RESEARCH ARTICLE

A NOTE ON STABILITY ANALYSIS OF COMPARTMENTAL MATHEMATICAL MODEL FOR THE SPREAD OF MALARIA.

A. Ali[1], R. Hussain[1] and M. Anayat[2].

1. Mirpur University of Science and Technology (MUST), Mirpur-10250(AJK), Pakistan.
2. International Islamic University Islamabad Pakistan.

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Manuscript Info	Abstract
Manuscript History ***Key words:-***	In this study, we present a compartmental model for the spread of malaria in a population where group of individuals were vaccinated. The purpose of this paper is to analyze the transmission dynamics of Malaria by using the compartmental model, including ordinary differential equations for human host and mosquito vector populations. A parallel system is obtained, which has two equilibriums: a disease-free equilibrium and an endemic equilibrium. The stability of the equilibrium points is verified by the basic reproduction number R_0. Asymptotically stable solution is obtained only for disease-free equilibrium and results are presented graphically.

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Introduction:-

Malaria is most common in Africa. The disease prevails in warmer climates and in areas where there is abundance of humidity and rain. According to latest WHO estimates released in December 2015, there were 214 million cases of malaria in 2015 and 438,000 deaths. At present five known species of plasmodium exists which are; P falciparum, P vivax, P ovale, P malariae and P knowlesi among them P. falciparum is responsible for most fatal infection and is widespread in the tropics. Clinical symptoms of malaria include: high fever, muscle and joint aches, headache, vomiting, chills, sweating and anemia etc. Young children and travellers (who do not have developed immunity) are at high risk of malaria. In highly endemic areas people develop a degree of acquired immunity which is boosted-up by new infections. Immunity lasts for a certain period in the absence of new infection. The duration of infection depends on many factors such as degree of infection, method and time of treatment, resistivity of parasite to drugs and biology of host.

Mathematical modeling has been frequently used in epidemiology and several other fields. Epidemiological modeling is very helpful in identifying important model parameters and suggests improvements in models for future predictions.

We modified the model of NidhiNirwani, R. Khandelwal and V.H. Badshah by performing the stability analysis. The purpose of this study is better understanding the dynamics of malaria.

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Corresponding Author:-A. Ali.
Address:-Mirpur University of Science and Technology (MUST), Mirpur-10250(AJK), Pakistan.

Description of Model:-
Let N_H and N_V denote human and mosquito population respectively with total population at time t. We assume that human and mosquito population has constant size with birth and death rates equal to μ_H and μ_V.

The human population of size N_H is composed of Susceptible S_H, Infective I_H and Recovered R_H whereas vector population consists of Susceptible S_V and Infective I_V.
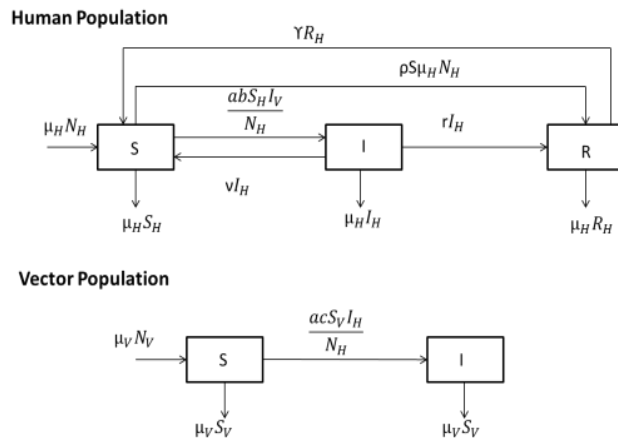
We say group of people ρ, $0 \leq \rho \geq 1$ of newborns host population be vaccinated. Assume that vaccine is not perfect and let the effectiveness of vaccine is s, then $\mu_H(1 - \rho s)N_H$ newborns remain susceptible, and $\mu_H \rho s N_H$ directly being removed to R_H. The governing equations are:

Human population:-
$$\frac{dS_H}{dt} = \mu_H(1 - \rho s)N_H - \frac{abS_H I_V}{N_H} + vI_H + \Upsilon R_H - \mu_H S_H$$
$$\frac{dI_H}{dt} = \frac{abS_H I_V}{N_H} - vI_H - rI_H - \mu_H I_H \qquad\qquad (1)$$
$$\frac{dR_H}{dt} = \mu_H \rho s N_H + rI_H - \Upsilon R_H - \mu_H R_H$$

Vector Population:-

$$\frac{dS_V}{dt} = \mu_V N_V - \frac{acS_V I_H}{N_H} - \mu_V S_V \quad (2)$$
$$\frac{dI_V}{dt} = \frac{acS_V I_H}{N_H} - \mu_V I_V$$

The human population of size N_H is formed of susceptible S_H, infective I_H and recovered R_H where vector population is composed of S_H and I_H.

Table 2.1:- Description of parameters of the model.

Variables	Interpretation
a	The average infection rate on man by single mosquito.
b	The proportion of bites on man that produce an infection.
c	The probability that a mosquito becomes infectious.
Υ	The per capita rate of loss of immunity in human hosts.
r	The rate at which human hosts acquire immunity.
v	The rate of recovery of human hosts from the disease.

Using $S_H + I_H + R_H = N_H$ and $S_V + I_V = N_V$, eqs (1) and (2) become

$$\frac{dS_H}{dt} = \mu_H(1 - \rho s)N_H - \frac{abS_H I_V}{N_H} + vI_H + \Upsilon(N_H + S_H + I_H) - \mu_H S_H$$

$$\frac{dI_H}{dt} = \frac{abS_H I_V}{N_H} - vI_H - rI_H - \mu_H I_H \qquad\qquad (3)$$

$$\frac{dI_V}{dt} = \frac{acI_H(N_V - I_V)}{N_H} - \mu_V I_V$$

Writing the eq (2.3) in population proportion

$$S_h = \frac{S_H}{N_H}, I_h = \frac{I_H}{N_H} \text{and } I_v = \frac{I_V}{N_V},$$

$$\frac{dS_h}{dt} = \mu_H(1 - \rho s) - ab\phi S_h I_v + vI_h + \Upsilon - \Upsilon(S_h + I_h) - \mu_H S_h$$

$$\frac{dI_h}{dt} = ab\phi S_h I_v - vI_h - rI_h - \mu_H I_h \qquad\qquad (4)$$

$$\frac{dI_v}{dt} = acI_h(1 - I_v) - \mu_v I_v$$

Where $\phi = \frac{N_V}{N_H}$ is the ratio of host and vector population.

Further we rescale t by ac and let $x = S_h, y = I_h$ and $z = I_v$

$$\frac{dx}{dt} = \mu(1 - x) - \sigma x - \eta xz + ky + \varphi - \varphi y$$

$$\frac{dy}{dt} = \eta xz - (k + m)y \qquad\qquad (5)$$

$$\frac{dz}{dt} = y(1 - z) - \omega z$$

Where

$$\mu = \frac{\mu_H}{ac}, \ \pi = \rho s, \eta = \frac{b\phi}{c}, \ m = \frac{\mu_H + r}{ac}, \ \omega = \frac{\mu_V}{ac}, \ k = \frac{v}{ac}, \sigma = \frac{\mu_H + \Upsilon}{ac}, \varphi = \frac{\Upsilon}{ac}$$

Euler Method:-

Values of parameters used were $\beta = 0.000318$ and $\mu = 0.0175$ and the initial conditions were S (0) =460, I (0) =12, R (0) =0

The Euler method

$$\begin{cases} w_0 = \alpha \\ w_{i+1} = w_i + hf(t_i, w_i) \end{cases}, \ i = 0, 1, 2, \dots\dots\dots, N - 1$$

The time interval was [0 90] and N=10 so

$h = \frac{b-a}{N}$

$h = \frac{90-0}{10} = 9$

$t_0 = 0, t_1 = 9, t_2 = 18, t_3 = 27, \dots\dots, t_{10} = 90$

$$w_0 = \begin{pmatrix} S(0) \\ I(0) \\ R(0) \end{pmatrix} = \begin{pmatrix} 460 \\ 12 \\ 0 \end{pmatrix} = \begin{pmatrix} w_{1,0} \\ w_{2,0} \\ w_{3,0} \end{pmatrix}$$

Iteration-1   for   i= 0

$$w_1 = w_0 + hf(t_0, w_0)$$

$$w_1 = \begin{pmatrix} w_{1,0} \\ w_{2,0} \\ w_{3,0} \end{pmatrix} + hf(0, w_0)$$

$$w_1 = \begin{pmatrix} 460 \\ 12 \\ 0 \end{pmatrix} + 9 \begin{pmatrix} -0.00038 \\ -0.20962 \\ 0.21 \end{pmatrix}$$

Steady State And Equilibrium Points:-
The system (5) has a disease-free equilibrium point E_0 ($\frac{\mu(1-\pi)+\varphi}{\sigma}$, 0, 0) and an endemic equilibrium point $E_1(x_e, y_e, z_e)$, where

$$x_e = \frac{(k+m)[\mu(1-\pi)+\varphi+(m+\varphi)\omega]}{\eta(m+\varphi)+\sigma(k+m)}$$

$$= \frac{(v+\mu_H+r)[ac\{\mu_H(1-\rho s)+Y\}+(\mu_H+r)\mu_V]}{ac[ab\phi(\mu_H+r+Y)+(\mu_H+Y)(v+\mu_H+r)]}$$

$$y_e = \frac{\eta[\mu(1-\pi)+\varphi]-\sigma(k+m)\omega}{\eta(m+\varphi)+\sigma(k+m)}$$

$$= \frac{a^2bc\phi[\mu_H(1-\rho s)+Y]-(\mu_H+Y)(v+\mu_H+r)\mu_V}{ac[ab\phi(\mu_H+r+Y)+(\mu_H+Y)(v+\mu_H+r)]}$$

$$z_e = \frac{\eta[\mu(1-\pi)+\varphi]-\sigma(k+m)\omega}{\eta[\mu(1-\pi)+\varphi+(m+\varphi)\omega]}$$

$$= \frac{a^2bc\phi[\mu_H(1-\rho s)+Y]-(\mu_H+Y)(v+\mu_H+r)\mu_V}{ab\phi[ac\{\mu_H(1-\rho s)+Y\}+(v+\mu_H+r)\mu_V]}$$

This has been obtained by setting the time derivatives of the Eq (5) equal to zero. Here the basic reproduction number R_0 is defined by

$$R_0 = \frac{\eta[\mu(1-\pi)+\varphi]}{\sigma(k+m)\omega} = \frac{a^2bc\phi[\mu_H(1-\rho s)+Y]}{(\mu_H+Y)(v+\mu_H+r)\mu_V}$$

And an endemic equilibrium E_1 (x_e , y_e , z_e) is stable when

$$R_0 = \frac{\eta[\mu(1-\pi)+\varphi]}{\sigma(k+m)\omega} > 0$$

$$w_1 = \begin{pmatrix} 459.99658 \\ 10.11342 \\ 1.89 \end{pmatrix}$$

Asymptotic Behaviour Of The Model:-
Theorem 1: If $R_0<1$, then the disease-free equilibrium is locally E_0 is locally stable and if $R_0=1$, E_0 is stable.
Proof:
To discuss the stability of the model, the governing dynamical system is
$F_1 = \mu(1-\pi)-\sigma x-\eta xz+ky+\varphi-\varphi y$ (6)
$F_2 = \eta xz-ky-my$ (7)
$F_3 = y(1-z)-\omega z$ (8)
The variation matrix of the above system is given by

$$J = \begin{bmatrix} -\sigma-\eta z & k-\varphi & -\eta x \\ \eta z & -k-m & \eta x \\ 0 & 1-z & -y-\omega \end{bmatrix}$$

For disease free equilibrium E_0 ($\frac{\mu(1-\pi)+\varphi}{\sigma}$, 0, 0) the variation matrix will be

$$J(E_0) = \begin{bmatrix} -\sigma & k-\varphi & \frac{-\eta[\mu(1-\pi)+\varphi]}{\sigma} \\ 0 & -k-m & \frac{\eta[\mu(1-\pi)+\varphi]}{\sigma} \\ 0 & 1 & -\omega \end{bmatrix}$$

The characteristic equation of it will be
$(\sigma+\lambda)\left[\lambda^2+(k+m+\omega)\lambda+(k+m)\omega-\frac{\eta[\mu(1-\pi)+\varphi]}{\sigma}\right] = 0$ (9)
By the above equation at eigenvalues, one can easily see that disease-free equilibrium E_0 is locally stable if

$$(k + m)\omega - \frac{\eta[\mu(1 - \pi) + \varphi]}{\sigma} > 0$$

i.e., $R_0 < 1$

Stability of disease-free equilibrium:-
The assumed values of all the parameters are given in the table below:

Parameters	Values
μ	1.16
η	0.00492
π	0.009
σ	2.1724
ϕ	0.9
k	0.0026
ω	1
m	0.011

With initial conditions $(x(0), y(0), z(0)) = (0.5, 0.5, 0.4)$
After substituting the values in equation (4.4) we get;
$(2.1724 + \lambda)(\lambda^2 + 1.0136\lambda) + 0.0089 = 0 (10)$
Where,
$\lambda_1 = -2.1724$
$\lambda_2 = -0.0089$
$\lambda_3 = -1.00475$
We see all Eigen values are real and negative, also $R_0 = 0.3413084471 < 1$, so the system is stable.

Stability of disease-free equilibrium:-
Taking equations (6) and (7); the variation matrix is given by

$$J_1 = \begin{bmatrix} -\sigma - \eta z & k - \varphi \\ \eta z & -k - m \end{bmatrix}$$

For disease free equilibrium E_0 $(\frac{\mu(1-\pi)+\varphi}{\sigma}, 0, 0)$ the variation matrix will be
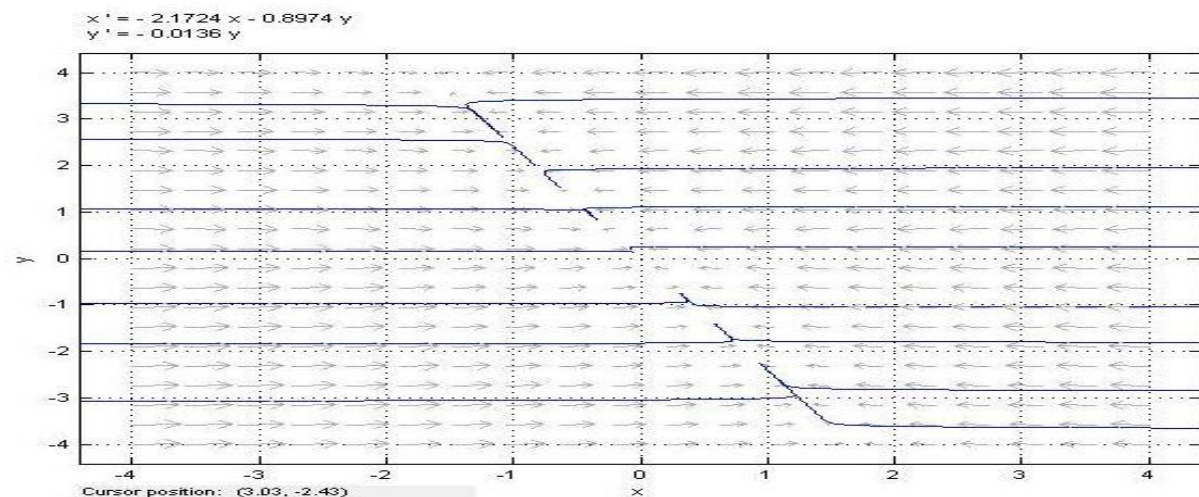
$$J_1 = \begin{bmatrix} -\sigma & k - \varphi \\ 0 & -k - m \end{bmatrix}$$

And putting the values from the table of disease-free equilibrium, we will get the following linear system;
$$\dot{x} = -2.1724x - 0.89747y$$
$$\dot{y} = -0.0136y$$
Now we take the graph of above equation through p-plane

Now, taking equations (6) and (7); the variation matrix is given by

$$J_2 = \begin{bmatrix} -k - m & \eta x \\ 1 - z & -y - \omega \end{bmatrix}$$
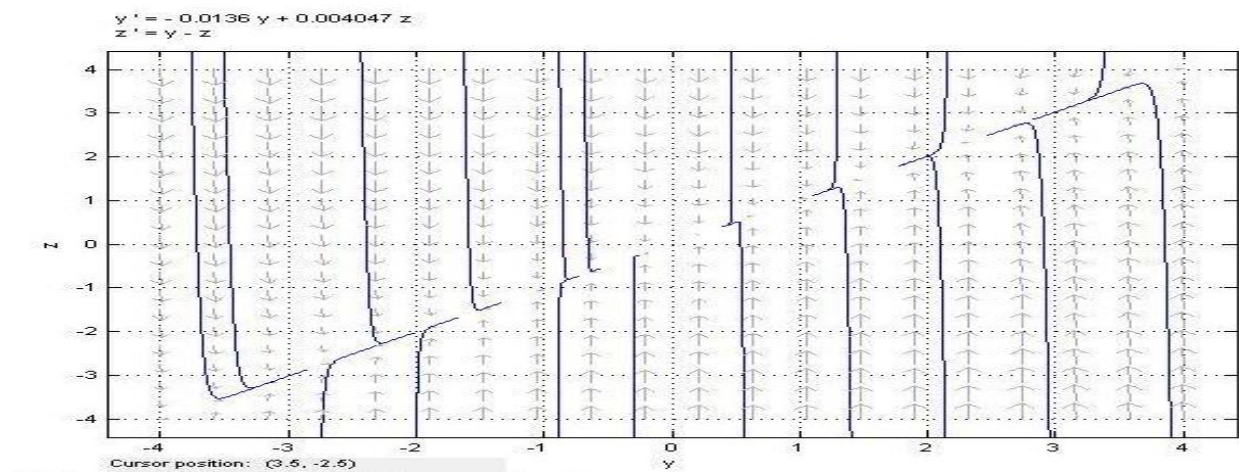
For disease free equilibrium E_0 $(\frac{\mu(1-\pi)+\varphi}{\sigma}, 0, 0)$ the variation matrix will be

$$J_1 = \begin{bmatrix} -k - m & \dfrac{\eta[\mu(1-\pi)+\varphi]}{\sigma} \\ 1 & -\omega \end{bmatrix}$$

And putting the values from the table of disease-free equilibrium, we will get the following linear system;

$$\dot{y} = -0.0136y + 0.004047z$$
$$\dot{z} = y - z$$

Now we take the graph of above equation through p-plane

Now, taking equations (6) and (9); the variation matrix is given by

$$J_3 = \begin{bmatrix} -\sigma - \eta z & \eta x \\ 0 & -y - \omega \end{bmatrix}$$
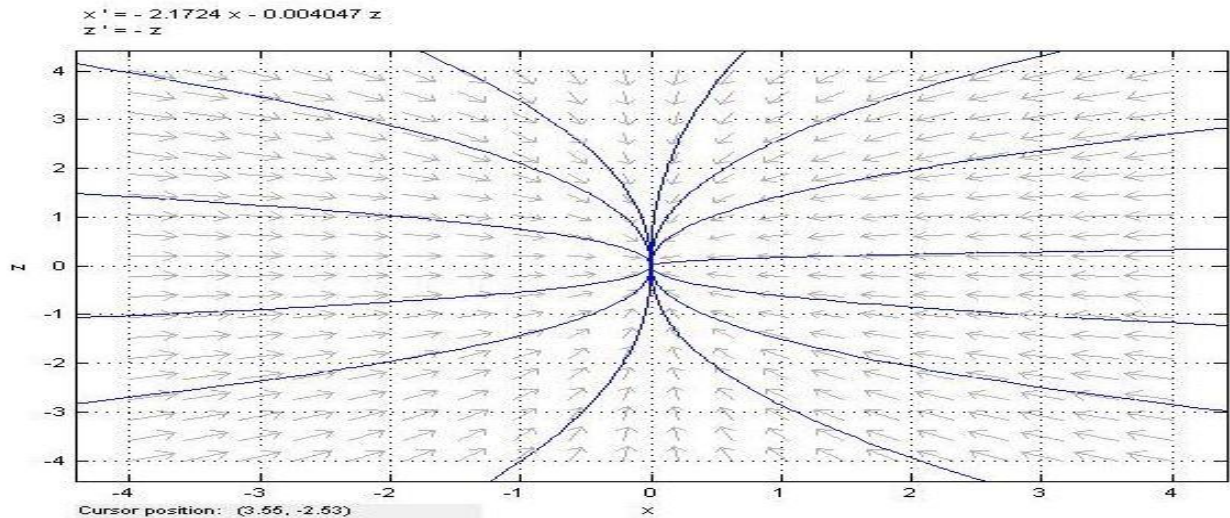
For disease free equilibrium E_0 $(\frac{\mu(1-\pi)+\varphi}{\sigma}, 0, 0)$ the variation matrix will be

$$J_1 = \begin{bmatrix} -\sigma & \dfrac{\eta[\mu(1-\pi)+\varphi]}{\sigma} \\ 0 & -\omega \end{bmatrix}$$

And putting the values from the table of disease-free equilibrium, we will get the following linear system;

$$\dot{x} = -2.1724x + 0.004047z$$
$$\dot{z} = -z$$

Now we take the graph of above equation through p-plane

x' = - 2.1724 x - 0.004047 z
z' = - z

Cursor position: (3.55, -2.53)

Conclusion

In this paper we present compartmental model for spread of malaria. An identical system is obtained which has two equilibrium points; a disease-free equilibrium and an endemic equilibrium. We discussed the stability of the disease-free equilibrium point numerically by computing Eigen-values and by using basic reproduction number. Further we perform stability analysis and graphically verify our results. All the graph indicate that the system is stable.

Future Work

The model presented here is multi-dimensional. In future we can perform stability analysis for endemic-equilibrium. Furthermore we can establish these results by using any of the numerical methods. Also we can work on its sensitivity analysis and parameter estimation.

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