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V2P (Vector to People) Disease Prediction : A Differential Equation Approach

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***Abstract*—**The devastating effect of vector-borne diseases is well-known in tropical and sub-tropical regions across the globe. Mosquitos serve as vectors to spread diseases such as dengue and malaria which cause wide-spread desolation on a yearly basis. By carrying contagious pathogens, they infect millions of people across various countries, putting the health of many at risk and causing numerous fatalities. Measures of prevention and control prove to be widely unsuccessful due to the lack of a targeted approach. This results in the sub-optimal allocation of over-stretched healthcare and financial resources. Moreover, traditional control methods prove to be hazardous when used excessively and indiscriminately. They are recommended to be used only where needed. By virtue of the factors discussed, there arises a need for a scientific method to predict areas with high susceptibility and a system designed to scale the model to larger geographical areas.

***Keywords*—**Human Mosquito Contact Rate, Infected Class, SIR Model, Susceptible Class.

I. INTRODUCTION

India is plagued with the annual epidemic of dengue which causes wide-spread devastation and panic. It puts the public in a helpless state, while the disease claims its victims, one at a time. The impact of Dengue and other vector-based epidemics such as Malaria and Yellow Fever present an urgent need for developing solutions to comprehensively tackle these epidemics. Just by looking at the records from previous years for the state of Delhi, it is evident how these deadly diseases afflict public health.

Year after year, countries spend billions in public health without a manifest translation of those resources into saving people's lives. A major cause of this is the lack of targeted solutions along with the unpredictable magnitude of the disease. Information which provides an estimate of the magnitude and distribution of the disease would prove invaluable in devoting our resources towards fighting the disease and would thus conserve resources as well as drastically improve the general well-being of the public.

There exist certain models, such as the Susceptible-Infected-Resistant (SIR) and SIRS models, which serve as tools for predicting and simulating the spread of disease. However, their structure is not suitably fit for analyzing the spread of vector-borne diseases.

In this paper, we aim to construct a mathematical model equipped with the fundamental parameters for accurately simulating the spread of dengue. We believe that our model would be an incredible aid in determining the trend and specific characteristics of the disease as well as proving extremely useful to epidemiologists for simulating vector-borne diseases.

Delhi Dengue Cases (2009-2016) :

Year	June	July	Aug	Sept	Oct	Nov	Dec	Total	Deaths
2009	0	2	2	33	337	713	66	1153	3
2010	1	51	885	2360	2246	678	38	6259	8
2011	1	10	51	179	512	328	46	1131	8
2012	3	4	4	55	951	1005	69	2093	4
2013	2	11	142	1962	2442	889	119	5574	6
2014	10	7	11	87	318	444	113	995	3
2015	6	36	778	6775	7283	841	137	15867	46
2016	15	121	782	1682	1794	825	133	5352	7

Literature Review

A. Basic SIR Model

a) The S − I − R model is a basic model in which a constant population is divided into three compartments of individuals depending on their infection status: susceptible S, infected I and recovered R.

b) This is usually known as the S−I−R model. These compartments are explained as follows:

(1) S is used to represent the number of individuals who are susceptible to the disease at time t

(2) I is used to express the number of individuals who have been infected with the disease and are capable of spreading the diFinal sease to those in the susceptible category

(3) R represents the number of individuals who have been infected and recovered from the disease. Those in this category are immune to infection and they would not transmit the infection to others.

c) Assumptions:

(1) Each compartment is assumed to be homogeneous. In other words, individuals in each compartment are randomly mixing with each other.

(2) The per capita rate of infection and the per capita rate of recovery are assumed to be independent of the length of time the person has spent in each compartment.

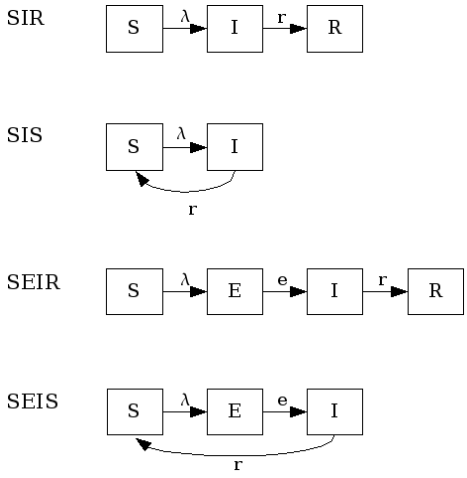
The above described model can be formulated as: -

$$\frac{dS}{dt} = -\frac{\beta SI}{N}$$
$$\frac{dI}{dt} = \frac{\beta SI}{N} - \gamma I$$
$$\frac{dR}{dt} = \gamma I$$

Where β is the force of infection, γ is the mean recovery rate and N is the total population. As consequence of a static population implies that $\frac{dS}{dt} + \frac{dR}{dt} + \frac{dI}{dt} = 0$

d) Other Models

The structure of the SIR model allows for addition of several new intermediary states to model more complex systems and many extensions of the SIR model have been developed such as the SEIR (such as in [1]) and MSIR models. The SEIR model adds an exposed population state into the dynamics of the model which can be viewed from the state diagram below without going into much detail.



Rest of the paper is organized as follows, Section II contains the methodology and functioning of the ODE, Section III is regarding the calculations undertaken to verify the model and to calculate its efficiency, Section IV contains the analysis of the results, Section V contains the conclusion of the paper, Section VI contains an appendix regarding a computer application which can be built on the basis of model in order to make it easier for civil authorities to use the model.

II. METHODOLOGY

We build the model on the base of the SIR and the SIRS models. However, as dengue and other vector-borne diseases are spread via viruses, there is no immunity to the disease and we do not have a recovered or immune category. Thus, we have only two classes: Susceptible(S) and Infected (I).

Let [N] denote the total population which is taken as constant at any interval in time. The overall population being static implies that $\frac{dS}{dt} + \frac{dI}{dt} = 0$.

To rigorously define a mathematical relation of the given system we take the following assumptions:

1. The distribution of the population for small regions is homogenous, this is done to establish a direct relationship with the human-mosquito contact rate β.
2. We assume a fixed population to study the dynamics of the infection.
3. We assume that the number of mosquitoes remains constant for a given time period and region.

To describe the rate of change of the infected population with time we introduce the following mechanism:

- Let the Human Mosquito Contact Rate be denoted by β, which refers to the total number of successful contacts (infections) made by a single mosquito in a day.

- Also, let M denote the total number of mosquitoes present in a given area, thus giving the total number of infectious contacts made in a certain region in one day equal to βM.
- $\frac{\mathbf{S}}{\mathbf{N}}$ denotes the fraction of the total population susceptible to the disease and also is the probability that any given successful infectious contact occurs with a susceptible individual.
- Thus, $\frac{\boldsymbol{\beta MS}}{\mathbf{N}}$ gives the total number of successful contacts made in a given time period. This term is subtracted from the susceptible category and added to the infected category since it represents the number of people essentially transforming from susceptible to infected.
- We also have to account for the recovery of infected individuals; let 1/ϒ denote the average infectious period, thus ϒ denotes the average recovery rate. ϒI represents the total number of infected individuals recovering from the disease on any given day. However, these recovered people will again go into the susceptible category as there is no immunity against dengue and most other vector-borne diseases. This term will be added to the susceptible category and subtracted from the infected category.

The completed equations are as follow:

$$\frac{dS}{dt} = -\frac{\beta SM}{N} + \gamma I$$

$$\frac{dI}{dt} = \frac{\beta SM}{N} - \gamma I$$

At any point in time:

N = S (t) + I (t)
For a quantitative analysis we must now isolate [S] and [I] purely as functions of time.

$$\frac{dI}{dt} = \frac{\beta SM}{N} - \gamma I$$

$$\frac{dI}{dt} = \frac{\beta (N - I)M}{N} - \gamma I$$

$$\frac{dI}{dt} = -I\left(\frac{\beta M}{N} + \gamma\right) + \beta M$$

$$\frac{1}{\left[-I\left(\frac{\beta M}{N} + \gamma\right) + \beta M\right]} dI = dt$$

We know that the differential of $-I\left(\frac{\beta M}{N} + \gamma\right) + \beta M$ is equal to $-(\frac{\beta M}{N} + \gamma)$, thus:

$$\frac{1}{\left[-I\left(\frac{\beta M}{N} + \gamma\right) + \beta M\right]} d\left[-I\left(\frac{\beta M}{N} + \gamma\right) + \beta M\right] = -dt(\frac{\beta M}{N} + \gamma)$$

$$\ln\left[-I\left(\frac{\beta M}{N} + \gamma\right) + \beta M\right] = -t\left(\frac{\beta M}{N} + \gamma\right) + c$$

$$\therefore -\mathbf{I}\left(\frac{\boldsymbol{\beta M}}{\mathbf{N}} + \boldsymbol{\gamma}\right) + \boldsymbol{\beta M} = \mathbf{e}^{-\mathbf{t}\left(\frac{\boldsymbol{\beta M}}{\mathbf{N}} + \boldsymbol{\gamma}\right)} . \mathbf{e}^{\mathbf{c}}$$

$$I = \frac{\left[\beta M - \mathrm{e}^{-\mathrm{t}\left(\frac{\beta M}{N} + \gamma\right)} . \mathrm{e}^{\mathrm{c}}\right]}{\frac{\beta M}{N} + \gamma}$$

Our final equation for the infected population as a function of time gives:

$$\boldsymbol{I = \frac{\left[\beta M - \mathrm{e}^{-\mathrm{t}\left(\frac{\beta M}{N} + \gamma\right)} . \beta M\right]}{\frac{\beta M}{N} + \gamma}}$$

The values of the total population and the average recovery rate are experimental, conversely, to determine the value of the human mosquito contact rate and the number of mosquitoes we choose to calculate the values out of data collected by the Delhi Dengue Control cell shown previously. As a field analysis to determine the values of **β** and **M** would be unfeasible, we can determine the value of **βM** from the collected data.
Given the values for the infected population during a certain time period, we may make the following calculations for **βM:**

$$I = \frac{\left[\beta M - \mathrm{e}^{-\mathrm{t}\left(\frac{\beta M}{N} + \gamma\right)} . \beta M\right]}{\frac{\beta M}{N} + \gamma}$$

$$I\left(\frac{\beta M}{N} + \gamma\right) = \beta M - \mathrm{e}^{-\mathrm{t}\left(\frac{\beta M}{N} + \gamma\right)} . \beta M$$

$$I\frac{\beta M}{N} - \beta M + \mathrm{e}^{-\mathrm{t}\left(\frac{\beta M}{N} + \gamma\right)} . \beta M = \gamma I$$

$$\beta M\left[\frac{I}{N} - 1 + \mathrm{e}^{-\mathrm{t}\left(\frac{\beta M}{N} + \gamma\right)}\right] = \gamma I$$

$$\beta M\left[\frac{I}{N}-1+e^{-\frac{t\beta M}{N}}.e^{-\gamma t}\right]=\gamma I$$

To proceed further, it is reasonable to make the approximation that as $t\beta M \ll N$ and $\frac{t\beta M}{N} \approx 0$

$$\therefore \beta M \approx \frac{\gamma I}{\left[\frac{I}{N}-1+e^{-\gamma t}\right]}$$

III. CALCULATIONS

In order to verify that the progression of the developed equation matches the spread of the disease, we input the data of the year 2016 and 2013 for the state of Delhi, (our model years as discussed earlier) to compare the number of infections predicted by our model against real-world data, to compute the value of **βM** we use the number of infected from the year 2013 for Delhi as follows:

$$\beta M \approx \frac{\gamma I}{\left[\frac{I}{N}-1+e^{-\gamma t}\right]}$$

Using data from the dengue control cell:

- N = 16.75 million
- I = 5574
- ϒ = 1/14
- t = 180 (days)

$$\beta M \approx \frac{\frac{1}{14}*5574}{\left[\frac{I}{16750000}-1+e^{-\frac{1}{14}*180}\right]}$$

$$\beta M \approx 398.275$$

Making use of our assumption regarding **βM,**

$$\beta M_{2013} = \beta M_{2016} = 398.275$$

Proceeding to the calculations for total infections for the year 2016, the variables are substituted as follows:

- N = 18.6 million
- I = 5574
- ϒ = 1/14
- t = 180 (days)

$$I=\frac{\left[\beta M-e^{-t\left(\frac{\beta M}{N}+\gamma\right)}.\beta M\right]}{\frac{\beta M}{N}+\gamma}$$

$$I=\frac{\left[398.275-e^{-180\left(\frac{398.275}{18600000}+\frac{1}{14}\right)}.398.275\right]}{\frac{398.275}{18600000}+\frac{1}{14}}$$

$$I=\frac{\left[398.275-e^{-180\left(\frac{398.275}{18600000}+\frac{1}{14}\right)}.398.275\right]}{\frac{398.275}{18600000}+\frac{1}{14}}$$

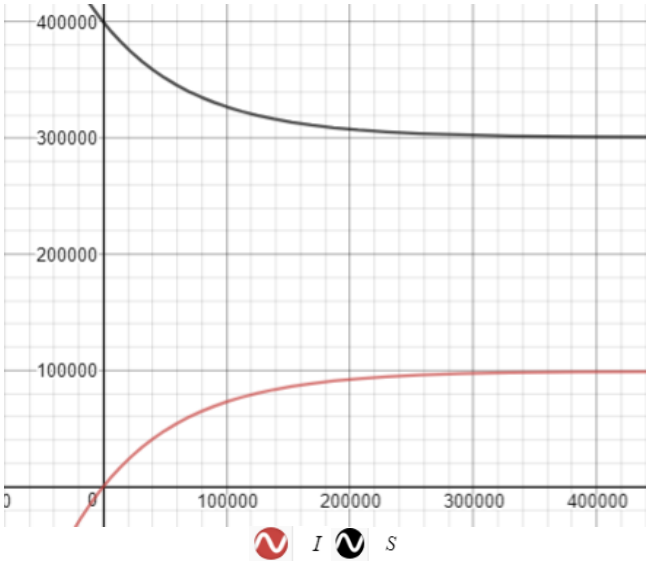
$$I \approx 5710$$

Referencing the data collected from the Dengue Control Cell, the actual number of infections for the year 2016 was approximately **5352**. Thus the margin of error of our result being **6.3%**

Given our results we must recognize that due to our assumption regarding the constancy of **βM,** the accuracy of our results depends heavily on the size of the region in question, since our assumption nears reality for smaller regions, the accuracy of the model is best represented through discreet sector wise computations.

IV. RESULTS AND DISCUSSION

Compartment models have been present largely through descriptions of person to person epidemics in the field of epidemiology, our project serving as an initial step towards modelling vector based epidemics provides an appreciable level of accuracy. To analyze the progression which our equation utilizes to simulate the spread of disease we may look at the following graph:



[Time period has been scaled by a factor of 10000 for observation]

We observe that the system tends to an equilibrium state after a given amount of time, which is not the case in the real world dynamics, however for our concerned time period it successfully replicates the progression of the disease since our model serves to approximate the key elements of the epidemic and cannot compensate for the real world complexities. The system is sensitive to variations in βM and ϒ. The equilibrium state is approached when the rate of infection is balanced by the rate of recovery, thus ϒ plays in an integral role in the extent of progression of the disease.
To consider the accuracy of the model in comparison to real world output, the model produces appreciably accurate results. However it is to be noted that the computation has been conducted on a large region. The model is structured towards simulating the spread of disease for smaller regions based around the initial assumption of the homogeneity of distribution of society, thus small area computations are expected to provide a higher degree of accuracy since the assumption comes closer to realistic systems. An important note is the benefit of small area computations in identifying hotspots within a region.

V. CONCLUSION

The main conclusions of the model are as follows: -

1. From the results, it is evident that although the model is not ideal, it is highly efficient and useful for use by civil authorities for prediction of spread of vector-borne diseases.
2. The degree of accuracy increases as the areas and time frames become smaller. This is true as our assumptions become more justifiable for a smaller area and time frame.
3. The model can be further enhanced by the addition of other natural variables such as the House Container Index Ratio (HCI).

VI. APPENDIX

To make the model scalable for a large area, we have also developed a computer application using Geographical Information System (GIS), creating Small Area Estimation Models based on official data and calculating the various values for **βM** for every small area in a city. GIS will be used as a planning tool [2], using which we can find the predicted number of infections in specific areas which helps to identify & divert resources to highly susceptible areas. This model can be used by civil authorities which are using rudimentary and ineffective methods of prediction currently. Also, the model is a useful tool to quantify number of mosquitoes in an area.

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Authors Profile

Ayush Sachdeva is a science student of Springdales School, Dhaula Kuan, New Delhi with a keen passion and interest in Applied Mathematics, Physics and Computer Science. He has been doing elementary and higher level research in fields such as Computational Biology and Theoretical Physics. Some of his projects have been recognised by Intel at the IRIS National Science Fair, Bill and Melinda Gates Foundation (BMGF), etc. His computational model regarding vector-borne diseases is also being evaluated by state governments in India and Nigeria for use.

