1 SIR EPIDEMIC MODEL

This model assumes that each member of a population is either susceptible to the disease (S), infected with the disease (I), or recovered from the disease with long-term immunity. If the disease is short-lived compared to the population, we can ignore vital dynamics (that is births and natural deaths).

In the case of airborne diseases or when infection occurs by respiratory secretion on hands, the rate of infections is modeled by a mass action term βSI where β is the disease transmission constant. If the mean infectious (or recovery) time is denoted by $1/\gamma$ (it is about 14 days for covid-19), the recovery rate can be modeled by γI. Let also f be the fraction of infected people who recover from the disease. With these assumptions, the disease dynamics can be simply described by the following system of ODEs:

$$\frac{dS}{dt} = -\beta SI \tag{1}$$

$$\frac{dI}{dt} = \beta SI - \gamma I \tag{2}$$

$$\frac{dR}{dt} = f\gamma I \tag{3}$$

The initial conditions are:

$$S(0) = S_0, \qquad I(0) = I_0, \qquad R(0) = 0 \tag{4}$$

where $I_0 \ll S_0$

By introducing the dimensionless variables

$$\overline{S} = \frac{S}{S_0}, \quad \overline{I} = \frac{I}{S_0}, \quad \overline{R} = \frac{R}{S_0}, \quad \tau = \gamma t$$

equations (1) to (4) become:

$$\frac{d\overline{S}}{d\tau} = -\frac{\beta S_0}{\gamma}\overline{S}\cdot\overline{I} \tag{5}$$

$$\frac{d\overline{I}}{d\tau} = \frac{\beta S_0}{\gamma}\overline{S}\cdot\overline{I} - \overline{I} \tag{6}$$

$$\frac{d\overline{R}}{d\tau} = f \cdot \overline{I} \tag{7}$$

with initial conditions:

$$\overline{S}(0) = 1, \qquad \overline{I}(0) = \frac{I_0}{S_0}, \qquad \overline{R}(0) = 0 \tag{8}$$

In the early stages of the epidemic and if the initial fraction of infected people is very small $\left(I_0 \ll S_0\right)$, the number of susceptible people will remain almost constant. That is $S(t) \approx S_0$ or $\overline{S} \approx 1$ for very small times. Then equation (6) becomes

$$\frac{d\overline{I}}{d\tau} = \frac{\beta S_0}{\gamma} \cdot \overline{I} - \overline{I} = \left(\frac{\beta S_0}{\gamma} - 1 \right) \overline{I} \tag{9}$$

whose solution is:

$$\overline{I} = \overline{I}_0 \exp\left[\left(\frac{\beta S_0}{\gamma} - 1 \right) \tau \right] \tag{10}$$

and in dimensional variables

$$I = I_0 \exp\left[\gamma \left(\frac{\beta S_0}{\gamma} - 1 \right) t \right] \tag{11}$$

If $$\frac{\beta S_0}{\gamma} < 1 \tag{12}$$

the number of infected people will decrease exponentially, and the disease will be extinguished. If $\frac{\beta S_0}{\gamma} > 1$, on the other hand, the number of infected people will increase exponentially.

The ratio $R_0 = \beta S_0 / \gamma$ is called the ***basic reproduction number*** of an infectious disease and is usually described as "the average number of secondary cases produced by introducing one infected individual into a population of susceptible individuals."

Figure 1 presents the infected and recovered population fractions for various values of the basic reproduction number R_0. As expected from the previous discussion on the intial stages of the epidemic, the disease spreads rapidly for large values of R_0 and 40% of the population will be infected 80 days after community spread begins with $R_0 = 4$. As more people recover, the infected fraction of the population decreases with time and eventually drops to less than 0.1% at

about 8 months after the first infection was observed. At that point, however, 97% of the population has recovered and only 3% of the population has not been infected.

Smaller values of the basic reproduction number lower the maximum (apex) of the infection curve and shift it to longer times (about 120 days from 80 when R_0 drops from 4 to 3). Figure 1 also shows that an increasingly larger fraction of the population will not get infected as R_0 decreases (about 7% for $R_0 = 3$ and about 21% for $R_0 = 2$.

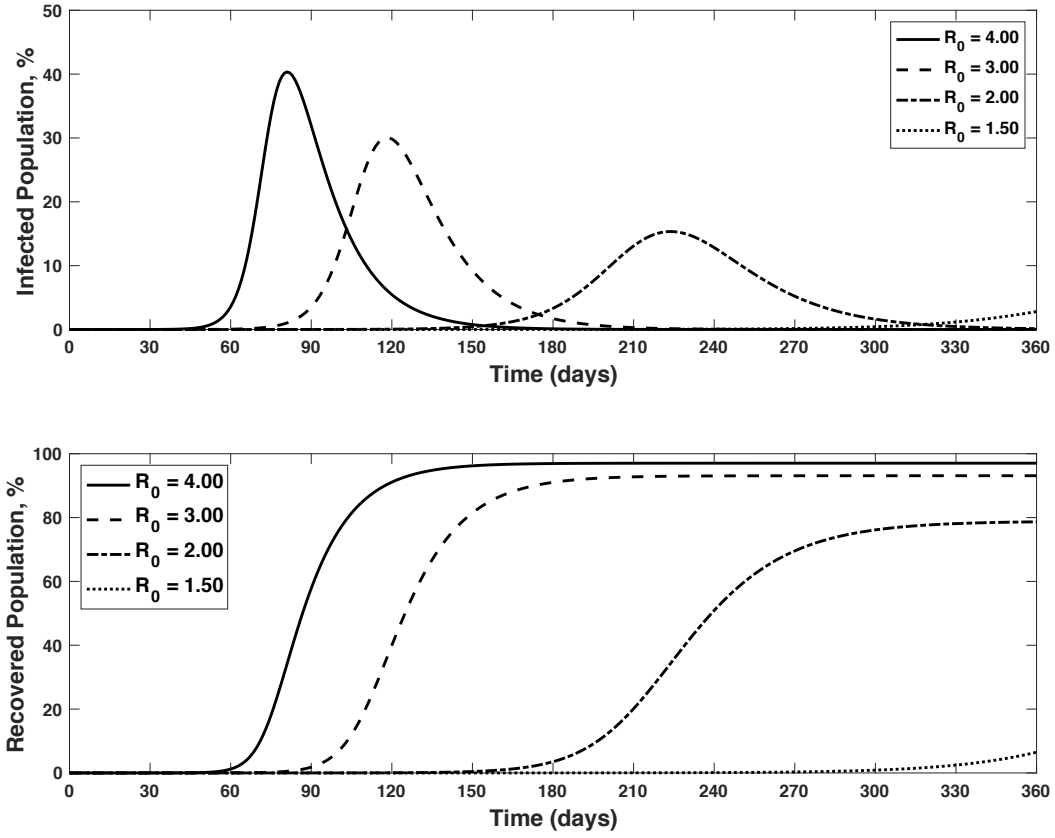

Figure 1: SIR model predictions for the percentages of infected people $I(t)/S_0$ (top panel) and recovered people $R(t)/S_0$ (bottom panel) for several values of the basic reproduction number R_0.
Data for these simulations: $1/\gamma = 14$ days; $\overline{I}_0 = 10^{-7}$; $f = 0.99$.

The rate at which the number of infections increases or, equivalently, the number of new infections per day is of critical importance. When this rate is very large, the number of new

infections and, thus, the number of new patients requiring hospitalization may exceed the ability of local health care systems to treat them. Figure 2 shows how the basic reproduction number R_0 affects the number of new infections per day. Reducing R_0 from 4 to 2 reduces by more than a factor of 4 the number of new patients per day who will seek treatment. The peak demand is also delayed giving the local health care systems time to adapt and expand their capacity.

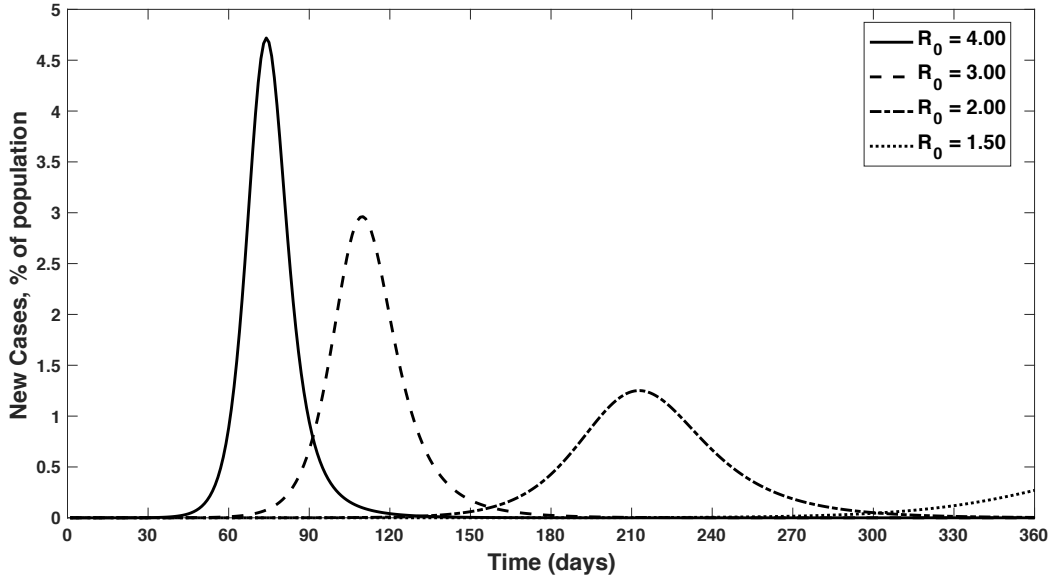

Figure 2: SIR model predictions for the number of new infections per day for several values of the basic reproduction number R_0.0
Data for these simulations: $1/\gamma = 14$ days; $\overline{I}_0 = 10^{-7}$; $f = 0.99$.

If the initial fraction of infected people is very small compared to the size of the population $\left(I_0 \ll S_0\right)$, the number of infected people in the early stages of the epidemic will increase exponentially and can be computed by Equation (11). If we know the recovery time $1/\gamma$, we can estimate the basic reproduction number R_0 by plotting $\log\left(I(t)/I_0\right)$ vs. time, fitting the data with a straight line and estimating R_0 from the slope $\gamma\left(R_0 - 1\right)$. Similarly, and if we are still in the early stages of the disease, the doubling time for the infection can be computed by:

$$t_{double} = \frac{\log(2)}{\gamma\left(R_0 - 1\right)} \tag{13}$$

Figure 3 shows that the assumption of exponential spreading of the disease is valid for a considerable length of time and until a significant fraction of the population has been infected.

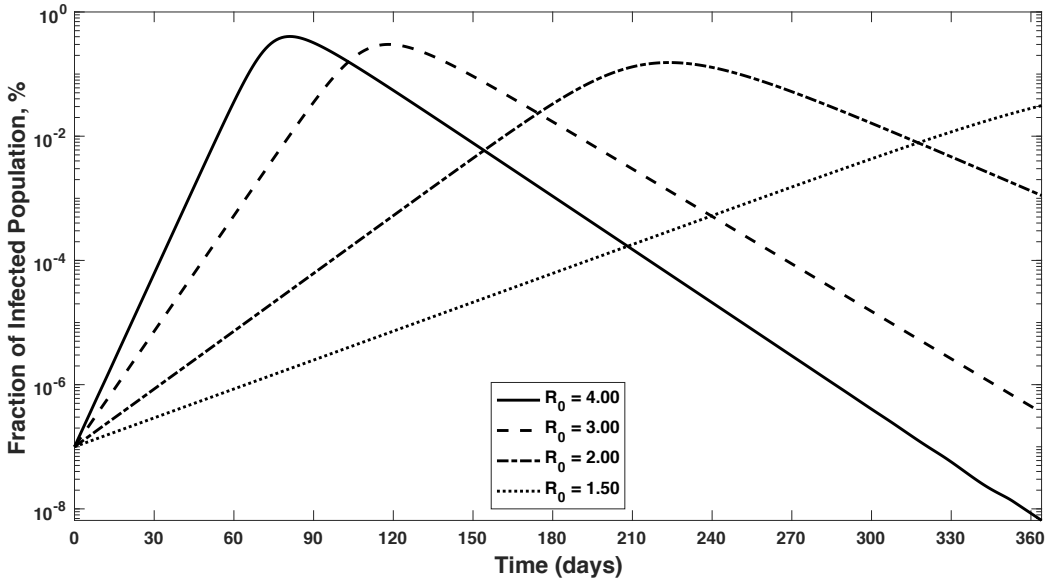

Figure 3: SIR model predictions showing in a semilogarithmic plot the percentage of infected people $I(t)/S_0$ for several values of the basic reproduction number R_0. Data for these simulations: $1/\gamma = 14$ days; $\overline{I}_0 = 10^{-7}$; $f = 0.99$.

2 SEIR MODEL

For many infectious diseases, there is a latent period between the time a person is infected and the time this person can transmit the disease to others. During this period the pathogen is present in the host in low enough numbers so that the ***host is not yet infectious***. This necessitates the introduction of a fourth subpopulation of exposed people (*E*) in addition to the susceptible, infected and recovered ones. If we assume that the mean duration of the latent or exposed period is $1/\kappa$, the rate at which exposed people move into the infected subpopulation is $\kappa E(t)$. If we again ignore the natural death rate, the dynamics of the epidemic can be described by the following system of ODEs:

$$\frac{dS}{dt} = -\beta SI \tag{14}$$

$$\frac{dE}{dt} = \beta SI - \kappa E \tag{15}$$

$$\frac{dI}{dt} = \kappa E - \gamma I \tag{16}$$

$$\frac{dR}{dt} = f\gamma I \tag{17}$$

The initial conditions are:

$$S(0) = S_0, \qquad E(0) = E_0, \quad I(0) = 0, \; R(0) = 0 \tag{18}$$

where again the initial fraction of exposed people is a small fraction of the population:

$$I_0 \ll S_0$$

By introducing the dimensionless variables

$$\overline{S} = \frac{S}{S_0}, \quad \overline{E} = \frac{E}{S_0}, \quad \overline{I} = \frac{I}{S_0}, \quad \overline{R} = \frac{R}{S_0}, \quad \tau = \gamma t$$

equations (14) to (17) become:

$$\frac{d\overline{S}}{d\tau} = -\frac{\beta S_0}{\gamma}\overline{S} \cdot \overline{I} \tag{19}$$

$$\frac{d\overline{E}}{d\tau} = \frac{\beta S_0}{\gamma}\overline{S} \cdot \overline{I} - \frac{\kappa}{\gamma}\overline{E} \tag{20}$$

$$\frac{d\overline{I}}{d\tau} = \frac{\kappa}{\gamma}\overline{E} - \overline{I} \tag{21}$$

$$\frac{d\overline{R}}{d\tau} = f \cdot \overline{I} \tag{22}$$

with initial conditions:

$$\overline{S}(0) = 1, \quad \overline{E}(0) = \frac{E_0}{S_0}, \quad \overline{I}(0) = 0, \quad \overline{R}(0) = 0 \tag{23}$$

In the early stages of the epidemic and if the initial fraction of exposed people is extremely small $\left(E_0 \ll S_0\right)$, the number of susceptible people will remain almost constant, that is $S(t) \approx S_0$ or $\overline{S} \approx 1$ for small times *t*. Under these conditions, the equations (20) and (21) that drive the dynamics of the epidemic become:

$$\frac{d\bar{E}}{d\tau} = -\frac{\kappa}{\gamma}\bar{E} + \frac{\beta S_0}{\gamma}\bar{I} \tag{24}$$

$$\frac{d\bar{I}}{d\tau} = \frac{\kappa}{\gamma}\bar{E} - \bar{I} \tag{21}$$

These equations are a system of first order ODEs with constant coefficients:

$$\begin{bmatrix} \frac{d\bar{E}}{d\tau} \\ \frac{d\bar{I}}{d\tau} \end{bmatrix} = \begin{bmatrix} -\frac{\kappa}{\gamma} & \frac{\beta S_0}{\gamma} \\ \frac{\kappa}{\gamma} & -1 \end{bmatrix} \begin{bmatrix} \bar{E}(\tau) \\ \bar{I}(\tau) \end{bmatrix} = \mathbf{A} \cdot \begin{bmatrix} \bar{E}(\tau) \\ \bar{I}(\tau) \end{bmatrix} \tag{25}$$

whose solution consists of linear combinations of terms $e^{\lambda_1 \tau}$ and $e^{\lambda_2 \tau}$ in which λ_1 and λ_2 are the eigenvalues of **A** obtained by solving the equation:

$$\det(\mathbf{A} - \lambda \mathbf{I}) = \begin{vmatrix} -\frac{\kappa}{\gamma} - \lambda & \frac{\beta S_0}{\gamma} \\ \frac{\kappa}{\gamma} & -1 - \lambda \end{vmatrix} = \left(-\frac{\kappa}{\gamma} - \lambda\right)(-1 - \lambda) - \frac{\beta S_0}{\gamma}\frac{\kappa}{\gamma}$$

or
$$\lambda^2 + \left(1 + \frac{\kappa}{\gamma}\right)\lambda + \frac{\kappa}{\gamma}\left(1 - \frac{\beta S_0}{\gamma}\right) = 0 \tag{26}$$

The exposed and infected subpopulations will decrease exponentially, and the disease will die out if both eigenvalues λ_1 and λ_2 are negative. Since

$$\lambda_1 + \lambda_2 = -\left(1 + \frac{\kappa}{\gamma}\right) \text{ and } \lambda_1 \cdot \lambda_2 = \frac{\kappa}{\gamma}\left(1 - \frac{\beta S_0}{\gamma}\right)$$

and $\left(1 + \frac{\kappa}{\gamma}\right) > \frac{\kappa}{\gamma} > 0$, both eigenvalues will be real and negative if and only if

$$1 - \frac{\beta S_0}{\gamma} > 0$$

or
$$\frac{\beta S_0}{\gamma} < 1 \tag{27}$$

When $R_0 = \dfrac{\beta S_0}{\gamma} > 1$, the exposed and infected subpopulations will increase exponentially, and the disease will spread. Note that this is the same criterion we used to determine whether a disease described by the SIR model will spread or die out.

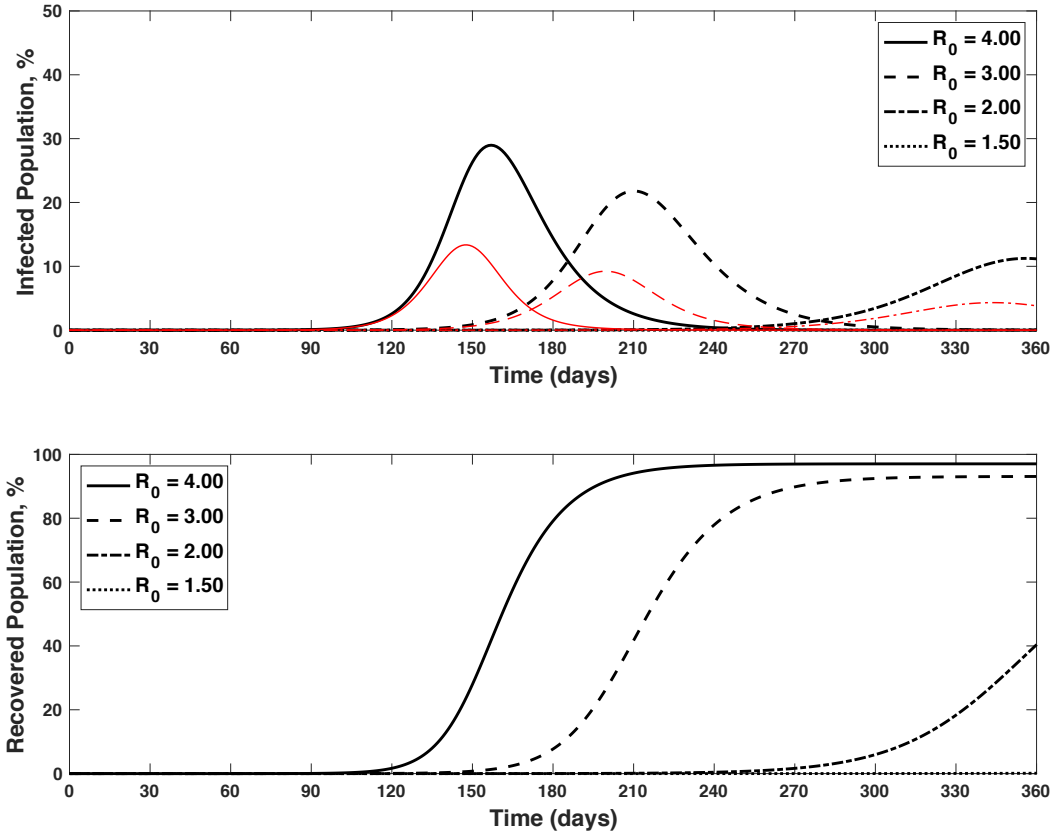

Figure 4: SEIR model predictions for the percentages of infected people $I(t)/S_0$ (top panel) and recovered people $R(t)/S_0$ (bottom panel) for several values of the basic reproduction number R_0. The thinner red lines in the top panel represent the SEIR model predictions for the percentage of exposed people $E(t)/S_0$ that peak before the infection curves.
Data for these simulations: $1/\gamma = 14$ days; $1/\kappa = 5$ days; $\bar{E}_0 = 10^{-7}$; $f = 0.99$.

Figure 4 presents the SEIR model predictions for the percentage of infected and recovered people for the same values of the basic reproduction number R_0 used for Figure 1 and the SIR

model. Again, the higher the basice reproduction number R_0 the more rapidly the disease will spread. When compared to the SIR model predictions, however, the infection curves predicted by the SEIR model are broader and take longer to reach their maximum (apex). This is because of the latent period during which the people exposed to the disease are not infectious. For $R_0 = 4$ and a latent period of 5 days, the SEIR infection curve reaches a maximum of 29% of the population at about 158 days (top panel of Fig. 1). The corresponding predictions of the SIR model were 40% of the population infected at 80 days (Figure 1). For $R_0 = 1.5$, the SEIR model predicts very low infections for a full year after the start of community spreading.

Again because of the latent period during which the exposed people are not infectious, the SEIR model predicts much lower numbers of new infections per day when compared to the SIR model (Figure 5).

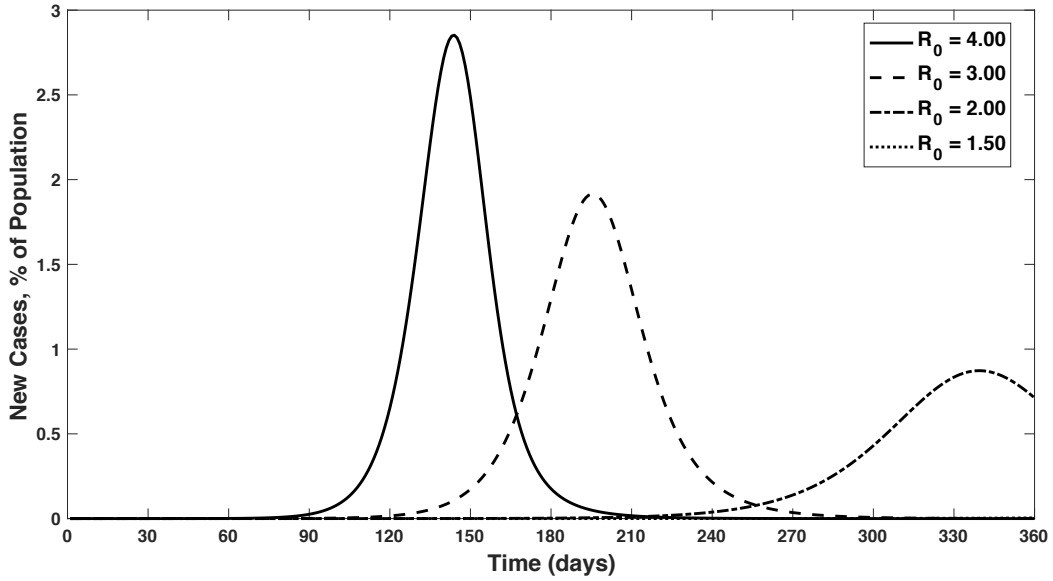

Figure 5: SEIR model predictions for the number of new infections per day for several values of the basic reproduction number R_0.
Data for these simulations: $1/\gamma = 14$ days; $1/\kappa = 5$ days; $\bar{E}_0 = 10^{-7}$; $f = 0.99$.

For the SEIR model, the early stages of the epidemic are described by the ODE system of Equation (25) whose solution is given by linear combinations of the terms $e^{\lambda_1 \tau}$ and $e^{\lambda_2 \tau}$, where

the eigenvalues λ_1 and λ_2 are solutions of the quadratic equation (26). For $1/\gamma = 14$ days, $1/\kappa = 5$ days and $R_0 = 4$, these eigenvalues are:

$$\lambda_1 = -5.366 \text{ and } \lambda_2 = 1.566$$

while for $R_0 = 1.5$ and the same values of γ and κ:

$$\lambda_1 = -4.138 \text{ and } \lambda_2 = 0.338$$

The SEIR model predictions are shown in Figure 6 for the R_0 values considered here. After a short initial transient, the positive eigenvalue dominates and the infection curve increases exponentially until it reaches the neighborhood of its maximum.

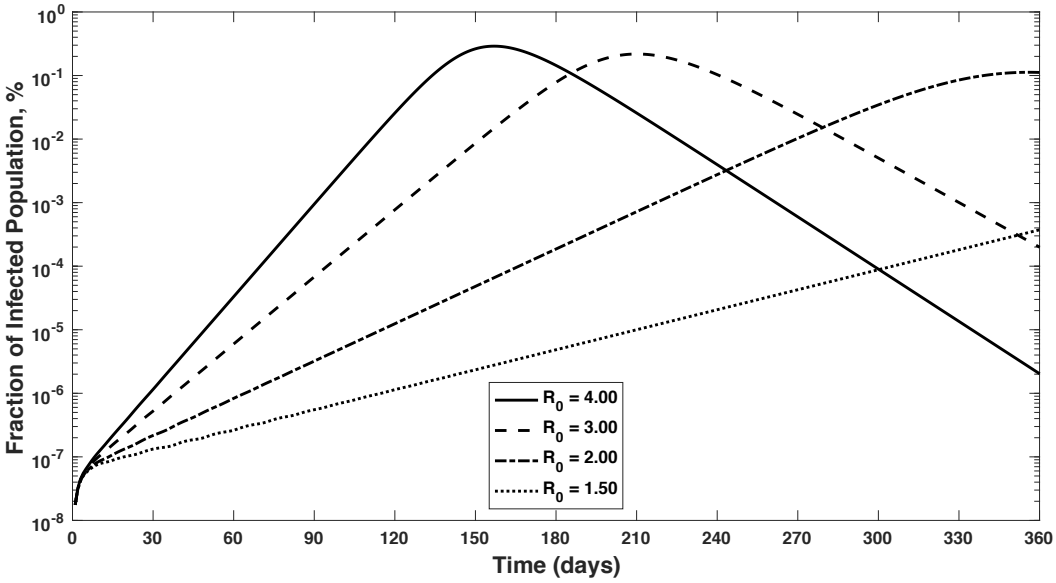

Figure 6: SEIR model predictions showing in a semilogarithmic plot the percentage of infected people $I(t)/S_0$ for several values of the basic reproduction number R_0. Data for these simulations: $1/\gamma = 14$ days; $1/\kappa = 5$ days; $\bar{E}_0 = 10^{-7}$; $f = 0.99$.

3 HOW DO MITIGATION MEASURES FLATTEN THE CURVE?

While COVID-19 has a latent period, people exposed to the SARS-CoV-2 virus are infectious before they exhibit any symptoms. Thus, the SIR model may be more appropriate to model the spread of COVID-19. Alternatively, we can modify the SEIR model by assuming that interactions between susceptible and exposed people will also contribute to the rate at which the number of exposed people increases.

For the sake of simplicity, we will use the SIR model to study how the spread of an infectious disease (like COVID-19) can be managed by mitigation measures (like shelter-in-place or physical distancing regulations) that modulate the basic reproduction number R_0.

We will consider the following four approaches for managing the spread of the disease:

1. No mitigation measures are adopted: $R_0 = 4$ at all times.
2. Mitigation measures are adopted 10 weeks after community spread begins and they lower R_0 to 0.95 within one week. After 4 weeks, the mitigation measures are relaxed and R_0 increases to 1.5.
3. Mitigation measures are adopted 8 weeks after community spread begins and they lower R_0 to 0.95 within one week. After 4 weeks, the mitigation measures are relaxed and R_0 increases to 1.5.
4. Mitigation measures are adopted 6 weeks after community spread begins and they lower R_0 to 0.95 within one week. After 4 weeks, the mitigation measures are relaxed and R_0 increases to 1.5.

Figures 7 and 8 show how the percentages of infected people and the number of new infections vary with time when the basic reproduction number R_0 remains constant varies with time as described above.

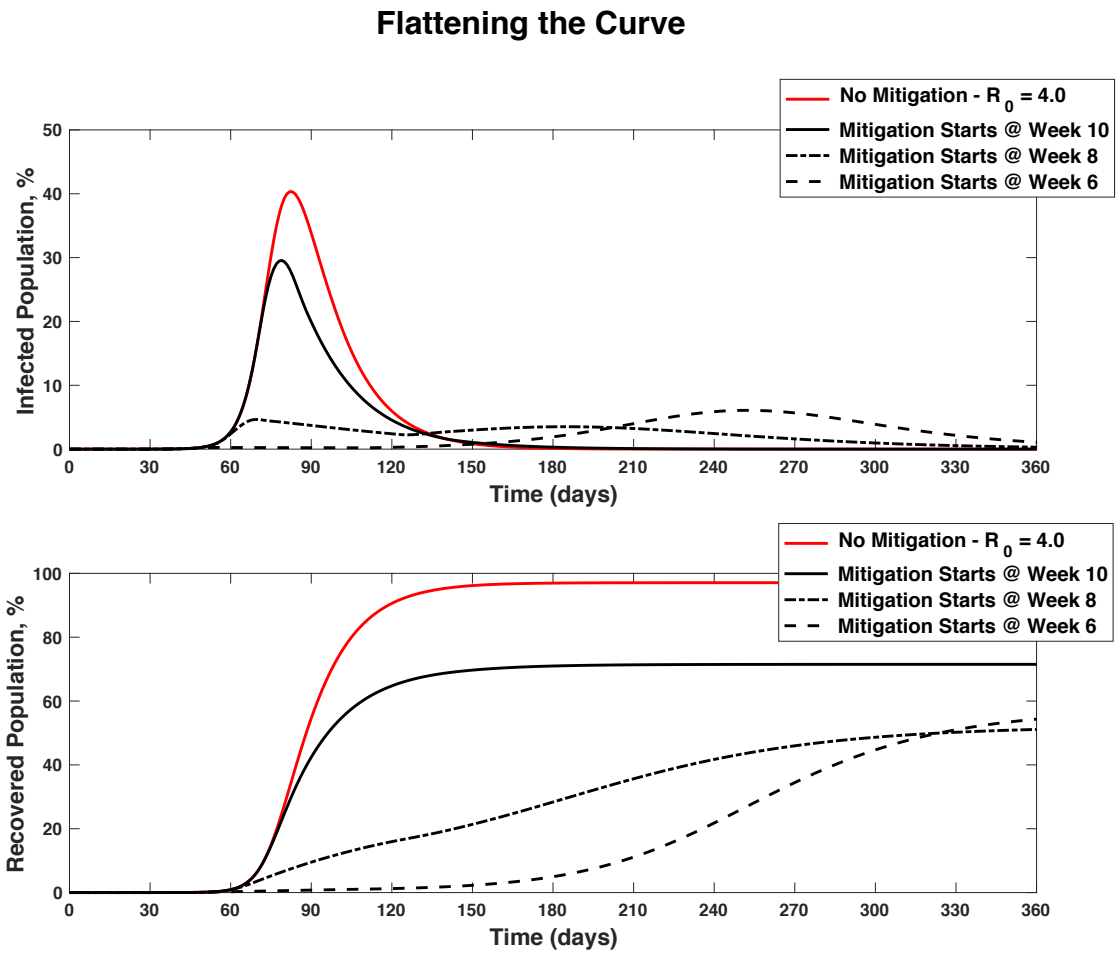

Figure 7: SIR model predictions for the percentages of infected people $I(t)/S_0$ (top panel) and recovered people $R(t)/S_0$ (bottom panel) for the following approaches to disease management:

1. No mitigation measures: Basic reproduction number R_0 is constant at 4.
2. Mitigation measures adopted at week 10 to reduce R_0 to 0.95. R_0 increases to 1.5 after 4 weeks.
3. Mitigation measures adopted at week 8 to reduce R_0 to 0.95. R_0 increases to 1.5 after 4 weeks.
4. Mitigation measures adopted at week 6 to reduce R_0 to 0.95. R_0 increases to 1.5 after 4 weeks.

Data for these simulations: $1/\gamma = 14$ days; $\overline{I}_0 = 10^{-7}$; $f = 0.99$.

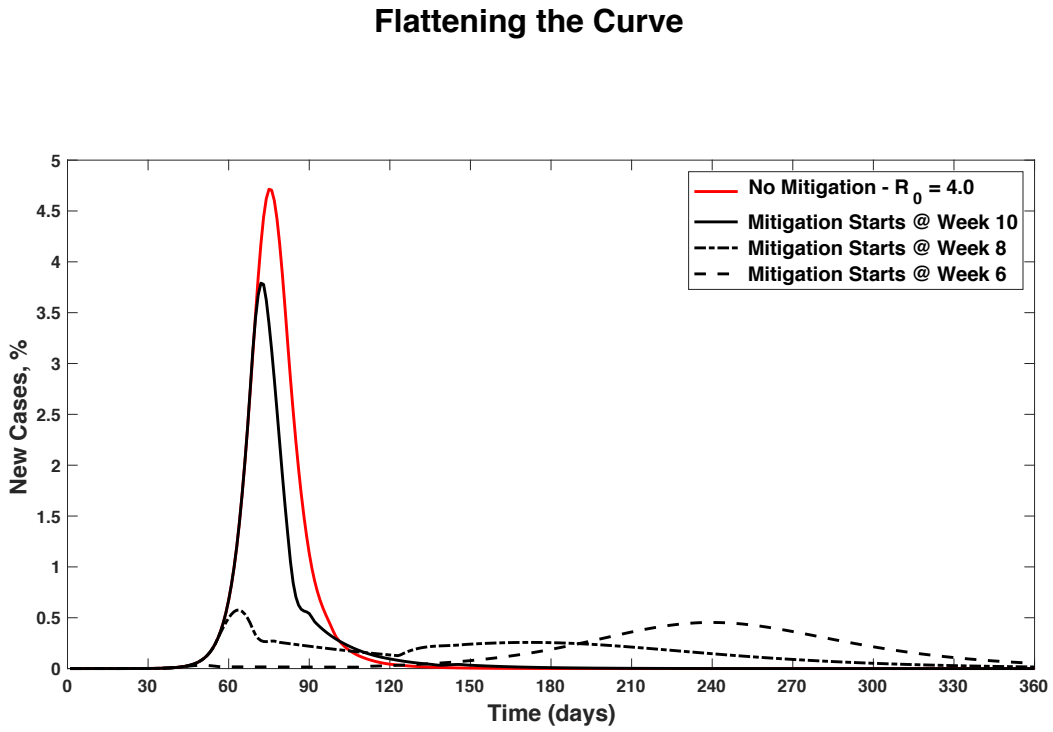

Figure 8: SIR model predictions for the number of new infections (or cases) for the following approaches to disease management:

1. No mitigation measures: Basic reproduction number R_0 is constant at 4.
2. Mitigation measures adopted at week 10 to reduce R_0 to 0.95. R_0 increases to 1.5 after 4 weeks.
3. Mitigation measures adopted at week 8 to reduce R_0 to 0.95. R_0 increases to 1.5 after 4 weeks.
4. Mitigation measures adopted at week 6 to reduce R_0 to 0.95. R_0 increases to 1.5 after 4 weeks.

Data for these simulations: $1/\gamma = 14$ days; $\overline{I}_0 = 10^{-7}$; $f = 0.99$.