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NUMERICAL SIMULATION OF SIR EPIDEMIOLOGICAL MODEL EMBEDDED IN SPATIO-TEMPORAL STATE

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Abstract:
In this paper a SIR epidemic model with spatial behavior of susceptible and infected populations has been studied by incorporating a diffusion term to the model. The SIR epidemic model is considered here in bi-dimensional case. Finite difference method based on Euler scheme has been used to solve the considered system. Finally numerical results have been shown.

Key words: Epidemic model, Spatial, Diffusion, Bi-dimensional

1.0 Introduction

W. Kermack and A. McKendrick [1] first proposed a model in 1927 to explain the rapid rise and fall in the number of infected patients observed in epidemics such as Cholera and Plague [2]. In 1979 M. Anderson and M. May revived the Kermack-McKendrick model as known as the SIR (Susceptible-Infected-Recovered) model. For the analysis of rapid spread of infectious diseases recently this simple epidemiological model consisting of three coupled ordinary differential equations has been used for a variety of epidemics, including HIV and SARS. Due to its applicability it has become the foundation for more complex and realistic epidemiological models.

A detailed history of mathematical epidemiology and basics of SIR epidemic models can be found in the classical books of Bailey [3], Murray [4] and Anderson and May [5]. After Kermack-McKendrick model different epidemiological models have been proposed and studied in the literature say Capasso and Serio [6], Hethcote and Tudor [7], Liu et al [8][9], Hethcote et al [10], Hethcote and Van den Driessche [11].

The population is divided into disjoint classes which change with time. The susceptible class consists of these individuals who can incur the disease but are not yet infective. The infective class consists of those who are removed from susceptible-infective interaction by recovery with immunity, isolation or death. The fractions of the total population in these classes are denoted by $S(t)$, $I(t)$ and $R(t)$ respectively.

Here the following assumptions are made:

(i) The only way a person can leave the susceptible group is to become infected.

(ii) The only way a person can leave the infected group is to recover from the disease

(iii) Once a per has recovered, the person received immunity
(iv) Probability of being infected is not depends on age, sex, social status and race.

2.0 Epidemic model

The mathematical model which is to be studied takes the following form:

$$\left.\begin{aligned}\frac{dS(t)}{dt} &= r_c S(t)\left(1-\frac{S(t)}{k}\right)-\frac{\alpha S(t)I(t)}{1+aI(t)}\\ \frac{dI(t)}{dt} &= \frac{\alpha S(t)I(t)}{1+aI(t)}-\gamma I(t)\end{aligned}\right\}-----(1)$$

The model has a susceptible group designated by $S(t)$, an infected group $I(t)$ and a recovered group $R(t)$ with permanent immunity, r_c is the intrinsic growth rate of susceptible, k is the carrying capacity of the susceptible in the absence of infective, α is the maximum values of per capita reduction rate of $S(t)$ due to $I(t)$, 'a' is half saturation constant, γ is the natural recovery rate from infection.

3.0 Spatio-Temporal model

In recent years, the problems of infection are gradually more present in our daily lives. Each individual is required to meet a number of people in a day either in the workplace or at various outlets (travel, cinema hall, shopping centers etc). We can cite models of spatial diffusion for Hunter [12], Gilg [13] and El Berrai et al [2] which deal with different types of epidemics. To model the spread of the epidemic for this SIR model it is assumed that the population moves: if the population is distributed in several cities, individuals can become infected within the same city, but more likely an individual can move in a city where it is an infectious, then bring the disease in his hometown, or another infected individual can move in another city to spread the disease. The fact can be modeled by using the following system:

$$\left.\begin{aligned}\frac{dS(t)}{dt} &= \nabla^2 S(t)+r_c S(t)\left(1-\frac{S(t)}{k}\right)-\frac{\alpha S(t)I(t)}{1+aI(t)}\\ \frac{dI(t)}{dt} &= \nabla^2 I(t)+\frac{\alpha S(t)I(t)}{1+aI(t)}-\gamma I(t)\end{aligned}\right\}-----(2)$$

The Laplacian is the spatial dispersion of individuals susceptible (infected respectively), the latter being modeled by a dissemination phenomenon that is to say a result of movements of individuals susceptible (infected respectively).

In the stationary problem, the system does not depend on time thus we obtain:

$$\left.\begin{aligned}\frac{\partial^2 S(t)}{\partial x^2}+\frac{\partial^2 S(t)}{\partial y^2} &= -r_c S(t)\left(1-\frac{S(t)}{k}\right)+\frac{\alpha S(t)i}{1+ai}\\ \frac{\partial^2 I(t)}{\partial x^2}+\frac{\partial^2 I(t)}{\partial y^2} &= -\frac{\alpha S(t)i}{1+ai}+\gamma I(t)\end{aligned}\right\}-----(3)$$

When this system depends on time then we obtained:

$$\left.\begin{aligned}\frac{dS(t)}{dt} &= \frac{\partial^2 S(t)}{\partial x^2}+\frac{\partial^2 S(t)}{\partial y^2}+r_c S(t)\left(1-\frac{S(t)}{k}\right)-\frac{\alpha S(t)i}{1+ai}\\ \frac{dI(t)}{dt} &= \frac{\partial^2 I(t)}{\partial x^2}+\frac{\partial^2 I(t)}{\partial y^2}+\frac{\alpha S(t)i}{1+ai}-\gamma I(t)\end{aligned}\right\}-----(4)$$

4.0 Approximation of the system

Here the spread of epidemics in 2-dimensions have been studied. Say people moves on a plane (digitally it is restricted to the polygon $]X_{\min}, X_{\max}[,]Y_{\min}, Y_{\max}[$)

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Thus the problem has been considered to the limits associated with the system (4).

We fixing $M_x > 0$ and $M_y > 0$ the number of domestic points in the polygon $]X_{\min}, X_{\max}[,]Y_{\min}, Y_{\max}[$. We note the discretization in space $\Delta_x = h_x = \frac{X_{\max} - X_{\min}}{M+1}$ and $\Delta_y = h_y = \frac{Y_{\max} - Y_{\min}}{M+1}$ with $x_i = X_{\min} + ih_x$ and $y_i = Y_{\min} + ih_y$. Now we divide the interval $[0,T]$ into N subintervals defined by $0 = t_0 < t_1 < t_2 < t_3 < \ldots\ldots < t_n = T$ with $l = \frac{T}{N}$. Now we will calculate an approximation of the solution denoted by $\left(s^n{}_{i,j}, I^n{}_{i,j}\right)$.

4.1 Proposition

We have a space-time discretization

$$\frac{\partial^2 u}{\partial x^2} = \frac{u^n{}_{i+1,j} - 2u^n{}_{i,j} + u^n{}_{i-1,j}}{\Delta x^2}, \quad \frac{\partial^2 u}{\partial y^2} = \frac{u^n{}_{i,j+1} - 2u^n{}_{i,j} + u^n{}_{i,j-1}}{\Delta y^2}, \frac{\partial u}{\partial t} = \frac{u^n{}_{i,j+1} - u^n{}_{i,j}}{\Delta t}$$

Now we put $H(S,I) = \frac{S^n{}_{i+1,j} + S^n{}_{i-1,j}}{\Delta x^2} + \frac{S^n{}_{i,j+1} + S^n{}_{i,j-1}}{\Delta y^2} + S^n{}_{i,j}\left[r_c\left(1 - \frac{S^n{}_{i,j}}{k}\right) - \frac{\alpha I^n{}_{i,j}}{1 + aI^n{}_{i,j}} - 2\left(\frac{1}{\Delta x^2} + \frac{1}{\Delta y^2}\right)\right]$

$$G(S,I) = \frac{I^n{}_{i+1,j} + I^n{}_{i-1,j}}{\Delta x^2} + \frac{I^n{}_{i,j+1} + I^n{}_{i,j-1}}{\Delta y^2} + I^n{}_{i,j}\left[\frac{\alpha I^n{}_{i,j}}{1 + aI^n{}_{i,j}} - \gamma - 2\left(\frac{1}{\Delta x^2} + \frac{1}{\Delta y^2}\right)\right]$$

Thus we obtain:

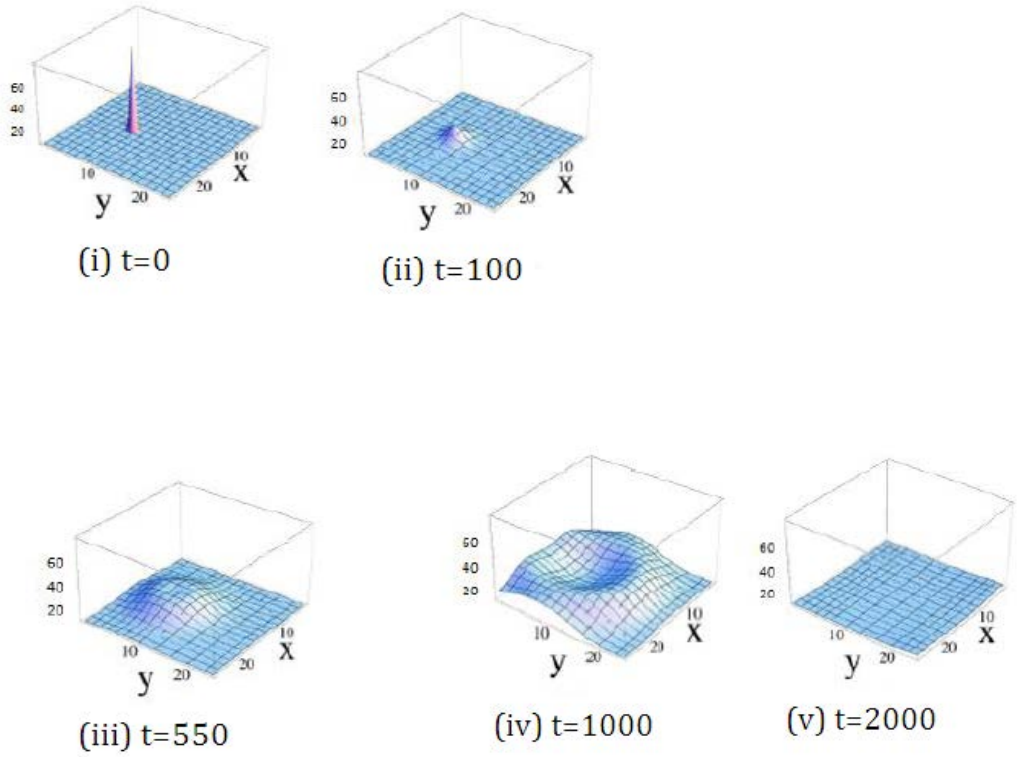
$$\left.\begin{aligned} S^{n+1}{}_{i,j} &= \Delta t\, H(S,I) + S^n{}_{i,j} \\ I^{n+1}{}_{i,j} &= \Delta t\, G(S,I) + I^n{}_{i,j} \end{aligned}\right] \text{-----(5)}$$

5.0 Numerical Simulation

For the numerical simulations following data have been used.

Parameter	S_0	I_0	a	α	γ	k	r_c
Value	50	30	2.3	1.49	0.611	100	2.5

Following diagrams are showing the spatial and temporal evolution of the infected populations for different times.



Initially at time $t = 0$, a proportion of infected is introduced. At time $t = 100$ in fig. (ii) the infected population begins to disseminate. At time $t = 550$ in fig. (iii) the dissemination is still amplifies. At time $t = 1000$ in fig. (iv) there is no longer a sick in the centre. Finally at the time $t = 2000$ in fig. (v) the epidemic is finite. The infected population is constant which is equal to zero.

6.0 Conclusions

The spatio-temporal epidemiological model 9STEM) tool is designed to help scientists and public health officials to create and use spatial temporal models of emerging infectious diseases. These models can support in understanding and potentially preventing the spread of such diseases. Computations of this model are based on compartment models that assume an individual is in a particular state, either susceptible (S), infected (I) or recovered (R) in classic SI(S), SIR(S) disease models. In this paper the SIR epidemic model of infectious diseases in populations is considered in bi-dimensional case. This model permits one hand to model the dynamic of spread of epidemic and on the other hand it permits to generalize the study proposed by El Berrai et al [2].

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