Minimisation of Medicine Inventory Costs Based on a Discretised SIS-Type Epidemic Model Involving Immigrants

Fransiska Eveline, Jonathan Hoseana, Dharma Lesmono

Abstract—Studies involving epidemic models are usually focused only on the dynamical analysis of the model itself or the evaluation of certain intervention strategies, thereby overlooking an important issue that may also arise during an epidemic: the optimal management of medicine inventory. In this paper, we address this issue by constructing a medicine inventory model based on an SIS-type epidemic model involving immigrants. We first study the epidemic model in its continuous form, verifying the non-negativity of its solutions, determining its equilibria and basic reproduction number, and analysing the stability of its equilibria. Since the model's exact solution is not easily obtainable, we discretise the model using the forward Euler method, and study the dynamical properties of the resulting discrete model. Using the estimates for the numbers of infected individuals at certain time steps provided by the discrete epidemic model, we then construct a finite-time-horizon medicine inventory model, in which the medicine's demand is assumed to be proportional to the number of infected individuals at any given time. The model takes the form of an expression for the medicine's total cost, which is the sum of its order, purchase, and holding costs, as a univariate function of the positive-integer inter-order time-interval. We conduct numerical simulations to illustrate the application of our epidemic and inventory models in determining the inter-order time-interval that minimises the medicine's total cost, using two sets of parameter values representing two qualitatively different cases: a disease-free and an endemic case. Finally, we carry out a sensitivity analysis, which reveals that in both cases, the disease's basic reproduction number depends most sensitively on the population's natural death coefficient, whereas the epidemic peak and the minimum total cost depends most sensitively on the disease's incidence rate.

Index Terms—medicine, inventory model, epidemic model, basic reproduction number, sensitivity analysis

I. Introduction

THE recent COVID-19 pandemic has led to a significant growth of the number of mathematical studies that analyse the transmission of infectious diseases using epidemic models [8], [10], [26], [30], [34], [39], [40], [50], [53]. In most of such studies, however, the primary focus has generally been on understanding the transmission dynamics of the disease itself, or assessing the effectiveness of various intervention strategies such as vaccinations, quarantines, or social restrictions. This leaves overlooked

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another equally important issue that may arise during an epidemic: the optimal management of pharmaceutical inventory. Indeed, the scarcity of pharmaceutical items resulting from suboptimal inventory management may undermine the disease's overall eradicative effort. A possible approach to address this issue is to study how pharmaceutical inventory can be managed with the aid of mathematical models for inventory management. While there has been a wealth of studies focusing solely on epidemic models, studies that construct pharmaceutical inventory models based on epidemic models appear to be relatively scarce.

An existing class of studies closely related to our present interest comprises those that develop inventory models for pharmaceutical items without the involvement of epidemic models. Such studies have been conducted particularly extensively by Uthayakumar and his collaborators. In 2016 and 2017, Uthayakumar and Karuppasamy constructed an inventory model for a pharmaceutical item that features a quadratic time-dependent demand and a linear time-dependent holding cost [43], and subsequently extended the model by incorporating shortages [44] and payment delays [45]. In these three models, the pharmaceutical item under consideration was assumed to undergo a constant deterioration. In 2018 and 2019, the same authors considered alternative forms of time-dependent demand [46] as well as time-proportional deterioration [47]. Also in 2018, Uthayakumar and Tharani incorporated complete backlogging into a modest inventory model for a pharmaceutical item with a quadratic time-dependent demand, a constant holding cost, and a constant deterioration [48].

Aside from Uthayakumar's contributions, Zhou et al. [52], in 2013, constructed a multi-item inventory model for deteriorating pharmaceutical items that accommodates both an arbitrary number of different items and space constraints. In 2018, Kumar and Srivastava [19] constructed an inventory model for a deteriorating pharmaceutical item with a ramp-type demand, while Li et al. [20] constructed an inventory model for a deteriorating pharmaceutical item that features a stochastic lead time. Rastogi and Singh, in 2019, constructed inventory models for a pharmaceutical item whose deterioration follows the Weibull distribution, with price-dependent demands and partial backlogging [31], [32], which were subsequently extended by Kumar et al. [18] in 2021 by taking into account inflation and lost sales. Most recently, Indrawati et al. [14], in 2024, constructed an inventory model for a pharmaceutical item with a linear time-dependent demand, a constant deterioration, and complete backlogging.

Each of the inventory models in the works cited above, although explicitly stated to be designed for pharmaceutical items, was constructed under the assumption that the item's demand follow a certain functional form, such as constant, a linear or a quadratic function of time, or an algebraic function of the item's selling price, often without any justification for whether such an assumption reasonably reflect the item's actual demand that arises at the time of an epidemic. The absence of such a justification subsequently raises the question of what distinguishes these inventory models, which were specifically designed for pharmaceutical items, compared to inventory models for generic items, the studies of which have been extremely abundant in the literature.

In this paper, we adopt a novel approach by constructing a modest inventory model for a pharmaceutical item under the assumption that the item's time-dependent demand is governed by a certain epidemic model. More precisely, we shall focus on a specific type of epidemic model: an SIS-type epidemic model, whereby at any given time each individual in the population is either susceptible or infected, and on a specific pharmaceutical item: medicine. In 2021, Saikh and Gazi [35] constructed an SIS-type epidemic model that takes into account the presence of immigrants, assuming that a certain fraction of the immigrants enter the population in an infected state. In this paper, we shall utilise a special case of this model by Saikh and Gazi, where the aforementioned fraction is set to be zero, meaning that all entering immigrants are susceptible. We shall construct a finite-time-horizon inventory model [27], [28], [29] for the disease's medicine, which takes the form of an expression for the total cost incurred by the medicine's monopolistic distributing company over a specified epidemic duration, which is to be minimised over all feasible constant positive-integer inter-order time-intervals. Drawing inspiration from the classical EOQ-type inventory model [25, Chap. 2], we shall assume that the total cost is the sum of three cost components: the medicine's order cost, purchase cost, and holding cost.

The rest of the paper is organised as follows. In the upcoming section II, we construct our epidemic model in its continuous form, verify the non-negativity of its solutions, analyse its dynamical properties, and construct the associated medicine inventory model. Since in the latter the demand is assumed to be proportional to the time-dependent number of infected individuals, whose explicit expression is not easily obtainable, in the subsequent section III we construct a discrete analogue of our epidemic model using the forward Euler method, and briefly study its dynamical properties. Using the estimates for the time-dependent number of infected individuals at certain time steps generated by our discrete epidemic model, we then construct a discrete analogue of our medicine inventory model. In section IV, we conduct numerical simulations to illustrate the applicability of both our epidemic and inventory models. We also analyse the sensitivity of three key quantities: the epidemic model's basic reproduction number, the epidemic peak, and the company's total cost, with respect to small changes in the involved parameters. In the final section V, we state our conclusions and discuss possible directions for future studies.

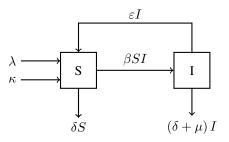


Fig. 1. Compartmental diagram of our model (1).

II. THE EPIDEMIC AND INVENTORY MODELS

In this section, we first construct our epidemic model in a continuous form and establish its biological feasibility (subsection II-A). Subsequently, we analyse the epidemic model dynamically, determining its equilibria, basic reproduction number, and stability of equilibria (subsection II-B). Finally, we construct our medicine inventory model, which takes the form of an expression for the total cost incurred by a company that distributes medicine for all infected individuals over a specified epidemic duration, as a function of the company's inter-order time-interval (subsection II-C).

A. Construction and biological feasibility of epidemic model

Suppose that a disease spreads across a population in such a way that at any given time, each individual in the population belongs to exactly one of the following two compartments: susceptible (S) and infected (I). We denote by S = S(t) and I = I(t) the numbers of individuals belonging to the susceptible and infected compartments, respectively, at any given time $t \ge 0$. Assume that the number of individuals in each compartment evolves over time in the way we now describe. First, the number of susceptible individuals increase due to the entries of newborns and immigrants at the constant rates of $\lambda, \kappa > 0$, respectively, and the entry of recovering infected individuals at the linear rate of εI , where $\varepsilon > 0$. The same number decreases due to infections occurring at the bilinear rate of βSI , where $\beta > 0$ and natural deaths occurring at the linear rate of δS , where $\delta > 0$. On the other hand, the number of infected individuals increases due to the infections at the rate of βSI and decreases due to recovery at the rate of εI and deaths due to the disease at the rate of $(\delta + \mu) S$, where $\mu > 0$. These assumptions lead to the compartmental diagram presented in Figure 1 and to the SIS-type epidemic model

$$\begin{cases} \frac{dS}{dt} = \lambda + \kappa - \beta SI - \delta S + \varepsilon I, \\ \frac{dI}{dt} = \beta SI - (\delta + \mu + \varepsilon) I, \end{cases}$$
(1)

Table I summarises the parameters involved in this model, along with their values used in our numerical simulations. Notice that we use days as the unit for time in our model. We remark that the above model is a special case of the SIS-type model constructed by Saikh and Gazi [35, eqn. (3.2)], obtained by setting r=0.

Let us now verify our epidemic model's biological feasibility. For this purpose, consider a solution (S, I) = (S(t), I(t)) associated to an initial condition in \mathbb{R}^2_+ , where

TABLE I
SUMMARY OF PARAMETERS INVOLVED IN OUR EPIDEMIC MODEL (1)
AND THEIR VALUES USED IN OUR NUMERICAL SIMULATIONS.

Parameter	Description	Unit	Value for simulation	Source
λ	entry rate of newborns	individual/day	0.14001904	[42], [51], [11], [12]
κ	entry rate of immigrants	individual/day	0.5	simulated
β	incidence coefficient	1/(individual × day)	0.00005 0.00006	simulated
δ	natural death coefficient	1/day	0.00024833	[13]
μ	death-by-disease coefficient	1/day	0.00036133	[13]
ε	recovery coefficient	1/day	0.1287	[49]
S(0)	initial number of susceptible individuals	individual	3,000	simulated
I(0)	initial number of infected individuals	individual	1	simulated

 $\mathbb{R}_+=[0,\infty)$. First, since at each $t^*\geqslant 0$ where $I\left(t^*\right)=0$ we have that $\mathrm{d}I/\mathrm{d}t=0$, then the value of I(t) remains non-negative for all $t\geqslant 0$. On the other hand, since at each $t^*\geqslant 0$ where $S\left(t^*\right)=0$ we have that $\mathrm{d}S/\mathrm{d}t\geqslant \lambda+\kappa>0$, then the value of S(t) also remains non-negative for all $t\geqslant 0$. This proves that the set \mathbb{R}_+^2 is positively invariant under our model (1).

Next, adding the two equations in (1) gives

$$\frac{\mathrm{d}N}{\mathrm{d}t} = \lambda + \kappa - \delta N - \mu I \leqslant \lambda + \kappa - \delta N,$$

i.e.,

$$\frac{\mathrm{d}N}{\mathrm{d}t} + \delta N \leqslant \lambda + \kappa,$$

where N=N(t)=S(t)+I(t). Multiplying both sides by $\mathrm{e}^{\delta t}$ gives

$$\frac{\mathrm{d}}{\mathrm{d}t} \left[\mathrm{e}^{\delta t} N(t) \right] \leqslant \frac{\mathrm{d}}{\mathrm{d}t} \left[\frac{\lambda + \kappa}{\delta} \mathrm{e}^{\delta t} + N(0) - \frac{\lambda + \kappa}{\delta} \right],$$

which, since the square-bracketed functions both evaluate to N(0) at t=0, implies that the following holds for all $t \ge 0$:

$$e^{\delta t}N(t) \leqslant \frac{\lambda + \kappa}{\delta}e^{\delta t} + N(0) - \frac{\lambda + \kappa}{\delta}$$

i.e.,

$$N(t) \leqslant \frac{\lambda + \kappa}{\delta} + \left\lceil N(0) - \frac{\lambda + \kappa}{\delta} \right\rceil \mathrm{e}^{-\delta t}.$$

Letting

$$\Omega = \left\{ (S, I) \in \mathbb{R}_+^2 : S + I \leqslant \frac{\lambda + \kappa}{\delta} \right\},\,$$

this shows that if $(S(0), I(0)) \in \Omega$ then the solution (S, I) remains forever in Ω . Our conclusion is the following theorem (cf. [35, p. 4]).

Theorem 1. The sets \mathbb{R}^2_+ and

$$\Omega = \left\{ (S, I) \in \mathbb{R}_+^2 : S + I \leqslant \frac{\lambda + \kappa}{\delta} \right\}$$

are both positively invariant under our epidemic model (1).

B. Equilibria and stability

Let us now discuss our epidemic model's equilibria and their stability [33], [38]. The equilibria of the epidemic model (1) satisfy the system

$$\left\{ \begin{array}{l} 0 = \lambda + \kappa - \beta SI - \delta S + \varepsilon I, \\ 0 = \beta SI - (\delta + \mu + \varepsilon) I, \end{array} \right.$$

The second equation can be written as

$$0 = (\beta S - \delta - \mu - \varepsilon) I,$$

which gives I=0 or $S=\left(\delta+\mu+\varepsilon\right)/\beta$. In the former case, the first equation gives $S=\left(\lambda+\kappa\right)/\delta$, leading to the disease-free equilibrium

$$\mathbf{e}_0 = (S_0, I_0) = \left(\frac{\lambda + \kappa}{\delta}, 0\right),$$

which exists in \mathbb{R}^2_+ for all sets of parameter values. In the latter case, the first equation gives

$$I = \frac{\beta (\lambda + \kappa) - \delta (\delta + \mu + \varepsilon)}{\beta (\delta + \mu)}$$

leading to the endemic equilibrium

$$\mathbf{e}_{1} = (S_{1}, I_{1}) = \left(\frac{\delta + \mu + \varepsilon}{\beta}, \frac{\beta(\lambda + \kappa) - \delta(\delta + \mu + \varepsilon)}{\beta(\delta + \mu)}\right). \tag{2}$$

Since on the right-hand side of the second equation of our epidemic model (1),

$$\frac{\mathrm{d}I}{\mathrm{d}t} = \beta SI - (\delta + \mu + \varepsilon) I,$$

the first term represents the entry rate of new infections to the infected compartment, while the second term contains all remaining transition rates to and from the infected compartment, the next-generation approach of van den Driessche and Watmough [4], [23] gives the following expression of our epidemic model's basic reproduction number:

$$\mathfrak{R}_0 = \beta S_0 \left(\delta + \mu + \varepsilon \right)^{-1} = \frac{\beta \left(\lambda + \kappa \right)}{\delta \left(\delta + \mu + \varepsilon \right)}$$

which enables us to rewrite our epidemic model's endemic equilibrium (2) as

$$\mathbf{e}_{1} = (S_{1}, I_{1}) = \left(\frac{\delta + \mu + \varepsilon}{\beta}, \frac{\delta (\delta + \mu + \varepsilon) (\mathfrak{R}_{0} - 1)}{\beta (\delta + \mu)}\right),$$

so that e_1 exists in \mathbb{R}^2_+ if and only if $\mathfrak{R}_0 \geqslant 1$.

Theorem 2. Our epidemic model (1) has the basic reproduction number

$$\mathfrak{R}_0 = \frac{\beta (\lambda + \kappa)}{\delta (\delta + \mu + \varepsilon)} \tag{3}$$

and two equilibria: a disease-free equilibrium

$$\mathbf{e}_0 = (S_0, I_0) = \left(\frac{\lambda + \kappa}{\delta}, 0\right),\tag{4}$$

which belongs to \mathbb{R}^2_+ for all sets of parameter values, and an endemic equilibrium

$$\mathbf{e}_{1} = (S_{1}, I_{1}) = \left(\frac{\delta + \mu + \varepsilon}{\beta}, \frac{\delta(\delta + \mu + \varepsilon)(\mathfrak{R}_{0} - 1)}{\beta(\delta + \mu)}\right),$$
(5)

which belongs to \mathbb{R}^2_+ if and only if $\mathfrak{R}_0 \geqslant 1$.

Next, since the Jacobian matrix of our epidemic model (1) is given by

$$\mathbf{J}(S,I) = \begin{bmatrix} -\beta I - \delta & \varepsilon - \beta S \\ \beta I & \beta S - (\delta + \mu + \varepsilon) \end{bmatrix},$$

the Jacobian matrix at the disease-free equilibrium \mathbf{e}_0 is the upper-triangular matrix

$$\mathbf{J}(\mathbf{e}_0) = \begin{bmatrix} -\delta & \varepsilon - \frac{\beta(\lambda + \kappa)}{\delta} \\ 0 & -(\delta + \mu + \varepsilon)(1 - \mathfrak{R}_0) \end{bmatrix}$$

whose eigenvalues are its diagonal entries $-\delta$ and $-(\delta + \mu + \varepsilon)(1 - \Re_0)$. Consequently, e₀ is locally asymptotically stable if $\Re_0 < 1$, is non-hyperbolic if $\Re_0 = 1$, and is unstable if $\Re_0 > 1$.

On the other hand, the Jacobian matrix of our epidemic model (1) at the endemic equilibrium e_1 ,

$$\mathbf{J}\left(\mathbf{e}_{1}\right) = \begin{bmatrix} -\frac{\delta\left(\delta + \mu + \varepsilon\right)\left(\mathfrak{R}_{0} - 1\right)}{\delta + \mu} - \delta & -\left(\delta + \mu\right) \\ \frac{\delta\left(\delta + \mu + \varepsilon\right)\left(\mathfrak{R}_{0} - 1\right)}{\delta + \mu} & 0 \end{bmatrix},$$

has the characteristic polynomial

$$|r\mathbf{I} - \mathbf{J}(\mathbf{e}_1)| = r^2 + \left[\frac{\delta(\delta + \mu + \varepsilon)(\mathfrak{R}_0 - 1)}{\delta + \mu} + \delta \right] r + \delta(\delta + \mu + \varepsilon)(\mathfrak{R}_0 - 1).$$

If $\mathfrak{R}_0 > 1$, then the non-leading coefficients of this polynomial are both positive, so that \mathbf{e}_1 is locally asymptotically stable by the Routh-Hurwitz criterion [1, sec. 4.5]. If $\mathfrak{R}_0 = 1$, then the matrix $\mathbf{J}(\mathbf{e}_1)$ has a zero eigenvalue, so that \mathbf{e}_1 is non-hyperbolic. If $\mathfrak{R}_0 < 1$, then the above polynomial has a negative discriminant, and hence real eigenvalues, but its constant coefficient's negativity ensures the existence of a positive eigenvalue, implying that \mathbf{e}_1 is unstable. We have therefore proved the following theorem, which indicates that our model's two equilibria cross and exchange their stability through a forward transcritical bifurcation at $\mathfrak{R}_0 = 1$.

Theorem 3. The following holds with regards to the disease-free and endemic equilibria \mathbf{e}_0 and \mathbf{e}_1 of our epidemic model (1). If $\mathfrak{R}_0 < 1$, then \mathbf{e}_0 is locally asymptotically stable, while \mathbf{e}_1 is unstable. If $\mathfrak{R}_0 = 1$, then $\mathbf{e}_0 = \mathbf{e}_1$ is non-hyperbolic. If $\mathfrak{R}_0 > 1$, then \mathbf{e}_0 is unstable, while \mathbf{e}_1 is locally asymptotically stable.

C. Construction of inventory model

To construct our inventory model, let us first fix an integer time horizon T>0 representing the duration of the epidemic. Recall that the time in our model is measured in days. We assume that each infected individual consumes a specific medicine at an average dosage of $\alpha>0$ units per day, where the distribution of this medicine is controlled entirely by a single company. Suppose that the company orders the medicine from a certain supplier at the per-unit purchase price of Π dollars, where the per-order ordering cost is Γ dollars, and that the medicine incurs a per-unit per-day holding cost of Λ dollars. Suppose also that to meet the medicine demands in the entire epidemic duration

—from day 0 to day T— the company places repeated orders with a regular inter-order time-interval of m days, which is assumed to be no longer than a certain maximum inter-order time-interval of m_{\max} days. More precisely, the company places $\lfloor T/m \rfloor + 1$ orders where, for $i \in \{0, \dots, \lfloor T/m \rfloor - 1\}$, the i-th order is placed on day im to meet the medicine demands on days im, ..., (i+1)m-1, and the $\lfloor T/m \rfloor$ -th order is placed on day $\lfloor T/m \rfloor m$ to meet the medicine demands on days $\lfloor T/m \rfloor m$, ..., T. We aim to formulate the company's total cost to meet the medicine demands in the entire epidemic duration as a univariate function of m, and later in our numerical simulation, determine the value of m that minimises the total cost.

As in the classical EOQ-type inventory model [25, Chap. 2], we assume that the company's total cost $\mathcal{TC}(m)$ is the sum of three cost components: the company's order cost $\mathcal{CC}(m)$, purchase cost $\mathcal{PC}(m)$, and holding cost $\mathcal{HC}(m)$, which we now construct separately. First, the fact that the company places $\lfloor T/m \rfloor + 1$ orders, where the per-order ordering cost is Γ dollars, implies the following expression for the company's order cost:

$$\mathcal{OC}(m) = \left(\left|\frac{T}{m}\right| + 1\right)\Gamma.$$
 (6)

Next, since for every $i \in \{0,\dots,\lfloor T/m\rfloor-1\}$, the total demand of medicine on days im, ..., (i+1)m-1 is $\alpha \sum_{j=im}^{(i+1)m-1} I(j)$ units, whereas the total demand of medicine on days $\lfloor T/m\rfloor m$, ..., T is $\alpha \sum_{j=\lfloor T/m\rfloor m}^T I(j)$ units, recalling that the medicine entails a per-unit purchase price of Π dollars, we obtain the following expression for the company's purchase cost:

$$\mathcal{PC}(m) = \Pi\alpha \left[\sum_{i=0}^{\lfloor T/m \rfloor - 1(i+1)m - 1} I(j) + \sum_{j=\lfloor T/m \rfloor m}^{T} I(j) \right]. \tag{7}$$

Finally, we notice that for every $i \in \{0,\dots,\lfloor T/m\rfloor-1\}$, since on day im the company purchases $\mathcal{Q}_i = \alpha \sum_{j=im}^{(i+1)m-1} I(j)$ units of medicine, then the number of stored medicines on each day $k \in \{im,\dots,(i+1)m-1\}$ are given by

$$\alpha \sum_{j=im}^{(i+1)m-1} I(j) - \alpha \sum_{j=im}^{k} I(j) = \alpha \sum_{j=k+1}^{(i+1)m-1} I(j).$$

Moreover, since on day $\lfloor T/m \rfloor m$ the company purchases $\mathcal{Q}_{\lfloor T/m \rfloor} = \alpha \sum_{j=\lfloor T/m \rfloor m}^T I(j)$ units of medicine, then the number of stored medicines on each day $k \in \{\lfloor T/m \rfloor m, \ldots, T\}$ are given by

$$\alpha \sum_{j=\lfloor T/m \rfloor m}^{T} I(j) - \alpha \sum_{j=\lfloor T/m \rfloor m}^{k} I(j) = \alpha \sum_{j=k+1}^{T} I(j).$$

Recalling that the medicine incurs a per-unit per-day holding cost of Λ dollars, this leads to the following expression for the company's holding cost:

$$\mathcal{HC}(m) = \Lambda \alpha \left[\sum_{i=0}^{\lfloor T/m \rfloor - 1} \sum_{k=im}^{(i+1)m-1} \sum_{j=k+1}^{(i+1)m-1} I(j) + \sum_{k=\lfloor T/m \rfloor m}^{T} \sum_{j=k+1}^{T} I(j) \right]. \tag{8}$$

TABLE II
SUMMARY OF PARAMETERS INVOLVED IN OUR INVENTORY MODEL (9)
AND THEIR VALUES USED IN OUR NUMERICAL SIMULATIONS.

Parameter	Description	Unit	Value for simulation	Source
T	time horizon	day	8,000	simulated
$m_{ m max}$	maximum inter-order time-interval	day	365	simulated
П	medicine's per-unit purchase price	\$/unit	1	simulated
Γ	medicine's per-order ordering cost	\$/order	500	[2]
Λ	medicine's per-unit per-day holding cost	\$/(unit × day)	0.00043836	[9]
α	medicine's average dosage	unit/day	3	simulated

Therefore, the company's total cost over the epidemic duration is given by

$$\mathcal{TC}(m) = \mathcal{OC}(m) + \mathcal{PC}(m) + \mathcal{HC}(m)$$

$$= \left(\left\lfloor \frac{T}{m} \right\rfloor + 1 \right) \Gamma + \Pi \alpha \left[\sum_{i=0}^{\lfloor T/m \rfloor - 1} \sum_{j=im}^{(i+1)m-1} I(j) \right]$$

$$+ \sum_{j=\lfloor T/m \rfloor m}^{T} I(j) \right]$$

$$+ \Lambda \alpha \left[\sum_{i=0}^{\lfloor T/m \rfloor - 1} \sum_{k=im}^{(i+1)m-1} \sum_{j=k+1}^{(i+1)m-1} I(j) \right]$$

$$+ \sum_{k=\lfloor T/m \rfloor m}^{T} \sum_{j=k+1}^{T} I(j) \right], \tag{9}$$

and the company's purchase quantity for each order $i \in \{0,\ldots,\lfloor T/m\rfloor+1\}$ is given by

$$Q_{i} = \alpha \sum_{j=im}^{\min\{(i+1)m-1,T\}} I(j),$$

On the other hand, the company's medicine inventory at the end of each day $t \in \{0, \dots, T\}$ is given by

$$\mathcal{I}\left(t\right) = \alpha \sum_{j=t+1}^{\min\left\{\left(\left\lfloor t/m\right\rfloor + 1\right)m - 1, T\right\}} I\left(j\right).$$

The parameters involved in our inventory model, along with their values used in our numerical simulations, are summarised in Table II.

III. DISCRETISATION

The expression of the company's total cost (9) can only be evaluated in an exact manner if an explicit expression for the number of infected individuals at any given time is available. In reality, such an expression is not easily obtainable. Accordingly, we generate a sequence of estimates for the number of infected individuals—and simultaneously for the number of susceptible individuals—at specified time steps, via discretisation. For this purpose, we utilise the simplest

discretisation method for systems of differential equations: the forward Euler method. In this section, we describe the discrete epidemic model obtained by applying the forward Euler method to our continuous epidemic model (1), before discussing its equilibria and their stability (subsection III-A). Subsequently, we derive an estimate for the company's total cost (9) using the estimates for the number of infected individuals at the specified time steps provided by our discrete epidemic model (subsection III-B).

A. Discretised epidemic model and equilibria

Fixing a step size $\Delta t > 0$ and defining the time steps $t_i = i\Delta t$ for every non-negative integer i, the forward Euler method [17, sec. 22.3] transforms our continuous epidemic model (1) into the discrete epidemic model

$$\begin{cases}
\overline{S}_{i+1} = \overline{S}_i + (\lambda + \kappa - \beta \overline{S}_i \overline{I}_i - \delta \overline{S}_i + \varepsilon \overline{I}_i) \Delta t, \\
\overline{I}_{i+1} = \overline{I}_i + \left[\beta \overline{S}_i \overline{I}_i - (\delta + \mu + \varepsilon) \overline{I}_i \right] \Delta t,
\end{cases} (10)$$

where $\overline{S}_i \approx S\left(t_i\right)$ dan $\overline{I}_i \approx I\left(t_i\right)$ for every non-negative integer i. In particular, $\overline{S}_0 = S\left(0\right)$ and $\overline{I}_0 = I\left(0\right)$. Clearly, the discrete epidemic model (10) possesses the same equilibria as our continuous epidemic model (1).

The Jacobian matrix of the discrete epidemic model (10) is given by

$$\overline{\mathbf{J}}\left(\overline{S},\overline{I}\right) = \begin{bmatrix} 1 - \left(\beta\overline{I} + \delta\right)\Delta t & \left(\varepsilon - \beta\overline{S}\right)\Delta t \\ \beta\overline{I}\Delta t & 1 + \left(\beta\overline{S} - \delta - \mu - \varepsilon\right)\Delta t \end{bmatrix}.$$

Evaluating this at the disease-free equilibrium e_0 gives the matrix

$$\overline{\mathbf{J}}(\mathbf{e}_{0}) = \begin{bmatrix} 1 - \delta \Delta t & \left[\varepsilon - \frac{\beta (\lambda + \alpha)}{\delta} \right] \Delta t \\ 0 & 1 - (\delta + \mu + \varepsilon) (1 - \Re_{0}) \Delta t \end{bmatrix}$$

having eigenvalues $1-\delta\Delta t$ and $1-(\delta+\mu+\varepsilon)\,(1-\mathfrak{R}_0)\,\Delta t$. In the case $\mathfrak{R}_0<1$, the disease-free equilibrium \mathbf{e}_0 is a locally asymptotically stable equilibrium of our discrete epidemic model (10) if these eigenvalues both lie inside the unit circle. The latter holds if and only if $\Delta t<2/\delta$ and

$$\Delta t < \frac{2}{\left(\delta + \mu + \varepsilon\right)\left(1 - \mathfrak{R}_0\right)},$$

respectively.

On the other hand, evaluating the Jacobian matrix $\overline{\mathbf{J}}(\overline{S}, \overline{I})$ at the endemic equilibrium \mathbf{e}_1 gives the matrix

$$\overline{\mathbf{J}}\left(\mathbf{e}_{1}\right) = \begin{bmatrix} 1 - \left[\frac{\delta\left(\delta + \mu + \varepsilon\right)\left(\mathfrak{R}_{0} - 1\right)}{\delta + \mu} + \delta\right] \Delta t - \left(\delta + \mu\right) \Delta t \\ \frac{\delta\left(\delta + \mu + \varepsilon\right)\left(\mathfrak{R}_{0} - 1\right)}{\delta + \mu} \Delta t & 1 \end{bmatrix}$$

whose characteristic polynomial reads

$$|r\mathbf{I} - \overline{\mathbf{J}}(\mathbf{e}_1)| = r^2 + \overline{\mathcal{A}}_1 r + \overline{\mathcal{A}}_2,$$

where

$$\overline{\mathcal{A}}_{1} = -2 + \left[\frac{\delta \left(\delta + \mu + \varepsilon \right) \left(\mathfrak{R}_{0} - 1 \right)}{\delta + \mu} + \delta \right] \Delta t,$$

$$\overline{\mathcal{A}}_{2} = 1 - \left[\frac{\delta \left(\delta + \mu + \varepsilon \right) \left(\mathfrak{R}_{0} - 1 \right)}{\delta + \mu} + \delta \right] \Delta t$$

$$+ \delta \left(\delta + \mu + \varepsilon \right) \left(\mathfrak{R}_{0} - 1 \right) \left(\Delta t \right)^{2}.$$

Suppose that $\Re_0 > 1$. By the Schur-Cohn criterion [5, sec. 5.1], \mathbf{e}_1 is locally asymptotically stable if $\left|\overline{\mathcal{A}}_1\right| < 1 + \overline{\mathcal{A}}_2 < 2$. The second inequality holds if and only if

$$\Delta t < \frac{1}{\delta + \mu} + \frac{1}{(\delta + \mu + \varepsilon)(\Re_0 - 1)},\tag{11}$$

while the first inequality holds if and only if $1 + \overline{\mathcal{A}}_1 + \overline{\mathcal{A}}_2 > 0$ and $1 - \overline{\mathcal{A}}_1 + \overline{\mathcal{A}}_2 > 0$. While the former is a tautology, the latter can be written as

$$\left[\Delta t - \frac{1}{\delta + \mu} - \frac{1}{(\delta + \mu + \varepsilon)(\Re_0 - 1)}\right]^2 > \overline{\Re}, \quad (12)$$

where

$$\widetilde{\Re} = \left[\frac{1}{\delta + \mu} + \frac{1}{(\delta + \mu + \varepsilon)(\Re_0 - 1)} \right]^2 - \frac{4}{\delta (\delta + \mu + \varepsilon)(\Re_0 - 1)}.$$

If $\overline{\mathfrak{K}} < 0$, then (12) is a tautology. Otherwise, since Δt must satisfy (11), the inequality (12) reduces to

$$\Delta t < \frac{1}{\delta + \mu} + \frac{1}{(\delta + \mu + \varepsilon)(\Re_0 - 1)} - \sqrt{\widehat{\Re}}.$$

Our conclusion is the following theorem.

Theorem 4. In the case $\mathfrak{R}_0 < 1$, the disease-free equilibrium \mathbf{e}_0 of our discrete epidemic model (10) is locally asymptotically stable if

$$\Delta t < \min \left\{ \frac{2}{\delta}, \frac{2}{\left(\delta + \mu + \varepsilon\right)\left(1 - \Re_0\right)} \right\}.$$

In the case $\Re_0 > 1$, the endemic equilibrium e_1 of the same model is locally asymptotically stable if

$$\Delta t < \frac{1}{\delta + \mu} + \frac{1}{(\delta + \mu + \varepsilon)(\Re_0 - 1)} - \sqrt{\max\left\{\overline{\Re}, 0\right\}}, (13)$$

where

$$\widetilde{\Re} = \left[\frac{1}{\delta + \mu} + \frac{1}{(\delta + \mu + \varepsilon)(\Re_0 - 1)} \right]^2 - \frac{4}{\delta (\delta + \mu + \varepsilon)(\Re_0 - 1)}.$$

B. Discretised inventory model

For computational convenience, let us choose $\Delta t \in (0,1]$ such that $1/\Delta t$ is an integer. After specifying the values of all involved parameters, given the initial numbers \overline{S}_0 and \overline{I}_0 of susceptible and infected individuals, our discrete epidemic model (10) provides the estimates $\overline{S}_{t/\Delta t}$ and $\overline{I}_{t/\Delta t}$ for the numbers of susceptible and infected individuals S(t) and I(t) on days $t \in \{0,1,\ldots,T\}$. The expressions (6), (7), and (8) for the company's order cost $\mathcal{OC}(m)$, purchase cost $\mathcal{PC}(m)$, and holding cost $\mathcal{HC}(m)$ as functions of the inter-order time interval m are thus estimated by

$$\begin{split} & \overline{\mathcal{OC}}\left(m\right) = \left(\left\lfloor\frac{T}{m}\right\rfloor + 1\right)\Gamma, \\ & \overline{\mathcal{PC}}\left(m\right) = \Pi\alpha \left[\sum_{i=0}^{\left\lfloor T/m\right\rfloor - 1}\sum_{j=im}^{(i+1)m-1}\overline{I}_{j/\Delta t} + \sum_{j=\left\lfloor T/m\right\rfloor m}^{T}\overline{I}_{j/\Delta t}\right], \end{split}$$

$$\overline{\mathcal{HC}}(m) = \Lambda \alpha \left[\sum_{i=0}^{\lfloor T/m \rfloor - 1} \sum_{k=im}^{(i+1)m-1} \sum_{j=k+1}^{(i+1)m-1} \overline{I}_{j/\Delta t} + \sum_{k=\lfloor T/m \rfloor m}^{T} \sum_{j=k+1}^{T} \overline{I}_{j/\Delta t} \right].$$

Consequently, the following expression estimates the company's total cost $\mathcal{TC}\left(m\right)$ as a function of the inter-order time interval m:

$$\overline{\mathcal{TC}}(m) = \left(\left\lfloor \frac{T}{m} \right\rfloor + 1 \right) \Gamma + \Pi \alpha \left[\sum_{i=0}^{\lfloor T/m \rfloor - 1} \sum_{j=im}^{(i+1)m-1} \overline{I}_{j/\Delta t} \right]$$

$$+ \sum_{j=\lfloor T/m \rfloor m}^{T} \overline{I}_{j/\Delta t}$$

$$+ \Lambda \alpha \left[\sum_{i=0}^{\lfloor T/m \rfloor - 1} \sum_{k=im}^{(i+1)m-1} \sum_{j=k+1}^{(i+1)m-1} \overline{I}_{j/\Delta t} \right]$$

$$+ \sum_{k=\lfloor T/m \rfloor m}^{T} \sum_{j=k+1}^{T} \overline{I}_{j/\Delta t}$$

$$+ \sum_{k=\lfloor T/m \rfloor m}^{T} \sum_{j=k+1}^{T} \overline{I}_{j/\Delta t} \right].$$

In the upcoming section, we conduct numerical simulations using two sets of parameter values representing two qualitatively different cases: $\mathfrak{R}_0 < 1$ and $\mathfrak{R}_0 > 1$, in each of which we determine the value of m that minimises $\overline{TC}(m)$, specify the company's purchase quantity \mathcal{Q}_i for each order $i \in \{0,\ldots,|T/m|+1\}$, which is estimated by

$$\overline{\mathcal{Q}}_i = \alpha \sum_{j=im}^{\min\{(i+1)m-1,T\}} \overline{I}_{j/\Delta t},$$

and visualise the company's medicine inventory $\mathcal{I}(t)$ at the end of each day $t \in \{0, \dots, T\}$, which is estimated by

$$\overline{\mathcal{I}}_{t/\Delta t} = \alpha \sum_{j=t+1}^{\min\{(\lfloor t/m \rfloor + 1)m - 1, T\}} \overline{I}_{j/\Delta t}.$$

IV. NUMERICAL SIMULATIONS AND SENSITIVITY ANALYSIS

In this section, we illustrate the applicability of both our epidemic and inventory models via numerical simulations. For this purpose, we employ two sets of parameter values presented in Tables I and II, representing two qualitatively different cases: a disease-free case $\Re_0 < 1$ and an endemic case $\Re_0 > 1$. These two sets of parameter values differ only in the value of the disease's incidence coefficient: $\beta = 0.00005$ in the former case and $\beta = 0.00006$ in the latter case. We begin by explaining how the parameter values the two tables are selected (subsection IV-A). Subsequently, we study numerically each of the two cases, calculating the values of the key epidemic quantities, observing how the number of susceptible and infected individuals evolve over time, and using our inventory model to solve the total-cost minimisation problem (subsection IV-B). We shall see that in both our disease-free and endemic cases, the number of infected individuals achieve a certain maximum -the so-called epidemic peak— before approaching its equilibrium value. Finally, we conclude our study by conducting a sensitivity analysis of the disease's basic reproduction number, the epidemic peak, and the minimum total cost with respect to the parameters involved in our epidemic and inventory models (subsection IV-C).

A. Selection of parameter values

Let us begin by justifying our selection of parameter values presented in Tables I and II.

- (i) The initial numbers of susceptible and infected individuals, $S\left(0\right)$ and $I\left(0\right)$, are both simulated to represent a scenario that begins with 3,000 susceptible individuals and only 1 infected individual. This implies that our initial population comprises 3,000+1=3,001 individuals.
- (ii) To estimate our population's birth rate λ , we assume an average number of births per female of 2.5 [42] and a female's average life expectancy of 73.4 years [51]. Further assuming that a year comprises 365 days, these lead to a female giving birth to approximately $2.5/(73.4 \cdot 365)$ individuals per day. Assuming a gender equidistribution [11], [12], in our initial population there are approximately 3,001/2 females. Consequently, we make the estimation $\lambda \approx (3,001/2) \cdot [2.5/(73.4 \cdot 365)] \approx 0.14001904$ individuals per day.
- (iii) Our population's natural death and death-by-disease coefficients δ and μ are derived from the work of Hoseana et al. [13], where these are assumed to be approximately 0.00745 and 0.01829-0.00745=0.01084 per month, respectively. Conducting the necessary unit conversion yields the estimations $\delta\approx0.00024833$ and $\mu\approx0.00036133$ per day.
- (iv) Our disease's recovery coefficient is directly acquired from the work of Wang et al. [49], namely, $\varepsilon\approx 0.1287$ per day.
- (v) A study by Cakici et al. [2] highlighted the potentially high per-order ordering cost of medicine, which practically includes expenses for manual counting, reordering, shipping and receiving, replenishment, invoice processing, and transportation. Following their observation, we assume that each medicine order incurs an ordering cost of $\Gamma \approx 500$ dollars per order.
- (vi) We set our medicine's purchase price at $\Pi=1$ dollar per unit. As noted by Gurtu [9], an item's annual holding cost is commonly assumed to be a certain percentage of the item's purchase price, with 16% as a possible choice. Consequently, we assume our medicine's holding cost as $\Lambda \approx 16\% \cdot 1/365 \approx 0.00043836$ dollars per unit per day.
- (vii) The values of all other parameters are simulated. In particular, as shown in Table II, we specify the epidemic period to be T=8,000 days and the maximum inter-order time-interval to be $m_{\rm max}=365$ days. Additionally, as shown in Table I, we specify two different values for the disease's incidence coefficient, namely, 0.00005 per individual per day to represent a disease-free case and 0.00006 per individual per day to represent an endemic case.

B. Numerical solution and total-cost minimisation

Let us now study numerically each of the two cases corresponding to the two different values of the disease's

incidence coefficient. For each case, we shall calculate the values of the key epidemic quantities, visualise the time evolution of the number of susceptible and infected individuals, and determine the inventory management strategy to be implemented by the medicine's distributing company in order to minimise the incurred total cost.

1) A disease-free case: Our disease-free case is characterised by the parameter values presented in Tables I and II with $\beta = 0.00005$. In this case, the disease's basic reproduction number (3) evaluates to $\Re_0 \approx 0.99655837 < 1$. By Theorem 4, one expects that the solution associated to the initial condition presented in Table I converges to the disease-free equilibrium $e_0 \approx (2577, 0)$, computed using equation (4), provided that the discretisation step size Δt is strictly less than the minimum value of $2/\delta \approx 8053.79938000$ and $2/[(\delta + \mu + \varepsilon)(1 - \Re_0)] \approx$ 4494.01540600. Recalling that Δt must be selected from the interval (0,1] such that $1/\Delta t$ is an integer, let us select $\Delta t = 1$. The time evolution of the number of susceptible and infected individuals over the epidemic period —from day 0 to day T— provided by our discrete epidemic model is visualised in Figure 2. Observe that the expected convergence to the disease-free equilibrium e₀ is achieved non-monotonically. Indeed, the number of susceptible individuals first decreases abruptly before gradually increasing towards its equilibrium value, while the the number of infected individuals initially rises towards a conspicuous maximum —which we refer to as the epidemic peak— of $I_{\rm max} \approx 343$ individuals on day 484, before progressively declining towards zero.

Let us now determine the company's optimal strategy for managing the medicine inventory over the epidemic period. First, the company's total cost $\overline{TC}(m)$ as a function of the inter-order time-interval $m \in \{1, \dots, m_{\text{max}}\}$ is plotted in Figure 3 (left). The plot, expectedly convex-shaped, reveals that the company may achieve the minimum total cost of $\overline{\mathcal{TC}}_{\min} \approx 2,033,258$ dollars by adopting an inter-order time-interval of $m_{\min} = 99$ days, thereby placing $\lfloor T/m_{\min} \rfloor + 1 = 81$ orders over the epidemic period. In such a scenario, the company's purchase quantity $\overline{\mathcal{Q}}_i$ for each order $i \in \{0, ..., |T/m_{\min}|\}$ is shown in Figure 3 (right), while the company's medicine inventory $\overline{\mathcal{I}}_{t/\Delta t}$ at the end of each day $t \in \{0, ..., T\}$ is displayed in Figure 4. Of note is that on the company's 5th order, placed on day 495, the company records a maximum purchase quantity of approximately 99, 253 units, which conforms with the fact that the epidemic peak is achieved on day 484.

2) An endemic case: For our endemic case, we consider the parameter values provided in Tables I and II with $\beta=0.00006$. For these parameter values, the formulae (3) and (5) yield the basic reproduction number $\Re_0\approx 1.19587004>1$ and the endemic equilibrium $e_1\approx (2155,172)$, respectively. Furthermore, the upper bound for the discretisation step size Δt prescribed by the inequality (13) evaluates to approximately 201.37476000, and so $\Delta t=1$ remains an admissible selection. Indeed, from Figure 5 we see the expected behaviour of our epidemic model's solution: convergence to the endemic equilibrium. As in the disease-free case, the convergence is non-monotonic, with the number of susceptible individuals exhibiting a sharp

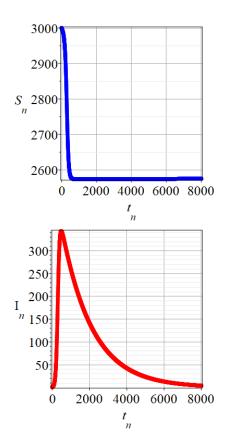


Fig. 2. The time evolution of the numbers of susceptible (left) and infected (right) individuals in our disease-free case where $\Re_0 \approx 0.99655837 < 1$.

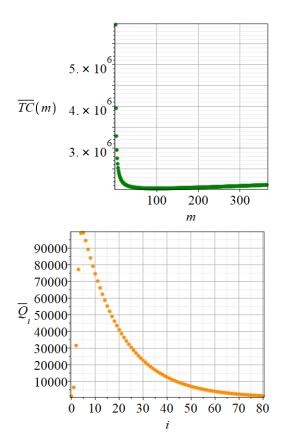


Fig. 3. The company's total cost $\overline{\mathcal{TC}}(m)$ as a function of the inter-order time-interval m (left) and the company's purchase quantity $\overline{\mathcal{Q}}_i$ for each order i (right) in our disease-free case where $\mathfrak{R}_0 \approx 0.99655837 < 1$.

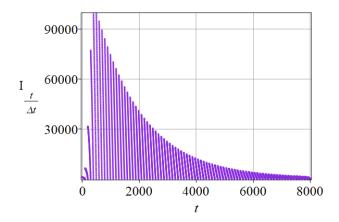


Fig. 4. The company's medicine inventory $\overline{\mathcal{I}}_{t/\Delta t}$ at the end of each day t in our disease-free case where $\mathfrak{R}_0 \approx 0.99655837 < 1$.

decrease before a steady increase and the number of infected individuals exhibiting a sudden increase towards an epidemic peak of $I_{\rm max} \approx 795$ individuals on day 230 before a moderate decay towards its positive equilibrium value.

A plot of the company's total cost \overline{TC} (m) as a function of the inter-order time-interval $m \in \{1,\ldots,m_{\max}\}$ in this endemic case is displayed in Figure 6 (left), the minimum total cost being $\overline{TC}_{\min} \approx 7,469,815$ dollars, achieved by adopting an inter-order time-interval of $m_{\min} = 51$ days and placing $\lfloor T/m_{\min} \rfloor + 1 = 157$ orders over the epidemic period. The company's purchase quantity \overline{Q}_i for each order $i \in \{0,\ldots,\lfloor T/m_{\min} \rfloor\}$ in this scenario is shown in Figure 6 (right), while the company's medicine inventory $\overline{I}_{t/\Delta t}$ at the end of each day $t \in \{0,\ldots,T\}$ is displayed in Figure 7. The company's 4th order, placed on day 204, is placed with the maximum purchase quantity of 1,189,874 units, anticipating the epidemic peak that is achieved on day 230.

C. Sensitivity analysis

Let us complement our results with a sensitivity analysis of three key quantities: the disease's basic reproduction number \mathfrak{R}_0 , the epidemic peak I_{\max} , and the company's minimum total cost $\overline{\mathcal{TC}}_{\min}$, with respect to the involved parameters. For this purpose, we recall that the sensitivity index of a quantity Q depending differentiably on a parameter p is defined as

$$\Upsilon_p^Q = \frac{\partial Q}{\partial p} \cdot \frac{p}{Q},\tag{14}$$

which provides a theoretical estimate for the ratio of the relative change in Q to the relative change in p [3]. The availability of the explicit expression (3) of the basic reproduction number as a differentiable function of our epidemic model's parameters implies an opportunity to compute the sensitivity index of the basic reproduction number in an exact manner. By contrast, the fact that analogous expressions for the epidemic peak and total cost are not readily obtainable forces us to compute the sensitivity indices of these quantities in a numerical manner.

1) Sensitivity analysis of the basic reproduction number: Substituting the expression (3) into the formula (14) and carrying out the algebraic simplification for $p \in \{\lambda, \kappa, \beta, \delta, \mu, \varepsilon\}$, we obtain the following expressions for the

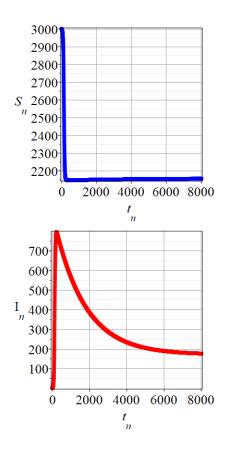


Fig. 5. The time evolution of the numbers of susceptible (left) and infected (right) individuals in our endemic case where $\Re_0 \approx 1.19587004 > 1$.

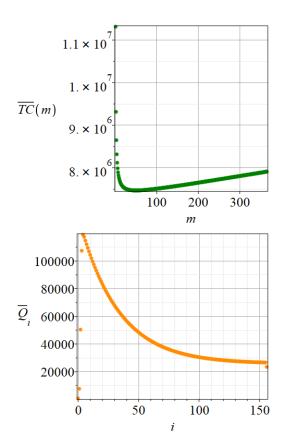


Fig. 6. The company's total cost \overline{TC} (m) as a function of the inter-order time-interval m (left) and the company's purchase quantity $\overline{\mathcal{Q}}_i$ for each order i (right) in our endemic case where $\mathfrak{R}_0 \approx 1.19587004 > 1$.

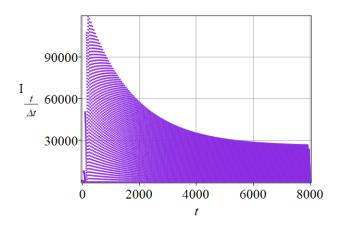


Fig. 7. The company's medicine inventory $\overline{\mathcal{I}}_{t/\Delta t}$ at the end of each day t in our endemic case where $\Re_0 \approx 1.19587004 > 1$.

basic reproduction number's sensitivity indices with respect to the parameters involved in our epidemic model:

$$\begin{split} \Upsilon_{\lambda}^{\mathfrak{R}_{0}} &= \frac{\lambda}{\lambda + \kappa}, & \Upsilon_{\kappa}^{\mathfrak{R}_{0}} &= \frac{\kappa}{\lambda + \kappa}, \\ \Upsilon_{\beta}^{\mathfrak{R}_{0}} &= 1, & \Upsilon_{\delta}^{\mathfrak{R}_{0}} &= -\frac{2\delta + \mu + \varepsilon}{\delta + \mu + \varepsilon}, \\ \Upsilon_{\mu}^{\mathfrak{R}_{0}} &= -\frac{\mu}{\delta + \mu + \varepsilon}, & \Upsilon_{\varepsilon}^{\mathfrak{R}_{0}} &= -\frac{\varepsilon}{\delta + \mu + \varepsilon}. \end{split}$$

Notice that none of these expressions depend on β . Since the two sets of parameter values representing our disease-free and endemic cases differ only in β , substituting these into the above expressions yields the same value of each index in both our disease-free and endemic cases:

$$\begin{split} \Upsilon_{\lambda}^{\mathfrak{R}_{0}} &\approx 0.21877324, & \Upsilon_{\kappa}^{\mathfrak{R}_{0}} &\approx 0.78122676, \\ \Upsilon_{\beta}^{\mathfrak{R}_{0}} &= 1.000000000, & \Upsilon_{\delta}^{\mathfrak{R}_{0}} &\approx -1.00192043, \\ \Upsilon_{\mu}^{\mathfrak{R}_{0}} &\approx -0.00279430, & \Upsilon_{\varepsilon}^{\mathfrak{R}_{0}} &\approx -0.99528527. \end{split}$$

Therefore, in both our disease-free and endemic cases, the basic reproduction number \mathfrak{R}_0 depends most sensitively on the natural death coefficient δ , with a 1% increase in the natural death coefficient leading to an approximately 1.00192043% decrease in the basic reproduction number.

2) Sensitivity analysis of the epidemic peak and total cost: The fact that explicit expressions for the epidemic peak I_{\max} and the company's minimum total cost $\overline{\mathcal{TC}}_{\min} = \overline{\mathcal{TC}}(m_{\min})$ as functions of our epidemic and inventory models' parameters are not easily obtainable forces us to compute the sensitivity indices of these two quantities numerically. For this purpose, let us fix a finite set Ψ of signed percentages and consider the following estimate for Υ_p^Q :

$$\overline{\Upsilon}_{p}^{Q}\left(\Psi
ight)=rac{1}{\left|\Psi
ight|}\sum_{v,v\in\Psi}rac{
ho_{Q,p}\left(\psi
ight)}{\psi},$$

where $\rho_{Q,p}\left(\psi\right)$ denotes the relative change in the value of Q resulting from a change of ψ in the value of p. Our goal is to compute $\overline{\Upsilon}_p^Q\left(\Psi\right)$ as an estimate for Υ_p^Q for every $Q\in\left\{I_{\max},\overline{\mathcal{TC}}_{\min}\right\}$ and $p\in\left\{\lambda,\kappa,\beta,\delta,\mu,\varepsilon,\Pi,\Gamma,\Lambda,\alpha\right\}$, using $\Psi=\left\{-1.0\%,-0.5\%,0.5\%,1.0\%\right\}$. We present our results in Table III.

Notice firstly that for every $p \in \{\Pi, \Gamma, \Lambda, \alpha\}$ we have that $\Upsilon_p^{I_{\max}} = 0$ since I_{\max} is independent of p. More notably,

TABLE III ESTIMATES $\overline{\Upsilon}_p^{I_{\max}}(\Psi)$ and $\overline{\Upsilon}_p^{\mathcal{T}C_{\min}}(\Psi)$ for the sensitivity indices $\Upsilon_p^{I_{\max}}$ and $\Upsilon_p^{\overline{\mathcal{T}C_{\min}}}$ of the epidemic peak and the company's minimum total cost with respect to $p \in \{\lambda, \kappa, \beta, \delta, \mu, \varepsilon, \Pi, \Gamma, \Lambda, \alpha\}$, computed using $\Psi = \{-1.0\%, -0.5\%, 0.5\%, 1.0\%\}$.

p	Disease-free case		Endemic case		
	$\overline{\Upsilon}_{p}^{I_{\mathrm{max}}}\left(\Psi ight)$	$\overline{\Upsilon}_p^{\overline{\mathcal{TC}}_{\min}}(\Psi)$	$\overline{\Upsilon}_{p}^{I_{\mathrm{max}}}\left(\Psi\right)$	$\overline{\Upsilon}_{p}^{\overline{\mathcal{TC}}_{\min}}(\Psi)$	
λ	0.16786883	1.68884659	0.03594191	0.59325683	
κ	0.59944848	6.01627266	0.12829593	2.11847186	
β	8.16131307	13.98903524	2.80012129	3.71303265	
δ	-0.89980672	-8.12764871	-0.19517287	-2.63643099	
μ	-0.07361513	-0.55946903	-0.03475499	-0.52039082	
ε	-7.95296654	-13.91562277	-2.73350371	-3.68128108	
П	0.000000000	0.95947246	0.00000000	0.97368140	
Γ	0.000000000	0.01991877	0.00000000	0.00539368	
Λ	0.00000000	0.02059185	0.00000000	0.02090774	
α	0.00000000	0.98008125	0.00000000	0.99460632	

in both our disease-free and endemic cases, both the the epidemic peak $I_{\rm max}$ and the company's minimum total cost $\overline{\mathcal{TC}}_{\rm min}$ depends most sensitively on the disease's incidence rate β . Indeed, in our disease-free case, a 1% increase in the incidence rate results in an approximately 8.16131307% increase in the epidemic peak and an approximately 13.98903524% increase in the minimum total cost. In our endemic case, on the other hand, a 1% increase in β results in an approximately 2.80012129% increase in the epidemic peak and an approximately 3.71303265% increase in the company's minimum total cost.

V. CONCLUSIONS AND FUTURE RESEARCH

We have studied the dynamical properties and the forward-Euler discretisation of a special case of an SIS-type epidemic model with immigrants introduced by Saikh and Gazi [35], in which all immigrants are assumed to be susceptible. We have also constructed a finite-time-horizon inventory model that can be used to determine a strategy to be implemented by a monopolistic medicine-distributing company in order to minimise the incurred total cost over a specified epidemic period. In the classical EOQ-type inventory model, we assumed that the total cost comprises three cost components: the medicine's order, purchase, and holding costs. Using two sets of parameter values representing a disease-free and an endemic case, we have conducted numerical simulations where we calculated the values of key epidemic quantities, visualised the time evolution of the numbers of susceptible and infected individuals, and determine the company's inter-order time-interval that minimises the incurred total cost. We have also conducted a sensitivity analysis, revealing that in both our disease-free and an endemic cases, the disease's basic reproduction number depends most sensitively on the population's natural death coefficient, whereas the epidemic peak and the company's minimum total cost both depend most sensitively on the disease's incidence coefficient.

The construction of inventory models for pharmaceutical items based on epidemic models constitutes the general theme of a collaborative study currently being conducted by the second and third authors of the present paper. In the near future, we plan to disseminate further results of this study, which includes a two-item medicine inventory model based on a two-age-group version of the SIS-type epidemic model utilised in the present study, medicine inventory models based on three different exactly solvable SIR-type epidemic models [24], [41], [6], and a vaccine inventory model based on an SIHV-type epidemic model [16]. Looking further ahead, studies on the same theme can be conducted by taking into account, for instance, multiple infection stages corresponding to different levels of medicine demands, as well as multiple vaccine doses. Moreover, one could modify the medicine inventory model constructed in the present paper by adopting different decision variables and incorporating additional factors such as deterioration, shortages, discounts, as well as storage and capital constraints [36], [37], [21], [22], [15], [7].

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