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Pathway to the Mathematical Modelling of Nipah Virus – A Review

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Abstract:

A virus is called zoonotic if it spreads to humans from animals. Nipah is one of the virulent zoonotic viruses that is reasoned to be the cause of deadly Nipah fever. Mathematical modelling takes its own space in the entire world not only for prediction but also in all the 360 degrees. There are many mathematicians provided various modelling techniques under different circumstances. This paper gives you the collected essence of the mathematical modelling works done by various mathematicians in connection with Nipah Virus. This paper also facilitate the researchers with chllenges in the modelling.

Keywords:*Nipah, Dengue, virus, review, communicable, fever.*

I. INTRODUCTION

Nipah virus can also be spread directly through people themselves or consumption of filthy food. This virus attacks not only humans but also animals. It is notated popularly by NiVand this notation will be used throughout this chapter to denote Nipah Virus. NiV can cause severe diseases in animals like pigs. The study of infections is called infectionology and the study deals with infectionology concept towards mathematical modelling. At the time of first outbreak of NiV, infection not only in pigs but other household creatures, for example, horses, goats, sheeps, etc were also reported. NiV profoundly infectious in pigs as they are irresistible during the incubation period, which keeps going from 4 to 14 days. A contaminated pig can display no indications, yet some create intense fever, issues in breathing, and neurological side effects like trembling, jerking and muscle fits. But the mortality is low with the exception of youthful piglets. NiV ought to be suspected if pigs additionally have an abnormal woofing hack or if human instances of encephalitis are available.The virus develops in the bladder, saliva, and face of fruit bats and is harbored naturally in fruit bats and microbats of numerous species. The fruit bat is also called as flying fox. It also infects bats when they eat the bites of the other bats and their urine and saliva. When humans come in close contact with infected domestic animals, they too become infected. Apart from pigs, the virus is also found in domestic cats, dogs, and horses. Also, bats can often live in high altitudes. Accordingly, in the pots tied to tall palm trees if the saliva and urine of the bats get mixed, it would spread quickly when humans drink it. This will result in significant economic loss for farmers. Post-mortem inspection showed critical NiV to be a systemic infection (Wong et al 2002)Canines were observed to be frequently diseased as well (Field H et al. 2001). Another hazard factor was found with caninesdying on farms frequently (Parashar UD et al. 2000). It also can be transmitted from human to human (H-H). It was Rahman SA et al. (2010) who discovered that Pteropus bats were exposed to be the reservoir of such a poisonous infection in Malaysia which diseased the magnifying hosts and vectors too by ingestion of bat-nibbled fruit and there is no proof of H-H transmission from these epidemics but later Stephen P. et al (2009) proposed the evidence

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of H-H transmission of disease. Here, especially in epidemiology modelling, one should know the few terminologies like host, vector, etc., (Source: Centers for Disease Control and Prevention. "Division of Vector-Borne Diseases")

Host (Intermediate stage): A living being tainted by a parasite whereas the parasite is in aninitial formative structure, not explicitly developed.

Host (Primary stage): An essential host is a life form that gives sustenance and haven to a parasite while enabling it to turn out to be explicitly full grown, while an auxiliary host is one involved by a parasite during the larval or agamic phases of its life cycle.

Reservoir: The creature or living being in which the infection or parasite regularly exist in.

Vector: Any mediator, living or something else, acting as a carrier and spreads parasites and infections. Likewise, a living being or chemical used to transporta gene into anotherhost.

de Wit, E., & Munster, V. J. (2015) have given animal models of disease that shed light on NiV pathogenesis and transmission. A beginner to such modelling can read this, to get more insight about the channels for the spread of the diseases, the factors causing it and how to develop a non-mathematical model initially. Hammoud, D. A et al (2018) proposed the model to determine the Aerosol exposure to intermediate size NiV particles that induces nervous illness in African green monkeys, though this work has deviated from the current objective.One might be interested in creating models and forecasting, hence, the author wishes to suggest this article for such aspirants whereas earlier Johnston, S (2015) has given a wonderfully detailed analysis of the African Green Monkey Model of NiV Disease. Middleton et al., (2007) detailed in their work based on an Investigational taint of Pteropus that bats with NiVhave not affected or given the disease in the fruit bats. Examinations of rodents and other faunae have not perceived further natural life repositories for NiV (Hsu VP 2004 &Yob JM 2001). Nowak (1994) stated in the work that around 50 kinds of Pteropus bats live in the South East Side of Asia.

II. Outbreaks

Despite the fact thatNiV has caused just a couple of known flare-ups in Asia, it taints a wide scope of creatures and causes extreme illness and demise in individuals, making it a general wellbeing concern. At the Malaysian peninsula, the pig farmers suffered due to encephalitis (brain inflammation). That is the first known human outbreak in the world in 1998-1999 where around 257 people suffered among which 157 died (Goh KJ et al 2000). NiV is a type of RNA the genus being Henipavirus order Mononegavirales. (Source: WHO NiV Infection 2018). The other genus and viruses of this genus are as follows respectively: Cedar henipavirus,Cedar virus (CedV), Ghanaian bat henipavirus, Kumasivirus (KV), Hendrahenipavirus, Hendra virus (HeV), Mojiang virus (MojV). In 1947, the probable origin of this virus was found. The 95% confidence interval for this virus statistically is between 1888 to 1988. The virus evolved two times; at 1985 and 2002. The mutation rate was estimated to be substitution/site/year with 95%confidence interval. (Lo Presti A et al 2015).The fatal death rate was estimated at50% to 75%. (Broder, C2013) NiV is named after the village Sungai Nipah, a river village in the Negeri Sembilan state in Malaysia. (Nipah Virus CDC 2017). To save people (infact the other animals too from infection) from the spread of the disease, more than 10 lakh pigs were euthanized (set to death without pain). Infact, that caused a great business loss to Malaysia. The reason for business trade loss is, the Pork consumption per capita in Malaysia from 2009 to 2018 (in kilograms) varies from 5.85 to 6.83, forecasted for 2020 and 2025 almost to 6 (Source: Statistica.com).Apart from this pork consumption, the adjoined business too encountered a great loss. After the euthanasia, there was no other outbreak reported neither from Malaysia nor from Singapore. The NiV but with different strains than identified in 1999 and found in 2001, again emerged in Bangladesh to give another outbreak. In 2014, an epidemic of NiVarose in Philippines. 17 cases were confirmed with the

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fatality rate of 82% in humans. It was observed that out of 17, 10 had adjacent connection with horses or consumption of horse meat. It was reported the deaths of 10 horses were found dead at 2014 epidemic of NiVin Philippines. Five health care nurses were infected at the same time while treating infected patients. (Ching PKG et al 2015).

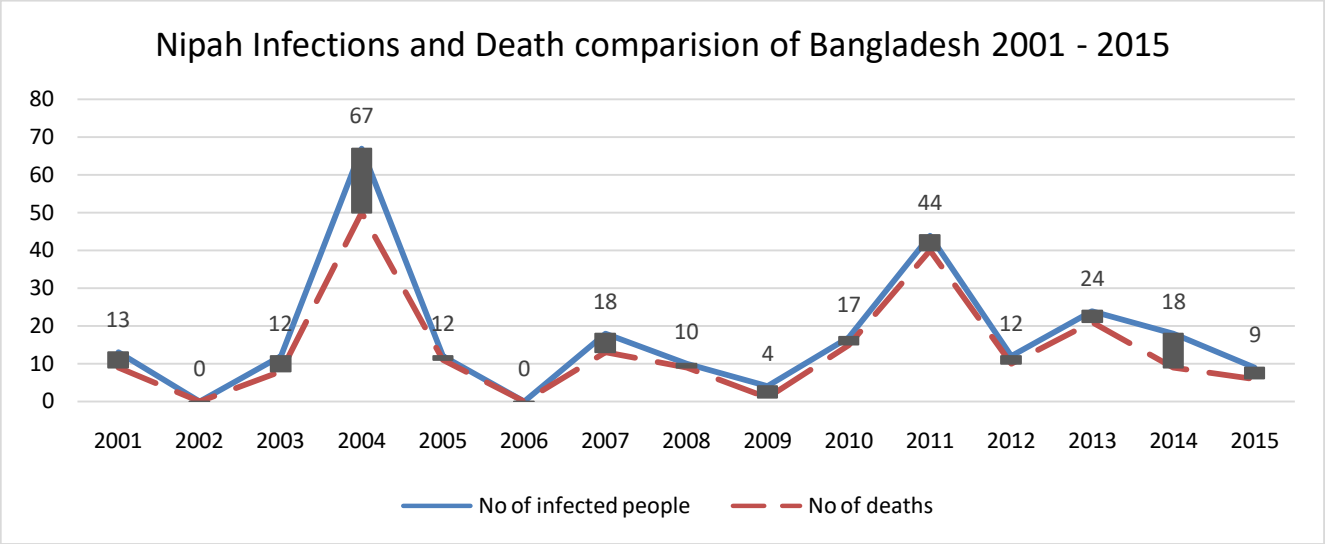

Figure 1 Nipah Epidemics in Bangladesh

III. Symptoms Andremedy

The incubation period (interval from infection to the onset of symptoms) of NiVvaries from 5 to 14 days. The infection later becomesan exposed state that varies from 3 to 14 days though reports say it can be till 45 days. The symptoms of NiV begins with mild fever. The virus affects the Blood vessels and parenchymal cells in most of the foremost organs. The symptoms of level exposing may include, drowsiness, mental confusion, fever, headache, disorientation etc. This exposure leads to infection and severe infection can lead to coma stage within 1 to 2 days. Few have shown pulmonary (related to lungs) signs and more than 50% have shown neurological symptoms. Other few have shown respiratory illness before reaching the exposed state of infections. It can lead to sequela (death as a result of nipa after the disease run out), and a sudden contraction in muscles and personality changes. It is to be noted that even after years of exposed state of the disease, latent infections with ensuring renaissance of NiV and morbid were also reported. ("Signs and Symptoms NiV", CDC, 2018). There were many people who recovered from coma. But those who went to the extent of coma to attack the virus must eventually die.

No specific drugs have been found yet and there are currently only pharmaceuticals to partially control them. Doctors say the best medicine is to give full support to those infected with virus. The victims should be away from food and others should not eat the leftovers of their food. Friends and relatives should personally take care of cough and colds if the victim has any. It is also good that others do not use the affected victim's clothes.. So far, 75 percent of those infected with the virus have died, as per reports.

In Siliguri, India, the NiVwas reported in2001, in the meantime, it was reported in Bangaladesh too. The outbreak emerged again in the years 2003,04, and 05 in districts, Naogaon, Rajbari, Manikganj, Tangail, and Faridpur. (Chadha et al 2006& Hsu 2004). In Kerala, India, at MalappuramKozhikode district an outbreak was reported in May 2018 in which 17 people died. The crucial thing is, out of 17 who were reported dead, one included aanurse (healthcare worker) who treated the infected people. (source: https:// www.ndtv.com/kerala-news/nurse-lini-who-treated-kerala- Nipah-victim- left-heartbreaking -

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note-for-husband- 1855625). Though in June 2018, the govt announced officially that the outbreak was over, it emerged again in May 2019. This shows the severity and re-emerging speed of the disease. A student admitted at Ernakulam, Kerala was infected and his treatment was confirmed with 2 months at the hospital. The infection of NiV was inveterate from RT-PCR tests. The communication rotations of NiV in Malaysia and Bangladesh are somewhat different. In Bangladesh, Nipah infection is believed to be communicated through the utilization of crude date palm sap. While date palm sap is gathered, bats enter the sap stream or accumulation pots and pollute the sap with NiV through their spit or pee. People become tainted with NiV after the utilization of this dingy date palm juice. Later these contaminated individuals can transmit NiV to others by means of close contact. In Malaysia, Nipah infection was transmitted from bats perching in organic product trees or on pig homesteads.. Pigs mainly inflicted NiV to people in close contact with them. (de Wit, Emmie, and Vincent J Munster, 2015). Figure 2 explains the way how NiVspreads among fruit bats, pigs, and humans.

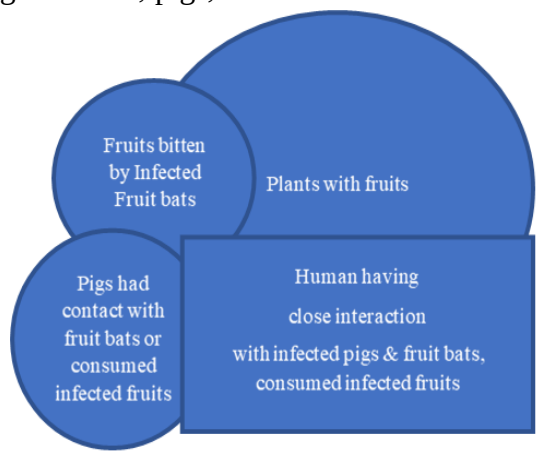

Figure 2 Schematic diagram of NiV infection

Ayush Kumar (2019) found many standards in the classical texts of Ayurveda, that can be compared with the concepts of epidemiology. Also, he stated that "Ayurveda labelsidea of the prevalence of disease and that can be compared with Janapadodhwans. Ayurveda summarizes the entire relevant concept in a single word as JanapadopdhwansaRogas".Though, being anorthodoxtherapeutic doctrine, it has its allure that can't be compared with the modern concepts of study of disease transmission.

Currently, neither vaccines nor medicines have been proven to be effective in treating NiV infection. However, health care providers may offer supportive therapy to manage symptoms. At this time duration of fever and the severity of diseases can be reduced and also may alleviate the symptoms of nausea, vomiting, and convulsions by ribavirin.

IV. Mathematical Modelling

An abstract model is said to be a Mathematical model if that utilizes the mathematical language to explain the behavior of a proposed system and it is likewise a helpful device for the estimation of the impact of various methodologies for controlling the spread of communicable diseases within a populace.There is no limitation discipline wise for the usage of Mathematical models. It is widely used in all disciplines, viz., computer science, engineering, management, all science and humanities, even political science too.Eykhoff(1974) defined a mathematical model as 'a representation of the essential aspects of an existing system (or a system to be constructed) which presents knowledge of that system in usable form'.Mathematical modeling has turned into a significant tool for analyzing the spread and for the control of communicable diseases. It is a helpful tool for the estimation of the impact of various methodologies for controlling the spread of irresistible infections within a population.One of the major epidemics in the U.S.A. was the Yellow Fever prevalent in Philadelphia in 1793. About 5000 individuals expired out of about 50,000, despite the fact that approximations propose that about 20,000 escaped the city; see the intriguing artifact by Foster et al. (1998) and the book by Powell (1993). The milestone book by McNeill (1989) is an enthralling story of the connection between diseases and individuals. The modeling literature is now extensively growing rapidly.Several kinds of modeling include claims about causality. This is

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typically (but not always) factual models concerning differential equations. The purpose of modeling is to upsurge the understanding of real-world problems. The validity of the models always sail on fitting it to the empirical data. It should have the ability to extrapolate to different circumstances. Mathematical modeling can be classified into two types based on the quantity of prior available information of the system which requires examination.

- Black box model - With no prior data
- White box model or glass box or clear box - all essential data

In the real scenario, all the examinations are in the intermediate stage between black and clear box model. So, the classification of the model concept acts as an intuitive guide to approaching a problem, not for the entire solution of the problem proposed. To propose an accurate model with high predictive power, it is advisable to use the available prior information as much as possible. One can use that information for better prediction and for checking the reliability of the modal. For example, if a researcher proposes a forecasting model for rainfall, the usage of the prior data can be used to check the reliability and error in the model. Based on that data, it is possible to check the current scenario and predict future values. On such predictions, the error obtained from the past data is useful to propose the limitations.A regularly utilized methodology for modeling is neural systems which for the most part don't accept nearly anything about the prior information. The issue with utilizing a huge arrangement of capacities to portray a framework is that evaluating the parameters turns out to be progressively troublesome when the number of parameters (and various kinds of capacities) increases. In recent years, the epidemiological modeling of such communicable disease transmission has had an upsurge impact on the various theories, spread and control management of the disease.Dheva Rajan et al (2013a) proposed a two compartmental model for the spread of Dengue fever. The model consists of set of 7 ordinary differential equations 4 for human and 3 for mosquito. The model is based on SEIR type model, which can be abbreviated as Susceptible, Exposed, Infectious and Recovered. There is no recovery of mosquito from infections, hence for mosquitoes it was only 3 states except recovery. The model was then developed to arbitrary n regions (Dheva Rajan et al 2013b). Again, with the help of work done by DhevaRajan et al (2013c,d)the stability analysis of the said model was discussed. The Bifurcation and sensitivity analysis has been performed by the same author in which the mosquito biting has the highest sensitive parameter value. (Dheva Rajan et al 2014 a,b,c,d). Though the model was proposed particularly for Dengue fever spread, it can also be used for other communicable diseases, by varying the respective parameters. As a future development, Dheva Rajan et.al (2014) proposed the inclusion of rainfall, climatic factors, temperature, humidity, impact of awareness programs, seasonality, self-prevention, etc., The said model is based on population dynamics model and is a reflection of the use in serving to comprehend the dynamic processes and in making predictions.It was developed from the basic concept birth-death, which people called as birth and death model. Consider any species. Let $TP(t)$ be the population at time t, then the rate of change $\frac{d(TP)}{dt}$ is the equation for the population. Hence,

$$\frac{d(TP)}{dt} = births - deaths + migration \quad \ldots(1)$$

The Right-hand side of the equation 1 demands to demonstrate the situation with which the proposers are concerned. The simplest model that has birth (b) and death (μ) terms are proportional tothe total population (TP) with the absence of migration.
That is,

$$\frac{d(TP)}{dt} = b(TP) - \mu(TP) \quad \ldots(2)$$

On integrating the equation 2, one can get,

$$TP(t) = (TP)_0 e^{(b-\mu)t} \quad \ldots(3)$$

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The RHS of Equation 3 is the abstract mathematical solution of LHS of Equation 2 with $TP(0) = (TP)_0$ the initial value of the population, b, $\mu > 0$ & constants. Hence, for Equation 3 one can get the following interpretation.

$\begin{cases} b > \mu & \text{grows exponentially} \\ b < \mu & \text{out} \end{cases}$

This approach proposed by Malthus (1790), is honestly impractical. A very good starter of reading the diverse problems and models for the spread and control of communicable diseases is the volume by Bailey (1975). Mathematical modeling of communicable disease commenced in 1911 with Ross's (Ross 1911). The most important biological incorporations are described in a book (MacDonald 1957). Let $S(t), I(t)$ and $R(t)$ denote the number of individuals in the susceptible, infectious and recovered classes at time t respectively. Hence, these susceptible, infectious and recovered classesare represented as a function of t, however, for the sake of simplicity, hereafter in this chapter it follows the notations by omitting the independent variable t, viz, Susceptible (S), Infection (I), and Recovery (R)and it is applicable for other state variables, if any defined for either host or vector. The total population at time t is represented by $TP(t) = S + I + R$. In this chapter it is assumed that the total population is $TP(t) = N$ and inconvenience is regretted for the usage of two parameters to denote the population. It is used only for the sake of convenience. This becomes asystem of non-linear differential equations. The advancement of the human population is schematically characterized by SIR. This SIR is one of the furthermost uncomplicated fundamental infectious disease model from 1927. Equation 2 gives a better idea to the ancient type of mathematical model SIR.

The basic SIR model can be expressed as follows with the parameters:

$$\frac{dS}{dt} = -\beta * S * I \qquad \ldots(4)$$

$$\frac{dI}{dt} = \beta SI - \gamma * I \qquad \ldots(5)$$

$$\frac{dR}{dt} = \gamma * I \qquad \ldots(6)$$

Equations 4,5 and 6 constitute a type of standard SIR model. Remember that, when giving the initial conditions on these type of models, values S & I should be at least one, and R is non-negative. The epidemic like fever is usually faster than that of birth and death, hence, birth and death in the above set of equations is omittedwith $S + I + R = N$, as assumed earlier. It is the choice of the experimenter to use the value of S,I and R directly or as the fraction value after dividing by the total number of population N. This is based on the basic logic that, in order to spread the disease, there should be at least one infective population and if found susceptible, it is evident that the recovery can be zero and cannot be in negative. This SIR type of model is a standard disease model that consists of a set of equations and can be used to explain the dynamics of NiV infections in society.

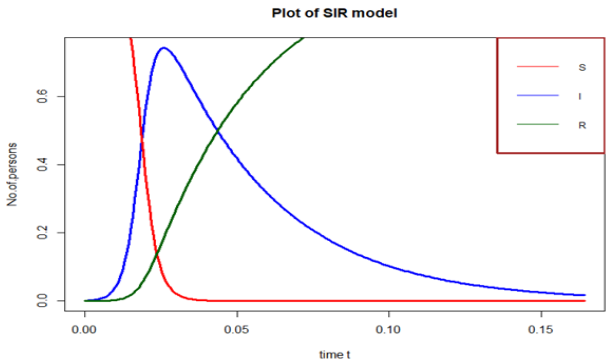

Figure3 SIR model with assumed values β =400, γ =365/13, *S=0.999,I=0.001,R=0.000*

The set of equations 4,5 and 6 together represents the SIR model. This model was proposed first by O. Kermack and Anderson Gray McKendrick. Hethcote H (2000) mentioned this as a specific case of the Kermack-McKendrick theory. (Kermack, W&McKendrick, A (1991a,b,c). Figure 1 describes the graph of the SIR model with different parameter values. To generate the graph like figure 3, one can use any mathematical programming language such as Matlab, Julia, Mathematica, etc., Usage of Mathematica is advisable but researchers have to

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think of the cost of the software also. Matlab is a widely used one to solve ODEs, especially using ODE 45 solver. Here, R programming language is used to generate as it is an open-source software. By seeing figure3, one can immediately find that the system is non-linear, hence it cannot have a standard plausible solution. However, the outcomes can be obtained using the replication methods specifically like Monte Carlo Simulation techniques and/or by using the process like Gillespie Algorithm (Gillespie D.T, 1976, 1977). Aron & May (1982) andNedelman (1985)haveproposedafew analyses on the Mathematical modeling of communicable diseases. Initially, the models are of two compartments, one for human and another one for vector-borne diseases. A significant accumulation of variables & parameters to the said replicas was the insertion of acquired immunity proposed by Dietz et.al (1990).Anderson & May (1991) and Koella (2003) have proposednotable contributions to the incorporation of biological factors and analyseson the SIR modeling of communicable diseases.

For the communicable diseases like yellow fever or malaria one can use the parameters for birth and death for better prediction. The model is given below with birth and death.

$$\frac{dS}{dt} = \text{birth} - \beta * S * I - \text{death} * S \quad \ldots(7)$$

$$\frac{dI}{dt} = \beta * S * I - \gamma * I - \text{death} * I \quad \ldots(8)$$

$$\frac{dR}{dt} = \gamma * I - \text{death}*R \quad \ldots(9)$$

The equations 7, 8 and 9 constitute a set representing the SIR model system with incorporation of birth and death parameters.

Figure 4 shows the solution of the SIR model with the incorporation of birth and death parameters.

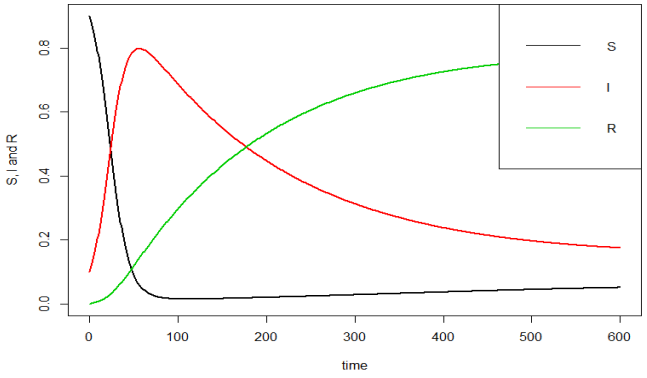

Figure 4: SIR model with birth and death & assumed values S = 0.9, I = 0.1, R = 0.005, beta = 0.1, death = 0.001, birth = 0.001.

Also, the assumption of values of birth and death may be equal or unequal. In equations 7,8 and 9 it is assumed to have different parameters for birth and death values. However, few researchers use the same parameters too. Though it is preferable to use the birth and death values separately, due to circumstances, the value becomes the same or at the start of the disease, the parameter value may not be available. Hence, few researchers use same value for birth and death parameters. The equations and the solution graph generated is given below. Usually a simple SIR Mathematical model forever forecasts hindered fluctuations for an equilibrium position. This is usually at odds among periodic epidemics which people can observe in various real circumstances with pathogens. Persistent fluctuations necessitate a few extra catalyst parameters for the proposed mathematical model. For instance, the infection of measles among children's contact rate follow seasonality as the children accumulate or gather at schools and there is a high chance during such gathering. Such circumstances can be explored by incorporating the seasonality parameters. It is the usual practice of assuming the sinusoidal curve forcing on β and can be defined as $\beta(t) = \beta_0\left(1 + \beta_0 Cos 2\pi t\right)$.

The SIR model along with the seasonality is given.

$$\frac{dS}{dt} = \text{birth}*(1\text{-}S) - \beta * S * I \quad \ldots(10)$$

$$\frac{dI}{dt} = \beta * S * I - \gamma * I - \text{birth} * I \quad \ldots(11)$$

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$$\frac{dR}{dt} = \gamma * I - \text{birth*R} \qquad \ldots(12)$$

Figure 5 shows the SIR model solutions with assumed values without incorporation of cyclic seasonal parameters

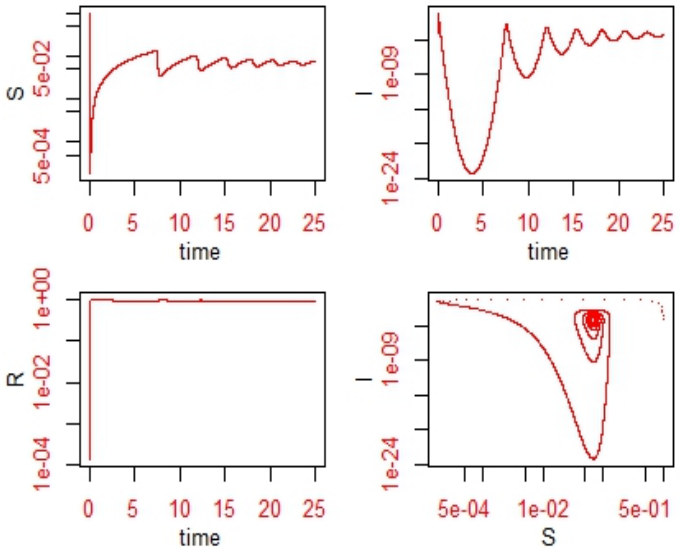

Figure 5: SIR model with values $S=0.999, I=0.001, R=0.000, \mu = 1/50, \beta = 400, \gamma = 365/12$ without cyclic seasonal parameter

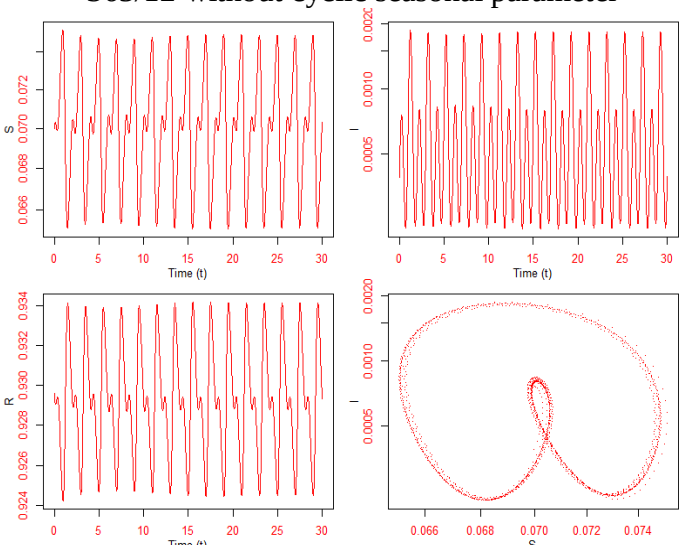

Figure 6: SIR model with initial conditions $\mu = 1/50$, $\beta_0 = 400$, $\beta_1 = 0.15$, $\gamma = 365/12$, $S=0.07$, $I=0.00039$, $R=0.92961$, $\beta(t) = \beta_0(1+\beta_1 Cos 2\pi t)$

Figure 6 shows the SIR model solutions with assumed values with the incorporation of cyclic seasonal parameters. If one wants to incorporate the rainfall as a parameter, the rainfall, $\log[R_A(t)] = \frac{a * R_A(t)}{b + R_A(t)}$, where $R_A(t)$ is the rainfall data with respect to time t, a and b are the respective parameters.If one replaces the value of β in equations 10,11 and 12 with the rainfall parameter $R_A(t)$, the one can change the model. Here it is to be noted that, by using programming, one can interpolate, especially extrapolate or predict the rainfall values using forecasting models. One such visualization is found in figure 7. The solution of the SIR model with respect to time for *S, I,* and *R* with incorporated rainfall data with respect to time with different initial conditions and forecasting is shown in figure 8.

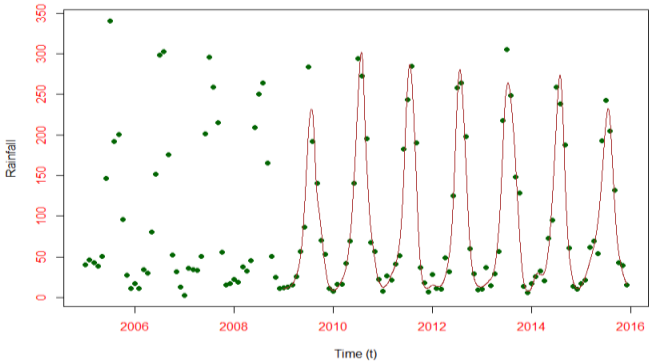

Figure 7: Sample forecasting for rainfall with respect to time

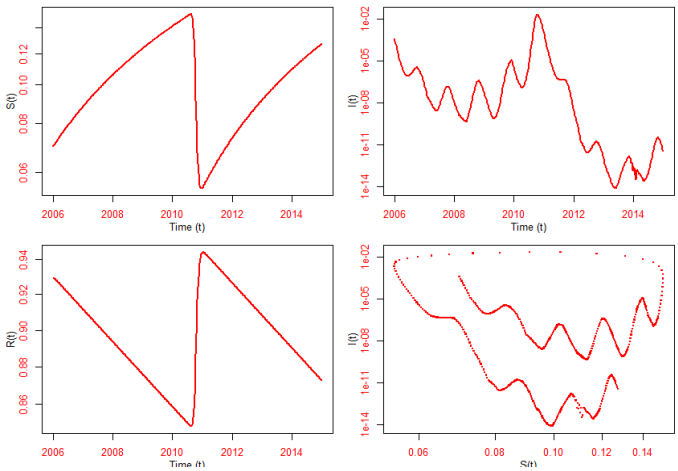

Figure 8: SIR solution with forecasted rainfall with respect to time with different initial conditions

As the seasonality becomes a specific case of SIR model formulation, it is continued without the sinusoidal assumption hereafter. There are various strategies for ascertaining the ideal control for a particular Mathematical model. As an example, Pontryagin's (1962) extreme principle permits the computation of the ideal control for a system of ordinary differential conditions with given

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restrictions. The ideal control approach is used to minimize the infected people and to amplify the number of recovered people. The book by Diekmann and Heesterbeek (2000) discusses the usage of biological assumptions in building replicas and current applications. The interesting thing is, the book covers both deterministic and stochastic modeling. The vaccinated population (v_a) has more immunity power and should be removed from the susceptible population and can be included in the recovered population. Since still no vaccination has been found for the deadly disease NiV, this variable v_a can be considered as the awareness level and /or self-prevention along with the immunity coefficient.

$$\frac{dS}{dt} = \text{birth} - \beta * S * I - \text{death} * S - v_a * S \quad \ldots(13)$$

$$\frac{dI}{dt} = \beta * S * I - \gamma * I - \text{death} * I \quad \ldots(14)$$

$$\frac{dR}{dt} = \gamma * I + v_a * S - \text{death} * R \quad \ldots(15)$$

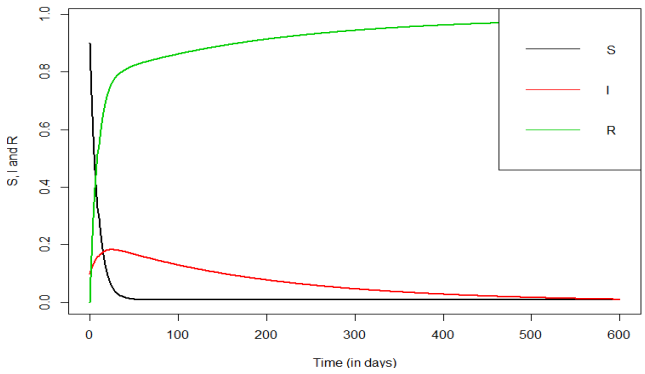

Figure 9: SIR model with birth, death, vaccination & assumed values *S=0.9, I=0.1, R=0*, beta = 0.1, recovery = 0.005, death = 0.001, birth = 0.001, vaccination = 0.1

Here, it is assumed that the value of v_a =0.1, as people don't have much awareness initially with the disease. Only after the spread of the disease, the Government and other organizations can start the awareness to people and provide vaccination if any. Hence, assumption of $v_a = 0.1$ is reasonable. As days roll on, the value of v_a can be increased which impact the decrease in S and increase in R. One can include the vaccination strategies in different aspects, and it can be expressed as the accumulation of awareness, vaccinations if any, cleanliness, self-awareness, etc., One can observe that figure 9 has quick and greater recovery than that of recovery curve in figure 4. The environmental effects for the spread and resistance to drug, evolution of immunity was proposed by Yang (2000) and Chen & Wilson (2006) for communicable diseases.

Sultana, J et al (2016) propose a model for NiVthat incorporates the awareness among people as conveyed by Dheva Rajan et al (2014d) too. A new design was proposed by Ngwa and Shu (2000) and Ngwa (2004) which consists of ordinary differential equation (ODE) compartmental model, a susceptible-exposed-infectious-recovered-susceptible (SEIRS) model for humans and a susceptible-exposed-infectious (SEI) pattern for vector. It is the choice of the researcher to propose the appropriate pattern for host and vector. The presumptions made about the transmission of the disease and incubation period are pivotal in any model; these are reflected in the terms of equations and parameters. One may get attracted to the modelling parameters of Heesterbeek, H (2015) due to his wonderful explanations in the article. In his article, he discussed several factors for notable achievements in control management of communicable diseases. The most significant factors like human connectivity, dynamic behavior of humans, etc., has been discussed in his work wonderfully.

V. Reproduction Number

The reproductive number R_0 is the most important parameter in studies related to the prevalence of disease and the respective mathematical models. By assuming all the individuals being susceptible to the disease infection, this number R_0 can be defined as the number of infected personalities (either host or vector) with one infected host results during its infectious period. The concept of R_0 was formerly established (1886) for the independent study for malaria 1911 and 1927 and & is nowcommonly applied and aimed at almost all communicable illness (1975) (Heesterbeek& Dietz, 1996).If the

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value R_0 is greater than 1, each infected person produces more than one new illness and, on average. Hence the disease can conquer the entire susceptible people. If the value R_0 is less than 1, the disease may go out of the population in the short run and that shows the effectiveness of the optimal control measures and the strategies followed. The effective reproduction rate is the average infection triggered by an infected person when only a cluster of a populace is susceptible. As discussed earlier, if $R_e > 1$, then the disease remains spreading or otherwise vanishes. The resisting power of people says immunity can be taken into account, whereas this becomes a challenging one while modeling initially at the time of emerging disease. The state of a population where the portion saved is enough to avert epidemicsay $R_e < 1$. Perilous removal edge p_c is a part of the vulnerable people's desires to be hoarded with effective measures or actions. For instance, one can obtain the perilous removal edge through vaccination. If the hosts are assumed to be mixed randomly, then p_c can be defined as $1-\frac{1}{R_0}$.

Nikolay B (2019) at PubMed published an article about 14 years examination for the Spread of NiV in Bangladesh. It is one of the most interesting articles that involves case studies and provides the following results. These results will be highly useful for future mathematical model developers while choosing the parameters and the values of different parameters. 82 caused by P-P transmission. This PP transmission yields $0.33\,R_0$.Nikolay B (2019) predicted the R_0 value as 1.1 for the infected people of age 45 and above along with struggle in breathing, which has a confidence interval of 0.4 to 3.2 at 95%. 0.05 times of association has been observed amongst the patients who did not have trouble breathing. Around 14% of the infected people are close spouses of the infected, 1.3% are close relatives and around 1% were others. It was observed that there was high positive correlation between infection and the body fluid.

VI. MODELLING WITH CONTROLS

Using the ideal philosophy of rheostat, Jakia& Chandra (2016) proposed a Mathematical model and did the analysis for NiV. Here, the classical SIR model is designed with incorporated parameters; different natural birth rate (b) and death rates (μ), disease-induced death rate (α), effective contact rate or transmission coefficient (β), and the recovery rate (γ). Hence, the equations 16, 17 and 18 can be enhanced with the incorporation of control strategies. Only two parameters namely awareness $u_1(t)$, and treatment $u_2(t)$ are included here as there is no vaccination found still now, hence one cannot include the effect of vaccination. The parameter $u_1(t)$ gives the decrease in β and the measure of $u_2(t)$ is required and determined by analyzing the health care facilities for the infected people, hence such measurements yield reduction in the infected stage I. Based on the above argument, the model has been proposed along with the initial conditions

$$S(0) = S_0 \geq 0, I(0) = I_0 \geq 0, R(0) = R_0 \geq 0, N(0) = N_0 \geq 0$$

$$\frac{dS}{dt} = b*N - \beta*S*I - \mu*S - u_1*S \quad \ldots(16)$$

$$\frac{dI}{dt} = \beta*S*I - \gamma*I - \mu*I - \alpha*I - u_2*I \quad \ldots(17)$$

$$\frac{dR}{dt} = \gamma*I - \mu*R + u_1*S + u_2*I \quad \ldots(18)$$

with

$$\frac{dN}{dt} = b*N - \alpha*I - \mu*N \quad \ldots(19)$$

This definition of the total population N gives a different idea to new researchers as infection and death are totally eliminated from the population. Bakare, E.A (2014) proposed the integration technique for minimization of the infected people, hence one can adopt the technique for the minimization of I. It is used in weight parameters say W_1 and W_2 which is required for the cost of treatment. After computation, the cost of awareness

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and cost of treatment is calculated as $W_1 * \frac{u_1^2}{2}$ and $W_2 * \frac{u_2^2}{2}$ respectively. For the set of ODE, it is mandatory to prove the existence of the solution and uniqueness, and it is the choice of the reader to adopt the different techniques to prove the same. Bakare, E.A (2014) used the assumed initial values of 0.90, 0.05 , 0.05, 0.03, 0.002, 0.005, 0.01, and 6 for S , I , R, $b, \mu\, \alpha, \gamma$ and number of years respectively. Bakare, E.A (2014) calculated the effective contact rate or the transmission coefficient β as 0.75, weight parameters W_1 and W_2 as 1 and 2 respectively. The model is proposed with simulated solutions, and one can develop by comparing it with actual data. Also, several assumed values are used in the model. As days roll by, one can get the epidemics and the much essential information with which the parameters can be updated with the current scenario. It was observed that the epidemic incidence is high during monsoon time and so the incorporation of seasonal parameters like rainfall, humidity, and temperature can be considered. One can think of next-generation reproductive number for NiVepidemics for better prediction. Though there is no significant predictions and publications on gender-wise differences in NiV epidemics, it is evident that women and children were affected more than males and a greater number of female infections is observed due to human interaction concerning social and family responsibilities. Hence, one can consider modelling with the inclusion of gender and age-wise infection levels.

Biswas (2014) has performed an investigation on "Optimal Control of NiV Infections: A Bangladesh Scenario". In his work, he used the scholastic campaigns and public dissociating as control measurement tools to prevent individuals from being affected by the epidemics of NiV. Nita et al (2018) proposed a two-compartment SEIR model with control strategies as a developmental work of Biswas (2014). In this work, Nita et al (2018) considered separate SEIR models for host and vector, that is, humans and bats. It is proposed to divide the human population to susscepible, exposed, infected, hospitalized and death and bat population as susscepible, exposed, infected, and removed. Figure 10 describes the transmission cycle, pathway and the stages of spread of NiV comprising of human and bat population. Nita et al (2018) proposed a model where the death stage is included in infectious stage. This assumption seems to be unrealistic, as the entire human death population cannot be included in the human exposed population, whereas the coefficient or parameter or additional transmission coefficient comprising of the spread of infections to human from the human death can be considered to incorporate. Hence, the future researcher may incorporate or modify the death stage to improve the predictive power of the proposed model. In the model, natural death rate is removed from every stage of human SEIHD while it is common to the total human and bat population. Hence one can get the accuracy error if the total death rate is removed from every stage and for future modelling one can think of removing different death rates at every stage.

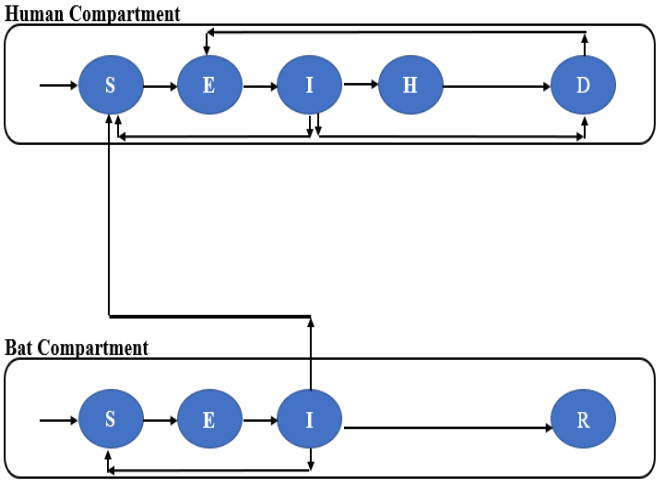

Figure 10: Two-compartment model for Human and Bat

The control strategies are divided into four parts in this model, spraying insecticides, buried bats, self-prevention and hospitalization denoted by u_1, u_2, u_3 and u_4 respectively. Such a division is an appreciable move, so that, one can evaluate each

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strategy separately to analyze its impact on the spread of the disease and to improve the model. The transmission coefficient α of bats is divided into five parts as susceptible to exposed, exposed to infected, infected to removed, infected to susceptible and infected to removed denoted by $\alpha_1, \alpha_2, \alpha_3$ α_4 and α_5 respectively. The transmission coefficient β of humans is divided into seven parts as susceptible to exposed, exposed to infected, infected to death (removed), infected to susceptible, infected to hospitalized, hospitalized to death, and death to exposed denoted by $\beta_1, \beta_2, \beta_3, \beta_4, \beta_5, \beta_6$ and, β_7 respectively. Modelling the transmission coefficients separately like this definitely will increase the predictive power, as the coefficients and the impacts are calculated separately. The local & global stability is discussed and it has been proved that the model is locally and globally asymptotically stable. The optimality is also discussed with strong mathematical calculations, shreds of evidence and numerical simulations with the effect of control strategies. The entire solution of the said model is not discussed here,as the reader can refer the work of Nita et al (2018) whenever necessary, however it is discussed the loop wholes and future development for the upcoming researchers.

VII. Challenges

Lloyd-Smith, J. O (2015) enlightened 9 most significant points in detail in modelling the novel pathogens. The challenges includes, finding the illness dynamics in non-human proximal types of species, intensifying the model for cross-species, detection of adaption and human-animal interface to map the transmission, incorporation of analyzation methods like stochasticity after pathogen introduction leads to observation errors, the data collection from the sporadic types, develop specific theories and case studies for intermediate hosts, incorporation of immunity of host in the models, developing a model that measure the fatality measurements of the diseases, designing the empirical studies of emerging pathogens for the most accurate scheming of risk.

This detailing by Grant, C (2016) traces the advantages of utilizing various ways to deal to improve a model and encourage multidisciplinary investigation into communicable illnesses, just as appearing and proposing down to earth instances of powerful incorporation. It takes a look at the advantages of utilizing participatory research related to conventional demonstrating techniques to possibly improve illness research, control, and the board. Incorporated methodologies can prompt increasingly reasonable numerical models which thusly can help with settling on strategy choices that lessen malady and advantage nearby individuals.Huyvaert, K. P (2018) analyzed the gaps of Lloyd-Smith, J. O (2015) and provided the most significant points in developing mathematical models. He discussed the challenges and opportunities too while modelling the pathogens of both wild and domestic animals. Also, Huyvaert, K. P (2018) suggested incorporating the separate mortality and birth rates of wild and domestic animals separately with the force of infection. Also, he suggested separating the population by gender-wise since there were changes in the immunity levels.

VIII. Conclusion

In this work it is discussed the extensive works done by many researchers starting from the mathematical modelling of diseases till the incorporation of different variables under various circumstances. This work may provide a very good insigt to the future researchers to learn about various works done on mathematical development of nipah virus modelling and for the further development of the proposed models.

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