S-I-R Model with Directed Spatial Diffusion

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Abstract

A S-I-R epidemic model is described in which susceptible individuals move away from foci of infection, and all individuals move away from overcrowded regions. It consists of hyperbolic partial differential equations, the sum of these equations being parabolic. Positivity and regularity of solutions are discussed and finite time blow-up of some solutions is illustrated through numerical simulations. A numerical test of the finite time blow-up of solutions is proposed.

1 Introduction

Kermack and McKendrick (1927) provided a mathematical description of the kinetic transmission of an epidemic in an unstructured population. The total population is assumed to be constant and divided into three classes: susceptible, infected (and infective), and removed (recovered with permanent immunity). The propagation of an infection governed by this simple model—which incorporates neither age or sex structure nor variability of infectivity or spatial position—gave rise to many models of various types of epidemics.

Few extensions have dealt with spatial issues. Webb (1981) proposed and analyzed a model structured by spatial position in a bounded onedimensional environment, [0, L], L > 0. Spatial mobility is assumed in Webb (1981) to be governed by random diffusion with coefficients $k_1$ and $k_2$ for the susceptible and infected classes. The infection is assumed to be transmitted from infected to susceptible at a rate per head $\alpha > 0$ by a “mass action” contact term, and the infected are assumed to recover at a rate per head $\gamma > 0$. Demographic changes are neglected under the assumption that the duration of the epidemic is short in comparison with the average life span.
of an individual and that the disease affects neither fertility nor mortality. This situation is typical, for example, of childhood diseases. Let \( S = S(x, t) \), \( I = I(x, t) \), and \( R = R(x, t) \) denote, respectively, the density of susceptible, infected, and removed individuals (recovered with immunity) at location \( x \) at time \( t \). The epidemic is described by the coupled system of parabolic partial differential equations:

\[
\begin{align*}
S_t &= k_1 S_{xx} - \alpha SI, \\
I_t &= k_2 I_{xx} + \alpha SI - \gamma I.
\end{align*}
\]  

The model is completed by homogeneous Neumann boundary conditions representing a closed environment,

\[
S_x(0, t) = S_x(L, t) = I_x(0, t) = I_x(L, t) = 0.
\]

Webb (1981) showed that Eq. (1)-(2), completed by appropriate initial conditions, is well-posed and has positive solutions for all time if the initial data are positive. Moreover, in the case \( k_1 = k_2 \), Webb (1981) showed that the infected class disappears while the susceptible tend to a spatially uniform steady state. A significant limitation is the fact that the spatial variable is one-dimensional, making the model of limited applicability: the spatial displacement of a ground-bound population is two-dimensional, while that of a water- or air-bound population is three-dimensional. Because the steady state is disease-free and spatially uniform, the spatial structure adds very little to the dynamics of the model, and nothing at all asymptotically.

Gurtin and MacCamy (1977) assumed that the susceptible move away from concentrations of the infected while the disease renders these individuals stationary. This model leads to overcrowding and, possibly, to a finite time blow-up, which biologically means overcrowding after short time.

We shall incorporate spatial mobility of the susceptible away from infected regions, and of all individuals away from overcrowding. We assume no incubation or latency period for this disease, so that the terms “infected” and “infective” are synonyms. Whenever such a model exhibits finite time blow-up, its interest and applicability is just for short time projection. Otherwise, it may be useful for long term projections as well. For one spatial dimension the model was first considered by Meade and Milner (1991). We shall describe the model in two space dimensions, analyze properties of its solution and, in case theoretical results are not available, carry out numerical simulations to show that, for example, the unrestricted movement away from infection can lead to catastrophic consequences from overcrowding that
leads to the impossibility of providing enough nourishment, housing, health care, and fresh water. Because demography is ignored, the model can also be applied to very lethal diseases by interpreting the removed class as those who die from the disease.

The model could be applied, for example, to the bubonic plague that killed almost half of the population of Europe in XIVth century, with $R$ representing the isolated infected who do not move nor transmit disease because of their isolation. The displacement of susceptible away from infected areas created regions with a high density of susceptible who were prone to cause large secondary outbreaks when an infected appeared among them.

Refugee displacements in areas of armed conflict constitute a more modern example of applicability of the model, with $S$ representing the non-battling and $I$ the battling individuals, and $R$ those wounded or otherwise immobilized and non-battling. The displacements of non-battling individuals away from the battle zones create large accumulations of non-battling individuals along the border of the embattled country, making them malnourished and prone to illness.

2 A Model with Avoidance of Infection and Overcrowding

Meade and Milner (1991) described an epidemic model with spatial diffusion designed to overcome the effects of overcrowding and which may lead to finite time blow-up in the Gurtin-MacCamy (1977) model. A second diffusion process parameterized by $k_2$ causes each of the three epidemic classes to disperse avoiding large concentrations of the total population $N = N(x, t) = S + I + R$:

$$
\begin{align*}
S_t &= k_1(SN_x)_x + k_2(SI_x)_x - \alpha SI, \\
I_t &= k_1(IN_x)_x + \alpha SI - \gamma I, \\
R_t &= k_1(RN_x)_x + \gamma I.
\end{align*}
$$

The differential system is completed by non-negative initial distributions $S_0(x), I_0(x), R_0(x)$, and no-flux boundary conditions

$$(k_1 N + k_2 I_x)(0, t) = (k_1 N + k_2 I_x)(L, t) = k_1 N_x(0, t) = k_2 N_x(L, t) = 0,$$

(4)

to represent a closed environment.
When \( k_1 > 0 \) and \( k_2 > 0 \), Eq. (4) implies that \( I_x = N_x = 0 \) on the boundary. However, to show that \( S_x = 0 \) and \( R_x = 0 \) on the boundary requires differential equations and the relation \( N = S + I + R \). The compatibility of the initial with boundary data is assumed. Some qualitative properties of the solution were given by Meade and Milner (1991, 1992).

Expanding \( N \) as \( S + I + R \) in Eq. (3) we obtain the equivalent system:

\[
\begin{align*}
S_t &= k_1 S(S_{xx} + I_{xx} + R_{xx}) + k_1 S_x(S_x + I_x + R_x) + k_2 SI_x x
+ k_2 S_x I_x - \alpha SI, \\
I_t &= k_1 I(S_{xx} + I_{xx} + R_{xx}) + k_1 I_x(S_x + I_x + R_x) + \alpha SI - \gamma I, \\
R_t &= k_1 R(S_{xx} + I_{xx} + R_{xx}) + k_1 R_x(S_x + I_x + R_x) + \gamma I,
\end{align*}
\]

(5)

which is, in terms of the unknown vector \( \vec{E} = [S, I, R]^T \):

\[
\vec{E}_t = A \vec{E}_{xx} + B_1 \vec{E}_x + C \vec{E},
\]

(6)

where

\[
A = \begin{pmatrix}
k_1 S & (k_1 + k_2) S & k_1 S \\
k_1 I & k_1 I & k_1 I \\
k_1 R & k_1 R & k_1 R
\end{pmatrix},
\]

\[
B_1 = \begin{pmatrix}
k_1 (S_x + I_x + R_x) + k_2 I_x & 0 & 0 \\
0 & k_1 (S_x + I_x + R_x) & 0 \\
0 & 0 & k_1 (S_x + I_x + R_x)
\end{pmatrix},
\]

\[
C = \begin{pmatrix}
-\alpha I & 0 & 0 \\
0 & \alpha S - \gamma & 0 \\
0 & \gamma & 0
\end{pmatrix}.
\]

The eigenvalues \( \lambda \) of the coefficient matrix \( A \) satisfy

\[
det (\lambda I_3 - A) = 0,
\]

(7)

where \( I_3 \) is the \( 3 \times 3 \) identity matrix.

Simplifying Eq. (7),

\[
\lambda^3 - k_1 (S + I + R) \lambda^2 - k_1 k_2 SI \lambda = 0.
\]

(8)

\( \lambda = 0 \) is always a root of Eq. (8), and when \( k_1 = 0 \) (movement away from infection but not away from overcrowding), it is the only root —with
algebraic multiplicity 3 and geometric multiplicity 2. In this case System (3) is first-order hyperbolic and it may exhibit blow-up in a finite time. For \( k_1 > 0 \), the other two eigenvalues of \( A \) are the roots of the quadratic

\[
\lambda^2 - k_1(S + I + R)\lambda - k_1k_2SI = 0,
\]

which for \( k_2, S, I, \) and \( R \) positive has one positive and one negative root. The three distinct eigenvalues allow for a linear change of unknowns. The diagonalization \( A \) leads to three equations which are semi-linearly coupled in their diffusion terms. Each corresponds a different behavior: one similar to the heat operator, one similar to the hyperbolic operator, and one similar to the backward heat operator. This coupling of different types of equations may lead to numerical instabilities. When \( k_2 = 0 \) there is a double eigenvalue 0 and a positive one, leading to a well-behaved system analyzed by Meade and Milner (1992).

We extend this model to the more realistic two-dimensional case. Let \( \Omega = [0, L_1] \times [0, L_2] (L_1 > 0, L_2 > 0) \) be the habitat for the population under consideration. For \((x, y) \in \Omega \) and \( t > 0 \), \( S(x, y, t), I(x, y, t), R(x, y, t) \) satisfy

\[
\begin{align*}
S_t &= k_1 \nabla \cdot (S \nabla N) + k_2 \nabla \cdot (S \nabla I) - \alpha SI, \\
I_t &= k_1 \nabla \cdot (I \nabla N) + \alpha SI - \gamma I, \\
R_t &= k_1 \nabla \cdot (R \nabla N) + \gamma I,
\end{align*}
\]

System (10) is completed by non-negative initial distributions \( S_0(x, y), I_0(x, y), R_0(x, y) \) and no-flux boundary conditions: for \((x, y) \in \partial \Omega, t > 0,\)

\[
\left( k_1 \frac{\partial N}{\partial n} + k_2 \frac{\partial I}{\partial n} \right) (x, y, t) = k_1 \frac{\partial N}{\partial n}(x, y, t) = 0,
\]

where \( n \) is the outward normal unit vector on \( \partial \Omega \).
Substituting $S + I + R$ for $N$, Eq. (10) becomes

$$
\begin{align*}
S_t &= k_1 S(S_{xx} + I_{xx} + R_{xx}) + k_1 S_x(S_x + I_x + R_x) \\
&\quad + k_1 S(S_{yy} + I_{yy} + R_{yy}) + k_1 S_y(S_y + I_y + R_y) \\
&\quad + k_2 S I_{xx} + k_2 S_x I_x + k_2 S I_{yy} + k_2 S_y I_y - \alpha S I, \\
I_t &= k_1 I(S_{xx} + I_{xx} + R_{xx}) + k_1 I_x(S_x + I_x + R_x) \\
&\quad + k_1 I(S_{yy} + I_{yy} + R_{yy}) + k_1 I_y(S_y + I_y + R_y) + \alpha S I - \gamma I, \\
R_t &= k_1 R(S_{xx} + I_{xx} + R_{xx}) + k_1 R_x(S_x + I_x + R_x) \\
&\quad + k_1 R(S_{yy} + I_{yy} + R_{yy}) + k_1 R_y(S_y + I_y + R_y) + \gamma I.
\end{align*}
$$

(12)

Using the same notation as for the one-dimensional problem, $\vec{E} = [S, I, R]^T$, we rewrite System (12) in terms of $\vec{E}$ as

$$
\vec{E}_t = A \Delta \vec{E} + B_1 \vec{E}_x + B_2 \vec{E}_y + C \vec{E}
$$

(13)

where $A, B_1, C$ are the same as before, $B_2$ is similar to $B_1$, with derivatives with respect to $x$ replaced by derivatives with respect to $y$.

We now prove that solutions of Eq. (10)-(11) are meaningful.

**Theorem 2.1** If $S_0, I_0, R_0 > 0$, any solution $(S, I, R)$ of Eq. (10)-(11) is positive as long as it exists.

Proof. Assume $(S, I, R)$ is a smooth solution. Extending on the technique in Meade and Milner (1992) for the porous medium equation, we first compute the solution $S$ along characteristics defined by the following family of initial value problems:

$$
\begin{align*}
X_t(p, t) &= -(k_1 N_x(X(p, t), Y(q, t), t) + k_2 I_x(X(p, t), Y(q, t), t)), \\
Y_t(q, t) &= -(k_1 N_y(X(p, t), Y(q, t), t) + k_2 I_y(X(p, t), Y(q, t), t)), \\
X(p, 0) &= p, \ Y(q, 0) = q.
\end{align*}
$$

(14)
Differentiating $X_t(p, t), Y_t(q, t)$ with respect to $p$ and $q$ respectively,

$$
\begin{align*}
X_{pt}(p, t) &= - [k_1 N_{xx}(X(p, t), Y(q, t), t) + k_2 I_{xx}(X(p, t), Y(q, t), t)] X_p(p, t), \\
Y_{qt}(q, t) &= - [k_1 N_{yy}(X(p, t), Y(q, t), t) + k_2 I_{yy}(X(p, t), Y(q, t), t)] Y_q(q, t), \\
X_p(p, 0) &= 1, \quad Y_q(q, 0) = 1.
\end{align*}
$$

(15)

For each $(p, q) \in \Omega$, $X_p(p, \cdot), Y_q(q, \cdot)$ is a solution of a system of homogeneous first-order linear ordinary differential equations with positive initial data. Hence $X_p$ and $Y_q$ are positive.

Let $S(p, q, t) := S(X(p, t), Y(q, t), t)$. Then

$$
\begin{align*}
S_t(p, q, t) &= S_t(X(p, t), Y(q, t), t) + S_x(X(p, t), Y(q, t), t)X_t(p, t) \\
&\quad + S_y(X(p, t), Y(q, t), t)Y_t(q, t)
\end{align*}
$$

(16)

$$
S(p, q, 0) = S(X(p, 0), Y(q, 0), 0) = S(p, q, 0) = S_0(p, q),
$$

(17)

and

$$
S(p, q, t) = \frac{S_0(p, q)}{X_p(p, t)Y_q(q, t)} \exp \left( -\alpha \int_0^t I(X(p, \tau), Y(q, \tau), \tau) d\tau \right).
$$

(18)

As $X_p, Y_q$ and $S_0$ are positive, the positivity of $S$ follows.

The positivity of $I$ and $R$ follows from an analogous argument with the characteristics defined by

$$
\begin{align*}
X_t(p, t) &= -k_1 N_x(X(p, t), Y(q, t), t), \\
Y_t(q, t) &= -k_1 N_y(X(p, t), Y(q, t), t), \\
X(p, 0) &= p, \quad Y(q, 0) = q.
\end{align*}
$$

(19)
3 Special Case I: Avoidance of infection

The model in which the susceptible move in avoidance of infection is similar to the Gurtin-MacCamy’s (1977) model, which is based on the assumption that the susceptible class moves to avoid concentrations of the infected with velocity \( v_S = k_2 \nabla I \), where \( k_2 \) is a positive constant. The infective have zero velocity \( v_I = 0 \). The resulting system of PDE is nonlinear and diffusion is degenerate.

In the one-dimensional case, System (3) reduces to:

\[
\begin{align*}
S_t &= k_2(SI_x)_x - \alpha SI, \\
I_t &= \alpha SI - \gamma I,
\end{align*}
\]

(20)

with nonnegative initial distribution \( S_0(x), I_0(x) \) and no-flux boundary conditions

\[
S_x(0, t) = S_x(L, t) = I_x(0, t) = I_x(L, t) = 0.
\]

(21)

Remark 3.1 Meade (1992) showed that the infected cannot spread out of their original support. The distribution of the other epidemic classes is stationary where the infected are absent. Moreover, if the solution exists at all time, the infected disappears asymptotically. Also, the susceptible may accumulate on the boundary of the compact support of the infected, and the solution may blow up in finite time.

We now estimate the rate of blow-up when it occurs in finite time through an example.

**Example 1:** We took the same parameters and initial data for Eq. (20)-(21) as Meade (1992) \( k_1 = 0, k_2 = 0.1, \alpha = 1, \gamma = 5, S_0(x) = 6, R_0(x) = 0 \), and

\[
I_0(x) = \begin{cases}
2 - 25x^2, & 0 \leq x \leq 0.1, \\
\frac{25}{7}(0.8 - x)^2, & 0.1 < x \leq 0.8, \\
0 & 0.8 < x \leq 1.
\end{cases}
\]

Meade (1992) conjectured that the solution of Eq. (20) may break down with the formation of a shock by rewriting Eq. (20) as a hyperbolic system. By tracking the characteristic line of the hyperbolic system in Example 1, Meade (1992) estimated that the solution breaks down (characteristic lines cross each other) at \( x = 0.8 \) and \( t = 0.7 \). We introduce a numerical test of
Table 1: Numerical solution of Eq. (20) using Scheme (38), with point values \( S \) at \( t = 0.7 \) and \( x = 0.8 - 1/M \) for different \( M \).

<table>
<thead>
<tr>
<th>Partition number ( M )</th>
<th>20</th>
<th>40</th>
<th>80</th>
<th>160</th>
<th>320</th>
<th>640</th>
<th>1280</th>
</tr>
</thead>
<tbody>
<tr>
<td>Numerical solution ( \bar{S} )</td>
<td>17.1</td>
<td>24.0</td>
<td>34.4</td>
<td>49.9</td>
<td>73.3</td>
<td>109.3</td>
<td>164.5</td>
</tr>
<tr>
<td>Ratio ( r )</td>
<td></td>
<td>1.41</td>
<td>1.43</td>
<td>1.45</td>
<td>1.47</td>
<td>1.49</td>
<td>1.51</td>
</tr>
</tbody>
</table>

finite time blow-up of solutions by looking at the numerical solution derived from the numerical scheme provided in Section 5. Numerical solutions of the susceptible at time \( t = 0.7 \) and \( x = 0.8 - 1/M \) are listed in Table 1, where \( M \) is the total number of spatial mesh points, \( \bar{S} \) the numerical solution at \( x = 0.8 - 1/M \), \( r \) the ratio between two consecutive values for \( \bar{S} \), corresponding to \( M \) and \( 2M \) spatial mesh points.

From Table 1, we conjecture that the ratios continue to increase when \( M \) increases. For a function of the form \( 1/(0.8 - x)^\alpha \) for some \( \alpha > 0 \), the ratio computed at \( x = 0.8 - 1/M \) is \( r = 2^\alpha \), a constant. The solution of susceptible blows up at \( x = 0.8 \), indeed faster than \( 1/(0.8 - x)^\alpha \). This happens because the susceptible cease to move as soon as they escape from the infection, when they reach the first infection-free point (\( x = 0.8 \), the boundary of the compact support of the infective).

**Remark 3.2** By comparing the ratios, we test whether a solution exhibits blow-up or not at a specific spatial location and a specific instant. Numerical simulations suggest that the blow-up happens where and when a ‘pseudo-oscillation’ first occurs, that is at the location and instant for which the numerical solution oscillates no matter how finely time and spatial intervals are divided.

In the two-dimensional case with avoidance of infection, Eq. (10) becomes

\[
\begin{align*}
S_t &= k_2 \nabla \cdot (S \nabla I) - \alpha SI, \\
I_t &= \alpha SI - \gamma I, \\
\end{align*}
\tag{22}
\]

with nonnegative initial distributions

\[
S(x, y, 0) = S_0(x, y), \quad I(x, y, 0) = I_0(x, y),
\tag{23}
\]

and no-flux boundary conditions,

\[
\frac{\partial S}{\partial n}(x, y, t) = 0, \quad \frac{\partial I}{\partial n}(x, y, t) = 0 \quad \text{on} \quad \partial \Omega.
\tag{24}
\]
Concerning the existence of solutions of Eq. (22), we know that global solutions do not exist in general, because in Example 2 System (22) exhibits finite time blow-up. As for local existence, we conjecture that the following result holds, though we do not have a proof for it yet.

**Theorem 3.1** Suppose $S_0 > 0$ and $I_0 > 0$ on $\Omega$. Then, there is a $T > 0$ such that Eq. (22) – (24) has a unique solution on $\Omega \times [0, T)$.

**Remark 3.3** If we let $\zeta(S, t) = e^{\int_0^t [\alpha S(\cdot, \cdot, \tau) - \gamma] d\tau}$, it follows from Eq. (22.ii) that

$$
\begin{align*}
I(\cdot, \cdot, t) &= I_0(\cdot, \cdot) \zeta(S, t), \\
\nabla I &= \zeta(S, \cdot) \nabla I_0 + I_0 \nabla \zeta(S, \cdot),
\end{align*}
$$

for any function $S(x, y, t)$. We rewrite Eq. (22.i) as

$$
S_t - k_2 \left( I_0 \nabla \zeta(S, \cdot) + \zeta(S, \cdot) \nabla I_0 \right) \cdot \nabla S + 2S \nabla I_0 \cdot \nabla \zeta(S, \cdot) \\
+ \frac{I_0}{\zeta} |\nabla \zeta|^2 + (\Delta I_0 - \alpha \frac{I_0}{k_2} S \zeta(S, \cdot)) = k_2 \alpha I_0 S \zeta \int_0^t \Delta S(\tau) d\tau.
$$

This equation is of the form

$$
S_t + \mathcal{F}(\nabla S) + \mathcal{G}(S) = \mathcal{H}(S) \int_0^t \Delta S(\tau) d\tau.
$$

Even though some existence results are available for the semi linear case with constant $\mathcal{H}$ and no integral in the gradient or Laplacian terms, such as in Smoller (1994), nothing is known about the quasi linear case with strong gradient nonlinearities in general.

**Theorem 3.2** If $S^* = S^*(x, y)$ and $I^* = I^*(x, y)$ are a steady state solution to Eq. (22)-(24), then $I^* \equiv 0$.

Proof. From Eq. (22.ii), $I^* = 0$ or $S^* = \frac{\gamma}{\alpha}$. If $S^* = \frac{\gamma}{\alpha}$, then the reduced boundary-value problem Eq. (22.ii)-(24),

$$
\begin{align*}
\Delta I^* - \frac{\alpha}{k_2} I^* &= 0, \quad \text{in } \Omega, \\
\frac{\partial I^*}{\partial n} &= 0, \quad \text{on } \partial \Omega,
\end{align*}
$$

where $\Delta = (\frac{\partial^2}{\partial x^2} + \frac{\partial^2}{\partial y^2})$, has the unique solution $I^* \equiv 0$. 

10
We now show that a finite time blow-up solution may exist in the two-dimensional case through an example.

**Example 2** For Eq. (22)-(24), we take $k_1 = 0$, $k_2 = 0.1$, $S_0(x, y) = 6$, $R_0(x, y) = 0$, and $I_0(x, y)$ equal to the tensor product of the initial distribution from Example 1 in $x$ and in $y$.

Our numerical scheme is capable of capturing shocks because shocks confront to a peak of the solution. Figure 1 shows the spatial distribution and contour plots of the density of the susceptible at $t = 0, 0.5, 1, 4$. The susceptible accumulate near the compact support of the initial distribution of infected $(0.8, y) \cup (x, 0.8)$, $0 \leq x, y \leq 0.8$.

We conjecture that a finite time blow-up solution exists, just as in the one-dimensional case. However, unlike the one-dimensional case, Eq. (22)-(24) cannot be written as a hyperbolic system. The characteristic method in Meade (1992) cannot be applied and we have to run many simulations to locate the ‘pseudo-oscillation’ to find the blow-up time and position.

**Remark 3.4** Example 2 can be viewed as representative of an outbreak of a severe infectious disease appearing in a limited environment such as an island. The susceptible individuals move away from the region of infection and the infected stay wherever they are located because they are too sick to move. If the infected do not occupy the entire habitat at the onset of the epidemic, the susceptible accumulate on the boundary of the support of the initial distribution of infection, because the infected can never spread out of their initial location and eventually disappear, while the susceptible from the infected region move towards the boundary of the infected region in their attempt to escape infection, but they stop moving as soon as they reach the boundary because there are no infected individuals there from whom to escape. This may lead to unhealthy overcrowding along the boundary of the infected region but it also suggests that this model cannot accurately represent the dynamics of the epidemic for a long time.

### 4 Special Case II: Avoidance of overcrowding

If $k_1 > 0, k_2 = 0$, diffusion is directed away from overcrowding but not away from infection, we then write $N = S + I + R$, sum all three equations, and obtain the porous media equation in one dimension:

$$N_t = \left(\frac{1}{2}N^2\right)_{xx}$$

(29)
with nonnegative initial distribution $N_0(x)$ and no-flux boundary conditions

$$N_x(0,t) = N_x(L,t) = 0. \quad (30)$$

In two dimensions, the resulting equation is

$$N_t = \nabla \cdot (N \nabla N) \quad (31)$$

with nonnegative initial distribution $N_0(x,y)$ and no-flux boundary conditions

$$\frac{\partial N}{\partial n} = 0 \quad \text{on } \partial \Omega. \quad (32)$$

Meade and Milner (1992) established the existence and uniqueness of the solution to the problem in one dimension under the condition $S_0 + I_0 > 0$. Using an identical argument, we obtain the same result in the two-dimensional case:

**Theorem 4.1** For $k_1 > 0$ and $k_2 = 0$, Eq. (10)-(11) admit a unique solution in $\Omega \times [0, \infty)$ for any initial data $S_0(x,y)$ and $I_0(x,y)$ such that $S_0(x,y) + I_0(x,y) > 0$ in any point $(x,y) \in \Omega$.

**Remark 4.1** Unlike in the case of avoidance of infection, a global solution exists here as long as $N_0 > 0$. Moreover, the steady state solution for the total population is spatially uniform, the infection vanishes, and the susceptible and removed densities converge to their steady states.

The next example shows that the total population can reach its steady state much faster than the epidemic classes do. Example 3 describes a population with an outbreak of a mild disease that is not symmetric across the line $x = y$ in the spatial domain, and all individuals move away from large concentrations of population but not from the infection, which is assumed to be mild.

**Example 3** We take $k_1 = 0.1$, $k_2 = 0$, $S_0(x,y) = 6$, $R_0(x,y) = 0$, and

$$I_0(x,y) = \begin{cases} 
3(2 - 25x^2) \exp \left( \frac{y^2}{y^2 - 0.8^2} \right), & 0 \leq x \leq 0.1, \ 0 \leq y < 0.8, \\
\frac{75}{4} (0.8 - x)^2 \exp \left( \frac{y^2}{y^2 - 0.8^2} \right), & 0.1 < x \leq 0.8, \ 0 \leq y < 0.8, \\
0, & 0.8 < x \leq 1, \ 0.8 \leq y \leq 1.
\end{cases}$$
The simulation is based on the numerical scheme described in Section 5. Figures 2 and 3 show the density of the susceptible, the infected, and the total population from the initial distribution to the steady state. The total population $N$ is close to its steady state at time $t = 4$. However, the subclasses $S$ and $I$ are close to their steady states only at time $t = 150$. This is because the equation for $N$ is independent of $S$ and $I$. At the beginning, the movement force away from overcrowding governs the spatial flow of all subclasses while, as soon as the total population is close to its steady state, the system behaves like the Kermack-McKendrick’s (1927) model.

**Remark 4.2** Meade and Milner (1992) claimed that the density at $t = 4$ was near a steady state for Eq. (3)-(4) when $k_1 = 0.1$, $k_2 = 0$, $\alpha = 1$, $\gamma = 5$, $R_0 = 0$, $S_0 = 6$ and

$$I_0(x) = \begin{cases} 3\exp\left(\frac{x^2}{x^2 - 0.8^2}\right), & 0 \leq x < 0.8, \\ 0, & 0.8 \leq x \leq 1. \end{cases}$$

However, our simulations show that the steady state cannot be reached in such a short time. Figure 4a shows that the steady state of Eq. (3)-(4) in Meade and Milner (1992) is reached only at time $t = 80$. If the infected invade the entire habitat before they disappear, the asymptotic behavior is governed by the Kermack-McKendrick model, because the total population converges to its steady state in a very short time. Figure 4b ($S_0 = 3$, other parameters unchanged) shows that the infected disappear before they invade the whole domain, so that only the susceptible occupy the habitat in the region that the infected never reached.

## 5 Numerical Schemes

In Section 2, we noted that Systems (3) and (10) behave as hyperbolic, forward or backward parabolic, depending on the diffusion coefficients and the sizes of the epidemic classes. In order to apply an appropriate numerical method, we treat the hyperbolic and the parabolic cases separately. For highly virulent epidemic diseases, the dynamics of the spatial displacements is more likely to be dominated by infection.

We introduce a numerical method combining a splitting method, Runge-Kutta Discontinuous Galerkin Method (RKDG) (Cockburn and Shu, 2001), and the standard Finite Element Method (FEM). As in Section 4, $N = S + I + R$ denotes the total population size. It satisfies the equation

$$N_t = k_1 \nabla \cdot (N \nabla N) + k_2 \nabla \cdot (S \nabla I).$$  (33)
Let $\overline{S}, \overline{S}, \overline{I}, \overline{T}, \overline{R}, \overline{R}$ represent the intermediate steps in the approximations to $S, I, R$. We solve Eq. (3) and (10) by approximating $N, I, S, R$ sequentially applying the standard finite element method to Eq. (33) for $N$, and splitting the equations for $S, I, R$ into conservation laws and residues. The conservation laws are solved by the Runge-Kutta Discontinuous Galerkin Method, the residues are solved analytically and the integrals approximated by trapezoids. For any time $t^n$, we solve Eq. (3) or (10) for $t^n \leq t \leq t^{n+1}$ using the scheme:

$$N_t = k_1 \nabla \cdot (N \nabla N) + k_2 \nabla \cdot (S^n \nabla I), \quad t^n \leq t \leq t^{n+1}, \quad (34)$$

$$\begin{align*}
T_t &= k_1 \nabla \cdot (T \nabla N), \\
\overline{T}^n &= I^n, \\
\overline{I}_t &= \alpha \overline{S} \overline{T} - \gamma \overline{I}, \\
\overline{I}^n &= \overline{I}^{n+1}, \\
I^{n+1} &= \overline{I}^{n+1};
\end{align*} \quad t^n \leq t \leq t^{n+1}, \quad (35)$$

$$\begin{align*}
\overline{S}_t &= k_1 \nabla \cdot (\overline{S} \nabla N) + k_2 \nabla \cdot (\overline{S} \nabla I), \\
\overline{S}^n &= S^n, \\
\overline{S}_t &= -\alpha \overline{S} \overline{I}, \\
\overline{S}^n &= \overline{S}^{n+1}, \\
S^{n+1} &= \overline{S}^{n+1};
\end{align*} \quad t^n \leq t \leq t^{n+1}, \quad (36)$$

$$\begin{align*}
\overline{R}_t &= k_1 \nabla \cdot (\overline{R} \nabla N), \\
\overline{R}^n &= R^n, \\
\overline{R}_t &= \gamma I, \\
\overline{R}^n &= \overline{R}^{n+1}, \\
R^{n+1} &= \overline{R}^{n+1}.
\end{align*} \quad t^n \leq t \leq t^{n+1}, \quad (37)$$

Because in the case of avoidance of infection, $k_1 = 0$, $k_2 > 0$, the system is closed in $S$ and $I$, we solve the first two equations and ignore the third one corresponding to $R$. The dynamics of infection does not depend on the size or spatial distribution of the immune (removed) class, because the variable
\( R \) appears neither in Eq. (3.a)-(3.b) nor in Eq. (6.a)-(6.b) for \( S \) or \( I \). The procedure for this case is:

\[
\begin{align*}
    I_t &= \alpha SI - \gamma I, \quad t^n \leq t \leq t^{n+1}, \\
    \overline{S}_t &= k_2 \nabla \cdot (\overline{S} \nabla I), \quad t^n \leq t \leq t^{n+1}, \\
    S^n &= S^{n+1}, \\
    \overline{S}_t &= -\alpha \overline{S} I_t, \quad t^n \leq t \leq t^{n+1}, \\
    S^{n+1} &= S^{n+1}.
\end{align*}
\]  

(38)

**Remark 5.1** In the case of avoidance of infection, computing \( \nabla I \) by differentiating the analytical solution of the ODE and then using the trapezoidal rule for spatial integration leads to numerical oscillations in the vicinity of the region where the solution blows up. In this case, we update \( \nabla I \) using centered differences of the values of \( I \).

We show that our numerical method is consistent to simulate epidemic classes and the total population through Example 3 (two-dimensional) and the example in Remark 4.2 (one-dimensional). The discrete \( L^1 \) and \( L^2 \) norms \( \| S + I + R - N \|_{L_1} \), \( \| S + I + R - N \|_{L_2} \) corresponding to different partitions and different time \( t \) are listed in Table 2, 3, 4, 5.

In Table 2, 3, 4, 5, let \( M \) denote the total number of mesh points in each space direction, and let \( L^1 \) and \( L^2 \) denote \( \| S + I + R - N \|_{L_1} \) and \( \| S + I + R - N \|_{L_2} \), respectively. Tables 2 and 3 show that the method is stable in the sense that the error stays bounded for chosen partition as time increases; Tables 4 and 5 show that the sum of \( S + I + R \) converges to \( N \) for chosen time as partition refines. Moreover, from Tables 4 and 5, the numerical scheme converges at first order in both \( L^1 \) and \( L^2 \).

Table 2: Numerical errors \( \| S + I + R - N \|_{L_1}, \| S + I + R - N \|_{L_2} \) for the example in Remark 4.2 (one-dimensional case), with partition \( M = 320 \), at \( t = 0.125, 0.25, 0.5, 1, 2, 4 \).

<table>
<thead>
<tr>
<th>Time</th>
<th>0.125</th>
<th>0.25</th>
<th>0.5</th>
<th>1</th>
<th>2</th>
<th>4</th>
</tr>
</thead>
<tbody>
<tr>
<td>( L^1 )</td>
<td>0.001611</td>
<td>0.001963</td>
<td>0.002147</td>
<td>0.002181</td>
<td>0.002180</td>
<td>0.002180</td>
</tr>
<tr>
<td>( L^2 )</td>
<td>0.001967</td>
<td>0.002302</td>
<td>0.002495</td>
<td>0.002531</td>
<td>0.002533</td>
<td>0.002533</td>
</tr>
</tbody>
</table>
Table 3: Numerical errors $\|S+I+R-N\|_{L^1}$, $\|S+I+R-N\|_{L^2}$ for Example 3 (two-dimensional case), with partition $M = 80$, at $t = 0.125, 0.25, 0.5, 1, 2, 4$.

<table>
<thead>
<tr>
<th>Time</th>
<th>0.125</th>
<th>0.25</th>
<th>0.5</th>
<th>1</th>
<th>2</th>
<th>4</th>
</tr>
</thead>
<tbody>
<tr>
<td>$L^1$</td>
<td>0.004807</td>
<td>0.005362</td>
<td>0.005715</td>
<td>0.005701</td>
<td>0.005847</td>
<td>0.005992</td>
</tr>
<tr>
<td>$L^2$</td>
<td>0.006470</td>
<td>0.007224</td>
<td>0.008088</td>
<td>0.008420</td>
<td>0.008487</td>
<td>0.008574</td>
</tr>
</tbody>
</table>

Table 4: Numerical errors $\|S+I+R-N\|_{L^1}$, $\|S+I+R-N\|_{L^2}$ for the example in Remark 4.2 (one-dimensional case), with partition $M = 20, 40, 80, 160, 320, 640$, at $t = 0.5$.

<table>
<thead>
<tr>
<th>M</th>
<th>20</th>
<th>40</th>
<th>80</th>
<th>160</th>
<th>320</th>
<th>640</th>
</tr>
</thead>
<tbody>
<tr>
<td>$L^1$</td>
<td>0.026973</td>
<td>0.015699</td>
<td>0.008316</td>
<td>0.004250</td>
<td>0.002147</td>
<td>0.001079</td>
</tr>
<tr>
<td>$L^2$</td>
<td>0.030938</td>
<td>0.017904</td>
<td>0.009557</td>
<td>0.004921</td>
<td>0.002495</td>
<td>0.001256</td>
</tr>
</tbody>
</table>

Table 5: Numerical errors $\|S+I+R-N\|_{L^1}$, $\|S+I+R-N\|_{L^2}$ for Example 3 (two-dimensional case), with partition $M = 20, 40, 80$, at $t = 0.25$.

<table>
<thead>
<tr>
<th>$M$</th>
<th>20</th>
<th>40</th>
<th>80</th>
</tr>
</thead>
<tbody>
<tr>
<td>$L^1$</td>
<td>0.019568</td>
<td>0.009969</td>
<td>0.005362</td>
</tr>
<tr>
<td>$L^2$</td>
<td>0.026260</td>
<td>0.013726</td>
<td>0.007224</td>
</tr>
</tbody>
</table>

**Remark 5.2** Figure 5 shows numerical results of Example 1 generated from the numerical scheme provided in this section. It has a great coincidence with the numerical simulations in Meade and Milner (1991), which shows that our scheme is just as reliable.

Avoidance of overcrowding is introduced in Curtin-MacCamy’s (1977) model so that the system does not blow up in finite time.

**Example 4** We compare the numerical solutions of Eq. (3)-(4), with parameter values $k_1 = 0, k_2 = 0.1$, with $k_1 = 0.0001, k_2 = 0.1$ and the rest are the same as in Remark 4.2.

Figure 6 displays side-by-side the density of the susceptible at time $t = 0.22$ for $k_2 = 0.1$, with $k_1 = 0$ and with $k_1 = 0.0001$. When the susceptible move away from a local infection ($I_0$ vanishes in part of $\Omega$), they accumulate at the interior boundary of the infected region and produce a finite time blow-up (the maximum value of $S(0.8, 0.22)$ grows unbounded as the space-time mesh is refined). In contrast, even with a little movement away from overcrowding, the blow-up stops ($S(0.8, 0.22)$ remains bounded as the mesh
is refined). The numerical method develops oscillations which prevent the simulation from proceeding further when the mesh is too fine.

6 Conclusion

We have partially analyzed an epidemic model of S-I-R type in which susceptible individuals move away from infection and from crowded areas. This model extends the spatially one-dimensional model (Meade and Milner, 1991, 1992) to two spatial dimensions.

The theoretical results and numerical simulations for the model with movement away from infection highlight that it may lead to overcrowding. Limiting such displacements by avoiding overcrowded regions increases the number of infected individuals through the course of the epidemic.

When the susceptible move away from infection but not away from overcrowded areas, numerical simulations show that the solution can blow up in finite time, both in one and two space dimensions. We provide a qualitative description of the type of blow up, as faster than $1/(0.8 - x)^{\alpha}$ for the special case presented.

Unlike the case of avoidance of infection, a global solution exists when there is movement away from overcrowding, as long as $N_0 > 0$. Moreover, the steady state solution for the total population is spatially uniform, the infection disappears, and the susceptible and removed densities converge to their steady states, which are not uniform in space. These results were already established in the case of one space dimension (Meade and Milner, 1992).

Numerical simulations for the case of avoidance of overcrowding, $k_2 = 0$, indicate that the total population may reach its steady state much faster than the subclasses. Initially the movement force away from overcrowding governs the spatial flow of all subclasses but soon, when the total population is close to its steady state, the system behaves according to Kermack-McKendrick because the gradient terms have vanished. A local infection can move out from its original location and become global. The infected may spread out to the whole habitat before disappearing. The susceptible and recovered individuals coexist everywhere asymptotically. Depending on the initial ratio of susceptible to infected, the infected may also disappear before they spread out to the whole domain so that only susceptible fill the habitat in some region once the infected disappear.

Numerical simulations for this case also indicate that susceptible and recovered converge to a given distribution in the region outside of the orig-
inal compact support of the infective, who disappear asymptotically. These steady state values depend on the infectivity and recovery rates, as well as on the initial distribution of susceptible.

The numerical method we described and used for the case of avoidance of overcrowding is consistent in the sense that the numerical approximations of $N$ and of $S + I + R$ are close to one another. The sum of the approximated values for the three subclasses, $S + I + R$, converges to the approximated value for the total population, $N$, for all time. We do not have a proof for this fact but it seems to hold for simulations over a wide parameter range.

The problem of existence of solutions for the model is a very difficult one and remains open.

References


Figure 1: Density plots (top four) and contour plots (bottom four) of susceptible for Example 2.
Figure 2: Density plots of susceptible (top four) and infected (bottom four) in Example 3.
Figure 3: Density plot of total population in Example 3.

Figure 4: Distribution of total population and subclasses at steady states corresponding to different initial data.
Figure 5: Distribution of susceptible (top) and infected (bottom) for infection with compact initial support and diffusion to avoid infection ($k_1 = 0, k_2 = 0.1$), as Example 1.
Figure 6: Comparison of the effect of avoidance of infection and avoidance of both infection and overcrowding. Left column is the density of susceptible for $k_1 = 0$ and right column for $k_1 = 0.0001$ at $t = 0.22$. 