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QUALITATIVE PROPERTIES OF THE FINITE DIFFERENCE SOLUTION OF A SPACE-TIME EPIDEMIC PROPAGATION MODEL

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Abstract. The compartmental models of disease propagation give only the number of the infected individuals but do not give any piece of information about the locations of them. One of the remedies can be to transform the system into an integro-differential equation. We give the known basic qualitative properties of this system: monotonicity, nonnegativity preservation and the formulation of epidemic waves. Then we construct a finite difference numerical scheme to the system and give conditions for the discrete equivalents of the qualitative properties of the continuous system. We give a sufficient condition that guarantees the nonnegativity and the monotonicity, and a condition that is sufficient to extinguish an epidemic wave. We demonstrate the results on numerical examples.

1. Introduction

One of the most devastating pandemics of the recorded human history was the so-called Black Death in the 14th century [2]. The plague, coming from

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Asia with rat fleas, reached Europe in Sicily in October 1347. The disease waved through Europe in four years and reached northwestern Russia killing about the 50% of Europe's total population. Countries with lower level trade relations with their neighbours were less involved in the disease. The greatest pandemics of the 20th century (and probably also the most devastating in the history of the human kind) broke out in the shadow of World War II: the so-called Spanish Flu. In two years, between 1918 and 1919, more than 30 million people died worldwide, more than those died in the war. One-quarter of the US and one-fifth of the world were infected with the influenza. The spread of the disease followed the path of its human carriers: trade routes, mass movements of the soldiers, etc. [9].

Albeit nowadays the hygiene and the vaccination protect the richer part of the human population, pandemics occur these days too. For example, the flu pandemic in 2009-2010 (the so-called swine flu) killed probably 200,000 people around the world [10].

As it can be seen from the previously listed cases, it is very important to understand the mechanism of epidemics and try to prevent their outbreak and propagation by efficient and affordable means (e.g. hygiene, vaccination). Mathematical models can be the tools to get deeper insight into the behaviour of an epidemic [1, 3, 7].

The most common and well-investigated mathematical models are the so-called compartmental models. In these models the population is divided into some subpopulations, so-called compartments, and the model describes the behaviour of the disease between these compartments. The most common compartments are susceptibles (those who can be infected by the disease), infectives (those who can infect others) and removed (those who cannot be infected – for example because of immunity or death) but according to the complexity of the model other compartments can be also introduced: for those who are in a latent period, or in incubation or in different state of the illness (e.g. HIV/AIDS) [4].

The first compartmental model was created by Kermack and McKendrick in 1927 [8]. The model is generally called also as SIR model and is written in the form of a system of ordinary differential equations

$$\begin{aligned} S' &= -aSI, \\ I' &= aSI - bI, \\ R' &= bI, \end{aligned} \tag{1.1}$$

where $I = I(t)$, $S = S(t)$ and $R = R(t)$ denote the number of infective, susceptible and removed individuals as a function of time t, respectively. The contact rate a and recovery coefficient b are positive known numbers. This model has been improved several times taking into the account also births, deaths, la-

tent periods, reinfections, incubations etc. [1, 3]. All of these compartmental models assume that the population is homogeneous, that is they do not handle the different spatial positions of the individuals. There are several methods to bring also spatial dependence into the picture. In this paper we will investigate the qualitative properties of the numerical solutions of one of these models. We extend our previous results [5, 6] to the more realistic homogeneous Dirichlet boundary case and give conditions for the numerical epidemic wave formation.

The paper is organized as follows. In section 2, we list the remedies for the inclusion of the spatial dependence into the model (1.1). We will investigate a system of integro-differential equations model in detail. We list its basic qualitative properties. Then, in section 3, the finite difference numerical solution of the model is given and sufficient conditions are obtained that guarantee the qualitative properties for the numerical solution. We close the paper with some numerical tests.

2. Spatial disease propagation models

The compartmental models in their original form are not able to model the spatial movements of the disease. They give only, for example, the number of the infective individuals as a function of time but do not give any piece of information about their location. The locations of the infectives and the relations between the neighbouring countries played an important role also in the historical cases listed in the introduction.

Spatial dependence can be included in several ways into the model. For example, it is possible to divide the habitat of the population into some geopolitical regions and write equation (1.1) for each region separately with different parameters (so-called meta-population model). This system must be extended with additional equations that describe the transmission of the disease from one region to the other [3].

Other possibility is to allow the motion of the individuals in the population [7]. This is done generally by the inclusion of a diffusion process into the model, that leads to a system of reaction diffusion equations.

As a third possibility, we can make some simplifications as follows: We assume that the speed of the motion of the individuals can be neglected compared to the speed of the disease and the infection is localized in that sense that a member of the population can infect only members in its well defined neighbourhood. The last property is brought into the model by integral coefficients that yields the system of integro-differential equations equipped with suitable

initial and boundary conditions

$$
\begin{aligned}
S'_t(x,t) &= -\left(\int\limits_{N(x)} W(|x'-x|)I(x',t)\,\mathrm{d}x'\right) S(x,t),\\
I'_t(x,t) &= \left(\int\limits_{N(x)} W(|x'-x|)I(x',t)\,\mathrm{d}x'\right) S(x,t) - bI(x,t),\\
R'_t(x,t) &= bI(x,t),
\end{aligned}
\tag{2.1}
$$

where now $S = S(x,t)$, $I = I(x,t)$ and $R = R(x,t)$ depend also on the spatial position and give the densities of the corresponding parts of the population (see e.g. [7]).

The nonnegative weighting function W is supposed to depend only on the distance of the points x' and x, and $N(x)$ denotes a prescribed neighbourhood of the point x. $N(x)$ represents the neighbourhood of action of the disease. Only those individuals can be infected from another one located at the point x who are in this neighbourhood. The intensity of the infection is given by the weighting function W.

In order to obtain a system of partial differential equations we simplify the model further. Let us suppose that the spatial dimension of the problem is one, and that $N(x) = [x-\delta, x+\delta]$ is a symmetric interval around any fixed point x. Let us approximate I with its second order spatial Taylor series. In this way we arrive at the system

$$
\begin{aligned}
S'_t &= -S\left(\vartheta I + \varphi I''_{xx}\right),\\
I'_t &= S\left(\vartheta I + \varphi I''_{xx}\right) - bI,\\
R'_t &= bI,
\end{aligned}
\tag{2.2}
$$

where

$$
\vartheta = \int\limits_{-\delta}^{\delta} W(|u|)\,\mathrm{d}u, \quad \varphi = \frac{1}{2}\int\limits_{-\delta}^{\delta} u^2 W(|u|)\,\mathrm{d}u \tag{2.3}
$$

are positive constants that can be computed from the model (namely from $N(x)$ and W) directly [7]. We call system (2.2) as spatial SIR system (shorly sSIR).

It can be an important requirement for the mathematical and numerical models of any real life phenomenon that the solutions of the models must

possess some basic qualitative properties of the original process. The basic qualitative properties of the sSIR system are already known.

Because the birth and death rates are set to be zero in the model, we can expect the following properties from the density functions.

P1 The size of the population at a given spatial position cannot change in time. This means that $S + I + R$ must be constant at any given spatial position.

P2 The number of the susceptibles cannot grow and the number of the recovered cannot decrease. That is S is a nonincreasing and R is a nondecreasing function of time at any fixed spatial point.

P3 The number of the susceptible, infective and recovered members must be nonnegative. S, I and R must be always nonnegative if $S > 0$, $I \geq 0$ and $R \equiv 0$ are satisfied at the initial time instant.

We showed that under the implicit condition (the condition depends on the solution itself)

$$\vartheta I + \varphi I''_{xx} \geq 0 \tag{2.4}$$

properties [P2] and [P3] are true for the solution of problem (2.2). Property [P1] is true without any restrictions [5, 6].

In [7], the authors show that under certain conditions system sSIR has wave form solutions. This means, for example, that the function $S(x,t)$ can be written in the form

$$S(x,t) = \tilde{S}(x - ct),$$

where $\tilde{S} : \mathbb{R} \to \mathbb{R}$ is the wave profile function that propagates at speed $c > 0$. Let us introduce the notations $\tilde{S}^{\infty} = \lim_{\xi \to \infty} \tilde{S}(\xi)$ and $\tilde{S}^{-\infty} = \lim_{\xi \to -\infty} \tilde{S}(\xi)$. The first value is the density of the susceptibles before the epidemic wave reaches a given point, and the second one is the density left behind by the wave. It can be shown that the condition

$$\tilde{S}^{\infty} > b/\vartheta \tag{2.5}$$

(the initial density of the susceptible members must be sufficiently large) is a necessary condition for the propagation of the disease. In this case $\tilde{S}^{-\infty} < b/\vartheta$, that is the epidemic wave does not leave enough susceptible members back to be able to sustain a new wave.

In the next section we construct the finite difference solution of (2.2) and give some sufficient conditions to guarantee the discrete equivalents of the qualitative properties.

3. Finite difference solution of the sSIR model and its qualitative properties

In [7] system (2.2) was investigated on an infinite domain. In order to construct the finite difference solution of the model we have to prescribe some boundary conditions. In papers [5, 6] we applied homogeneous Neumann boundary conditions but now we think that homogeneous Dirichlet boundaries are more realistic. Homogeneous Neumann condition would mean that there is no in or outflow on the boundary but in the present case it is not clear what is the quantity that flows from one place to the other. In contrast, homogeneous Dirichlet condition can be interpreted as follows. Outside the considered domain conditions are incompatible with life, thus the densities must be zero on the boundaries.

Now we construct the finite difference solution of (2.2) on the spatial interval $[0, L]$ $(L > 0)$ applying homogeneous Dirichlet boundary conditions. We define a uniform spatial grid $\omega_h = \{x_k \in [0, L] \,|\, x_k = kh,\ k = 0, \ldots, N+1, h = L/(N+1)\}$ and a time step $\tau > 0$. The functions S, I and R are approximated respectively by the grid functions s^n, i^n and r^n at the nth time level $t = n\tau$. For $n = 0$, the grid functions are known from certain initial conditions.

Let us consider the explicit Euler discretization scheme

$$
\begin{aligned}
\frac{s_k^{n+1} - s_k^n}{\tau} &= -s_k^n \left(\vartheta i_k^n + \varphi \frac{i_{k-1}^n - 2i_k^n + i_{k+1}^n}{h^2} \right), \\
\frac{i_k^{n+1} - i_k^n}{\tau} &= s_k^n \left(\vartheta i_k^n + \varphi \frac{i_{k-1}^n - 2i_k^n + i_{k+1}^n}{h^2} \right) - b i_k^n, \\
\frac{r_k^{n+1} - r_k^n}{\tau} &= b i_k^n,
\end{aligned}
\tag{3.1}
$$

for the indices $k = 1, \ldots, N$, where we define the values with the spatial indices 0 and $N + 1$ to be zero (homogeneous Dirichlet boundary).

System (3.1) can be rewritten is a more compact form when we consider the grid functions s^n, i^n and r^n as column vectors, we define the product of two column vectors and the some of a real number and a vector elementwise and we introduce the matrix notation $Q = \mathrm{tridiag}(1, -2, 1) \in \mathbb{R}^{N \times N}$:

$$
\begin{aligned}
s^{n+1} &= s^n - \tau s^n p^n, \\
i^{n+1} &= (1 - \tau b) i^n + \tau s^n p^n, \\
r^{n+1} &= r^n + \tau b i^n,
\end{aligned}
\tag{3.2}
$$

where

$$p^n = \vartheta i^n + \frac{\varphi}{h^2} Q i^n. \tag{3.3}$$

The discrete versions of the qualitative properties [P1]–[P3] can be easily formulated for the numerical solution simply changing the functions S, I and R to the mesh functions s^n, i^n and r^n. Because it is not confusing, we will denote the discrete properties also by [P1]–[P3].

The next theorem provides a sufficient condition that guarantees the properties [P1]–[P3]. A numerical scheme that satisfies the properties [P1]–[P3] is called qualitatively adequate scheme.

Theorem 3.1. *Let us suppose that at the initial state $s^0 \geq 0$, $i^0 \geq 0$, $r^0 \geq 0$, and $p^0 \geq 0$, moreover assume that*

$$\tau \leq \min\left\{ \frac{1}{b + 2\varphi M/h^2}, \frac{1}{M(\vartheta + 2\varphi/h^2)} \right\}, \tag{3.4}$$

where $M = \max(s^0 + i^0 + r^0)$. Then the finite difference scheme (3.2) *with p^n given in* (3.3) *satisfies the qualitative properties* [P1]–[P3].

Proof. Property [P1] is satisfied automatically. We note that this implies that, provided that the statement of the theorem is true, the maximum norms of the vectors s^n, i^n and r^n are bounden by M. That is the numerical scheme is stable. In order to verify [P2]-[P3], it is enough to show that under the condition (3.4) the implication

$$s^0 \geq 0,\ i^0 \geq 0,\ r^0 \geq 0,\ p^0 \geq 0 \quad \Rightarrow \quad s^1 \geq 0,\ i^1 \geq 0,\ r^1 \geq 0,\ p^1 \geq 0$$

is true. Then the statement follows by induction.

The vector r^1 is trivially nonnegative. From the condition (3.4), the relation $\tau b \leq 1$ follows. Thus $i^1 \geq 0$. Based on condition (3.4) and the estimate $0 \leq i^0 \leq M$ we have

$$\tau p^0 = \tau\left(\vartheta i^0 + \frac{\varphi}{h^2} Q i^0\right) \leq \tau\left(\vartheta i^0 + \frac{\varphi}{h^2} 2M\right) \leq \tau M\left(\vartheta + \frac{2\varphi}{h^2}\right) \leq 1. \tag{3.5}$$

This means that s^1 is also nonnegative. Thus the state vectors are nonnegative at the first time level. From this fact and from the equality $s^0 + i^0 + r^0 = s^1 + i^1 + r^1$ we can state that $0 \leq s^1 \leq M$.

Now we show that $p^1 \geq 0$. Let us consider the relation

$$\begin{aligned} p^1 &= \vartheta i^1 + \frac{\varphi}{h^2} Q i^1 = \\ &= \vartheta(\tau s^0 p^0 + (1 - b\tau) i^0) + \frac{\varphi}{h^2} Q(\tau s^0 p^0 + (1 - b\tau) i^0) = \\ &= (1 - b\tau) \underbrace{\left(\vartheta i^0 + \frac{\varphi}{h^2} Q i^0\right)}_{p^0} + \tau\vartheta s^0 p^0 + \tau \frac{\varphi}{h^2} Q(s^0 p^0) = \\ &= (1 - b\tau + \tau\vartheta s^0) p^0 + \tau \frac{\varphi}{h^2} Q(s^0 p^0). \end{aligned} \tag{3.6}$$

Due to the nonnegativity of the vector $s^0 p^0$ we have $Q(s^0 p^0) \geq -2 s^0 p^0$. Hence, based on (3.6),

$$p^1 \geq (1 - b\tau + \tau\vartheta s^0 - 2\tau \frac{\varphi}{h^2} s^0) p^0 = (1 - \tau(b - \vartheta s^0 + \frac{2\varphi}{h^2} s^0)) p^0.$$

The nonnegativity of p^1 can be guaranteed by the condition

$$\tau \left(b - \vartheta s^0 + \frac{2\varphi}{h^2} s^0 \right) \leq 1,$$

which follows from the first term of the right hand side of the assumption (3.4). This completes the proof. ■

Now we consider the question of the propagation of a numerical epidemic wave. We proof a necessary condition.

Theorem 3.2. *Let us suppose that the qualitatively adequate numerical solution of* (2.2) *describes a numerical wave of speed c for the infectious individuals. If this wave has a strictly concave, monotonically decreasing part in the direction of the moving and $\tau < h/c$ then the density of the susceptibles must be greater than b/ϑ on that part of the wave profile* (*compare with* (2.5)).

Proof. Let us suppose that the wave front moves to the positive direction and the monotonically decreasing concave part of this front is the vector $[i^n_{k-1}, i^n_k, i^n_{k+1}]$. Thus we have $i^n_{k-1} \geq i^n_k \geq i^n_{k+1}$ and $i^n_{k-1} + i^n_{k+1} < 2i^n_k$. In view of the upper bound $\tau < h/c$ and the direction of the moving of the wave the relation $i^{n+1}_k \geq i^n_k$ must be true.

Let us suppose indirect that $s^n_k \leq b/\vartheta$. After rearranging the second equation in (3.2) we have

$$\frac{i^{n+1}_k - i^n_k}{\tau} = (s^n_k \vartheta - b) i^n_k + s^n_k \frac{\varphi}{h^2} (Q i^n)_k.$$

Here the first term on the right hand side is non-positive due to the indirect assumption. At the same time the second term is negative because of the strict concavity. Thus $i_k^{n+1} < i_k^n$, which is a contradiction. This completes the proof. ■

A direct consequence of the theorem is as follows. If an epidemic wave with the properties given in the statement of the theorem reaches a region with not enough individuals (density is less than b/ϑ) then the wave amplitude will decrease, and – when the shape of the wave does not change then – the wave passes.

4. Numerical examples

Now we verify the results of the previous section numerically. We have seen that if we choose the mesh appropriately then the numerical solution will possess the properties [P1]-[P3], and epidemic waves can occur for sufficiently large susceptible density.

We set $L = 1$, $\delta = 0.01$ and $b = 0.03$. The weighting function is defined to be $W(|u|) = 1 - |u|/\delta$ for $|u| \in [0, \delta]$ and zero otherwise, which is the usual tent function on the interval $[-\delta, \delta]$. This function models the situation that an infectious individual infects stronger if he is located closer. With this choice, formulas in (2.3) give $\vartheta = \delta$ and $\varphi = \delta^3/12$. The spatial step size is set to $h = 1/60$ ($N = 59$). We use the initial conditions seen in Figure 1. The infectives are located in the middle third part of the interval. The number of susceptibles tends to zero in the directions of the interval ends. With this initial conditions we have $M = 17$.

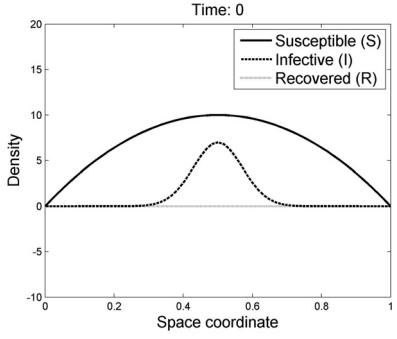

Figure 1. The initial conditions on the interval $[0, 1]$.

The upper bound (3.4) for the time step is $\tau \leq 5.5494$. First we choose $\tau = 15$, thus above the bound that guarantees the qualitative properties [P1]-[P3]. On the left panel of Figure 2 the density functions can be seen at the second time level ($t = 30$). The figure shows a qualitatively incorrect solution, namely the density function of the susceptibles has also negative values. Contrary, choosing the time step to be $\tau = 5$, thus below the bound (3.4), we will get a qualitatively correct solution (right panel of Figure 2). This supports the theoretical results of the previous section.

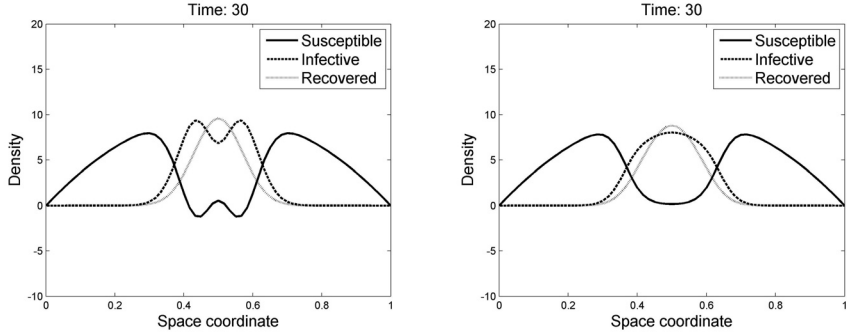

Figure 2. Left panel: The density functions at $t = 30$ in the case when the time step ($\tau = 15$) is chosen above the bound given by the sufficient condition. Right panel: The density functions at $t = 30$ in the case when the time step ($\tau = 5$) is chosen according to the bound of the sufficient condition.

Let us turn to the investigation of epidemic waves. The necessary condition $s > b/\vartheta = 3$ of Theorem 3.2 is satisfied in the middle region of the interval. Thus we may expect the appearance of epidemic waves. In the middle of the interval there are enough susceptibles to sustain the wave. Albeit, the condition is only necessary, in our numerical test the wave does appear. On the left panel of Figure 3 the density functions at time instant $t = 260$ can be seen. The peak of the infectives on the left hand side moves to the left and the right peak to the right.

When we follow the propagation of the waves, we can observe that the waves die out approximately at the points $x = 0.1$ and $x = 0.9$, thus susceptibles outside the interval $[0.1, 0.9]$ are not infected by the disease. This phenomenon can be explained by Theorem 3.2 that says that the regions where the density of susceptibles is not greater than $b/\vartheta = 3$ are not able to conduct epidemic waves. By means of this observation we may be able to obtain an immunization strategy. We can give that how many individuals must be immunized before the epidemic wave reaches a given region and we can stop the propagation of the disease.

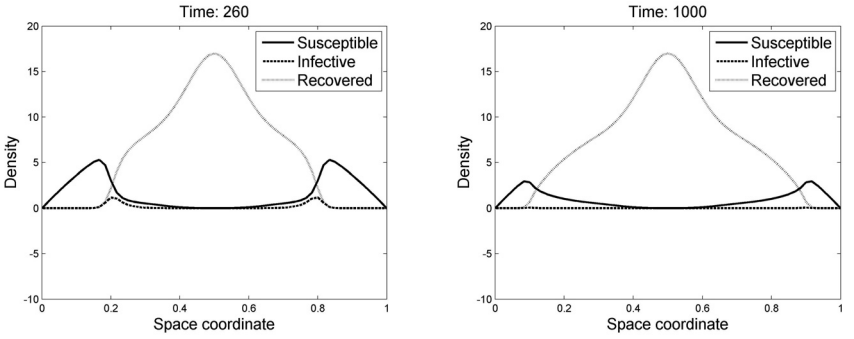

Figure 3. Left panel: The case of an epidemic wave. Right panel: The epidemic waves die out when the number of susceptibles is not enough to sustain the wave.

5. Summary, future work

In this paper we formulated a system of partial differential equations model of the one-dimensional spatial disease propagation. After discretizing the system by the finite difference method, we gave two sufficient conditions to guarantee the characteristic qualitative properties of the model. We obtained that if the time-step is sufficiently small then the qualitative properties are satisfied. Moreover, we showed that if the number of susceptibles is sufficiently small then the epidemic waves are not able to move. We demonstrated our results by numerical tests. Our future plan is to extend the result of this paper to the more realistic two-dimensional case.

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