has semiwidth of one std of simulations. Top row utilizes the exponential matrix; the bottom row utilizes the linearized approximation for the transition matrix. The Euler scheme has a stepsize $h = 0.001$. 
The SIR Model: Numerical Solution vs. Agent Based Modeling (5)

Figure: Results over 1000 simulations for $T_0 = 1.0$, with parameters $\beta = 2$ and $\alpha = 1$. The shaded area has semiwidth of one std of simulations. Top row utilizes the exponential matrix; the bottom row utilizes the linearized approximation for the transition matrix. The Euler scheme has a stepsize $h = 0.001$. 
The SIR Model

Analytic expressions

For the normalized systems of equations, divide the equation for $i$ by equation for $s$ and use chain rule:

$$\frac{di}{ds} = -1 + \frac{\alpha}{\beta} \frac{1}{s}$$

The ratio $R_0 = \frac{\beta}{\alpha}$ is known as the *reproduction ratio*, or the *contact number*. Its meaning: $\beta$ represents the number of close contacts per day per one infected individual; $\frac{1}{\alpha}$ is the average infectious period (or, the average number of days an infected person remains contagious). Hence $R_0$ represents the average number of close contacts per infected individual.

Use separability of this Diff Eq. and integrate both sides:

$$i(t) - i(0) = s(0) - s(t) + \frac{1}{R_0} \left( \log(s(t)) - \log(s(0)) \right)$$

Thus $i + s - \frac{1}{R_0} \log(s)$ must stay constant over time.
The SIR Model

Analytic calibrations

We obtained that \( i + s - \frac{1}{R_0} \log(s) \) must stay constant over time.

**Approximation:** At time \( t = 0 \), \( s(0) \approx 1 \) (assuming little infections and recovered people) and \( i(0) \approx 0 \) (very few infected people compared to the total population).

\[
i(t) + s(t) - \frac{1}{R_0} \log(s(t)) = 1
\]

What happens for \( t \to \infty \)?

One thing for sure: \( i(\infty) = 0 \). What happens with \( s(\infty) \)? We obtain the following equations:

\[
1 = s(\infty) - \frac{1}{R_0} \log(s(\infty))
\]

\[
R_0 = \frac{\log(s(\infty))}{s(\infty) - 1}
\]
With the approximation $i(0) = 0$, $s(0) = 1$, the plot of $\log(s(\infty))/(s(\infty) - 1)$ as function of $s(\infty)$ is rendered in the left figure. For instance, if the contact number is $R_0 = 2$, then $s(\infty) \approx 0.2$. Thus 20% of population get protection from the 80% who have gotten infected and recovered.
The SIR Model

Herd Immunity

With the approximation \( i(0) = 0, \ s(0) = 1 \), the plot of \( \log(s(\infty))/(s(\infty) - 1) \) as function of \( s(\infty) \) is rendered in the left figure.

For instance, if the contact number is \( R_0 = 2 \), then \( s(\infty) \approx 0.2 \). Thus 20% of population get protection from the 80% who have gotten infected and recovered.

But what happens if \( R_0 < 1 \)?
In reality, $i(0) > 0$ and $s(0) < 1$. Assume that still $r(0) = 0$, thus $s(0) + i(0) = 1$, but $\log(s(0)) < 0$. We obtain:

$$i(t) + s(t) - \frac{1}{R_0} \log(s(t)) = 1 - \frac{\log(s(0))}{R_0} \implies R_0 = \frac{\log(s(\infty)) - \log(s(0))}{s(\infty) - 1}$$

For $s(0) = 2000/2023$ we obtain the left plot. For $R_0 >> 1$, the previous approximation is still good. For $R_0 < 1$, it follows that a significant number of susceptible individual do not get infected.
SIR Model with Two Outcomes

Since \( I(t) \), or \( i(t) \), is not monotone increasing sequence, the SIR model is appropriate for the time series of the daily rates of the number of infections. On the hand, the removed sequence \( R(t) \), or \( r(t) \), is monotone increasing. The “removed” compartment contains only two types of individuals: (1) individuals that recovered and gained full immunity \( X(t) \), (so they will never get infected again), and (2) people who died, \( Y(t) \). Thus \( R(t) = X(t) + Y(t) \).

Assumption 1: \( Y(t) = \gamma R(t) \) for all \( t \). In other words, a fixed fraction \( \gamma \) of people who get infected eventually die, with the same infectious period as the individuals that eventually recovered and gained immunity:

\[
\begin{align*}
\frac{dS}{dt} &= -\beta S \frac{I}{N}, \quad S(0) \\
\frac{dI}{dt} &= \beta S \frac{I}{N} - \alpha I, \quad I(0) \\
\frac{dX}{dt} &= (1 - \gamma) \alpha I, \quad X(0) = (1 - \gamma)R(0) \\
\frac{dY}{dt} &= \gamma \alpha I, \quad Y(0) = \gamma R(0)
\end{align*}
\]

Note: For obtaining \((S, I, X, Y)\) you need only to solve the SIR system and find \( S(t), I(t), R(t) \), and then allocate, \( X(t) = (1 - \gamma)R(t) \) and \( Y(t) = \gamma R(t) \).
The two-outcome SIR model has the form:

\[
\begin{align*}
\frac{dS}{dt} &= -\beta S \frac{I}{N}, \quad S(0) \\
\frac{di}{dt} &= \beta S \frac{I}{N} - \alpha i, \quad I(0) \\
\frac{dx}{dt} &= (1 - \gamma)\alpha i, \quad X(0) = (1 - \gamma)R(0) \\
\frac{dy}{dt} &= \gamma \alpha i, \quad Y(0) = \gamma R(0)
\end{align*}
\]

Its normalized form in variables \(s, i, r, x = \frac{X}{N}, y = \frac{Y}{N}\) is given by:

\[
\begin{align*}
\frac{ds}{dt} &= -\beta si , \quad s(0) = \frac{S(0)}{N} \\
\frac{di}{dt} &= \beta si - \alpha i , \quad i(0) = \frac{I(0)}{N} \\
\frac{dx}{dt} &= (1 - \gamma)\alpha i , \quad x(0) = (1 - \gamma)\frac{R(0)}{N} \\
\frac{dy}{dt} &= \gamma \alpha i , \quad y(0) = \gamma \frac{R(0)}{N}
\end{align*}
\]

Note the conservation laws: \(N = S(t) + I(t) + X(t) + Y(t)\), \(s(t) + i(t) + x(t) + y(t) = 1\). The deterministic system is initialized by \((S(0), I(0), R(0))\) and its evolution is determined by the choice of three parameters: \((\alpha, \beta, \gamma)\). \(X(t)\) and \(Y(t)\) are computed from \(R(t)\).
SIR Model Analysis

The three parameters have the following meaning:

1. $\beta$ represents the number of close contacts per day per one infected individual; differently said, it is the probability of disease transmission per contact (dimensionless) times the number of contacts per unit of time. Unit: $day^{-1}$

2. $\alpha$ is the removing rate of infectious individuals; its reciprocal is the infectious period. If no death, $\alpha$ represents the recovery rate from infections. Unit: $day^{-1}$

3. $\gamma$ represents the probability of a fatal infection (death) once an individual gets infected. Unit: dimensionless.

$R_0 = \frac{\beta}{\alpha}$ is the reproduction ratio (or, the contact number) and represents the average number of infections caused by one infected individual.

Note: $\alpha$ and $\gamma$ are parameters that characterize the infectious disease and cannot be controlled. Instead, $\beta$ and $\rho$ depend on human interactions, and therefore can be controlled by society/individuals (e.g., during a complete shut-down, $\beta \approx 0$).
SIR Model Calibration: LSE

For calibration and testing we are using two pieces of measured data: the daily infection rates, \{I(0), \cdots, I(T_{max})\}, and the time series of cumulative deaths, \{Y(0), \cdots, Y(T_{max})\}. Note that, if we know \(\gamma\) and \(N\) we can compute
\[ R(0) = \frac{Y(0)}{\gamma} \quad \text{and} \quad S(0) = N - I(0) - R(0). \]

At the onset of an infectious disease it is likely the case that \(R(0) = Y(0) = 0\) and \(I(0)\) is small and given by the first detected cases. Then \(S(0) = N\).

**Assumption 2:** The time series of detected infections undercounts the actual number of infections. Specifically we assume \(I(t) \approx \rho I_{\text{sim}}(t)\), where \(\rho \leq 1\) is a parameter that represents the undercounting factor.

The least-squares estimator (LSE) finds parameters \(\alpha, \beta, \gamma, \rho\) that minimize:

\[
\begin{align*}
&\text{minimize} \quad I(\alpha, \beta, \gamma, \rho) := c_I \sum_{t=0}^{T_{max}} (I(t) - \rho I_{\text{sim}}(t))^2 + c_Y \sum_{t=0}^{T_{max}} (Y(t) - \gamma R_{\text{sim}}(t))^2. \\
&\alpha, \beta, \gamma, \rho \geq 0 \\
&\gamma, \rho \leq 1 
\end{align*}
\]

Weights \(c_I, c_Y \geq 0\) are chosen by user depending on how accurate are the two measured time series. If infections go unreported, set \(c_I = 0, c_Y = 1\). Alternatively, choose \(c_I = c_Y = 1\).
The procedure works like this: \((S_{\text{sim}}(t), I_{\text{sim}}(t), R_{\text{sim}}(t))\) are simulated with a numerical solver for the SIR model with parameters \((\alpha, \beta)\) initialized at \((S(0), I(0), R(0))\). Parameters \(\gamma\) and \(\rho\) are then obtained by solving two independent optimization problems:

\[
\hat{\rho} = \arg\min_{0 \leq \rho \leq 1} \sum_{t=0}^{T_{\max}} (I(t) - \rho I_{\text{sim}}(t))^2, \quad \hat{\gamma} = \arg\min_{0 \leq \gamma \leq 1} \sum_{t=0}^{T_{\max}} (Y(t) - \gamma R_{\text{sim}}(t))^2
\]

Then compute the objective function \(J(\alpha, \beta) = I(\alpha, \beta, \hat{\gamma}, \hat{\rho})\) and minimize over the set of pairs \((\alpha, \beta)\) used in simulations.
A simple modification of the SIR vanilla model is to consider vital signals, such as births and deaths at separate processes. In normalized form this becomes:

\[
\begin{align*}
\frac{ds}{dt} &= \frac{\Lambda}{N} - \beta si - \mu s, \quad s(0) = \frac{S_0}{N} \\
\frac{di}{dt} &= \beta si - \alpha i - \mu i, \quad i(0) = \frac{I_0}{N} \\
\frac{dr}{dt} &= \alpha i - \mu r, \quad r(0) = \frac{R_0}{N}
\end{align*}
\]

(SIR Model)

where \( \Lambda \geq 0 \) is the constant source of births (=number of births/day) and \( \mu \geq 0 \) is the natural death rate (i.e., in the absence of this virus). Its reciprocal \( 1/\mu \) represents the average life expectancy.