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MATHEMATICAL MODELING OF THE DYNAMICS WITH RESPECT TO DOG RABIES DISEASE

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ABSTRACT

A SEIR model for rabies between dogs with vaccination effect is formulated. The basic reproduction ratio for this model is derived using the Next Generation Matrix Method. Graphical solutions of the differential equations are produced using Matlab. Stability analysis is performed and the impact of vaccination is analyzed.

Key Words: Rabies, Model, Ordinary differential equation

1. Introduction:

Mathematical modeling has become an important tool in analyzing the epidemiological characteristics of infectious diseases. Several mathematical models have been proposed for modeling the spread of infectious diseases. The earliest account of the mathematical modeling of the spread of a disease was carried out in 1766 by Daniel Bernoulli. Trained as a physician, Bernoulli created a mathematical model to defend the practice of inoculating against smallpox. The calculations from this model showed that universal inoculation against smallpox would increase the life expectancy from 26 years 7 months to 29 years 9 months [5]. In the years since, mathematicians, biologists, physicians, epidemiologists, and others have contributed to the maturing discipline of mathematical epidemiology. Several books have played a significant role in the development of theory. Mathematical models associated with the study of rabies in various

countries have existed over the years [8]. Early models of rabies dynamics followed the SEIR frame-work where populations were subdivided into specific classes corresponding to susceptible (S), exposed (E), infectious (I), and removed (R) individuals [9]. The dynamics were encapsulated through the construction of a system of ordinary differential equations (ODEs) representing either single populations or linked Meta populations from which a variety of predictions can be drawn concerning temporal and spatial pattern. These early models made use of the basic SEIR compartmental framework and these models were used to derive several critical features of disease emergence and spread. The models were used to calculate the critical threshold for epidemic emergence and the basic reproductive number (*R*0) for the virus. When *R*0 is greater than 1, the infection will spread and an epidemic will result. Using *R*0, it is possible to suggest what level of population culling would be necessary in order to bring threshold density below epizootic level. Although the construction of their model followed the SEIR compartmental framework, they failed to include the *R* class since there was evidence of natural recovery or development of natural immunity and vaccination which translates susceptible into the removed category was not considered by them.

Translating the dynamics portrayed in the flow chart into the following set of ODEs gave them;

$$\frac{dS}{dt} = rs - \gamma SN - \beta SI, \qquad \frac{dE}{dt} = rSI - (\alpha + \beta + \gamma N)E \quad , \qquad \frac{dI}{dt} = \alpha E - (\alpha + \beta\gamma N),$$
$$N = S + E + I$$

Where S, E and I represented densities of susceptible hosts, exposed, and infectious individuals respectively. The rate at which individuals were exposed (E) in the population is proportional to the densities of susceptible and infectious individual.

Anderson et al., 1981 was developed, fox rabies was continuing to advance south westerly into France and Switzerland. Descriptive studies then begun to investigate ecological factors that could influence the spatial propagation of virus, such as habit quality or fox densities [10]. Following these studies, Murray et al., 1986 developed a reaction-diffusion model to describe the behavior of this propagating wave. This model allowed predictive modeling of how a transmission barrier might be implemented at the wave front in order to halt the expansion of the epizootic [11]. The framework of the reaction diffusion formulation used by [13] consisted of coupled partial differential equations (PDEs) which were one-dimensional reaction diffusion framework identical to the model of (Anderson et al., 1981). The stochastic spatial model was used by [2] to analyze data from Ohio. Members of this team later authored another paper using

an ODE model to show that the spread of rabies may be controlled by distributing vaccine behind barriers such as rivers. This SIR model included the three classes in nine spatial compartments giving a total of 27 ODEs. Results showed that a higher rate of vaccination is needed for a large population and a lower rate with a higher cost.

Taking into account the actual situation of rabies spreading in China [15] formulated two mathematical models to study both the spreading dynamics of rabies in dogs and human, and the control strategies. They compared the efficiency of three strategies for controlling rabies: culling, vaccination, culling and vaccination and found that vaccination is the best choice to control rabies.

2. MODEL FORMULATION

2.1.1. SEIR model of Rabies transmission with vaccination

In this paper we formulate *SEIR* model for Dog rabies. We categorize Dog population into susceptible, exposed, infected and recovered groups. Susceptible groups have no disease, but they are likely to be infected in case of contact with rabid dogs, Exposed individuals are those who contracted the virus via bites or scratch, but still they have not shown symptoms. Infected individuals are those who develop clinical symptoms and they are unlikely to recover due to the nature of rabies [3]. The Recovered classes are those who recovered through vaccination before they reach to infectious stage, whereas the rest get infected and die eventually.

2.1.2. Methodology

The mathematical model will be formulated using differential equations. Furthermore investigate the existence and stability of the disease-Free State of the modified model by linearization approach. And also investigate the existence of the endemic equilibrium state of the modified model. The Computer software Mat lab (*ode*45) will be used to simulate the model.

In this section we can develop $SEIR$ epidemic model, Susceptible $\rightarrow$ Expose $\rightarrow$ Infected $\rightarrow$ Recovered, epidemic model. We will also conduct a simulation study by assigning different valid values to the parameters of the model. The present model has a compartmental structure and is designed based on the assumptions described as follows:

2.1.3. Model Assumptions

- The individuals in the susceptible compartment are subjected to get infection due to contact with infected population at a rate of β.
- The susceptible population on getting infection enters in to the exposed compartment.

- The susceptible population and the exposed population getting recovery centers in to the recovered compartment at the rate of Θ.
- The individuals in the exposed compartment are subjected to get infection due to contact with infected population at a rate of ρ.
- The individuals in all compartments there is natural death at the rate of μ and α stands for the annual birth rate of dog population.

All the parameters of the model are positive and they are introduced in Table 1.

Parameters	**Description**
α	The annual birth rate of dog population
δ	Death rate due to rabies for dog population
γ	The loss rate of vaccination immunity for dog population
μ	Natural death rate of dog population
β	The rate of infectious dogs infects susceptible dog population
θ	Vaccination rate of susceptible and exposed dog population
ρ	The incubation period in dog population

Table 1: Description of parameters

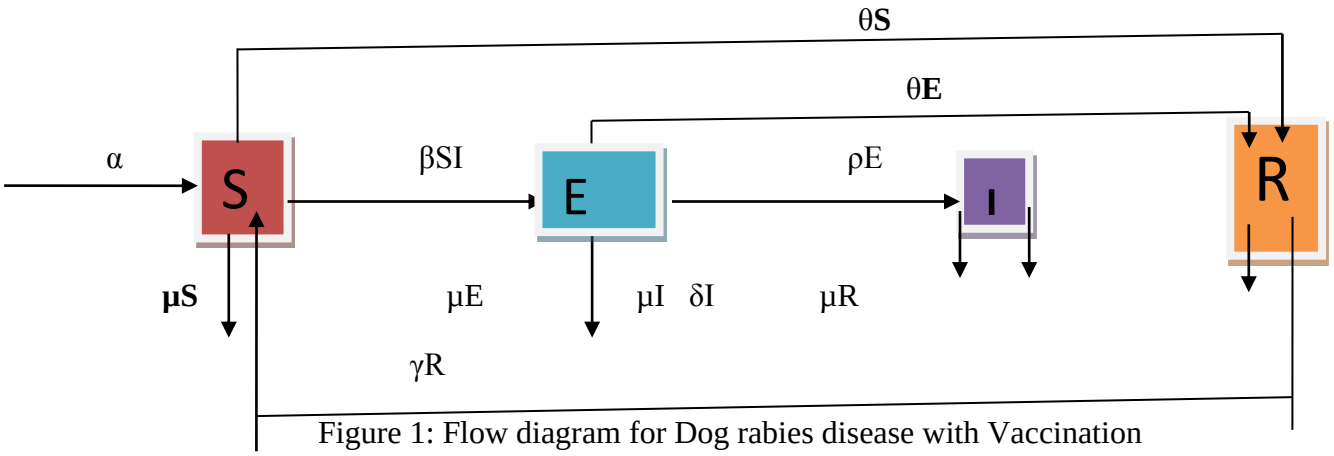

Figure 1: Flow diagram for Dog rabies disease with Vaccination

The mathematical formulation of $SEIR$ model can be expressed as systems of nonlinear differential equations as follows:

$$\frac{dS}{dt} = \alpha + \gamma R - (\mu + \theta + \beta I)S \qquad (1a)$$

$$\frac{dE}{dt} = \beta SI - (\theta + \rho + \mu)E \qquad (1b)$$

$$\frac{dI}{dt} = \rho E - (\delta + \mu)I \qquad (1c)$$

$$\frac{dR}{dt} = \theta S + \theta E - (\gamma + \mu)R \qquad (1d)$$

The total population for $N(t)$ are $N(t) = S(t) + E(t) + I(t) + R(t)$

Therefore adding each of the differential equations of system (1) of the dog population will give

$$N(t) = \frac{dS}{dt} + \frac{dE}{dt} + \frac{dI}{dt} + \frac{dR}{dt}$$

2.2. Positivity of the solutions of the modified model

In order to show that the general model equations (1a -1d) above to be epidemiologically meaningful and well posed, it is needed to prove that all the state variables are non-negative. This fact has been stated as a theorem and proved in what follows.

Theorem 2.2.1: If the initial conditions are non-negative i.e.$S(0) > 0, E(0) > 0, I(0) > 0, R(0) > 0$, the solutions $\{S(t), E(t), I(t), R(t)\}$ of the system of equation (1a-1d) above are non negative for all $t > 0$.

Proof: To show that the positivity of the solution of the dynamical system comprising the equations $(1a - 1d)$ above, we have to consider and verify each differential equation and show that their solution is positive. From the first equation, we have

$$\frac{dS}{dt} = \alpha + \gamma R - (\mu + \theta + \beta I)S$$

$$\frac{dS}{dt} \geq -(\mu + \theta + \beta I)S$$

$$\frac{dS}{S} \geq -(\mu + \theta + \beta I)dt$$

$$\int \frac{dS}{s} \geq \int -(\mu + \theta + \beta I)dt$$

$$\ln S \geq -(\mu + \theta + \beta I)t + C$$

$$S(t) \geq e^{-(\mu+\theta+\beta I)t+C}$$

$$S(t) \geq e^{C} e^{-(\mu+\theta+\beta I)t}$$

$$S(t) \geq S(0) e^{-(\mu+\theta+\beta I)t} \geq 0$$

Where $S(0) = e^{C}$ at $t = 0$

From the second equation (1b) $\frac{dE}{dt} = \beta SI - (\theta + \rho + \mu)E$

$$\frac{dE}{dt} = \beta SI - (\theta + \rho + \mu)E \geq -(\theta + \rho + \mu)E$$

$$\frac{dE}{dt} \geq -(\theta + \rho + \mu)E$$

$$\frac{dE}{E} \geq -(\theta + \rho + \mu)dt$$

Integrating inequality

$$\int \frac{dE}{E} \geq \int -(\theta + \rho + \mu)dt$$

$$\ln E \geq -(\theta + \rho + \mu)t + C$$

$$E(t) \geq e^{-(\theta+\rho+\mu)t+C}$$

$$E(t) \geq e^{C} e^{-(\theta+\rho+\mu)t} \geq 0$$

$$E(t) \geq E(0) e^{-(\theta+\rho+\mu)t} \geq 0$$

Where $E(0) = e^{C}$ for $t = 0$

From the third equation (1c) we have $\frac{dI}{dt} = \rho E - (\delta + \mu)I$

$$\frac{dI}{dt} = \rho E - (\delta + \mu)I \geq -(\delta + \mu)I$$

$$\frac{dI}{dt} \geq -(\delta + \mu)I$$

$$\frac{dI}{I} \geq -(\delta + \mu)dt$$

Integrating inequality

$$\int \frac{dI}{I} \geq \int -(\delta + \mu)dt$$

$$\ln I \geq -(\delta + \mu)t + C$$

$$I(t) \geq e^{-(\delta+\mu)t+C}$$

$$I(t) \geq e^{C} e^{-(\delta+\mu)t} \geq 0$$

$$I(t) \geq I(0) e^{-(\delta+\mu)t} \geq 0$$

Where $I(0) = e^C$ at $t = 0$

From the fourth (1d) equation we have $\frac{dR}{dt} = \theta S + \theta E - (\gamma + \mu)R$

$$\frac{dR}{dt} = \theta S + \theta E - (\gamma + \mu)R \geq -(\gamma + \mu)R$$

$$\frac{dR}{dt} \geq -(\gamma + \mu)R$$

$$\frac{dR}{R} \geq -(\gamma + \mu)dt$$

Integrating the differential equation, $\int \frac{dR}{R} \geq \int -(\gamma + \mu)dt$

$$\ln R \geq -(\gamma + \mu)t + C$$

$$R(t) \geq e^{-(\gamma+\mu)t+C}$$

$$R(t) \geq e^C e^{-(\gamma+\mu)t} \geq 0$$

$$R(t) \geq R(0)e^{-(\gamma+\mu)t} \geq 0$$

Where $R(0) = e^C$ at $t = 0$

Hence the solution set $\{S(t), E(t), I(t), R(t)\}$ of equations $(1a - 1d)$ are positive for all $t \geq 0$

2.3. Invariant Region

The model under consideration monitors population as such, we assume that all the variables and parameters of the model are positive for al l$t \geq 0$. In order to show that the solution of general model equations (1a-1d) is bounded it is needed to prove that the total population size *N*(t) is bounded. This fact is stated in the form of a theorem below accompanied by the proof.

Theorem 2.3.1: All solutions $S(t), E(t), I(t), R(t)$ of the system of differential equations $(1a - ad)$ above are bounded.

Proof: In order to show that the population sizes of each compartment is bounded we prefer to show that the total population size of the whole system $N(t)$ is bounded. The total dog population size $N(t)$ of the whole system is the sum of the populations of the four compartments and is given by

$$N(t) = S(t) + E(t) + I(t) + R(t)$$

Up on differentiating with respect to time we obtain

$$\frac{dN}{dt} = \frac{dS}{dt} + \frac{dE}{dt} + \frac{dI}{dt} + \frac{dR}{dt}$$

From the model we have

$\frac{dN}{dt} = \alpha + \gamma R - (\mu + \theta + \beta I)S + \beta SI - (\theta + \rho + \mu)E + \rho E - (\delta + \mu)I + \theta S + \theta E - (\gamma + \mu)R$

$\frac{dN}{dt} = \quad \alpha + \gamma R - \mu S - \theta S - \beta IS + \beta IS - \theta E - \rho E - \mu E + \rho E - \delta I - \mu I + \theta S + \theta E - \gamma R - \mu R$

Up on cancelling like terms but opposite in sign, we get

$\frac{dN}{dt} = \alpha - \mu S - \mu E - \delta I - \mu I - \mu R$

$\frac{dN}{dt} = \alpha - \delta I - \mu(S + E + I + R)$

$\frac{dN}{dt} = \alpha - \delta I - \mu N$

Since $\delta I \geq 0$ and $\delta I \leq \delta N$

$\frac{dN}{dt} \leq \alpha + \delta N - \mu N$ or equivalently

$\frac{dN}{dt} \leq \alpha + N(\delta - \mu)$

$\frac{dN}{\alpha + N(\delta - \mu)} \leq dt$

On integrating the foregoing differential inequality on both sides and applying the initial conditions we get its analytical solution as

$\int \frac{dN}{\alpha + N(\delta - \mu)} \leq \int dt$

$\ln \frac{(\alpha + N(\delta - \mu))}{(\delta - \mu)} \leq t + C$

$\ln\big(\alpha + N(\delta - \mu)\big) \leq (t + C)(\delta - \mu)$

$\alpha + N(\delta - \mu) \leq e^{(t+C)(\delta - \mu)}$

$N(\delta - \mu) \leq e^{(t+C)(\delta - \mu)} - \alpha$

$N(t) \leq \frac{e^{(t+C)(\delta - \mu)} - \alpha}{(\delta - \mu)}$

Let $N(0) = N_0$

$\rightarrow \frac{e^{(0+C)(\delta - \mu)} - \alpha}{(\delta - \mu)} = N_0$

$\rightarrow \frac{e^{C(\delta - \mu)} - \alpha}{(\delta - \mu)} = N_0$

$e^{C(\delta - \mu)} - \alpha = N_{0(\delta - \mu)}$

$e^{C(\delta - \mu)} = N_{0(\delta - \mu)} + \alpha$

$C(\delta - \mu) = \ln(N_{0(\delta - \mu)} + \alpha)$

$C = \frac{\ln(N_{0(\delta - \mu)} + \alpha)}{(\delta - \mu)}$

$N(t) \leq \frac{e^{t(\delta - \mu)} N_{0(\delta - \mu)} + \alpha - \alpha(\delta - \mu)}{(\delta - \mu)(\delta - \mu)}$

$$N(t) \leq \frac{e^{t(\delta-\mu)}N_{0(\delta-\mu)}-\alpha(\delta-\mu)+\alpha}{(\delta-\mu)(\delta-\mu)}$$

$$N(t) \leq \frac{e^{t(\delta-\mu)}(\delta-\mu)(N_0-\alpha)+\alpha}{(\delta-\mu)(\delta-\mu)}$$

$$N(t) \leq \frac{e^{t(\delta-\mu)}(\delta-\mu)(N_0-\alpha)}{(\delta-\mu)(\delta-\mu)} + \frac{\alpha}{(\delta-\mu)(\delta-\mu)}$$

$$N(t) \leq \frac{e^{-t(\mu-\delta)}(N_0-\alpha)}{(\delta-\mu)} + \frac{\alpha}{(\delta-\mu)^2}$$

$$N(t) \leq \frac{(N_0-\alpha)}{(e^{t(\mu-\delta)})(\delta-\mu)} + \frac{\alpha}{(\delta-\mu)^2}$$

As $t \to \infty$, $N(t) \leq \frac{\alpha}{(\delta-\mu)^2}$ which is an upper boundary

Hence $0 < N(t) \leq \frac{\alpha}{(\delta-\mu)^2}$ which is bounded

Therefore, $\Omega = \{\{S, E, I, R \in |R^4\}; 0 < N(t) \leq M\}$,Where $M = \frac{\alpha}{(\delta-\mu)^2}$ invariant

Therefore the solution of the given system of differential equation of the model is bounded.

2.4. Disease free equilibrium point

Let $E_0 = S^*, E^*, I^*, R^*)$ represents the disease free equilibrium point of $SEIR$ model with vaccination. Disease free equilibrium points are steady state solutions of mathematical model indicating that there is no disease. The compartmental classification of dog population reveals that the diseased dog population is distributed only in exposed and infected compartments. Hence, in the absence of infection we have $E^* = I^* = 0$ and an equilibrium points are and equilibrium points are obtained by setting zero for left sides in the equations (1a-1d),then the disease free equilibrium point E_0 will be obtained as

$\alpha + \gamma R^* - (\mu + \theta)S^* = 0$ (1) From (1a)

$\theta S^* - \gamma R^* - \mu R^* = 0$ (2) From (1d)

$\alpha + \gamma R^* - (\mu + \theta)S^* = 0$

$\alpha + \gamma R^* - \mu S^* - \theta S^* = 0$ From equation (1)

$-\mu S^* - \theta S^* + \gamma R^* = -\alpha$

$S^*(\mu + \theta) - \gamma R^* = \alpha$ (3)

$\theta S^* - \gamma R^* - \mu R^* = 0$ From (1d)

$\theta S^* - R^*(\gamma + \mu) = 0$ (4)

We proceed to solve (3) and (4) simultaneously

$S^* = \frac{(\gamma+\mu)}{\theta} R^*$ (5)

$\alpha + \gamma R^* - (\mu + \theta)S^* = 0$ From (1) (6)

Substitute equation (5) in to equation (6) to solve for R^*

$\alpha + \gamma R^* - (\mu + \theta)S^* = 0$

$\alpha + \gamma R^* - (\mu + \theta)\frac{(\gamma+\mu)}{\theta} R^* = 0$

$\gamma R^* - (\mu + \theta)\frac{(\gamma+\mu)}{\theta} R^* = -\alpha$

$\theta\gamma R^* - (\mu + \theta)(\gamma + \mu)R^* = -\alpha\theta$

$\theta\gamma R^* - \mu\boldsymbol{\gamma R}^* - \mu^2\boldsymbol{R}^* - \theta\gamma R^* - \theta\mu R^* = -\alpha\theta$

$-\mu\boldsymbol{\gamma R}^* - \mu^2\boldsymbol{R}^* - \theta\mu R^* = -\alpha\theta$

$\boldsymbol{R}^*(\mu\boldsymbol{\gamma} + \mu^2 + \theta\mu) = \alpha\theta$

$\boldsymbol{R}^* = \frac{\alpha\theta}{\mu\boldsymbol{\gamma}+\mu^2+\theta\mu} = \frac{\alpha\theta}{\mu^2+(\boldsymbol{\gamma}+\theta)\mu}$ **(7)**

Insert equation (7) in to equation (5) to solve for S^*

$S^* = \frac{(\gamma+\mu)}{\theta} R^*$

$S^* = \frac{(\gamma+\mu)}{\theta}(\frac{\alpha\theta}{\mu^2+(\boldsymbol{\gamma}+\theta)\mu})$

$S^* = \frac{\alpha(\gamma+\mu)}{\mu^2+(\boldsymbol{\gamma}+\theta)\mu}$

Therefore the disease free equilibrium

$(S^*, E^*, I^*, R^*) = (\frac{\alpha(\gamma+\mu)}{\mu^2+(\boldsymbol{\gamma}+\theta)\mu}, 0, 0, \frac{\alpha\theta}{\mu^2+(\boldsymbol{\gamma}+\theta)\mu})$

2.5. Endemic Equilibrium point of the model

Endemic equilibrium point of the model is obtained by finding each parameters of the system (1a 1d) above by setting the left side terms zero.

$\alpha + \gamma R - (\mu + \theta + \beta I)S = 0$ (8)

$\beta SI - (\theta + \rho + \mu)E = 0$ (9)

$\rho E - (\delta + \mu)I = 0$ (10)

$\theta S + \theta E - (\gamma + \mu)R = 0$ (11)

From (10) we have $\rho E - (\delta + \mu)I = 0$

$I = (\frac{\rho}{\delta + \mu})E$ (12)

From (9) we have

$\beta SI - (\theta + \rho + \mu)E = 0$

$\beta SI = (\theta + \rho + \mu)E$

$S = \left(\frac{\theta + \rho + \mu}{\beta I}\right)E$ (13)

Insert (12) in (13)

$S = \frac{(\delta + \mu + \rho)(\delta + \mu)}{\beta \rho}$ (14)

From (11) we have

$\theta S + \theta E - (\gamma + \mu)R = 0$

$R = \frac{\theta S + \theta E}{\gamma + \mu}$ (15)

Insert (14) in (15)

$R = \frac{\theta(\theta + \mu + \rho)(\delta + \mu)}{\beta \rho(\gamma + \mu)} + \frac{\theta E}{\gamma + \mu}$ (16)

We know that

$\beta SI = (\theta + \rho + \mu)E$ insert this in equation(8) and calculate for E

$\alpha + \gamma R - (\mu + \theta + \beta I)S = 0$

$\alpha + \gamma R - \mu S - \theta S - \beta SI = 0$

$\alpha + \gamma R - \mu S - \theta S - (\theta + \rho + \mu)E = 0$

$E = \frac{\alpha - \gamma R - (\theta + \mu)S}{\theta + \rho + \mu}$ but $S = \frac{(\delta + \mu + \rho)(\delta + \mu)}{\beta \rho}$ and $R = \frac{\theta(\theta + \mu + \rho)(\delta + \mu)}{\beta \rho(\gamma + \mu)} + \frac{\theta E}{\gamma + \mu}$ from (14) and (16) respectively

Up on substitution endemic equilibrium point is given by

$$(S^*, E^*, I^*, R^*) = \left(\frac{(\theta+\mu+\rho)(\mu+\delta)}{\beta\rho(\theta+\rho+\mu)(\mu+\delta)-\theta\beta\rho}, \frac{\alpha\beta\rho-\mu(\delta+\mu+\rho)(\mu+\delta)}{\beta\rho(\theta+\rho+\mu)(\mu+\delta)-\theta\beta\rho}, \frac{\alpha\beta\rho-\mu\rho(\theta+\rho+\mu)(\mu+\delta)}{(\mu+\delta)\beta\rho(\theta+\rho+\mu)(\mu+\delta)-\theta\beta\rho)}, \frac{1}{\mu+\gamma}\left(\frac{\theta(\mu+\delta)(\theta+\rho+\mu)-\mu}{\beta\rho(\gamma+\mu)}+\frac{\theta\alpha}{(\gamma+\mu)(\theta+\rho+\mu)-\theta}\right)\right)$$

2.6. Basic Reproductive Number

The basic reproductive number R_0 is a threshold parameter defined as the average number of secondary infection caused by an infectious individual by introducing in to a completely susceptible population. The basic reproductive number provides an invasion criterion for the initial spread of the infection in susceptible population. It is also called basic reproduction ratio or basic reproductive rate. If more than one secondary infection is produced from one primary infection that is, $R_0 > 1$ then an epidemic occurs. When $R_0 < 1$ 1then there is no epidemic and it means that the disease dies out over a period of time. When $R_0 = 1$then the disease becomes endemic, meaning the disease remains in the population at a constant rate as one infected dog transmits the disease to one susceptible [4].

We can calculate R_0 using using the Next Generation Matrix Approach. The Next Generation Matrix comprises two matrices *F* and *V*. The elements in matrix *F* constitute the new infections that will arise, while that of matrix *V* constitute the transfer of infections from one compartment to another. R_0 is the dominant Eigen value of the matrix$G = FV^{-1}$.

Linearizing the disease free equilibrium, reordering the states (E, I, S, R) and separating new infections F from other transitions V we get.

$$\frac{dE}{dt} = \beta SI - (\theta + \rho + \mu)E \qquad A(E, I, S, R)$$

$$\frac{dI}{dt} = \rho E - (\delta + \mu)I \qquad B(E, I, S, R)$$

$$\frac{dS}{dt} = \alpha + \gamma R - (\mu + \theta + \beta I)S \qquad C(E, I, S, R)$$

$$\frac{dR}{dt} = \theta S + \theta E - (\gamma + \mu)R \qquad D(E, I, S, R)$$

Linearizing the $SEIR$ model gives the Generation matrix (G) evaluated at disease free equilibrium

$$G = \begin{bmatrix} A_E & A_I & A_S & A_R \\ B_E & B_I & B_S & B_R \\ C_E & C_I & C_S & C_R \\ D_E & D_I & D_S & D_R \end{bmatrix} \qquad (8)$$

According to the next generation matrix approach, the G matrix above can be divided in to 2X2 sub matrices. Elements in the top left matrix is said to be $F-V$, the upper right sub matrix is always a zero matrix, Elements in the lower left sub matrix gives as J_1 and the lower right sub matrix termed as J_2.

$$G = \begin{bmatrix} F-V & 0 \\ J_1 & J_2 \end{bmatrix} \quad (9)$$

From equation (8) above we get our generation matrix as

$$G = \begin{bmatrix} -\theta-\rho-\mu & \beta & 0 & 0 \\ \rho & -\delta-\mu & 0 & 0 \\ 0 & -\beta & -\mu-\theta & \gamma \\ \phi & 0 & \phi & -\gamma-\mu \end{bmatrix}$$

$$F-V = \begin{bmatrix} -\theta-\rho-\mu & \beta \\ \rho & -\delta-\mu \end{bmatrix}$$

$$= \begin{bmatrix} 0 & \beta \\ 0 & 0 \end{bmatrix} - \begin{bmatrix} \theta+\rho+\mu & 0 \\ -\rho & \delta+\mu \end{bmatrix}$$

$$F = \begin{bmatrix} 0 & \beta \\ 0 & 0 \end{bmatrix} \text{ and } V = \begin{bmatrix} \theta+\rho+\mu & 0 \\ -\rho & \delta+\mu \end{bmatrix}$$

$$V^{-1} = \begin{bmatrix} \frac{1}{\theta+\rho+\mu} & 0 \\ \frac{\rho}{(\theta+\rho+\mu)(\delta+\mu)} & \frac{1}{\delta+\mu} \end{bmatrix}$$

$$FV^{-1} = \begin{bmatrix} 0 & \beta \\ 0 & 0 \end{bmatrix} \begin{bmatrix} \frac{1}{\theta+\rho+\mu} & 0 \\ \frac{\rho}{(\theta+\rho+\mu)(\delta+\mu)} & \frac{1}{\delta+\mu} \end{bmatrix}$$

$$FV^{-1} = \begin{bmatrix} \frac{\beta\rho}{(\theta+\rho+\mu)(\delta+\mu)} & \frac{\beta}{\delta+\mu} \\ 0 & 0 \end{bmatrix}$$

R_0 is the dominant eigen value of the matrix $\begin{bmatrix} \frac{\beta\rho}{(\theta+\rho+\mu)(\delta+\mu)} & \frac{\beta}{\delta+\mu} \\ 0 & 0 \end{bmatrix}$

$$|FV^{-1} - \lambda I_2| = 0$$

$$\begin{vmatrix} \frac{\beta\rho}{(\theta+\rho+\mu)(\delta+\mu)} - \lambda & \frac{\beta}{\delta+\mu} \\ 0 & -\lambda \end{vmatrix} = 0$$

$$\left(\frac{\beta\rho}{(\theta+\rho+\mu)(\delta+\mu)} - \lambda\right)(-\lambda) - \left(\frac{\beta}{\delta+\mu}\right)(0) = 0$$

$$\lambda^2 - \frac{\beta\rho\lambda}{(\theta+\rho+\mu)(\delta+\mu)} = 0$$

$$\lambda\left(\lambda - \frac{\beta\rho}{(\theta+\rho+\mu)(\delta+\mu)}\right) = 0$$

$\lambda_1 = 0$ and $\lambda_2 = \frac{\beta\rho}{(\theta+\rho+\mu)(\delta+\mu)}$

Therefore the dominant eigen value is $\lambda_2 = \frac{\beta\rho}{(\theta+\rho+\mu)(\delta+\mu)}$ and

Hence $R_0 = \frac{\beta\rho}{(\theta+\rho+\mu)(\delta+\mu)}$

2.7. Local Stability of Disease-Free Equilibrium point of Rabies transmission with vaccination

Theorem: If $R_0 < 1,$ then

a. The disease free equilibrium E_0 $of\ the$ system (1a-1d) is locally asymptotically stable.
To determine the local stability of the system at the disease-free equilibrium, we will consider the linearized system of equations below about the equilibrium point.

$$\frac{dS}{dt} = \alpha + \gamma R - \beta\left(\frac{S}{N}\right)I - (\mu+\theta)S$$

$$\frac{dE}{dt} = \beta(\frac{S}{N})I - (\theta + \rho + \mu)E$$

$$\frac{dI}{dt} = \rho E - (\delta + \mu)I$$

$$\frac{dR}{dt} = \theta S + \theta E - (\gamma+\mu)R$$

The Jacobian is therefore given by

$$J = \begin{bmatrix} -\mu-\theta-\beta I & 0 & -\beta S & \gamma \\ \beta I & -\theta-\rho-\mu & \beta S & 0 \\ 0 & \rho & -\delta-\mu & 0 \\ \phi & \theta & 0 & -\gamma-\mu \end{bmatrix}$$

Since $S = 1$ and $I = 0$ at disease-free equilibrium, the Jacobian matrix becomes

$$J = \begin{bmatrix} -(\mu+\theta) & 0 & -\beta & \gamma \\ 0 & -(\theta+\mu+\rho) & \beta & 0 \\ 0 & \rho & -(\delta+\mu) & 0 \\ \theta & \theta & 0 & -(\gamma+\mu) \end{bmatrix}$$

.The trace of the above matrix will be

$$Tr\left(J_{E_o}\right) = -(\mu + \theta) - (\theta + \rho + \mu) - (\delta + \mu) - (\gamma + \mu) < 0$$

$$\text{Det}(J_{E_o}) = -(\mu+\theta)\begin{vmatrix} -(\theta+\mu+\rho) & \beta & 0 \\ \rho & -(\delta+\mu) & 0 \\ \theta & 0 & -(\gamma+\mu) \end{vmatrix} - \theta \begin{vmatrix} 0 & -\beta & \gamma \\ -(\theta+\mu+\rho) & \beta & 0 \\ \rho & -(\delta+\mu) & 0 \end{vmatrix}$$

$$\text{Det}(J_{E_0}) = -(\mu+\theta)\left[-(\gamma+\mu)\left[\begin{vmatrix} -(\theta+\mu+\rho) & \beta \\ \rho & -(\delta+\mu) \end{vmatrix}\right]\right] - \theta[\gamma\left[\begin{vmatrix} -(\theta+\mu+\rho) & \beta \\ \rho & -(\delta+\mu) \end{vmatrix}\right]]$$

$$\text{Det}(J_{E_0}) = (\mu+\theta)(\gamma+\mu)[(\theta+\mu+\rho)(\delta+\mu) - \beta\rho] - \theta\gamma[(\theta+\mu+\rho)(\delta+\mu) - \beta\rho]$$

$$\text{Det}(J_{E_0}) = [(\theta+\mu+\rho)(\delta+\mu) - \beta\rho][(\mu+\theta)(\gamma+\mu) - \theta\gamma]$$

$$= [(\theta+\mu+\rho)(\delta+\mu) - \beta\rho][\mu\gamma + \mu^2 + \theta\gamma + \theta\mu - \theta\gamma]$$

$$= [(\theta+\mu+\rho)(\delta+\mu) - \beta\rho][\mu(\gamma+\mu+\theta)]$$

$$= \mu(\gamma+\mu+\theta)[(\theta+\mu+\rho)(\delta+\mu) - \beta\rho]$$

$$= \mu(\gamma+\mu+\theta)\frac{(\theta+\mu+\rho)(\delta+\mu)}{(\theta+\mu+\rho)(\delta+\mu)}[(\theta+\mu+\rho)(\delta+\mu) - \beta\rho]$$

$$= \mu(\gamma+\mu+\theta)(\theta+\mu+\rho)(\delta+\mu)[\frac{(\theta+\mu+\rho)(\delta+\mu)}{(\theta+\mu+\rho)(\delta+\mu)} - \frac{\beta\rho}{(\theta+\mu+\rho)(\delta+\mu)}$$

Since $R_0 = \frac{\beta\rho}{(\theta+\mu+\rho)(\delta+\mu)}$, we have

$$= \mu(\gamma+\mu+\theta)(\theta+\mu+\rho)(\delta+\mu)[1 - R_0]$$

Therefore $\text{Det}(J_{E_0}) = \mu(\gamma+\mu+\theta)(\theta+\mu+\rho)(\delta+\mu)(1-R_0)$

Since $R_0 = \frac{\beta\rho}{(\theta+\mu+\rho)(\delta+\mu)}$ for $R_0 < 1$, we have $\text{Tr}(J_{E_0}) < 0$ and $\text{Det}(J_{E_0}) > 0$ then the disease free Equilibrium (DFE) is locally asymptotically stable otherwise it is unstable if $R_0 > 1$.

3. MODEL ANALYSIS AND SIMULATION

Numerical simulations of the model have been carried out using MATLAB inbuilt function ode45; using the Runge-Kutta method of of order four. The main focus of the simulation is to investigate the response of model parameters for rabies epidemic

3.1.Simulation of SEIR model for rabies transmission with Vaccination

The simulations and analysis made are based on these parameters values which are displayed below in Table.

Parameter	Value	Description	Source	Unit
α	0.041	Annual birth rate of dog Population	Assumption	$Year^{-1}$
δ	0.985	Death rate of dog Population due to rabies Disease	Assumption	$Year^{-1}$
γ	0.02	The loss rate of vaccination immunity for dog population	Assumption	$Year^{-1}$
μ	0.41	Natural death rate of dog population	Assumption	$Year^{-1}$
β	0.997	The rate of infectious dogs infects susceptible dog population	Assumption	$Year^{-1}$
θ	1	Vaccination rate of susceptible and exposed dog population	Assumption	$Year^{-1}$
ρ	0.998	The incubation period in dog population	Assumption	$Year^{-1}$

Table 2: Assumption of the parameters values for SEIR model With Vaccination

The following initial conditions have been considered for simulation

$S(0) = 300, E(0) = 8, I(0) = 15$ *and* $R(0) = 20$

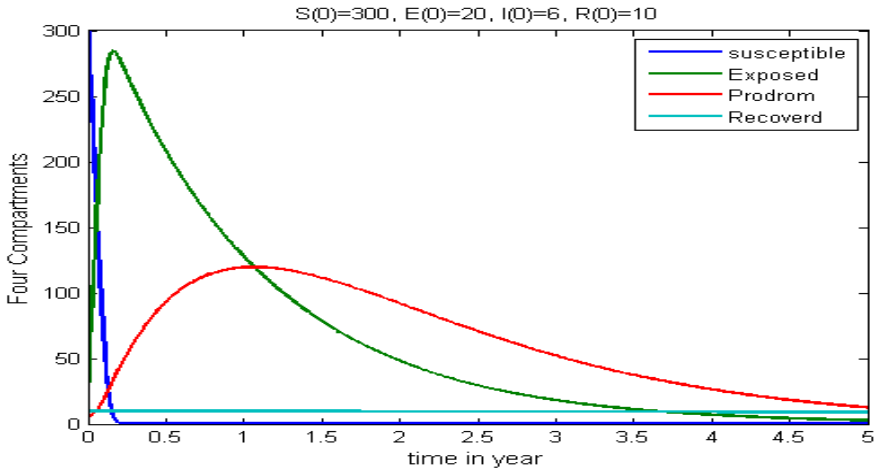

Figure 2: Numerical Simulation of Dog rabies model with $\boldsymbol{\theta = 0}$ ***and*** $\boldsymbol{R_0 = 1.46}$

As observed from the above figure if there is no vaccination, the sucstiple dog population is decreasing simultaneously and this shows that the existence of the disease. The recovered compartment is also decreasing.

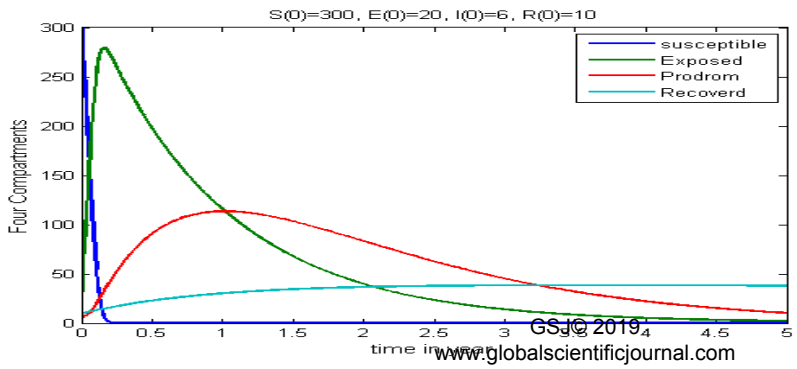

Figure 3: Numerical Simulation of dog rabies model with $\boldsymbol{\theta = 0.1}$ $\boldsymbol{and}$ $\boldsymbol{R_0 = 1.33}$

From the above figure we observed that when we introduce vaccination on the model the number of recovered compartment increases and the number of the infected compartment decreases.

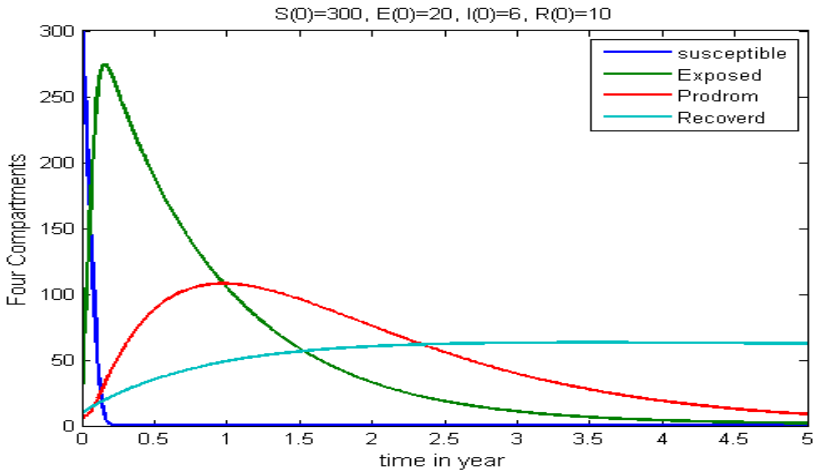

Figure 4: Numerical Simulation of dog rabies model with $\boldsymbol{\theta = 0.2}$ $\boldsymbol{and}$ $\boldsymbol{R_0 = 1.2}$

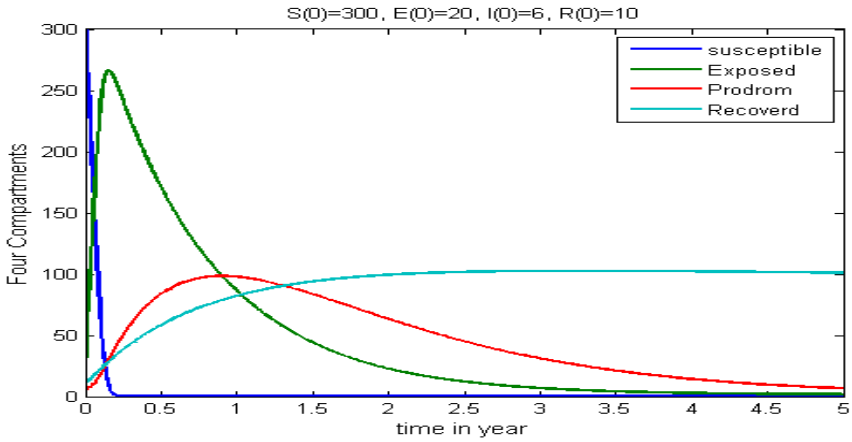

Figure 5: Numerical Simulation of dog rabies model when $\theta = 0.4$ and $R_0 = 1.04$

From the above figure we observed that as we increases the vaccination rate the number of infected compartments decreases and the number of recovered compartment increases.

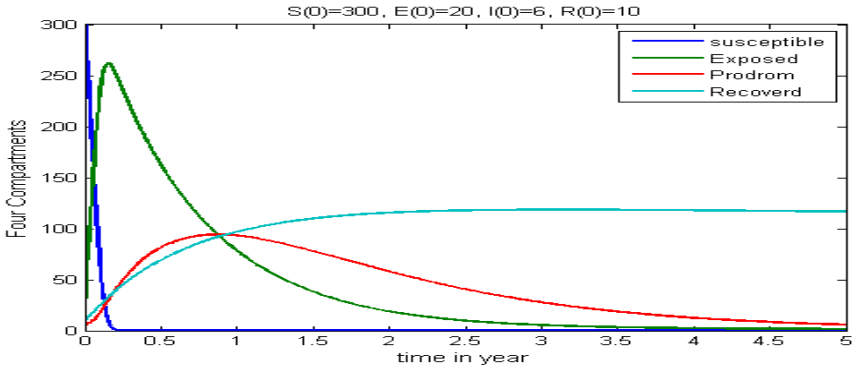

Figure 6: Numerical Simulation of dog rabies model when $\boldsymbol{\theta = 0.587}$ $\boldsymbol{and}$ $\boldsymbol{R_0 = 0.97}$

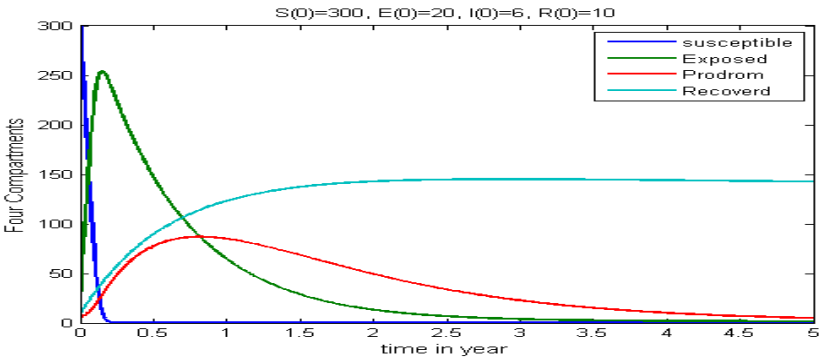

Figure 7: Numerical Simulation of dog rabies model when $\boldsymbol{\theta = 0.7}$ $\boldsymbol{and}$ $\boldsymbol{R_0 = 0.85}$

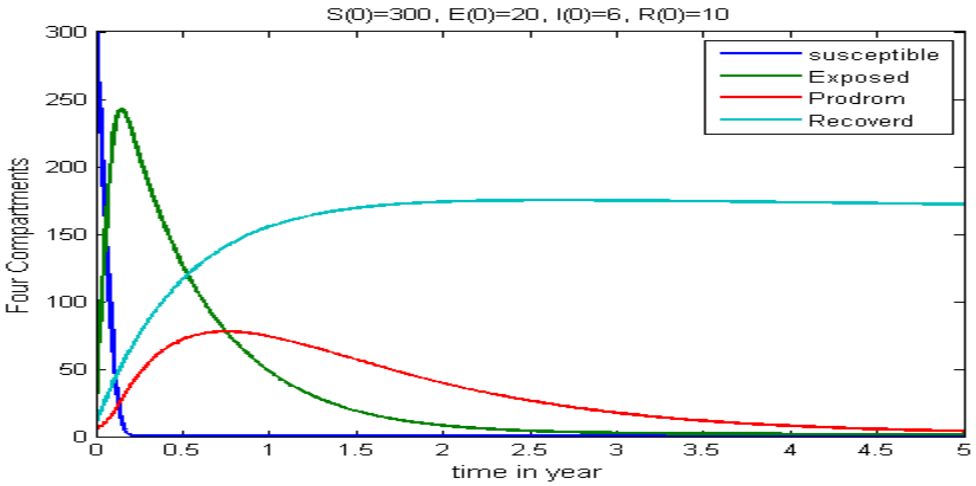

Figure 8: Numerical Simulation of dog rabies model when $\boldsymbol{\theta = 1}$ $\boldsymbol{and}$ $\boldsymbol{R_0 = 0.72}$

As we observed from the above figure, the graph of the recovered compartment increases and the number of infected dog population decreases. As observed from the graph the recovered graph is completely above the graph of the infected compartment and as time goes the graph of the

infected compartment approaches coincides with the graph of time axis which indicates that the number of infected dog population is near to zero.

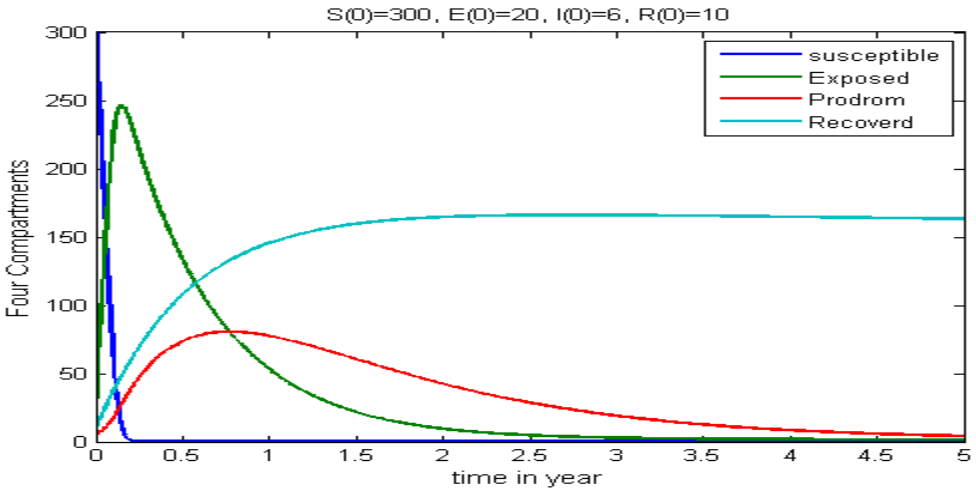

Figure 9: Numerical Simulation of dog rabies model when $\boldsymbol{\theta = 0.98}$ $\boldsymbol{and}$ $\boldsymbol{R_0 = 0.76}$

4. Conclusion

In the present study we have formulated and analyzed a Compartmental mathematical model for the dynamics of rabies transmission. Vaccination of dogs is the best controlling strategy for rabies disease. Increasing the vaccination coverage will decrease in the rate of transmission of rabies diseases. The basic reproduction number has been computed using next generation matrix method. We discussed the existence and stability of the disease free equilibrium points driven by using the Routh - Hurwitz criteria. The diseases free equilibrium points are shown locally asymptotically stable. Also disease endemic equilibrium point of the model has been derived. Simulation study and analysis of the model are performed by varying the vaccinated rate. It is Observed that increasing of the vaccination rate of rabies has a significant impact on the rate of spread of rabies transmission. Further, reducing the vaccination rate of rabies had decreased the number of recovered in the model.

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