

S–I–R Epidemic Models with Directed Diffusion

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Abstract. A generalization of the Gurtin–MacCamy model for an S–I–R epidemic is described. The new model, which includes diffusion away from overcrowded regions, retains many of the interesting qualitative features of previous models. In addition, the global-in-time existence of solutions is proved for a special case. Qualitative properties of the solution are discussed and illustrated with a numerical example.

1. Introduction. Mathematical models for epidemics have been evolving in complexity and realism during the past 60 years. From the simple, unstructured model of Kermack and McKendrick of 1927 [7], many models incorporating, for example, age structure, time delays corresponding to incubation periods, spatial diffusion, and variable infectivity have been proposed (see, e.g., [2], [3], [4], [6]). The effects of dispersion on the spatial distribution of the subpopulations are of primary interest in this work.

In addition to allowing for more realistic descriptions of the observed phenomena, more complex models have solutions which can be qualitatively very different from the solutions of simpler ones. In this fashion the solutions can vary from exponentially increasing or decreasing populations in the simplest setting, to periodic or oscillatory solutions when delays are introduced, or to populations that “blow up” in a finite time for some nonlinear models. In the case of spatially distributed populations, there is have a fairly complete analysis for a model with “random” diffusion [12]. Global existence and uniqueness results have been obtained for the case of equal diffusivities in all classes, and all solutions originating from non-negative (positive) initial data remain non-negative (positive). Furthermore, the infection always dies out and the spatial distribution of susceptibles tends to a constant function. For the case of unequal diffusion coefficients the questions of global existence and asymptotic behavior are open. Just as is observed with the heat equation, the speed of transmission of the infection is infinite, making this model rather unrealistic for many applications.

From an epidemiological perspective, a more reasonable assumption than random motion of susceptibles is that they move away from infection. This is the basis for the Gurtin–MacCamy model [8]. Solutions to this model may tend asymptotically to spatially inhomogeneous distributions. The only analytic results for this model are positivity, uniqueness and local existence of solutions [9]. Numerical evidence indicates that the solution may actually “blow up” in finite time due to the accumulation of susceptibles at the boundary of the support of the infected individuals (when the initial distribution of

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the latter is compactly supported in the total domain) [10]. Although the disease propagates with a finite speed, the particular form of the diffusion is too restrictive for real-life applications: the infection cannot spread to regions in which the disease was not present initially.

In order to overcome this unwanted feature we propose a new model which incorporates a “directed” diffusion away from overcrowding. The new model also has more physical propagation characteristics. Whereas the Gurtin–MacCamy model has finite propagation speed it does not allow for the spread of an infection beyond its initial support. In contrast, the new model retains the finite speed of transmission and does permit the spread of the infection beyond its initial support.

2. Models with Directed Diffusion. Although several types of diffusion terms have been proposed for various demographic models, for human epidemics it is fairly reasonable to assume that uninfected individuals will move away from the infected, as considered by MacCamy [8]. Models based on just this kind of motion (“directed away from infection”) may result in an unwanted accumulation of susceptibles on the boundary of the infected region [10]. To overcome this limitation we propose a model which contains additional diffusion away from large concentrations of individuals.

Let $N = N(x, t)$ be the spatial distribution of a population at time $t \geq 0$ in the one-dimensional domain $\Omega = [0, L]$. The population is subdivided into classes of susceptible, infected (and infective, as we shall assume no incubation period), and removed or “recovered” (usually by immunity) individuals with spatial distributions $S(x, t)$, $I(x, t)$, and $R(x, t)$, respectively. In this model we shall not consider the demography (that is, there are no births or deaths) but just the transition from one epidemic class to another. Consequently, the dynamics are given by the following system of PDE’s:

$$(2.1) \quad \begin{cases} S_t = k_1(SN_x)_x + k_2(SI_x)_x - \alpha SI, \\ I_t = k_1(IN_x)_x + \alpha SI - \gamma I, \\ R_t = k_1(RN_x)_x + \gamma I, \end{cases}$$

where the x and t subscripts indicate partial differentiation in those variables, $\alpha > 0$ is a mean infectivity per individual so that αI is the “force of infection”, $\gamma > 0$ is the recovery rate, $k_1 \geq 0$ is the coefficient of diffusion away from overcrowding and $k_2 \geq 0$ the one away from infection. The case $k_1 = 0$, $k_2 > 0$ corresponds to the Gurtin–MacCamy model [8]. We shall use “no flux” (homogeneous Neumann) boundary conditions to maintain a closed population (no immigration or emigration):

$$(2.2) \quad \begin{cases} (k_1 N_x + k_2 I_x)(0, t) = (k_1 N_x + k_2 I_x)(L, t) = 0, \\ k_1 N_x(0, t) = k_1 N_x(L, t) = 0. \end{cases}$$

Note that, for $k_1, k_2 > 0$, these yield $N_x(0, t) = N_x(L, t) = I_x(0, t) = I_x(L, t) = 0$. We shall assume that the initial distributions for the three classes are non-negative (for obvious

reasons) and C^2 on $[0, L]$,

$$(2.3) \quad S(x, 0) = S_0(x), \quad I(x, 0) = I_0(x), \quad R(x, 0) = R_0(x) \equiv 0.$$

A solution of (2.1)–(2.3) on $[0, T]$, $0 < T \leq \infty$, is a triple (S, I, R) of functions $C^1([0, T]; C^2(\Omega))$ which are non-negative on $\Omega \times [0, T]$ and satisfy (2.1)–(2.3). Note that this imposes some compatibility conditions on the initial and boundary data, e.g. $I_{0,x}(0) = I_{0,x}(L) = 0$. The following lemma shows that any solution of the system (2.1)–(2.3) with non-negative initial data remains non-negative.

LEMMA 2.1. *Let (S, I, R) be a solution of (2.1)–(2.3) on $\Omega \times [0, T]$. Then, S, I , and R are non-negative and, if $S_0 > 0, I_0 > 0$ everywhere, then S and I are positive on $\Omega \times [0, T]$.*

Proof. Consider the characteristic curve $X(s; t)$, with parameter $s \in \Omega$, which is the solution of the initial value problem

$$(2.4) \quad \begin{cases} X_t(s, t) = -k_1 N_x(X(s; t), t) - k_2 I_x(X(s; t), t), \\ X(s; 0) = s. \end{cases}$$

Existence and uniqueness are guaranteed, for instance, if N_x and I_x are continuous in $\Omega \times [0, T]$, and uniformly Lipschitz continuous in x , which we have assumed. It follows that

$$X_{st}(x; t) = -(k_1 N_{xx}(X(s; t), t) - k_2 I_{xx}(X(s; t), t)) X_s(s; t).$$

As in [9], let $\mathfrak{S}(s, t) = S(X(s; t), t)$. Then

$$\mathfrak{S}_t(s, t) = - \left(\frac{X_{st}(s; t)}{X_s(s; t)} + \alpha I(X(s; t), t) \right) \mathfrak{S}(s, t),$$

with $\mathfrak{S}(s, 0) = S(X(s; 0), 0) = S(s, 0) = S_0(s) \geq 0$. Also, since $X_s(s; 0) \equiv 1 > 0$, it follows that

$$X_s(s; t) > 0, \quad s \in \Omega, \quad 0 \leq t < T.$$

Thus,

$$\mathfrak{S}(s, t) = \frac{S_0(s)}{X_s(s; t)} \exp \left(-\alpha \int_0^t I(X(s; \tau), \tau) d\tau \right)$$

is non-negative, and positive whenever S_0 is.

Similarly, let $Y(s; t)$, $s \in \Omega$, be the solution of the initial value problem

$$(2.5) \quad \begin{cases} Y_t(s; t) = -k_1 N_x(Y(s; t), t) \\ Y(s; 0) = s. \end{cases}$$

Then

$$Y_{st}(s; t) = -k_1 N_{xx} Y_s(s; t),$$

and $\mathcal{J}(s, t) = I(Y(s; t), t)$ is seen to satisfy

$$\mathcal{J}_t(s, t) = - \left(\frac{Y_{st}(s; t)}{Y_s(s; t)} - \alpha S(X(s; t), t) + \gamma \right) \mathcal{J}(s, t),$$

with $\mathcal{J}(s, 0) = I(Y(s; 0), 0) = I(s, 0) = I_0(s) \geq 0$. As above, we have $Y_s(s; t) > 0$, $s \in \Omega$, $t \in [0, T)$, and thus

$$\mathcal{J}(s, t) = \frac{I_0(s)}{Y_s(s; t)} \exp \left(\gamma t - \alpha \int_0^t S(X(s, \tau), \tau) d\tau \right)$$

is always non-negative, and positive whenever I_0 is.

Finally, with $\mathcal{R}(s, t) = R(Y(s; t), t)$ we obtain, as in the previous two cases,

$$\mathcal{R}_t(s, t) = - \frac{Y_{st}(s; t)}{Y_s(s; t)} \mathcal{R}(s, t) + \gamma \mathcal{J}(s, t),$$

which gives

$$\mathcal{R}(s, t) = \frac{\gamma}{Y_s(s; t)} \int_0^t Y_s(s; \tau) \mathcal{J}(s, \tau) d\tau \geq 0,$$

since $R_0 = 0$, $Y_s(s; \tau) > 0$, $s \in [0, L]$, $t \geq 0$, and $I \geq 0$ (as just shown). This completes the proof.

Remark 2.1. For any fixed $s \in \Omega$, the characteristics $X(s; \cdot)$ and $Y(s; \cdot)$ remain in Ω so long as they exist. More specifically, the no-flux boundary conditions (2.2) imply that any characteristic originating at an endpoint must be vertical (i.e. $X(0; t) = Y(0; t) = 0$ and $X(L; t) = Y(L; t) = L$ for all $t \geq 0$). Then, using the continuity with respect to s , it is seen that each family of characteristic curves must cover all of Ω for each $t \geq 0$ for which they exist. Note also that this confirms the claim that transmission of the disease occurs with finite speed.

Next we observe that the boundary conditions, (2.2), imply that the total population,

$$\bar{N}(t) = \int_{\Omega} N(x, t) dx,$$

is, as expected due to the absence of births, deaths, immigration, and emigration, constant. Consequently,

$$\bar{N}(t) \equiv \bar{N}_0 = \|S_0\|_{L^1(\Omega)} + \|I_0\|_{L^1(\Omega)}.$$

We now let

$$(2.6) \quad \bar{S}(t) = \int_{\Omega} S(x, t) dx, \quad \bar{I}(t) = \int_{\Omega} I(x, t) dx, \quad \bar{R}(t) = \int_{\Omega} R(x, t) dx,$$

denote, respectively, the total number of susceptible, infected, and removed individuals at time t . It follows from (2.1) and (2.2) that

$$(2.7) \quad \bar{S}'(t) = -\alpha \int_{\Omega} I(x, t)S(x, t)dx \leq 0$$

since, by Lemma 2.1, I and S are non-negative. Under the assumption that the solution to (2.1)–(2.3) exists for all time, we see that the total number of susceptibles has a limit, \bar{S}_{∞} . Since $\bar{S}(0) = \|S_0\|_{L^1(\Omega)}$ and \bar{S} is non-negative and non-increasing, this limit satisfies

$$(2.8) \quad 0 \leq \bar{S}_{\infty} = \lim_{t \rightarrow \infty} \bar{S}(t) = \lim_{t \rightarrow \infty} \int_{\Omega} S(x, t)dx \leq \|S_0\|_{L^1(\Omega)}.$$

We also obtain, from (2.1) and (2.2),

$$(2.9) \quad \begin{cases} \bar{I}'(t) = \alpha \int_{\Omega} I(x, t)S(x, t)dx - \gamma \bar{I}(t), \\ \bar{R}'(t) = \gamma \bar{I} \geq 0. \end{cases}$$

In particular, \bar{R} is non-negative, non-decreasing, and bounded by \bar{N}_0 , therefore it has a limit \bar{R}_{∞} ,

$$(2.10) \quad 0 \leq \bar{R}_{\infty} = \lim_{t \rightarrow \infty} \bar{R}(t) \leq \bar{N}_0.$$

Finally, $\bar{I}(t) = \bar{N}_0 - \bar{S}(t) - \bar{R}(t)$ must also have a limit \bar{I}_{∞} ,

$$(2.11) \quad 0 \leq \bar{I}_{\infty} = \lim_{t \rightarrow \infty} \bar{I}(t) \leq \bar{N}_0.$$

We can show now that, just as in other $S - I - R$ model without demography, the disease dies out everywhere.

LEMMA 2.2. *Assume the solution of (2.1)–(2.3) exists for all time. Let \bar{S} , \bar{I} , \bar{R} be the functions defined by (2.6) and let \bar{I}_{∞} be given by (2.11). Then $\bar{I}_{\infty} = 0$, and $\lim_{t \rightarrow \infty} I(x, t) = 0$ for all $x \in \Omega$.*

Proof. Integration of (2.9)₂ yields

$$(2.12) \quad \bar{R}(t) = \gamma \int_0^t \bar{I}(\tau)d\tau.$$

Thus, from the existence of \bar{R}_{∞} , it is seen that $\bar{I}(t) \rightarrow 0$ as $t \rightarrow \infty$. The non-negativity of I implies $I(x, t) \rightarrow 0$ almost everywhere and hence, by continuity, everywhere.

Remark 2.2. Note that (2.12) says that the cumulative number of “recovered” individuals is equal to the recovery rate times the cumulative number of infected individuals, as one would intuitively expect.

Remark 2.3. A generalization of the well-known threshold phenomenon for the Kermack–McKendrick model is obtained from (2.7) and (2.9)₁: if there exists $t^* \geq 0$ for which $\alpha \int_{\Omega} S(x, t^*)I(x, t^*)dx > \gamma \bar{I}(t^*)$, then $\bar{I}'(t^*) > 0$ and the total number of infectives increases. This gives a sufficient condition for a “local-in-time” epidemic. Note that this does not say that the infectives increase pointwise on all of Ω . Moreover, it is not clear that this condition is also necessary, since, for $\alpha \int_{\Omega} S(x, t)I(x, t)dx \leq \gamma \bar{I}(t)$ there may still be regions of Ω in which the infective population increases.

Further analytical information about the asymptotic behavior of solutions is more difficult to obtain. It is interesting to note that once it is known that $I \rightarrow 0$ all of the time-independent equations are formally satisfied. As a result there is no reason to believe that the steady-state distribution of S or R will be homogeneous. This is illustrated in the numerical example in the next section.

Next we concentrate on the questions of existence and uniqueness of solutions to (2.1)–(2.3). Numerical evidence [10] suggests that one should not expect global-in-time existence of solutions without imposing some additional constraints on the data. We shall show that, when $k_2 = 0$ (that is, there is diffusion directed away from overcrowding but not away from infection) we do have global existence and uniqueness.

THEOREM 2.1. *Let $k_1 > 0$ and $k_2 = 0$ in (2.1) and (2.2). Then (2.1)–(2.3) admits a unique solution on $\Omega \times [0, \infty)$ for any initial data such that $S_0 + I_0 > 0$.*

Proof. In this case the total population, N , is a solution of the following initial–boundary value problem for the porous medium equation:

$$(2.13) \quad \begin{cases} N_t = \frac{k_1}{2}(N^2)_{xx}, & x \in \Omega, \quad t > 0, \\ N_x(0, t) = N_x(L, t) = 0, & t \geq 0, \\ N(x, 0) = N_0(x) = S_0(x) + I_0(x) > 0, & x \in \Omega. \end{cases}$$

From the positivity of N_0 it follows that there is a unique classical solution of (2.13) which is positive (see, e.g., [1], [11]). Furthermore, both N_x and N_{xx} are continuous and bounded. Thus S and I are solutions of the following almost linear first-order system (linear with quadratic perturbations in the zero-order terms):

$$(2.14) \quad \begin{cases} S_t = (k_1 N_x)S_x + (k_1 N_{xx} - \alpha I)S, \\ I_t = (k_1 N_x)I_x + (k_1 N_{xx} + \alpha S - \gamma)I. \end{cases}$$

Note that, in general, not even the single linear equation $S_t = a(t, x)S_x$ admits a global solution (consider, for example, $a(x, t) = x^2$; then, no point (x_1, t_1) with $x_1 t_1 > 1$ lies on

a characteristic originating at $(x_0, 0)$, $x_0 > 0$). Consequently, (2.1) may not be globally solvable in general.

It is possible, however, to derive an a priori L^∞ -bound for $W = S + I$. In fact, (2.14) implies that

$$(2.15) \quad W_t = (k_1 N_x)W_x + (k_1 N_{xx})W - \gamma I.$$

From $S, I \geq 0$ it follows that so long as W exists, it satisfies the differential inequality

$$W_t - (k_1 N_x)W_x \leq \bar{K}W,$$

with $\bar{K} = \sup\{k_1 |N_{xx}|, |k_1 N_{xx} - \gamma|\} < +\infty$.

Let $x_0 \in \Omega$ be given and consider the characteristic curve $x = Y(x_0; t)$. The function $\mathcal{W}(t) = W(Y(x_0; t), t)$ is non-negative and satisfies the differential inequality

$$\frac{d}{dt}\mathcal{W} \leq \bar{K}\mathcal{W}.$$

Therefore,

$$\begin{aligned} 0 \leq \mathcal{W}(t) &\leq \mathcal{W}(0)e^{\bar{K}t} = (S_0(x_0) + I_0(x_0))e^{\bar{K}t} \\ &\leq (\|S_0\|_{L^\infty} + \|I_0\|_{L^\infty(\Omega)}) \exp\{(k_1 \|N_{xx}\|_{L^\infty} + \gamma)t\}. \end{aligned}$$

Hence $W = S + I$ will exist for all $t \geq 0$, $x \in \Omega$ which can be reached via a Y -characteristic. The fact that N_x is uniformly Lipschitz continuous in x and uniformly bounded implies the global solvability of (2.5). Combined with the observations in Remark 2.1, W is seen to exist globally in space and time.

To complete the proof, note that explicit formulae for S and I can be obtained from (2.15) and the definition of W :

$$\begin{cases} I = \frac{1}{\gamma}(k_1(N_x W)_x - W_t), \\ S = W - I. \end{cases}$$

Remark 2.4. The situation in which the initial data is not strictly positive is also of interest, e.g. a compactly supported population. In this case solutions to (2.13) exist only in a “weak” sense; discontinuities in N_x can occur at points where $N = 0$. The analysis of the resulting almost linear system for S and I must also be modified.

3. Numerical Example. The families of characteristic curves are also well-suited to numerical implementation [5]. In this section we describe a numerical method for the solution of (2.1)–(2.3) with $k_1 > 0$ and $k_2 = 0$, i.e. diffusion to avoid overcrowding only.

An example which illustrate some of the properties discussed in the previous section is also provided.

Let Y satisfy (2.5) and redefine the auxiliary functions

$$\mathcal{S}(s, t) = S(Y(s; t), t)Y_s(s, t), \quad \mathcal{J}(s, t) = I(Y(s; t), t)Y_s(s, t), \quad \mathcal{N}(s, t) = N(Y(s; t), t)Y_s(s, t).$$

It is a simple exercise to verify that these new functions satisfy the equations

$$(3.1) \quad \begin{cases} \mathcal{S}_t(s, t) = -\alpha \frac{\mathcal{J}(s, t)}{Y_s(s; t)} \mathcal{S}(s, t), \\ \mathcal{J}_t(s, t) = \left(\alpha \frac{\mathcal{S}(s, t)}{Y_s(s; t)} - \gamma \right) \mathcal{J}(s, t), \\ \mathcal{N}_t(s, t) = 0, \end{cases}$$

with initial conditions

$$(3.2) \quad \mathcal{S}(s, 0) = S_0(s), \quad \mathcal{J}(s, 0) = I_0(s), \quad \mathcal{N}(s, 0) = S_0(s) + I_0(s).$$

Moreover, the governing equation for the characteristic curves takes the form

$$(3.3) \quad Y_t(s; t) = -k \left(\frac{\mathcal{N}_s(s, t)}{Y_s(s; t)^2} - \frac{\mathcal{N}(s, t)Y_{ss}(s; t)}{Y_s(s; t)^3} \right).$$

The algorithm for the numerical solution of (3.1)–(3.3) is a standard (and simple) finite difference method. Discretize both the time, t , and spatial parameter, s . The explicit Euler method is used to advance from one timestep to the next. This proceeds in two steps. Second-order centered difference approximations of the spatial derivatives in (3.3) are used to compute the position of each characteristic at the next timestep. Then equations (3.1) can be “integrated” to obtain approximate values of \mathcal{S} , \mathcal{J} , and \mathcal{N} along each characteristic.

An example on $\Omega = [0, 1]$ is used to illustrate the properties discussed in the preceding section. Suppose the initial distributions of susceptibles and recovereds are constant ($S_0 = 6$, $R_0 = 0$) while the infectives are given by

$$I_0(x) = \begin{cases} 3 \exp\left(\frac{x^2}{x^2 - 0.8^2}\right), & 0.0 < x < 0.8, \\ 0, & 0.8 \leq x \leq 1.0. \end{cases}$$

Note that $I_0 \in C^\infty(\Omega)$. The values of the diffusion coefficients and infectivity and recovery rates are selected to be $k_1 = 0.1$, $k_2 = 0$, $\alpha = 1.0$, and $\gamma = 5.0$. Snapshots of the solution at several representative times are given in Figure 1.

It is interesting to note that the total population approaches the anticipated uniform distribution very rapidly (see Figure 1.b). Although the threshold condition is satisfied only in a very small neighborhood of $t = 0$, each of the graphs indicates some local growth in the infection. Of course, all of the infectives eventually disappear.

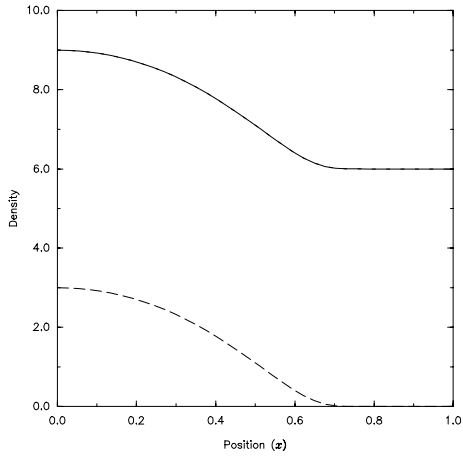
The steady-state solution is essentially that shown in Figure 1.f. This figure is consistent with the previous observation that the steady-state susceptible and recovered populations are not required to be constants.

Conclusion. The Gurtin–MacCamy model has been generalized with the inclusion of diffusion to avoid overcrowding. While the analysis of the full model is far from complete, the results for the special case without diffusion to avoid concentrations of the infection are promising.

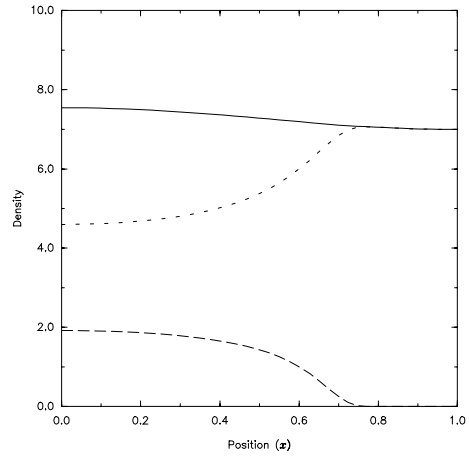
It remains to analyze both the case with compactly supported initial data and the full model with both diffusions. Preliminary results on these problems indicate that most of the features of the simple model are present in the more complicated models. The results of these investigations are forthcoming.

References

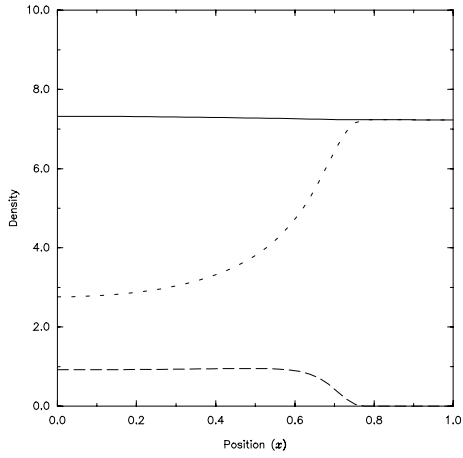
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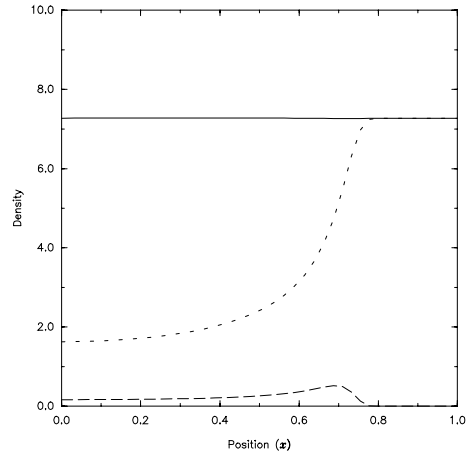
a. ($t = 0.0$)



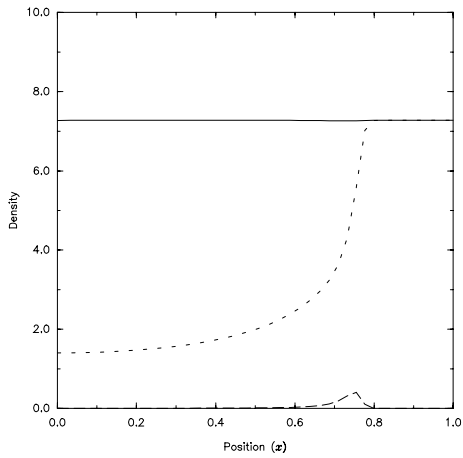
b. ($t = 0.25$)



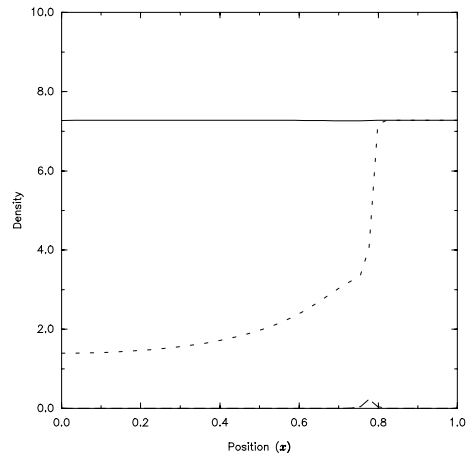
c. ($t = 0.5$)



d. ($t = 1.0$)



e. ($t = 2.0$)



f. ($t = 4.0$)

Population distributions at selected times ranging from the initial distribution (a.) to near steady-state (f.). The solid line indicates the total population. The infectives occupy the region below the dashed line, the susceptibles the region between the dashed and dotted lines, and the recovered the region between the dotted and solid lines.