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Voting Rule Based Cellular Automata Epidemic Spread Model for Leptospirosis

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Abstract

This paper is focused on a cellular automata based computational model for the spread of disease named Leptospirosis using voting rules. Leptospirosis is most commonly found in bovine rats and the humans get infected when they come into contact with them. The disease spread is modelled in terms of Susceptible-Infective-Recovered-Susceptible (SIRS) model through one of the efficient computational modeling tool–Cellular Automata (CA); and requires strategic change in the rule set of the traditional CA. An idea of voting based rule on the neighborhood environment is studied for modeling the Leptospirosis and compared with real data of such infection in Thailand during the year 2000 and 2001. The simulation of the model is done with real data of Leptospirosis infection in Thailand during 2000 and 2001 and the results yielded from this model were closely in match with the real time data.

Keywords: Cellular Automata, Leptospirosis, SIRS Epidemic Model , Voting Rules

1. Introduction

The first type in Compartmental model-the SIR model proposed by Kermack and Mckendrick in 1927 consists of only human population[1]. Leptospirosis has two groups of population namely humans and animals, the latter being responsible for the transmission of the disease[2,3]. The human population is divided into three categories: Susceptible (S_H), Infective (I_H) and Recovered (R_H). The vector animal population is divided in to two categories: Susceptible (S_A), Infective (I_A). The schematic of the SIRS compartment model is shown in the following Figure 1.

2. Assumptions of the Model

Total human population NH is divided into three compartments: susceptible, infective and removed (or immunised) having populations S_H, I_H, and R_H respectively. Also, the human population has a birth rate λ_H which is balanced by an equal death rate μ_H, so the population during the epidemic period remains constant.

Vector animal population N_A is homogeneously mixed with the human population and has susceptible animal population S_A and infected animal population I_A, the latter being responsible for transmitting the Leptospirosis to human susceptible.

There is no incubation period for the disease. So the new born human children become susceptible immediately after their birth.

The disease is not transmitted by any individual of infected human population I_H but it is caused by an infected animal population I_A. It is assumed that every vector animal infects a susceptible human with a constant transmission rate β_H per month, as a result of which the susceptible human population S_H decreases with a rate of $\beta_H I_A S_H$ per month and increases the infected human population with the same amount.

The infected humans can recover from the disease with a rate r_1 per month per infected human, thus decreasing the infected population with a rate $r_1 I_A$ per month and correspondingly increasing the removed population with the same rate. The recovered humans become susceptible after some lapse of time, thus decreasing the recovered human

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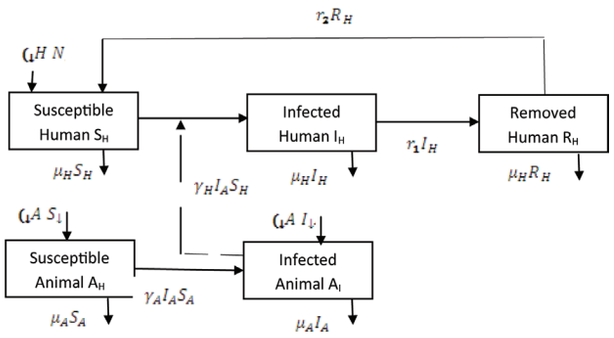


Figure 1. Flow chart of the dynamics of transmission of leptospirosis.

population and increasing susceptible human population with the same rate r_2R_H.

Both susceptible animal population and infective animal population have same birth rate λ_A which is balanced by an equal death rate μ_A, thus keeping the animal population N_A a constant during the period of disease.

An infective animal infects a susceptible animal with a constant transmission rate β_A per month. This decreases the susceptible animal population and increases the infective vector animal population with a rate of $\beta_A I_A S_A$ per month.

3. The Cellular Automata Model

The cellular automata model for modeling Leptospirosis requires certain modifications from the basic model of cellular automata[4]. They are:

States: A cell could be in one of the following states: Susceptible human, Susceptible Animal, Infected Human, Infected Animal, and Recovered Human. The CPV (critical population value) would be calculated in two parts as CPV_H(Human) and CPV_A(Animal) refer to equations (2.1, 2.2).

$$CPV_H = \frac{IPC_H(x,y)}{TPC_H(x,y)} \quad (2.3)$$

$$CPV_A = \frac{IPC_A(x,y)}{TPC_A(x,y)} \quad (2.4)$$

Where, $IPC_H(x,y)$ and $TPC_H(x,y)$ are critical infected human population and total human population respectively in a cell (x, y); $IPC_A(x,y)$ and $TPC_A(x,y)$ are corresponding critical infected animal population and total animal population in the cell (x, y).

If the CPV_H is greater or equal to CPV_A then cell (x, y) is considered to be in infected human state I_H=1; and if CPV_H is less than CPV_A, the cell is considered to be in infected animal state I_A=1.

3.1 The Cell Status Word

The Cell Status Word (CSW) would be modified slightly compared to the basic ones used in our earlier work[5,6] for fitting into the conditions of this model.

The CSW has five parameters as shown below and in Table 1:

(1) Cell_id which is the current cell denoted by C(x, y),

(2) CPV (Critical Population Value) which is the fraction of infected population over total population in the cell, which is split in to two- one for the CPV_H another one for CPV_A,

(3) I Value (Infection value) which is further split into two I_HValue and I_AValue which takes Boolean value 0/1 depending upon the human infection (I_H =1) or an animal infection (I_A=1); 0 means the cell is free of any infection, 1 means some percentage of cell is infected so we consider that the cell is infected (human/animal),

(4) R Value (Recovery Value) that may also take either 0 or 1 depending upon whether the population inside the cell is recovered from the disease or not,

(5) M Value, the Movement flag for a particular cell is used to control the movement of the population from one cell to another. M Value is 0 means no movement possible from the cell.

Table 1. Structure of the cell status word

Cell_id	CPV_H	CPV_A	I_HValue	I_AValue	R Value	M Value

Neighborhood Structure: The neighborhood structure is assumed to be Moore neighborhood that considers all cells around the cells to be updated currently.

3.2 Voting Transition Rules

Voting rules are the ones which update the center cell values according to the popularity of the values found in their local neighborhood. Each cell in the neighborhood is given one vote as to whether update the center cell with a particular value, and the center cell is given the voted-on value on the next time level t+1 from the present time level *t*, if the number of votes exceeds some threshold value. The general form of voting is a rule (1) as given in the following equation (2.5).

$$I_H = \begin{cases} 1 & if \ \ CPVH > CPV_A \\ 0 & Otherwise \end{cases} \quad (2.5)$$

Where, τ is the threshold value and N(i) is the neighborhood around i^{th} cell and C_j is the voted on value by j^{th} cell in the neighborhood of the i^{th} cell.

The transition rules from various states S_H, I_H, R_H, S_A and I_A of cell C(x, y) to one of these states are as follows:

3.3 Transition Rule from S_H to I_H

If State of C_{xy} = 'S_H' then

$$N_i = \sum_{j}^{nh} I_A$$

If N_i>5 then

q = (random (0, 1))

If q >1- $(1-b_A)^{Ni}$ then

$C_{x,y}$ = 'S_H'

else if q <1- $(1-b_A)^{Ni}$

$C_{x,y}$ = 'I_H'

End if

End if

End if

A Susceptible human S_H cell state changes to infected human I_H state, if the maximum votes of the neighborhood cells which is the sum of the I_A Values exceeds 5. This means more than five out of 9 cells are in infected animal state I_A then current cell state of human susceptible changes its state to human infected I_H. The random value is used to add the noise factor into the model since the real word should be modeled with some uncertainty.

3.4 Transition Rule from S_A to I_A

If State of C_{xy} = 'S_A' then

$$N_i = \sum_{j}^{nh} I_A$$

If N_i >5 then

q = (random(0,1))

If q >1- $(1-b_A)^{Ni}$ then

$C_{x,y}$ = 'S_A'

else if q <1- $(1-b_A)^{Ni}$

$C_{x,y}$ = 'I_A'

End if

End if

End if

A Susceptible animal S_A cell state changes to infected animal I_A state only if the maximum votes of the neighborhood cells which is the sum of the I_A Values exceeds 5. This means that if more than five out of 9 cells are in infected animal state I_A, then current cell state of animal susceptible changes its state to human infected IH.

3.5 Transition Rule from I_H to R_H

If State of C_{xy} = 'I_H' then

q = (random(0,1))

If q > r1→ then

C_{xy} = 'I_H'

else if q < r_1

C_{xy} = 'R_H'

End if

End if

Infected Human cell would be become recovered or removed based on the treatment obtained after some fixed amount of time. Then the recovered human would become susceptible after certain period of time according to the following transition rule.

3.6 Transition Rule from R_H to S_H

If State of C_{xy} = 'R_H' then

q = (random(0,1))

If q > r2→ then

C_{xy} = 'R_H'

else if q < r2

C_{xy} = 'S_H'

End if

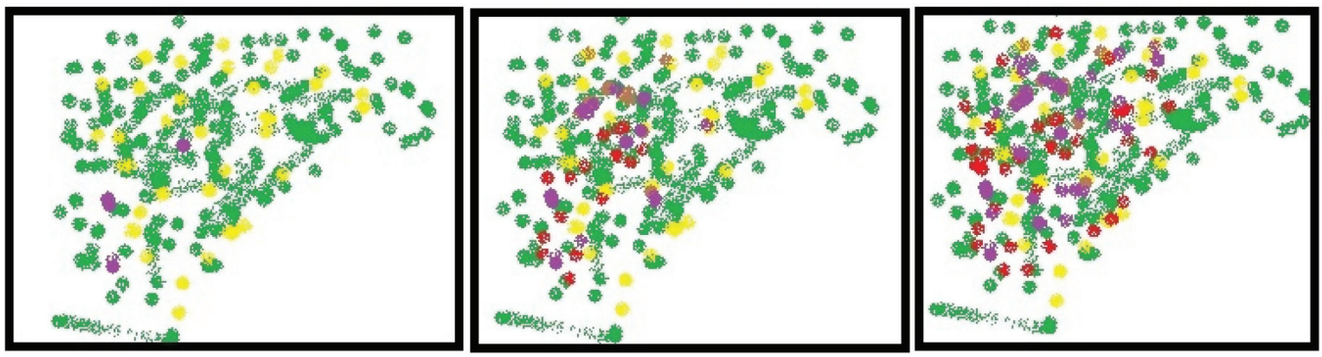
End if

3.7 Algorithm for Homogeneous Mix of Human Population and Vector Population without Movement of Vector Population

Step 1: Get the input from the user the value of tr (time period for recovery), tg (number of generations), ti (time period for immunity). Block the boundary cells so as to control the infection spread.

Step 2: Initialise the generation counter to 0

Step 3: Initialise all the cells with equal number of populations



Generation 30 Generation 60 Generation 90

Figure 2. Green dots are human susceptibles, yellow dots are animal susceptibles, violet dots are animal infected and red dots are human infected.

Step 4: Initialise the M value of the CSW of all cells to 0 to control the movement of animal population.

Step 5: Infect the desired cells.

Step 6: Increment the generation counter by 1.

Step 7: Find out the region of cells which are infected humans and infected animals.

Step 8: Depending on the voting based transition rules, change the state of the cell.

Step 9: If Rvalue is 1 then go to step 10
Else
Calculate the CPV_H value and CPV_A value based on the cellular automata update rule to find the fraction of infected population.

Step 10: If the number of generations is less than tg then go to step 4.

Step 11: Stop.

4. Results and Discussion

The model has been simulated for 360 generations with $\beta_H = 0.05$, $\beta_A = 0.25$, $r_1 = 1.25$, $r_2 = 0.08$. The mix of susceptible human, animal susceptibles, human and animal infected are shown in the Figure 2 during various generations.

The Figures 2.1 and 2.2 gives the comparison graph between in the simulated and observed data of Leptospirosis infected population for Nakhon Ratchsima and Phrae provinces in Thailand during the year 2000 and 2001[7,8].

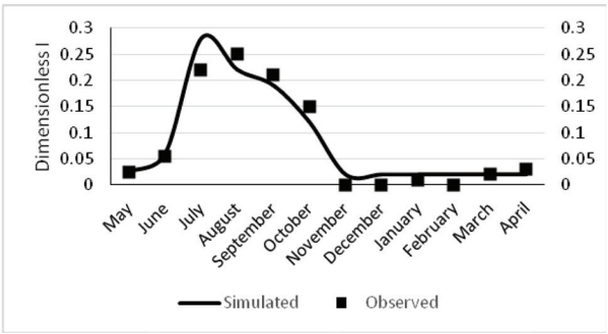


Figure 2.1. Simulated values vs. observed values for the Leptospirosis infected population in Nakhon Ratchsima-Year 2000.

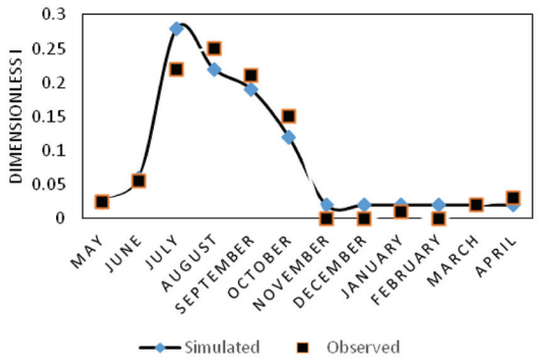


Figure 2.2. Simulated values vs observed values for the Leptospirosis infected population in Phrae province-year 2000.

5. Conclusion and Future Scope

Diseases like Leptospirosis where the human population is not infected by infected human population but by the infected animal population is quite rare but cannot be ignored. The spread of this type of disease has been simulated using cellular automata with voting rule neighborhood principle and the results that were compared with the real data gives us good results. In this model we assumed the population do not move. This model could be improvised by involving the movement of the vector animal population across the grid.

6. References

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