Fluid models for infective disease propagation

D. Deplano and A. Giua

DIEE, University of Cagliari, 09123 Cagliari, Italy.

Email: diego.deplano@unica.it, giua@unica.it

14 May 2020

1 Introduction

This short note provides a brief introduction to two of the the most common epidemic models, SIR and SEIR following the material presented in [1, 2, 4].

The spread of an epidemic is intrinsically a discrete event process. The state of an epidemic in a population can be represented by discrete variables, such as the number of individuals that are susceptible to the infection, the number of persons that have been exposed or that are infective, the number of people that have recovered or are immune because have been vaccinated, etc. The evolution of such a system depends on the asynchronous and random occurrence of events such as "a new person has been infected", "an infective has recovered", etc.

However, given the large number of individuals in a population, the formulation and analysis of a *microscopic* model, where the state of each person is individually taken into account, is not always possible. This is why it is common to abstract these models via a technique called *fluidization*, which consists in approximating the discrete state value of a high-populated system by means of continuous average variables so that a *macroscopic* time-driven model, in terms of differential or difference equations, can be formulated. Fluidification [3] is an efficient relaxation technique to tackle classical state explosion problems in discrete event systems and has often been used for performance analysis and optimization.

Although the epidemic models we present in this note are purely continuous, we emphasize that a full understanding of their dynamics and of the physical meaning of their parameters is rooted in the theory of stochastic discrete-event and fluid processes.

As a final comment, we point out that continuous macroscopic models, based on average values,

are very useful to decision makers: they allow them to study different scenarios depending on which measure to contrast an epidemic are taken, or to predict its spread in a quantitative way and thus plan an appropriate use of resources. However, when the number of infected individuals is quite small — e.g., at the beginning or at the tail of an infection spread — microscopic models, where all infective individuals are identified and they movements are tracked, are of greater use.

2 The SIR model structure

We want to study how an infective disease caused by a germ can spread in a population. To this aim we define the following variables.

- $S(t)$: the number of *susceptible* individuals at time t. These are individuals which are at risk of being infected.
- $I(t)$: the number of *infective* individuals at time t. These are individuals that have been infected with the germ and may transmit it to susceptible individuals.
- $R(t)$: the number of *removed* individuals at time t. These are individuals that are immune and cannot transmit the infection to others.
- $N(t) = S(t) + I(t) + R(t)$: the *size of the population* at time t.

Such a partitioning of the total population into disjoint classes can be seen as a *compartmental model*[1]. We assume that individual may move from one class to another one according to specified dynamics.

Here we consider the so-called *SIR model* which is based on several assumptions.

Assumption 1. The size of the population is constant, i.e., $N(t) = N$ for all t. This is a reasonable assumption if the following conditions both hold: (a) the epidemic spread has a short duration with respect to the nominal population dynamics characterized by nominal births and deaths; (b) population is isolated, with no arrivals or departures from/to the external world. Note that deaths from the disease are possible but will not affect the size of the population (see Assumption 3 below).

Assumption 2. No vaccine is available. Hence susceptible individuals can be infected (moving to class S) but cannot be removed (moving directly to class R).

Assumption 3. Infected individuals may either recover (and in this case they develop immunity to the disease) or may also die as a result of the infection. In both cases they move to class R.

[1]Compartmental models describe how material or energy flows are transmitted between different parts (compartments) of a system. Each compartment is an homogenous entity, i.e., the distribution of material or energy within it can be considered uniform. They are also often used to model population dynamics: in such a case, a compartment represent a class of individuals with the same property.

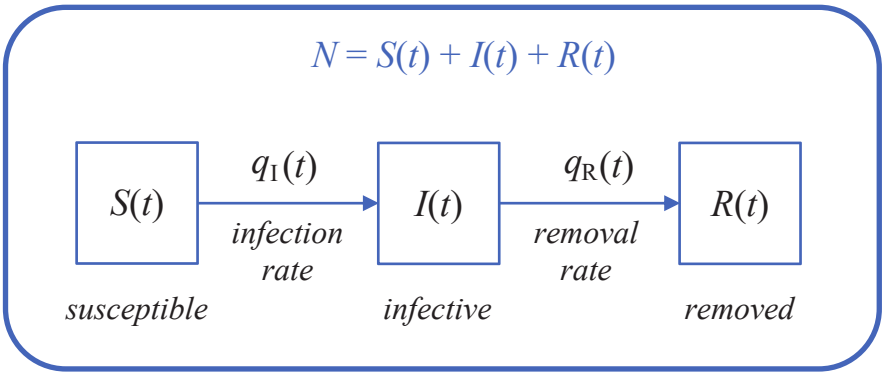

Figure 1: Compartmental view of a SIR model.

Based on these three assumptions we have a three-compartment model as shown in Figure 1 characterized by two flows.

- $q_I(t)$: *infection rate*. This is the number of susceptible individuals that, at time t, become infected in a unit of time.
- $q_R(t)$: *removal rate*. This is the number of infective individuals that, at time t, recover or die in a unit of time.

Note that the two rates are expressed in *num. of individuals / time*, e.g., 300 persons/day or 21,000 persons/week.

The last assumption we consider is the following.

Assumption 4. The number of individuals in the population is very large and we can assume all variables S, I, R, q_I and q_R take real nonnegative values (as opposed to nonnegative integer values). This allow us to consider a continuous-time fluid model involving these variables and their derivatives.

Based on all previous assumptions we can present a first SIR model in continuous-time where the exact dynamics (the precise value of the infection and removal rates) need not be specified.

Definition 1 (Abstract SIR model). *The model in Figure 1 is ruled by the following dynamical equations:*

$$\begin{cases} \frac{d}{dt}S(t) &= -q_I(t) \\ \frac{d}{dt}I(t) &= q_I(t) - q_R(t) \\ \frac{d}{dt}R(t) &= q_R(t) \end{cases} \tag{1}$$

▲

From this abstract model we can verify that, starting from an initial condition $S(0), I(0), R(0)$, the total number of individuals $N(t) = S(t) + I(t) + R(t)$ is constant because:

$$\frac{d}{dt}N(t) = \frac{d}{dt}S(t) + \frac{d}{dt}I(t) + \frac{d}{dt}R(t) = -q_I(t) + (q_I(t) - q_R(t)) + q_R(t) = 0,$$

and thus it holds that $N = S(0) + I(0) + R(0)$.

In addition we observe that:

- The number of susceptible individuals $S(t)$ is non-increasing because its derivative can never be positive (by definition $q_I \geq 0$).
- The number of removed individuals $R(t)$ is non-decreasing since its derivative can never be negative (by definition $q_R \geq 0$).
- On the contrary, depending on the current values of the infection and removal rates the number of infective individuals $I(t)$ may increase or decrease.

Finally, it is worth noticing that an equivalent second order model can be obtained considering only the first two equations in (1), where the variable R does not appear. Once this system of two differential equations is solved to determine $S(t)$ and $I(t)$, one can directly determine $R(t)$ using the algebraic equation $R(t) = N - S(t) - I(t)$.

3 Formulation of the SIR model

We now provide a more precise formalization of the flows between compartments in the SIR model shown in Figure 1. The two flows are the infection rate $q_I(t)$ and the removal rate $q_R(t)$. Suitable expressions for these variables can be derived averaging the underlying discrete-event microscopic dynamics of individuals.

3.1 Infection rate

We assume that the infection can be transmitted when a susceptible and an infective individual engage in a contact. Let us first define two parameters.

- *Transmission factor* τ: denotes the probability that an individual is infected when exposed to the infective agent. This parameter is nondimensional.
- *Risky contact rate* ϱ: denotes the number of risky contacts that an individual engages in during a unit of time. A contact is called risky if it may expose an individual to the infective agent. This parameter has the dimension of the inverse of a time, e.g., day^{-1} or $week^{-1}$.

A risky contact, depending on the disease, may have different definitions: sexual act, physical proximity, indirect contact via contaminated surfaces, etc. The transmission factor is related to the infectivity or virulence of the diseases but may also vary according to the type contact: as an example, there may exist high-risk and low-risk contacts. The risky contact rate also varies from one individual to another one, depending on lifestyle, profession, etc. Here we consider for both parameters an average value over all the population and all type of risky contacts.

***Example* 1.** *During the COVID-19 epidemic in early 2020, many countries have adopted measures to limit the spread of the disease. Regulations requiring the use of a face mask or the frequent disinfection of surfaces in public places aim to reduce the transmission factor of the infection. Regulations such as the closing of schools or other lockdown measures aim to reduce the risky contact rate.* ◇

Combining these two values, one can define a fundamental parameter characterizing the SIR model.

Definition 2 (**Adequate contact rate).** *The* adequate contact rate

$$\beta = \tau \cdot \varrho \tag{2}$$

denotes the average number of contacts leading to disease transmission in which an individual engages in a unit of time. This parameter has the dimension of the inverse of a time. ▲

In the literature is also common to directly define the parameter β without mentioning its two factors τ and ϱ: in such a case β may be simply called *contact rate*, not being necessary to distinguish it from ϱ.

***Example* 2.** *The virus of Hepathitis B, called HBV, is sexually trasmissible. Assume that the transmission factor during a risky intercourse is $\tau = 0.7$. If in a population the average individual engages in $\varrho = 2$ risky intercourses per year, the adequate contact rate if $\beta = \tau \cdot \varrho = 1.4$ intercourses per year.* ◇

Let us now look at the disease spread from the point of an infective person. The average number of susceptible persons infected by an infective individual in a unit of time is

$$\phi_{I \to S}(t) = \beta \cdot \frac{S(t)}{N} \tag{3}$$

since the rate of adequate contacts is β and when the contact is with a susceptible individual (with probability $S(t)/N$) the disease is transmitted. The inverse of this rate is the time

$$\delta_{I \to S}(t) = \frac{1}{\phi_{I \to S}(t)} = \frac{N}{\beta \cdot S(t)} \tag{4}$$

that passes, on average, between two different transmissions caused by the same infective individual.

Dually, we can look at the disease spread from the point of a susceptible person. The rate at which a susceptible individual can be infected is

$$\phi_{S \to I}(t) = \beta \cdot \frac{I(t)}{N} \tag{5}$$

since the rate of adequate contacts is β and when the contact is with an infective individual (with probability $I(t)/N$) the disease is transmitted. The inverse of this rate is the time

$$\delta_{S\to I}(t) = \frac{1}{\phi_{S\to I}(t)} = \frac{N}{\beta \cdot I(t)} \tag{6}$$

that passes, on average, before the susceptible individual gets infected.

We can finally compute the total infection rate $q_I(t)$ at time t.

Definition 3 (Infection rate). *The infection rate in eq. (1) has the following expression:*

$$q_I(t) = \phi_{I\to S}(t) \cdot I(t) = \phi_{S\to I}(t) \cdot S(t) = \beta \cdot \frac{S(t) \cdot I(t)}{N}, \tag{7}$$

which can be obtained multiplying for the number $I(t)$ of infectives the rate of infection (3) caused by each of them or, equivalently, multiplying for the number $S(t)$ of susceptibles the rate (5) at which each of them is infected. ▲

***Example* 3.** *In a given country with a population of $20M$, the number of individuals infected by HBV is $0.2M$ and $10M$ are vaccinated. Thus we can write $I = 0.2M$, $R = 10$ and $S = 9.8M$.*

Assume the adequate contact rate per year is $\beta = 1.4$. Then the average infective individual in one year transmits the disease to $\phi_{I\to S} = \beta \cdot \frac{S}{N} = 0.69$ persons. On the average a susceptible individual can expect to be infected after $\delta_{S\to I} = \frac{N}{\beta \cdot I} = 71$ years.

The total infection rate is $q_I = \beta \cdot \frac{S \cdot I}{N} = 137,000$ persons per year. ◇

3.2 Removal rate

Typically a disease is characterized by a random time from infection to recovery, or more generally from infection to removal (including also disease induced deaths).

Let us consider a stationary condition, where, on the average, the number of infective people remains constant. In such a case, the infective compartment can be seen as a stationary queuing system where *Little's law* applies (see Appendix A) and can be rewritten as follows:

$$\bar{I} = \bar{q} \cdot \theta_I \qquad \text{or equivalently} \qquad \bar{q} = \frac{\bar{I}}{\theta_I} \tag{8}$$

where

- $\bar{I}$ is the average number of infectives (averaged over time).
- $\bar{q} = \bar{q}_I = \bar{q}_R$ is the average infection/removal rate (averaged over time). Note that the two average rates coincide due to the stationarity assumption).
- θ_I is the average *infective period*, i.e., the duration of the infection (averaged over all infective individuals).

***Example* 4.** *The world population affected by common cold at any given time is estimated around $\bar{I} = 60M$ people. Assume the average duration of a cold is: $\theta_I = 5$ days $= 0.7$ weeks. The average number of people that recover by cold in a week is $\bar{q}_R = I/\theta_I = 84M$. Note that the process can be assumed stationary: this means that also the average number of people that catch a cold in a week is $\bar{q}_I = \bar{q}_R = 84M$.* ◇

Although eq. (8) holds for the average values (over time) of the variables $I(t)$ and $q_R(t)$, it is common to use the same law to compute the instantaneous removal rate, which depends on the removal coefficient.

Definition 4 (**Removal coefficient).** *The* removal coefficient

$$\gamma = \frac{1}{\theta_I} \tag{9}$$

denotes the average number of recovered or dead divided by the total number of infected in a unit of time. This parameter has the dimension of the inverse of a time. ▲

Definition 5 (**Removal rate).** *The removal rate in eq. (1) has the following expression:*

$$q_R(t) = \gamma \cdot I(t). \tag{10}$$

which can be obtained multiplying for the number $I(t)$ of infectives the removal coefficient (9). ▲

It should be remarked that eq. (10) may introduce a significant error but leads to a very simple dynamics for the infective population:

$$\frac{d}{dt} I(t) = q_I(t) - \gamma \cdot I(t), \tag{11}$$

where the infection rate $q_I(t)$ can be seen as an input term.

A more precise model should take into account the effective probability distribution of the infective period. Following the notation in Appendix B, assume the duration of the infection is a random variable $\Theta \sim (R_{\geq 0}, f)$ with probability density function $f(\theta)$ and complementary probability function $F'(\theta) = Pr(\Theta > \theta) = 1 - \int_0^\theta f(s) \cdot ds$.

In such a case the solution of eq. (11) starting from initial condition $I(0)$ takes the form:

$$I(t) = I(0) \cdot F'(t) + \int_0^t q_I(s) \cdot F'(t-s) \cdot ds, \tag{12}$$

where the first term $I(0) \cdot F'(t)$ denotes the number of initially infective individual which have not been removed at time t because their infective period is longer, while in the second term $q_I(s) \cdot F'(t-s) \cdot ds$ denotes the number of new individuals infected during the time interval $[s, s+ds]$ which which have not been removed at time t because their infective period is greater than $t - s$. This equation can be used to compute a more accurate evolution of the infective population when $f(\theta)$ is known.

We conclude this analysis considering the particular case in which the length of the infective period is an exponentially distributed random variable of parameter $\lambda > 0$, i.e., it holds (see Appendix B):

$$f(\theta) = \lambda \cdot e^{-\lambda\theta}, \qquad F'(\theta) = e^{-\lambda\theta}, \qquad \text{and} \qquad \theta_I \stackrel{\text{def}}{=} E[\Theta] = \frac{1}{\lambda}.$$

Thus eq. (12) becomes:

$$I(t) = I(0) \cdot e^{-\lambda t} + \int_0^t q_I(s) \cdot e^{-\lambda(t-s)} \cdot ds = I(0) \cdot e^{-\lambda t} + e^{-\lambda t} \cdot \int_0^t q_I(s) \cdot e^{\lambda s} \cdot ds. \tag{13}$$

Taking the derivative with respect to time of both sides we get

$$\begin{aligned} \frac{d}{dt} I(t) &= -\lambda \cdot I(0) \cdot e^{-\lambda\theta} + e^{-\lambda t} \cdot q_I(t) \cdot e^{\lambda t} - \lambda \cdot e^{-\lambda t} \cdot \int_0^t q_I(s) \cdot e^{\lambda s} \cdot ds \\ &= q_I(t) - \lambda \cdot \left[I(0) + \int_0^t q_I(s) \cdot e^{-\lambda(t-s)} \cdot ds \right] \\ &= q_I(t) - \lambda \cdot I(t) = q_I(t) - \frac{1}{\theta_I} \cdot I(t) \end{aligned}$$

where to compute the derivative of the integral we used the standard rule $\frac{d}{dt} \int_0^t g(s)ds = g(t)$ and in the second line we used (11).

As a result we obtain that the expression in eq. (11) is actually correct when the length of the infection period is an exponentially distributed random variable.

3.3 The standard and normalized SIR model

The expression previously derived in eq. (7) and (10) for infection and removal rates can be substituted in the abstract SIR model (1) to obtain the so-called standard model

Definition 6 (Standard SIR model).

$$\begin{cases} \frac{d}{dt} S(t) &= -\beta \cdot \frac{S(t) \cdot I(t)}{N} \\ \frac{d}{dt} I(t) &= \beta \cdot \frac{S(t) \cdot I(t)}{N} - \gamma \cdot I(t) \\ \frac{d}{dt} R(t) &= \gamma \cdot I(t) \end{cases} \tag{14}$$

▲

The standard model defined in eq. (14) can be normalized considering as variables

- $s(t) = S(t)/N$: the fraction of susceptible individuals on the total population;

- $i(t) = I(t)/N$: the fraction of infective individuals on the total population;
- $r(t) = R(t)/N$: the fraction of removed individuals on the total population.

Using these new variables, eq. (14) can be rewritten as follows.

Definition 7 (Normalized SIR model).

$$\begin{cases} \frac{d}{dt}s(t) &= -\beta \cdot s(t) \cdot i(t) \\ \frac{d}{dt}i(t) &= \beta \cdot s(t) \cdot i(t) - \gamma \cdot i(t) \\ \frac{d}{dt}r(t) &= \gamma \cdot i(t) \end{cases} \tag{15}$$

▲

In the standard model, two important epidemic measures can be immediately recognized.

- *Prevalence* of the disease: it is variable $i(t) = I(t)/N$ which represents the fraction of the population that is infective.
- *Incidence* of the disease: it is the term $\beta \cdot s(t) \cdot i(t) = q_I(t)/N$ which represents the infection rate as a fraction of the total population.

***Example* 5.** *In a population of $1.6M$ individuals there are about $80k$ carriers of a disease and 40 new cases are reported in a given year. The prevalence of the disease is 80,000/1,600,000 = 5% and its yearly incidence is 80/1,600,000=0.005%. It also common to express the prevalence as 500/100,000 inhabitants and the yearly incidence as 500/100,000 inhabitants.* ◇

4 Evolution of the SIR model

We will consider the normalized SIR model (15).

Note that this is a *positive* system, i.e., starting from a nonnegative initial condition such that $s(0), i(0), r(0) \geq 0$, for all $t \geq 0$ it also holds $s(t), i(t), r(t) \geq 0$. To prove this for the first two variables, we observe that in (15) as $s(t)$ (resp., $i(t)$) goes to zero, its derivative also goes to zero hence it cannot further decrease. Finally if $i(t)$ is nonnegative, then $r(t)$ is obviously nondecreasing.

Furthermore, by definition, we assume that the initial condition is such that

$$s(0) + i(0) + r(0) = \frac{S(0)}{N} + \frac{I(0)}{N} + \frac{R(0)}{N} = \frac{S(0) + I(0) + R(0)}{N} = 1.$$

Then for all $t \geq 0$ it also holds $s(t) + i(t) + r(t) = 1$ because

$$\frac{d}{dt}\left(s(t) + i(t) + r(t)\right) = \frac{d}{dt}s(t) + \frac{d}{dt}i(t) + \frac{d}{dt}r(t) = 0.$$

We also observe from (15) that $s(t)$ is always nonincreasing because its derivative is nonpositive while, as we have already observed, $r(t)$ is always nondecreasing because its derivative is nonnegative.

Before we discuss the evolution of the infective population $i(t)$, which may increase or decrease, let us define two important parameters.

Definition 8 (Contact number (or basic reproduction number)). *The* contact number

$$\sigma = \beta/\gamma \tag{16}$$

denotes the average number of adequate contacts that an infective individual has during the infective period. This parameter is also called basic reproduction number *and in this case it is denoted* $\mathcal{R}_0$. ▲

The contact number is a structural parameter that does not depend on the current state. Note that it is given by the product of the adequate contact rate β and the average length of the infective period θ_I, i.e., $\sigma = \beta \cdot \theta_I$.

Definition 9 (Reproduction number). *The* reproduction number

$$\mathcal{R}(t) = \sigma \cdot s(t) \tag{17}$$

denotes the average number of new contagions that an infective individual causes during the infective period. ▲

The reproduction number is not a structural parameter and thus it depends on the current state of the system (it changes over time). Note that it is given by the product the average number of adequate contacts during an infective period σ and the probability that a contact transmit the infection $s(t)$.

We can finally discuss, in qualitative terms, the evolution of the infective population $i(t)$. Assuming $i(t) > 0$, the prevalence (fraction of the infectives) will increase if and only

$$\frac{d}{dt}i(t) = \beta \cdot s(t) \cdot i(t) - \gamma \cdot i(t) > 0 \quad \Longrightarrow \quad \beta \cdot s(t) - \gamma > 0 \quad \Longrightarrow \quad \sigma \cdot s(t) > 1$$

i.e., when the reproduction number $\mathcal{R}(t) = \sigma \cdot s(t)$ is greater than 1. In fact, according to its definition this parameter expresses the average number of new infections caused by a single infective individual and a value greater that 1 determines an increase in the prevalence of the disease. Note, however, that the reproduction number will continuously decrease as the fraction of susceptible individuals $s(t)$ left in the population decreases and in particular as soon as the threshold value $s(t) = 1/\sigma$ is crossed the number of infectives will monotonically decrease.

We point out that the contact number σ is equal to the reproduction number when $s(t) \simeq 1$: this is what happens when a single infective is introduced into a completely susceptible host population.

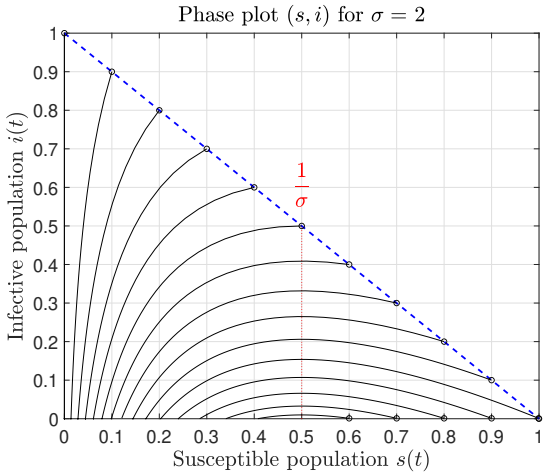

Figure 2: State space plot of the SIR model in Example 6 with contact number $\sigma = 2$ and average infective period $\theta_I = 20$ days.

Note that when $\sigma < 1$ even if the initial condition is such that $s(0) \simeq 1$ the number of infectives will monotonically decrease.

Finally we remark that (15) has an infinite number of equilibrium points:

$$\{(s, i, r) \in \mathbb{R}^3_{\geq 0} \mid i = 0,\ s + i + r = 1\}$$

since a value $i = 0$ causes all derivatives to go to zero.

Example 6. *Considers a normalized SIR model with adequate contact rate $\beta_I = 0.1$ and average infective period $1/\gamma = 20$ days: this corresponds to a contact number $\sigma = 2$.*

Figure 2 shows the state space plot for different initial conditions (denoted by a circle). In such a case, only the plane $s(t) - i(t)$ is considered for the sake of simplicity:

- *Initial conditions on the blue line, correspond to $s(0) + i(0) = 1$. Evolutions starting from an initial state $s(0) > 1/\sigma$ — which determines a reproduction number $\mathcal{R}(0) > 1$ — are characterized by a number of infectives that is initially increasing until the threshold $s = 1/\sigma$ is reached: after the crossing $i(t)$ will monotonically decrease to zero, reaching an equilibrium point. Evolutions starting from an initial state $s(0) \leq 1/\sigma$ — which determines a reproduction number $\mathcal{R}(0) \leq 1$ — are characterized by a number of infectives that is monotonically decreasing.*
- *All points on axis $i = 0$ are equilibrium points. Equilibrium points on the right of the threshold $s = 1/\sigma$ are instable: perturbing the system with the introduction of a single infective, i.e., $i(0) = 1/N$, will cause the disease to spread (reproduction number $\mathcal{R}(0) > 1$). All equilibrium points on the left of the threshold $s(t) = 1/\sigma$ are stable (not asymptotically).*

Figure 4 shows an evolution from the initial condition $(s(0), i(0), r(0)) = (0.9999, 0.0001, 0)$ with time measured in days. Note that although the initial prevalence is very small, the disease will

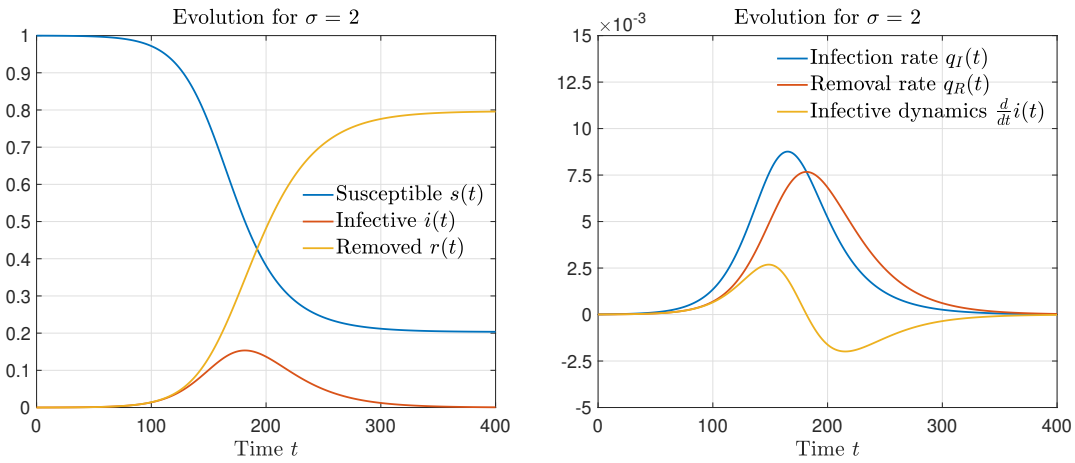

Figure 3: Time evolution of the SIR model in Example 6 with contact number $\sigma = 2$, average infective period $\theta_I = 20$ days and initial condition $i(0) = 0.0001$.

reach about 80% *of the population with a peak of infectives close to* 18% *about 5 months later. It should also be noted that it takes more than 240 days (8 months) for the disease to disappear.* $\diamond$

Example 7. *As a second example, consider a normalized SIR model with adequate contact rate* $\beta_I = 0.04$ *and average infective period* $1/\gamma = 20$ *days: this corresponds to a contact number* $\sigma = 0.8$.

In particular, Figure 4 shows the state space plot for different initial conditions (denoted by a circle). Since the contact number is $\sigma < 1$, *for all values of* $s(t)$ *the reproduction number* $\mathcal{R}(t)$ *will always be smaller than* 1 *and the number of infectives will constantly decrease to zero. All points on axis* $i = 0$ *are stable equilibrium points.*

Figure 4 shows an evolution from the initial condition $(s(0), i(0), r(0)) = (0.9, 0.1, 0)$ *with time measured in days. Note that the constant decrease of the number of infectives does not mean that no new infections occur, i.e., that the incidence of the disease is zero. As can be seen from the figure, the number of susceptibles decrease from* $s(0) = 0.9$ *to almost* 0.72*: this decrement corresponds to newly infected individuals.*

5 Formulation of the SEIR model

Many variations of the SIR model have been considered. Depending on the epidemic nature, the population can be partitioned into more than the three classes that characterize the standard SIR model, namely *susceptible* S, *infected* I, *removed* R.

Here we list some of the most common classes that could be considered in an epidemic model:

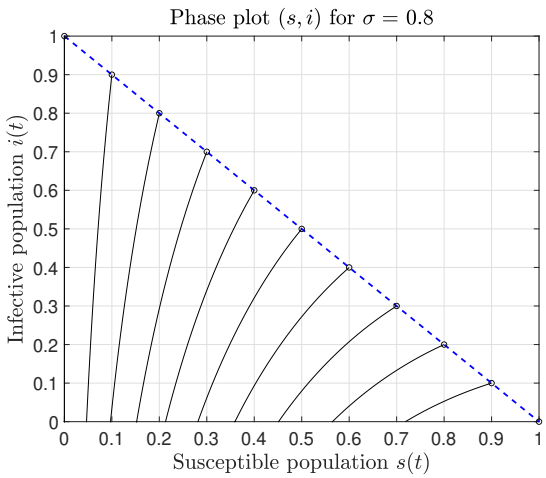

Figure 4: State space plot of the SIR model in Example 7 with contact number $\sigma = 0.8$ and average infective period $\theta_I = 20$ days.

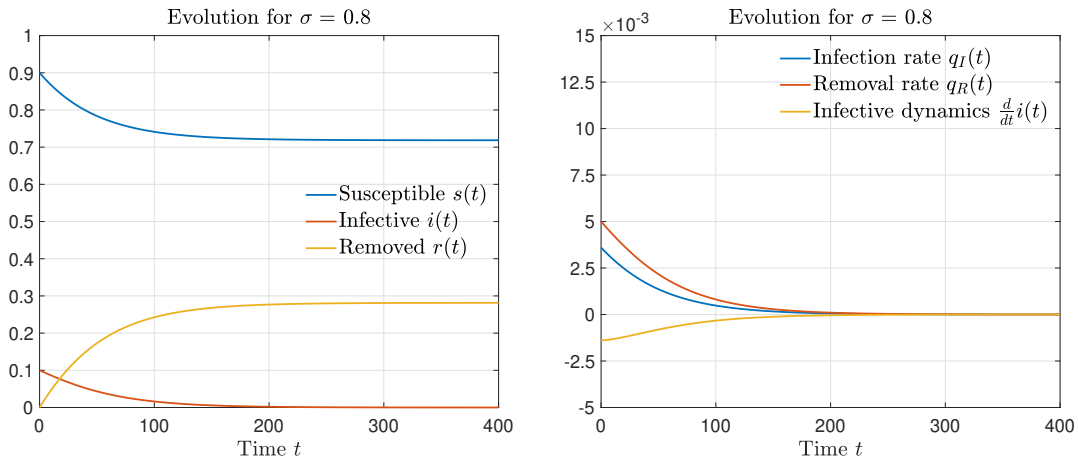

Figure 5: Time evolution of the SIR model in Example 7 with contact number $\sigma = 0.8$, average infective period $\theta_I = 20$ days and initial condition $i(0) = 0.1$.

- $D(t)$: the number of *deceased* individuals at time t. These are individuals which die because of the infection. With the introduction of this class, the class R takes on the meaning of *recovered* individuals.
- $A(t)$: the number of *asymptomatic* individuals at time t. These are individuals that have been infected with the germ, may transmit it to susceptible individuals but are not showing any symptoms. With the introduction of this class, the class I takes on the meaning of *infective* individuals showing symptoms.
- $M(t)$: the number of *maternally-derived immunity* individuals at time t. These are individuals (usually newborns) which may have temporary passive immunity due to protection from maternal antibodies.
- $C(t)$: the number of *carrier* individuals at time t. These are individuals that have (not completely) recovered from the disease but continue to carry the germ with the probability to transmit it to the susceptibles.
- $E(t)$: the number of *exposed* individuals at time t. These are individuals which are incubating the virus and may transmit (depending on the disease) the infection.

In next section we are going to describe a modified SIR model in which the class of *exposed* population is introduced.

5.1 The SEIR model

We want to study an infective disease caused by a germ whose incubation period is not negligible. In this case, after contracting the disease, an individual passes through two phases. In the first phase, before the onset of the symptoms of the the disease, the is called *exposed*. In second phase, after the onset of the symptoms of the the disease, the individual is called *infective*. Note, however, that an individual may transmit the disease in both phases: for this reason we call *infectious* all exposed and infective individuals and we denote *infectious period* the total period spent as exposed or infective. Distinguishing the two phases allows one to derive a more precise model where the adequate contact rate may vary from one phase to the other one.

Based on the Assumptions 1-4 made in Section 2 and taking inspiration from [4], we consider in this case a four-compartment model as shown in Figure 6 characterized by three flows.

- $q_I(t)$: *infection rate*. This is the number of susceptible individuals that, at time t, contract the disease in a unit of time and will enter the first stage of infection becoming exposed. Note that $q_I(t) = q_{I.E}(t) + q_{I.I}$, where:
  - $q_{I.E}(t)$ is the *infection rate caused by exposed*. This is the number of susceptible individuals that, at time t, contract the disease in a unit of time from an exposed individual.

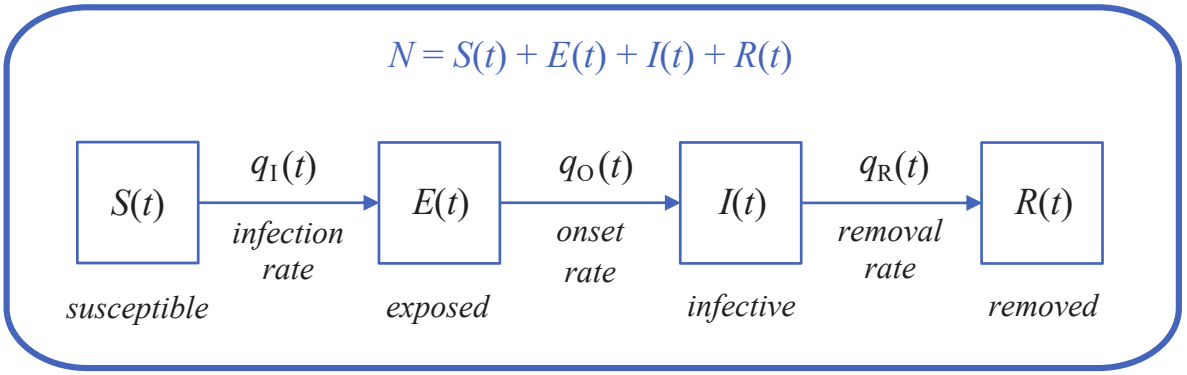

Figure 6: Compartmental view of a SEIR model.

  - $q_{I.I}(t)$ is the *infection rate caused by infective*. This is the number of susceptible individuals that, at time t, contract the disease from an infective individual in a unit of time from an infective individual.

- $q_O(t)$: *onset rate*. This is the number of exposed individuals that, at time t, show the onset of symptoms in a unit of time.

- $q_R(t)$: *removal rate*. This is the number of infective individuals that, at time t, recover or die in a unit of time.

We can present a first SEIR model in continuous-time where the exact dynamics (the precise value of the infection and removal rates) need not be specified.

Definition 10 (Abstract SEIR model). *The model in Figure 6 is ruled by the following dynamical equations:*

$$\begin{cases} \frac{d}{dt}S(t) &= -q_I(t) \\ \frac{d}{dt}I(t) &= q_I(t) - q_O(t) \\ \frac{d}{dt}I(t) &= q_O(t) - q_R(t) \\ \frac{d}{dt}R(t) &= q_R(t) \end{cases} \tag{18}$$

▲

The expression previously derived in eq. (7) for the infection rate $q_I(t)$ can be generalized for the infection rates $q_{I.E}(t)$ and $q_{I.I}(t)$ as follows

$$q_{I.E}(t) = \phi_{E\to S}(t) \cdot E(t) = \phi_{S\to E}(t) \cdot S(t) = \beta_E \cdot \frac{S(t) \cdot E(t)}{N},$$

$$q_{I.I}(t) = \phi_{I\to S}(t) \cdot I(t) = \phi_{S\to I}(t) \cdot S(t) = \beta_I \cdot \frac{S(t) \cdot I(t)}{N},$$

where

- the *exposed adequate contact rate* $\beta_E = \tau_E \cdot \rho_E$ is given by the product between the exposed transmission factor τ_E and the exposed risky contact rate ρ_E.
- the *infective adequate contact* rate $\beta_I = \tau_I \cdot \rho_I$ is given by the product between the infective transmission factor τ_I and the infective risky contact rate ρ_I;

Similarly, the expression previously derived in eq. (10) can be used for the onset rate and the removal rate as follows

$$q_O(t) = \gamma_E \cdot I(t), \qquad q_R(t) = \gamma_I \cdot I(t),$$

where

- the onset coefficient $\gamma_E = 1/\theta_I$ is the inverse of the average incubation period θ_E.
- the removal coefficient $\gamma_I = 1/\theta_I$ is the inverse of the average infective period θ_I,

Finally, substituting these expressions in the abstract SEIR model (18), we obtain the following standard model.

Definition 11 (Standard SEIR model).

$$\begin{cases} \frac{d}{dt}S(t) &= -\beta_E \cdot \frac{S(t) \cdot E(t)}{N} - \beta_I \cdot \frac{S(t) \cdot I(t)}{N} \\ \frac{d}{dt}E(t) &= \beta_E \cdot \frac{S(t) \cdot E(t)}{N} + \beta_I \cdot \frac{S(t) \cdot I(t)}{N} - \gamma_E \cdot E(t) \\ \frac{d}{dt}I(t) &= \gamma_E \cdot E(t) - \gamma_I \cdot I(t) \\ \frac{d}{dt}R(t) &= \gamma_I \cdot I(t) \end{cases} \tag{19}$$

▲

The standard model defined in eq. (19) can be normalized considering as variables

- $s(t) = S(t)/N$: the fraction of susceptible individuals on the total population;
- $e(t) = E(t)/N$: the fraction of exposed individuals on the total population;
- $i(t) = I(t)/N$: the fraction of infective individuals on the total population;
- $r(t) = R(t)/N$: the fraction of removed individuals on the total population.

Using these new variables, eq. (14) can be rewritten as follows.

Definition 12 (**Normalized SEIR model).**

$$\begin{cases} \frac{d}{dt}s(t) &= -\beta_E \cdot s(t) \cdot e(t) - \beta_I \cdot s(t) \cdot i(t) \\ \frac{d}{dt}e(t) &= \beta_E \cdot s(t) \cdot e(t) + \beta_I \cdot s(t) \cdot i(t) - \gamma_E \cdot e(t) \\ \frac{d}{dt}i(t) &= \gamma_E \cdot e(t) - \gamma_I \cdot i(t) \\ \frac{d}{dt}r(t) &= \gamma_I \cdot i(t) \end{cases} \tag{20}$$

▲

We can give the expression of the contact number for the SEIR model.

Definition 13 (**Contact number).** *The* contact number

$$\sigma = \frac{\beta_I}{\gamma_I} + \frac{\beta_E}{\gamma_E}, \tag{21}$$

denotes the average number of adequate contacts that an infectious (exposed or infective) individual has during the total period in which they are infectious. This parameter is also called basic reproduction number *and denoted* $\mathcal{R}_0$. ▲

Note that the contact number is in this case the sum of two terms: β_I/γ_I is the average number of adequate contacts that an exposed individual has during the incubation period θ_E, while β_I/γ_I is the average number of adequate contacts that an infective individual has during the infective period θ_I.

***Example* 8.** *Figure 5.1 compares the evolution of the SIR model that was discussed in Example 6 with that of an equivalent SEIR model: time is measured in days.*

The parameters for the two models are consistent in the the sense that the SEIR model has:

- *Infective adequate contact rate* $\beta_I = 0.05$*;*
- *Exposed adequate contact rate* $\beta_E = 5 \cdot \beta_I = 0.25$
- *Average infective period* $\theta_I = 15$ *days;*
- *Average incubation period* $\theta_E = 5$ *days;*
- *Contact number* $\sigma = 2$*.*

while the SIR model, as previously mentioned, has,

- *Adequate contact rate* $\beta = 0.1$*;*

- *Average infective period* $\theta_I = 20$ *days;*
- *Contact number* $\sigma = 2$.

The SEIR model has initial condition $(s(0), e(0), i(0), r(0)) = (0.9999, 0, 0.0001, 0)$ *while the SIR model has initial condition* $(s(0), i(0), r(0)) = (0.9999, 0.0001, 0)$.

Note that, even if the initial condition and the contact number is the same, the spread of the disease is faster according to the SEIR models although the final number of removed remains the same. $\diamond$

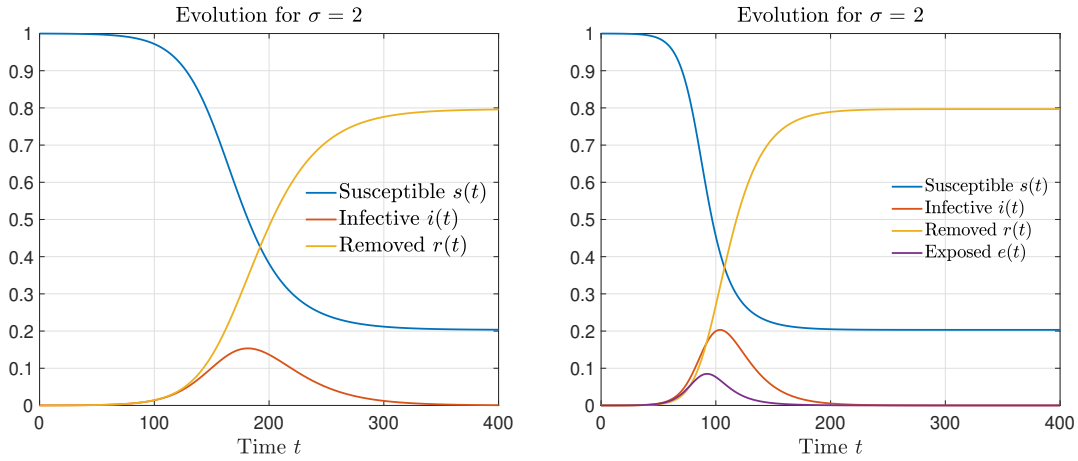

Figure 7: Comparison between the evolution of the SIR model in Example 6 (left) and an equivalent SEIR model in Example 8 (right). Both models have contact number $\sigma = 2$.

References

[1] H.W. Hethcote, "Three Basic Epidemiological Models," in *Applied Mathematical Ecology*, S.A. Levin, T.G. Hallam and L.J. Gross (eds), Series on Biomathematics, vol. 18, pp. 119–144. Springer, 1989.

[2] H.W. Hethcote, "The Mathematics of Infectious Diseases," *SIAM Review*, vol. 42, no. 4, pp. 599–653, 2000.

[3] M. Silva, J. Júlvez, C. Mahulea, C.R. Vázquez, "On fluidization of discrete event models: observation and control of continuous Petri nets," *Discrete Event Dynamic Systems*, vol. 21, no. 4, pp. 427-497, Springer, 2011.

[4] Z. Yang, et al. "Modified SEIR and AI prediction of the epidemics trend of COVID-19 in China under public health interventions," *Journal of Thoracic Disease*, vol. 12, no. 3, pp. 165-182, AME Pubblications, 2019.

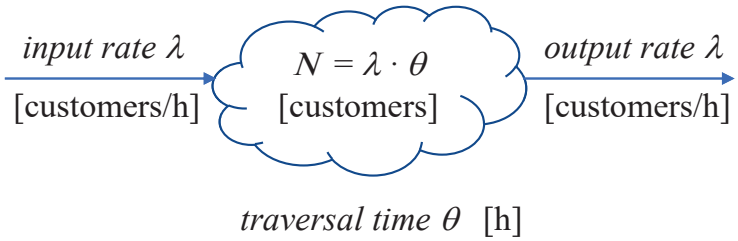

Figure 8: A stationary queuing system illustrating Little's law (time is measured in hours).

Appendix

A Little's Law

Consider a *queuing system* where customers arrive according to a stochastic process, remain in the system for a random time and finally leave. Assume this system reaches a *stationary* condition, which can be informally described as a situation in which the *average values* of the variables of interest do not change over time.

In stationary condition (see Figure 8) *Little's law* holds:

$$N = \lambda \cdot \theta \tag{22}$$

where;

- N is the average number of *customers in the system*;
- λ is the average *arrival rate*, which by the stationary assumption is also equal to the average *departure rate*;
- θ is the average *traversal time*, i.e., the time spent in the system by a customer.

It is important to stress the generality of Little's law (22): it holds regardless of the distribution of the random variable describing the arrival and traversal processes: it only requires the stationarity assumption.

Example 9. *In a large supermarket, the number of customers during a Saturday afternoon can be considered stationary. Suppose one observes an input flow* $\lambda = 30$ customers/min *and an average number of* $N = 600$ customers*: the average time spent in the shop is* $\theta = N/\lambda = 20$ min.

Note that computing λ *and* N *is not difficult: one just needs to count the number of customers entering and leaving the shop at all time. Measuring* θ*, on the contrary, would require identifying each single customer when entering and leaving so that individual traversal time could be computed and averaged over all customers.* ◇