MATH MODEL RESEARCH GROUP

DEPARTMENT OF MATHEMATICS

FEDERAL UNIVERSITY OF TECHNOLOGY (FUT), MINNA, NIGERIA

BOOK OF PROCEEDINGS

for the

International Conference on MATHEMATICAL MODELLING, OPTIMIZATION AND ANALYSIS OF DISEASE DYNAMICS (ICMMOADD 2024)

HYBRID (VIRTUAL & PHYSICAL)

Theme:

CONTEMPORARY ISSUES ON THE CONTROLS OF DISEASES EPIDEMICS AND PANDEMIC

DATE: Thursday 22nd February, 2024 **TIME:** 10:00am Prompt

VENUE: Department of Mathematics, Federal University of Technology Minna, Nigeria

PROFESSOR N. I. AKINWANDE FNMS

Convener

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An Appraisal on the Application of Reproduction Number for the Stability Analysis of Disease - Free Equilibrium State for S-I-R Type Models

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Abstract

One of the key ideas in mathematical biology is the basic reproduction number, which can be utilized to comprehend how a disease epidemic profile might evolve in the future. The basic reproduction number, represented by R_0, is the anticipated number of secondary cases that a typical infectious individual would cause in a population that is fully susceptible. This threshold parameter is highly valuable in characterizing mathematical problems related to infectious diseases. If $R_0 < 1$, this suggests that, on average, during the infectious period, an infected individual produces less than one new infected individual, suggesting that the infection may eventually be eradicated from the population. On the other hand, if $R_0 > 1$, every infected person develops an average of multiple new infections, it suggests that the disease may continue to spread throughout the population. We discuss the Reproduction number in this work and provide some examples, both for straightforward and complicated situations.

1.0 The Basic Reproduction Number

One of the key ideas in mathematical biology that is used to predict the future of an epidemic is the basic reproduction number. Diekmann O. & Heesterbeck, 2000), (Murray, 2002) state that the basic reproduction number, represented by, is the anticipated number of secondary cases that a typical infectious individual would cause in a fully susceptible population. This threshold parameter is highly valuable as it describes mathematical issues related to the dynamics of infectious diseases.

If $R_0 < 1$, this implies that, on average, an infected individual produces less than one new infected individual during the infectious period and the infection can be brought under control or totally eliminated from the population. Conversely, if $R_0 > 1$, then each infected individual produces, on average, more than one new infection, and the disease persists in the population. For a single infected compartment, R_0 is simply the product of the infection rate and the mean duration of the infection. But for complicated models, this simple computation of R_0 is not applicable and the need for a more robust computation is required and will be demonstrated in the second example after giving the analytical framework. We therefore compute the basic reproduction number R_0, using the next generation operator approach by (Van de Driessche, 2002). The method is described as illustrated next.

1.1 Computation of Basic Reproduction Number

Suppose that there are a total number of n compartments in the S-I-R model under consideration with m compartments corresponding to the infected classes.

Let

$F_i(x)$ = the rate of appearance of new infections in compartment i.

$V_i^+(x)$ = the rate of transfer of individuals into compartment i by all other means; (inflow).

$V_i^-(x)$ = the transfer of individuals out of the compartment i. (outflow)

The disease transmission model is given by the system of equations

$$x_i' = f_i(x) = F_i(x) - V_i(x) \tag{1.1}$$

where,

$$V_i = V_i^-(x) - V_i^+ \tag{1.2}$$

One other important step is to obtain the disease-free equilibrium point x_0. We then compute matrices F and V which are $m \times m$ matrices, where m represents number of the infected classes, defined by

$$F = \left[\frac{\partial F_i}{\partial x_j}(x_0) \right] \tag{1.3}$$

and

$$V = \left[\frac{\partial V_i}{\partial x_j}(x_0)\right] \text{ with } 1 \le i, \quad j \le m, \tag{1.4}$$

and F is non-negative and V is a non-singular M-matrix (a matrix with inverse, belonging to the class of positive matrices). Since F is non-negative and V is non-singular, then V^{-1} is non-negative and also FV^{-1} is non-negative. We then compute matrix FV^{-1}, defined as the next generation matrix (Diekmann O. & Heesterbeck, 2000).

The basic reproduction number (reproduction ratio) R_0 is then defined as

$$R_0 = \rho\left(FV^{-1}\right) \tag{1.5}$$

where

$\rho(A)$ = the spectral radius of matrix A, (or the maximum modulus of the eigenvalues of A).

The following steps are followed in computing the basic reproduction number using the next generation operator approach:

1. Identify classes for which:
   (i) An infection event increases this class (gain/inflow terms).
   (ii) Loss from this class means of current or future infection (loss/outflow terms)
2. Compute the disease-free equilibrium
3. List the gain and loss terms for each class.
4. Create a matrix (F) of gain terms of each class partially differentiated with respect to each and evaluated at the disease-free equilibrium
5. Create a matrix (V) of loss terms of each class partially differentiated with respect to each and evaluated at the disease-free equilibrium
6. Invert matrix V to get V^{-1}
7. Evaluate matrix $G = FV^{-1}$
8. R_0 is the dominant Eigen-value of G.

2.0 Example 1

Consider the following SIR model

$$\frac{dS}{dt} = \pi - \beta SI - \mu S \tag{1}$$

$$\frac{dI}{dt} = \beta SI - (\mu + \gamma)I \tag{2}$$

$$\frac{dR}{dt} = \gamma I - \mu R \tag{3}$$

We compute the basic reproduction number for the above model.

The disease-free equilibrium state for the model is given by $(S, I, R) = \left(\frac{\pi}{\mu}, 0, 0\right) = E_0$.

Gains to class $I =$ βSI (4)

Loss from class $I =$ $(\mu + \gamma)I$ (5)

$$F_i = (\beta SI) \tag{6}$$

And so

$$V_i = (\mu + \gamma)I \tag{7}$$

Differentiating (6) and (7) partially with respect to I at E_0

$$F = \left(\frac{\beta\pi}{\mu}\right) \tag{8}$$

$$V = (\mu + \gamma) \tag{9}$$

$$V^{-1} = \left(\frac{1}{(\mu + \gamma)}\right) \tag{10}$$

The product of (8) and (10) yields

$$FV^{-1} = \left(\frac{\beta\pi}{\mu}\right)\left(\frac{1}{(\mu+\gamma)}\right) = \frac{\beta\pi}{\mu(\mu+\gamma)} \tag{11}$$

The basic reproduction number R_0, is therefore given by

$$R_0 = \frac{\beta\pi}{\mu(\mu+\gamma)} \tag{12}$$

Analysis and interpretation

The Disease-Free equilibrium DFE is stable if

$$R_0 = \frac{\beta\pi}{\mu(\mu+\gamma)} < 1 \tag{13}$$

i.e if

$$\beta < \frac{\mu(\mu+\gamma)}{\pi} = \beta_{max} \tag{14}$$

Which gives the threshold for the infection rate β.

For the effective control of the disease from the population we must have

$$\beta < \beta_{max} \tag{15}$$

Otherwise, the disease will persist in the population.

3.0 Example 2 - Scabby Mouth Disease Model

3.1 Preamble

Abdurrahman *et al.* (2021) in their work titled A Mathematical Model of Scabby Mouth Disease Incorporating the Quarantine Class obtained the Reproduction Number and analyzed the DFE stability. The aspect of the work relating to this application is presented in this section.
The authors proposed a mathematical model to study the transmission and control of scabby mouth disease in sheep, incorporating the vaccinated and quarantine classes. The Disease-free equilibrium (DFE) was obtained and the reproduction number was also computed. The DFE was analyzed for local stability using the condition that the DFE is locally stable if $R_0 < 1$.

3.2 Model Equation Formulation

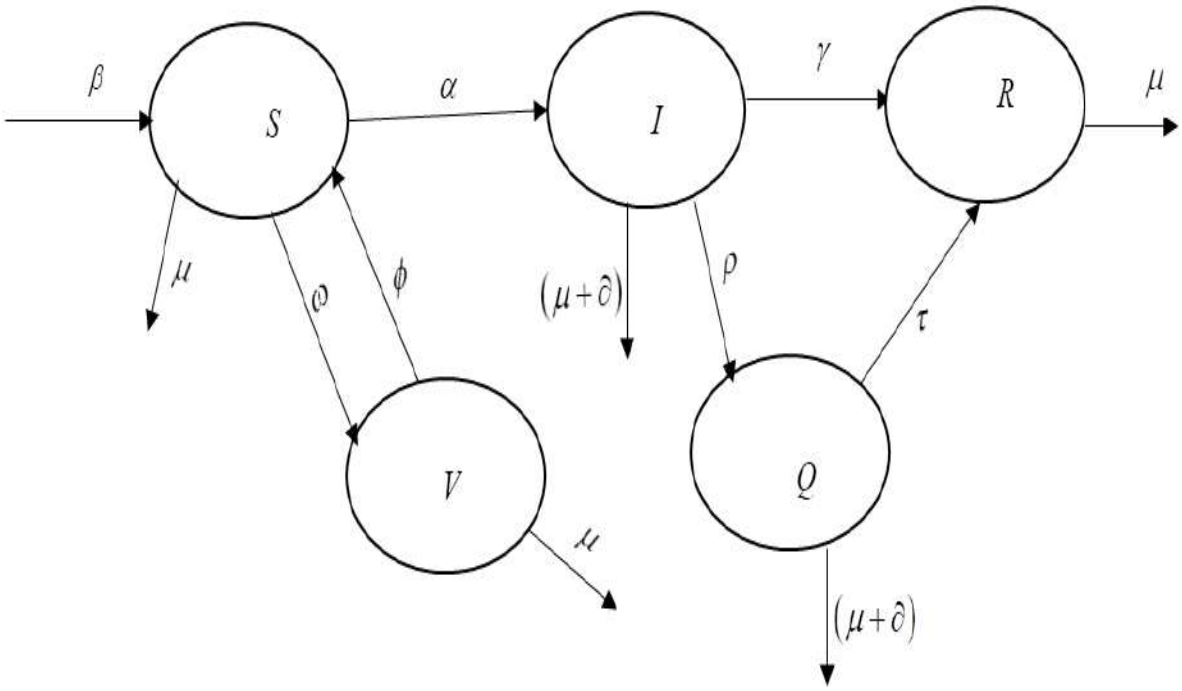

Figure 1: Schematic Diagram

The governing equations are given as:

$$\frac{dS}{dt} = \beta + \phi V - \frac{\alpha SI}{N} - (\omega + \mu)S \tag{16}$$

$$\frac{dI}{dt} = \frac{\alpha SI}{N} - (\gamma + \rho + \mu + \partial)I \tag{17}$$

$$\frac{dQ}{dt} = \rho I - (\tau + \mu + \partial)Q \tag{18}$$

$$\frac{dV}{dt} = \omega S - (\phi + \mu)V \tag{19}$$

$$\frac{dR}{dt} = \gamma I + \tau Q - \mu R \tag{20}$$

Table 3.1: Definition of Variables and Parameters.

Variables and Parameters	Description
S	Susceptible class
I	Infected Class

V	Vaccinated Class
Q	Quarantine Class
R	Recovered Class
β	Recruitment/Birth Rate
α	infection rate
ρ	Rate at which the infected class is quarantined
∂	death due to complication from infection
ω	Vaccination rate
ϕ	loss of immunity
μ	natural death rate
γ	recovery rate
τ	treatment rate

Let

$$k_1 = (\omega + \mu), k_2 = (\gamma + \rho + \mu + \partial), k_3 = (\tau + \mu + \partial), k_4 = (\phi + \mu)\,; \tag{21}$$

3.4 Equilibrium state of the model

At equilibrium state,

$$\frac{dS}{dt} = \frac{dI}{dt} = \frac{dQ}{dt} = \frac{dV}{dt} = \frac{dR}{dt} = 0 \tag{22}$$

Let $\begin{pmatrix} S \\ I \\ Q \\ V \\ R \end{pmatrix} = \begin{pmatrix} S_0^* \\ I_0^* \\ Q_0^* \\ V_0^* \\ R_0^* \end{pmatrix}$ (23)

We have the following equations

$$\beta + \varphi V_0^* - \frac{\alpha S_0^* I_0^*}{N_0^*} - k_1 S_0^* = 0 \tag{24}$$

$$\frac{\alpha S_0^* I_0^*}{N_0^*} - k_2 I_0^* = 0 \tag{25}$$

$$\rho I_0^* - k_3\, Q_0^* = 0 \tag{26}$$

$$\omega S_0^* - k_4 V_0^* = 0 \tag{27}$$

$$\gamma I_0^* + \tau Q_0^* - \mu R_0^* = 0 \tag{28}$$

From equation (25)

$$(\alpha S_0^* - k_2)\, I_0^* = 0 \tag{29}$$

$$\Rightarrow I_0^* = 0 \tag{30}$$

From (24)

$$\beta + \phi V_0^* - k_1 S_0^* = 0 \tag{31}$$

$$\Rightarrow V_0^* = \frac{k_1 S_0^* - \beta}{\phi} \tag{32}$$

From equation (27),

$$V_0^* = \frac{\omega S_0^*}{k_4} \tag{33}$$

comparing equation (32) and (33), we have

$$\frac{\omega S_0^*}{k_4} = \frac{(k_1 S_0^* - \beta)}{\phi} \tag{34}$$

$$S_0^* = \frac{\beta k_4}{k_1 k_4 - \omega\phi} \tag{35}$$

Substituting equation (35) into (33), we have

$$V_0^* = \frac{\omega\beta}{k_1 k_4 - \omega\phi} \tag{36}$$

Substituting equation (30) into (26), we have

$$k_3\, Q_0^* = 0 \tag{37}$$

$$\Rightarrow Q_0^* = 0 \tag{38}$$

substituting equations (30) and (36) into equation (28),

$$\mu R_0^* = 0 \tag{39}$$

$$\Rightarrow R_0^* = 0 \tag{40}$$

$$\begin{pmatrix} S_0^* \\ I_0^* \\ Q_0^* \\ V_0^* \\ R_0^* \end{pmatrix} = \begin{pmatrix} \frac{\beta k_4}{k_1 k_4 - \omega\phi} \\ 0 \\ 0 \\ \frac{\omega\beta}{k_1 k_4 - \omega\phi} \\ 0 \end{pmatrix} \tag{41}$$

$$N_0^* = \frac{\beta k_5}{k_1 k_4 - \omega\phi} \tag{42}$$

Where $k_5 = k_4 + \omega$ (43)

3.5 Computation of the Reproduction Number R_0

he basic reproduction number is the average number of secondary infections produced when one infective is introduced into the host population where everyone is susceptible (Benyah, 2009)

When$R_0 < 1$ The infection will die out over time while if $R_0 > 1$ the infection will persist in the population. In this model the reproduction number is given as the largest eigen-value or spectral radius of FV^{-1} . WhereF_i is the rate of appearance of new infection in compartment i, $V_i$is the transfer of infection from one compartment i to another.

$$FV^{-1} = \left(\frac{dF_i}{dx_i}\right)\left(\frac{dV_i}{dx_i}\right)^{-1} \tag{44}$$

$$F_i = \begin{pmatrix} \frac{\alpha SI}{N} \\ \rho I \end{pmatrix} \tag{45}$$

At DFE,

$$F = \begin{pmatrix} \frac{\alpha S_0^*}{N_0^*} & 0 \\ \rho & 0 \end{pmatrix} = \begin{pmatrix} \frac{\alpha k_4}{k_5} & 0 \\ \rho & 0 \end{pmatrix} \tag{46}$$

$$\frac{S_0}{N_0} = \frac{k_4}{k_5} \tag{47}$$

$$V_i = \begin{pmatrix} k_2 I \\ k_3 Q \end{pmatrix} \tag{48}$$

$$V_i = \begin{pmatrix} \frac{dV_i}{dI} \\ \frac{dV_i}{dQ} \end{pmatrix} = \begin{pmatrix} k_2 & 0 \\ 0 & k_3 \end{pmatrix} \tag{49}$$

$$|V| = \left|\begin{pmatrix} k_2 & 0 \\ 0 & k_3 \end{pmatrix}\right| = (k_2 k_3) \tag{50}$$

$$AdjV = \begin{pmatrix} k_3 & 0 \\ 0 & k_2 \end{pmatrix} \tag{51}$$

$$V^{-1} = \begin{pmatrix} \frac{1}{k_2} & 0 \\ 0 & \frac{1}{k_3} \end{pmatrix} \tag{52}$$

$$FV^{-1} = \begin{pmatrix} \frac{\alpha k_4}{k_2 k_5} & 0 \\ 0 & 0 \end{pmatrix} \tag{53}$$

$$|FV^{-1} - I\lambda| = 0 \tag{54}$$

$$\begin{vmatrix} \frac{\alpha k_4}{k_2 k_5} - \lambda & 0 \\ 0 & -\lambda \end{vmatrix} = 0 \tag{55}$$

$$-\lambda\left(\frac{\alpha k_4}{k_2 k_5} - \lambda\right) = 0 \tag{56}$$

$$\lambda_1 = 0, \lambda_2 = \frac{\alpha k_4}{k_2 k_5} \tag{57}$$

Therefore, the reproduction number

$$R_0 = \frac{\alpha k_4}{k_2 k_5} \tag{58}$$

3.6 Local Stability Analysis of the DFE

$$J(E^0) = (S_0^* I_0^* Q_0^* V_0^* R_0^*) \tag{59}$$

$$J(E^0) = \begin{pmatrix} -\alpha I - k_1 & -\alpha S & 0 & \phi & 0 \\ \alpha I & \alpha S - k_2 & 0 & 0 & 0 \\ 0 & \rho & -k_3 & 0 & 0 \\ \omega & 0 & 0 & -k_4 & 0 \\ 0 & \gamma & \tau & 0 & -\mu \end{pmatrix} \tag{60}$$

Substituting (39) into (54) we have that

$$\begin{pmatrix} -k_1 & -\frac{\alpha\beta k_4}{k_1 k_4 - \omega\phi} & 0 & \phi & 0 \\ 0 & \frac{\alpha\beta k_4}{k_1 k_4 - \omega\phi} - k_2 & 0 & 0 & 0 \\ 0 & \rho & -k_3 & 0 & 0 \\ \omega & 0 & 0 & -k_4 & 0 \\ 0 & \gamma & \tau & 0 & -\mu \end{pmatrix} \tag{61}$$

$$\begin{pmatrix} -k_1 & -\frac{\alpha\beta k_4}{k_1 k_4 - \omega\phi} & 0 & \phi & 0 \\ 0 & \frac{\alpha\beta k_4}{k_1 k_4 - \omega\phi} - k_2 & 0 & 0 & 0 \\ 0 & \rho & -k_3 & 0 & 0 \\ \omega & 0 & 0 & -k_4 & 0 \\ 0 & \gamma & \tau & 0 & -\mu \end{pmatrix} \tag{62}$$

$$\begin{vmatrix} -k_1 & -\frac{\alpha k_4(k_1-\beta)}{\omega\phi} & 0 & \phi & 0 \\ 0 & \frac{k_2\phi\omega+\alpha k_4(k_1-\beta)}{\omega\phi} & 0 & 0 & 0 \\ 0 & 0 & -k_3 & 0 & 0 \\ 0 & 0 & 0 & \frac{\phi\omega-k_1k_4}{k_1} & 0 \\ 0 & 0 & 0 & 0 & -\mu \end{vmatrix} \tag{63}$$

$$\begin{pmatrix} -k_1-\lambda_1 & -\frac{\alpha k_4(k_1-\beta)}{\omega\phi} & 0 & \phi & 0 \\ 0 & \frac{k_2\phi\omega+\alpha k_4(k_1-\beta)}{\omega\phi} - \lambda_2 & 0 & 0 & 0 \\ 0 & 0 & -k_3-\lambda_3 & 0 & 0 \\ 0 & 0 & 0 & \frac{\phi\omega-k_1k_4}{k_1} - \lambda_4 & 0 \\ 0 & 0 & 0 & 0 & -\mu-\lambda_5 \end{pmatrix} \tag{64}$$

$$\begin{pmatrix} \lambda_1 = -k_1 \\ \lambda_2 = \frac{-k_2\phi\omega+\alpha k_4(k_1-\beta)}{\omega\phi} \\ \lambda_3 = -k_3 \\ \lambda_4 = \frac{\phi\omega-k_1k_4}{k_1} \\ \lambda_5 = -\mu \end{pmatrix} \tag{65}$$

For the Disease-Free state to be achieved λ_2 and $\lambda_4$have to be negative. For $\lambda_2$to be negative we have that

$$-k_2\phi\omega + \alpha k_4(k_1-\beta) < 0 \tag{66}$$

$$\Rightarrow \alpha k_4(k_1-\beta) < k_2\phi\omega \tag{67}$$

$$\frac{\alpha k_4(k_1-\beta)}{k_2\phi\omega} < 1 \tag{68}$$

Comparing (58) to (68)

$\Rightarrow R_0 < 1$which implies that the disease will die out if this inequality holds.

On the other hand, $\lambda_4 < 0$ implies that

$$\Rightarrow \phi\omega < k_1 k_4 \tag{69}$$

$$\Rightarrow \phi\omega < (\omega+\mu)(\phi+\mu) \tag{70}$$

$$\Rightarrow \phi\omega < \phi\omega + \omega\mu + \mu\phi + \mu^2 \tag{71}$$

$$\Rightarrow -\omega\mu < \mu\phi + \mu^2 \tag{72}$$

$$\omega > -(\phi+\mu) \tag{73}$$

3.7 Conclusion

The DFE is locally stable if $R_0 = \frac{\alpha k_4}{k_2 k_5} < 1$ which implies that

$$\alpha < \frac{k_2 k_5}{k_4} < \frac{(\gamma+\rho+\mu+\partial)(\phi+\mu+\omega)}{(\phi+\mu)} = \alpha_{max} \tag{74}$$

Hence, the infection rate should not exceed α_{max} in order to effectively control the disease.

4.0 Example 3 - A TB model

Ashezual *et al*. (2017), in their work titled A Mathematical Model of Scabby Mouth Disease Incorporating the Quarantine Class obtained the Reproduction Number and analyzed of the DFE stability.

$$\left.\begin{aligned}
\frac{dS}{dt} &= \pi - (1-k)\alpha_1\lambda S - k\alpha_2\lambda S - \mu S \\
\frac{dL}{dt} &= (1-k)\alpha_1\lambda S - (\phi\alpha_3\lambda + \gamma)L - \mu L \\
\frac{dI}{dt} &= k\alpha_2\lambda S + (\phi\alpha_3\lambda + \gamma)L - (\upsilon + \mu + d)I + \alpha_4\lambda\omega R \\
\frac{dR}{dt} &= \upsilon I - \alpha_4\lambda\omega R - \mu R
\end{aligned}\right\} \tag{75}$$

With, $$\lambda = \beta c \frac{I}{N} \tag{76}$$

$S(t)$ Number of susceptible individuals at time t

$L(t)$ Number of exposed individuals at time t

$I(t)$ Number of infected individuals at time t

$R(t)$ Number of recovered individuals at time t

The disease-free equilibrium state for the model is given by

$$(S, L, I, R) = \left(\frac{\pi}{\mu}, 0, 0, 0\right) = E_0. \tag{77}$$

This represents the state in which there is no TB infection and is known as the disease-free equilibrium point.

$$F_i = \begin{pmatrix} (1-k)\alpha_1 \beta c \dfrac{I}{N} S \\ k\alpha_2 \beta c \dfrac{I}{N} S \\ 0 \\ 0 \end{pmatrix} \tag{78}$$

and

$$V_i = \begin{pmatrix} (\phi\alpha_3\lambda + \gamma)L + \mu L \\ -(\phi\alpha_3\lambda + \gamma)L - \alpha_4\lambda\omega R + (\upsilon + \mu + d)I \\ -\pi + (1-k)\alpha_1\lambda S + k\alpha_2\lambda S + \mu S \\ -\upsilon I + \alpha_4\lambda\omega R + \mu R \end{pmatrix} \tag{79}$$

We then obtain the partial derivatives of (78) and (79) with respect to (L, I) and by substituting the disease-free equilibrium point E_0 we get a 2×2 matrix since there are two infectious classes.

$$F = \begin{pmatrix} 0 & (1-k)\alpha_1 \beta c \dfrac{S}{N} \\ 0 & k\alpha_2 \beta c \dfrac{S}{N} \end{pmatrix} \tag{80}$$

and

$$V = \begin{pmatrix} (\gamma+\mu) & 0 \\ -\gamma & (\upsilon+\mu+d) \end{pmatrix} \tag{81}$$

Taking the inverse of (81) gives:

$$V^{-1} = \begin{pmatrix} \frac{1}{(\gamma+\mu)} & 0 \\ \frac{\gamma}{(\gamma+\mu)(\upsilon+\mu+d)} & \frac{1}{(\upsilon+\mu+d)} \end{pmatrix} \tag{82}$$

By computing the product of (80) and (82), we obtain

$$FV^{-1} = \begin{pmatrix} \frac{(1-k)\alpha_1 c\beta\gamma}{(\gamma+\mu)(\upsilon+\mu+d)} & \frac{(1-k)\alpha_1 c\beta}{(\upsilon+\mu+d)} \\ \frac{k\alpha_2 c\beta\gamma}{(\gamma+\mu)(\upsilon+\mu+d)} & \frac{k\alpha_2 c\beta}{(\upsilon+\mu+d)} \end{pmatrix} \tag{83}$$

From (83), we calculate the eigenvalues to determine the basic reproduction number, R_0 by taking the spectral radius (dominant eigenvalue) of the matrix FV^{-1}. This is computed by $|J-\lambda I| = 0$, hence the matrix becomes

$$\begin{vmatrix} \frac{(1-k)\alpha_1 c\beta\gamma}{(\gamma+\mu)(\upsilon+\mu+d)} - \lambda & \frac{(1-k)\alpha_1 c\beta}{(\upsilon+\mu+d)} \\ \frac{k\alpha_2 c\beta\gamma}{(\gamma+\mu)(\upsilon+\mu+d)} & \frac{k\alpha_2 c\beta}{(\upsilon+\mu+d)} - \lambda \end{vmatrix} = 0 \tag{84}$$

From (84), we obtain two eigenvalues, λ_1 and λ_2 which are given by

$$\lambda_1 = \frac{c\beta[\alpha_2 k(\gamma+\mu)+\alpha_1\gamma(1-k)]}{(\gamma+\mu)(\upsilon+\mu+d)} \tag{85}$$

and

$$\lambda_2 = 0 \tag{86}$$

Clearly, λ_1 is the dominant eigenvalue and therefore becomes the effective reproduction number R_{es} for the model. This is called the effective reproduction number because of the control parameters contained in the dominant eigenvalue.

5.0 Example 4 Vector-Host Model

In their research, Akinwande (2017) described the relationship between a population of humans and mosquitoes, with the human population represented as $S_h \to I_h \to S_h$ and the mosquito dynamics represented in $S_m \to I_m$ a model where S_h denotes susceptible humans, I_h is the human population that is infected, and S_M stands for both susceptible mosquitoes and I_M infected mosquitoes.

According to such a model, the mode of transmission occurs in each population in two stages:
Humans become infected (I_h) when they come into contact (i.e. λ_h, biting rate) with mosquitoes carrying the infection, which then spreads to other susceptible humans (S_h). When a susceptible mosquito (S_m) bites a human who is infected, it can spread the virus to other mosquitoes. Infected humans move into the removed compartment at a rate α and the removed compartment move to the susceptible compartment at a rate r. Additionally, we take into account that while infected humans die at a rate υ, mosquitoes and humans also have constant natural death rates w_h and w_m. Human and mosquito birth rates are b_h and b_m, respectively.

$$\dot{S}_h = b_h + rR_h - \lambda_h S_h I_m - w_h S_h \tag{87}$$

$$\dot{I}_h = \lambda_h S_h I_m - (w_h + \alpha + \upsilon) I_h \tag{88}$$

$$\dot{R}_h = \alpha I_h - (w_h + r) R_h \tag{89}$$

while that for mosquitoes is

$$\dot{S}_m = b_m - \lambda_m S_m I_h - w_m S_m \tag{90}$$

$$\dot{I}_m = \lambda_m S_m I_h - w_m I_m \tag{91}$$

with

$$T_h = S_h + I_h + R_h \tag{92}$$

$$T_m = S_m + I_m \tag{93}$$

The disease-free equilibrium state of the system (87) - (91) is:

$$x_0 = \left(\frac{b_h}{w_h}, 0, 0, \frac{b_m}{w_m}, 0 \right) \tag{94}$$

The Jacobian for system (87) - (91) for new infections and transfer from one compartment to another is provided by the next generation method as follows:

$$F_i = \begin{pmatrix} 0 \\ \lambda_h S_h I_m \\ 0 \\ 0 \\ \lambda_m S_m I_h \end{pmatrix} \tag{95}$$

and

$$V_i = \begin{pmatrix} w_h S_h - b_h - r R_h \\ (w_h + \alpha + \upsilon) I_h \\ (w_h + r) R_h - \alpha I_h \\ w_m S_m - b_m \\ w_m I_m \end{pmatrix} \tag{96}$$

Taking the partial derivatives with respect to I_h and I_m, and solving at the disease-free equilibrium produces

$$F = \begin{pmatrix} 0 & \lambda_h \\ \lambda_m & 0 \end{pmatrix} \tag{97}$$

and

$$V = \begin{pmatrix} (w_h + \alpha + \upsilon) & 0 \\ 0 & w_m \end{pmatrix} \tag{98}$$

The inverse of (98) yields

$$V^{-1} = \begin{pmatrix} \frac{1}{(w_h + \alpha + \upsilon)} & 0 \\ 0 & \frac{1}{w_m} \end{pmatrix} \tag{99}$$

The product of (97) and (99) gives

$$FV^{-1} = \begin{pmatrix} 0 & \frac{\lambda_h}{w_m} \\ \frac{\lambda_m}{(w_h + \alpha + \upsilon)} & 0 \end{pmatrix} \tag{100}$$

Next, we compute

$\left|FV^{-1} - \lambda I\right| = 0$ as

$$\begin{vmatrix} -\lambda & \frac{\lambda_h}{w_m} \\ \frac{\lambda_m}{(w_h + \alpha + \upsilon)} & -\lambda \end{vmatrix} = 0 \tag{101}$$

The evaluation of (101) gives

$$\lambda^2 - \frac{\lambda_m \lambda_h}{w_m (w_h + \alpha + \upsilon)} = 0 \tag{102}$$

From (102), we obtain the eigenvalues

$$\lambda = \pm \sqrt{\frac{\lambda_m \lambda_h}{w_m (w_h + \alpha + \upsilon)}} \tag{103}$$

From (103) we define our basic reproduction number, R_0 as the spectral radius (dominant eigenvalue) of the next generation matrix FV^{-1} since the basic reproduction number cannot be negative. Therefore

$$R_0 = + \sqrt{\frac{\lambda_m \lambda_h}{w_m (w_h + \alpha + \upsilon)}} \tag{104}$$

Interpretation and Analysis

$\frac{\lambda_h}{(w_h+\alpha+\upsilon)}$ represents the average number of newly infected humans that an infected mosquito spreads throughout the course of its infectivity from a population of humans that are only susceptible to the virus, and $\frac{1}{(w_h+\alpha+\upsilon)}$ is the average amount of time that each infected person spends prior to any kind of transfer. Also, $\frac{\lambda_m}{w_m}$ represents the quantity of infected mosquitoes that an infected human generates during its infectious period from a population of purely susceptible mosquitoes close to the DFE and $\frac{1}{w_m}$ is the average number of hours an infectious mosquito stays within the infectious chamber. The following scenarios will be taken into consideration for the system's stability:

(i) If $\lambda_m\lambda_h > w_m(w_h+\alpha+\upsilon) \Rightarrow R_0 > 1$, hence, the equilibrium is unstable, which implies that if a disease is introduced into the human and mosquito populations, it will persist.

(ii) If $\lambda_m\lambda_h < w_m(w_h+\alpha+\upsilon) \Rightarrow R_0 < 1$, thus there is stability in the equilibrium. In that case, the illness might not persist.

As a result, this provides guidance to the vector control and public health agencies regarding the efforts to be made to stop the disease's spread.

6.0 Example 5 - A COVID-19 Pandemic Mathematical Model

Akinwande *et al.* (2023) proposed a model on Covid-19 pandemic, the disease Free Equilibrium was computed, the effective reproduction number was calculated and the stability analysis of the DFE was performed. Below is the model formulation:

6.1 Model Formulation

By dividing the entire human population $N(t)$ at time t nine sub-populations of susceptible $S(t)$, first dose vaccinated $V_1(t)$, second dose vaccinated $V_2(t)$, latently infected $L(t)$, quarantined $Q(t)$, asymptomatic infectious $I_a(t)$, symptomatic infectious $I_s(t)$, hospitalized (isolated) $P(t)$ and removed $R(t)$. a model for the dynamics of COVID-19 transmission within a population in the presence of first and second doses of vaccination is fomulated.

Susceptible individuals are recruited at a constant rate Λ. The individuals in susceptible class are infected through contact with an infected person at the probability τ_1 and effective contact rate $\tau_1 c$ and moved to latent class. The individuals in first dose vaccinated class are infected through contact with an infected

person at the probability τ_2 and effective contact rate $\tau_2 c$ and moved to latent class. Also, the susceptible vaccinated individuals moved to first dose vaccinated class at vaccination rate ρ_1. First dose vaccinated individuals moved to second dose vaccinated class at vaccination rate ρ_2 after getting second dose of vaccine. First dose vaccinated individuals moved to susceptible class at waning rate ω. Second dose vaccinated individuals moved to removed class at progression rate ρ_3. People in latent class move to quarantine class and infected class at the quarantine rate θ and progression rate σ respectively. Some individuals in latent class recovered from the disease through natural immune and move to removed class at the recovery rate γ_1. The individual in quarantine class move to isolation class and removed class at the isolation rate ϕ_1 and recovery rate γ_2 respectively. The individuals in infected classes move to isolation class at the isolation rates ϕ_2 and ϕ_3. Those in isolation class are moved to the removed class at the recovery rate γ_3. Those in symptomatic infectious class and hospitalized (isolated) class can die due to COVID - 19 at disease-induced death rate δ_1 and δ_2 respectively. Those in symptomatic infectious class have reduced infectiousness compared to asymptomatic infectious class at the rates η.

The formulation of our model is guided by the following assumptions:

1. Individual in first dose vaccinated class can reverse back to susceptible class as a result of the waning of the vaccine.

2. There is permanent immunity after recovery.

3. While all infected classes are contagious, both hospitalized (isolated) and quarantined individuals have negligible contact rates and are therefore thought to be non-infectious under ideal (normal) conditions.

4. The risk of infection is further decreased with the second dosage.

5. Every individual has equal chance of contracting the disease.

The above description leads to the flow diagram in Figure 6.1.

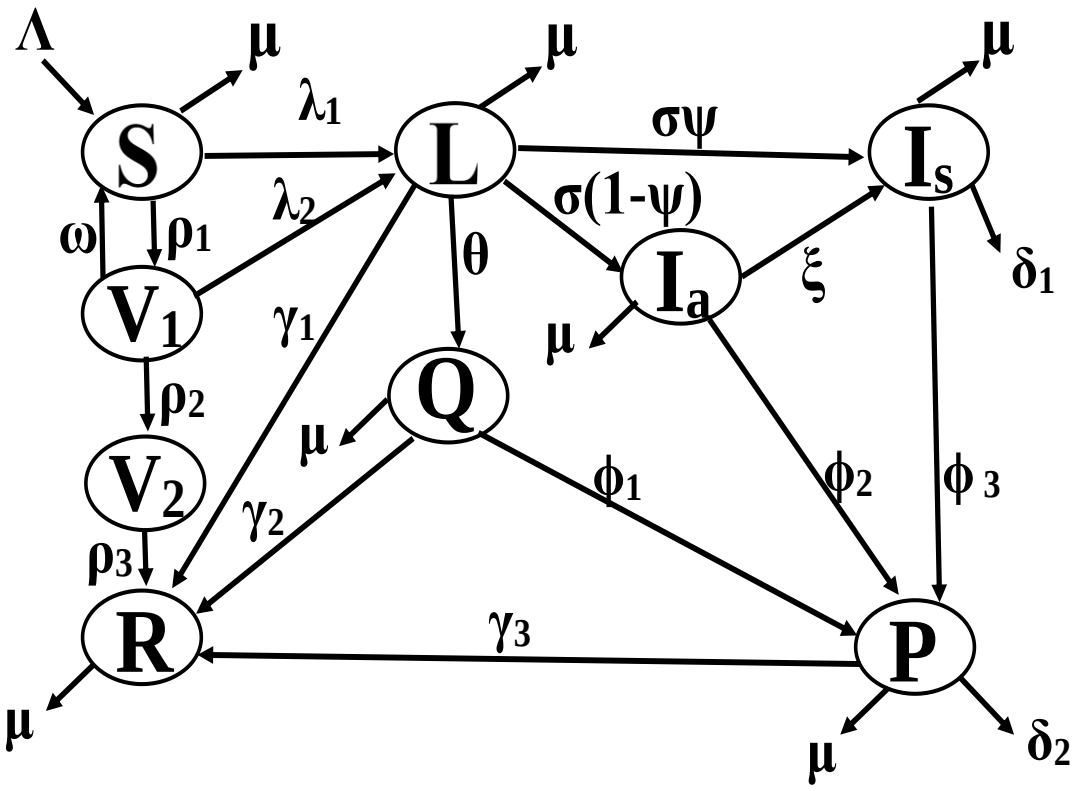

Figure 6.1: Flow diagram of COVID-19 dynamics

Using these definitions, assumptions and Figure 6.1 we arrive at the following non-linear system of equations that model the transmission dynamics and control of COVID-19 pandemic in a homogeneously mixing population:

$$\frac{dS}{dt} = \Lambda + \omega V_1 - \lambda_1 S - (\rho_1 + \mu)S \tag{105}$$

$$\frac{dV_1}{dt} = \rho_1 S - \lambda_2 V_1 - (\omega + \rho_2 + \mu)V_1 \tag{106}$$

$$\frac{dV_2}{dt} = \rho_2 V_1 - (\rho_3 + \mu)V_2 \tag{107}$$

$$\frac{dL}{dt} = \lambda_1 S + \lambda_2 V_1 - (\sigma + \theta + \gamma_1 + \mu)L \tag{108}$$

$$\frac{dQ}{dt} = \theta L - (\phi_1 + \gamma_2 + \mu)Q \tag{109}$$

$$\frac{dI_a}{dt} = \sigma(1-\psi)L - (\phi_2 + \xi + \mu)I_a \tag{110}$$

$$\frac{dI_s}{dt} = \sigma\psi L + \xi I_a - (\phi_3 + \delta_1 + \mu)I_s \tag{111}$$

$$\frac{dP}{dt} = \phi_1 Q + \phi_2 I_a + \phi_3 I_s - (\gamma_3 + \delta_2 + \mu)P \tag{112}$$

$$\frac{dR}{dt} = \rho_3 V_2 + \gamma_1 L + \gamma_2 Q + \gamma_3 P - \mu R \tag{113}$$

With initial conditions:

$$S(0) = S_0,\ V_1(0) = V_{10},\ V_2(0) = V_{20},\ L(0) = L_0,\ Q(0) = Q_0,\ I_a(0) = I_{a0},\ I_s(0) = I_{s0},\ P(0) = P_0,\ R(0) = R_0 \tag{114}$$

Movement out of the susceptible class, S into latently infected class, L occurs at a rate

$$\lambda_1 = \frac{\tau_1 c(1-\varepsilon\varphi)(I_a + \eta I_s)}{N} \tag{115}$$

Movement out of the first dose vaccinated class, V_1 into latently infected class, L occurs at a rate

$$\lambda_2 = \frac{\tau_2 c(1-\varepsilon\varphi)(I_a + \eta I_s)}{N} \tag{116}$$

where,

$$N(t) = S(t) + V_1(t) + V_2(t) + L(t) + Q(t) + I_a(t) + I_s(t) + P(t) + R(t) \tag{117}$$

The parameters and variables of the model indicated in Figure 6.1 are defined in Tables 6.1 and 6.2.

Table 6.1: Description of Variables

S/N	Variable	Description
1	S	Susceptible class.
2	V_1	First Dose Vaccinated class
3	V_2	Second Dose Vaccinated class
4	L	Latent class
5	Q	Quarantined class
6	I_a	Asymptomatic Infectious class
7	I_s	Symptomatic Infectious class.
8	P	Hospitalized (Isolated) class
9	R	Removed class
10	N	Total Population

Table 6.2: Description of Parameters

S/N	Parameters	Description
1	Λ	Constant recruitment into the population via birth or immigration
2	ρ_1	First Dose Vaccination rate
3	ρ_2	Second Dose Vaccination rate
4	ρ_3	Progression rate from V_2 to R
5	ω	Waning rate of first dose
6	μ	Natural death rate
7	δ_1	The disease-induced death rate of I_a.
8	δ_2	The disease-induced death rate of P.
9	τ_1	Covid-19 transmission probability per contact from S.
10	τ_2	Covid-19 transmission probability per contact from V_1.
11	c	Average contact rate, and thus $\beta = \pi c$ is the effective contact rate in the absence of any control measure.
12	ε	Efficacy of public enlightenment
13	φ	Rate of compliance to public enlightenment.
14	ϕ_1	Rate of hospitalization of L.

15	ϕ_2	Rate of hospitalization of I_a.
16	ϕ_3	Rate of hospitalization of I_s.
17	θ	Rate of quarantine L to Q
18	η	Modification parameter associated with reduced infectiousness of I_s compared to I_a.
19	σ	Progression rate of disease from L to I_a and I_s
20	ψ	Proportion of L that goes to I_s.
21	γ_1	Self- immune recovery of the L individuals
22	γ_2	Self- immune recovery of the Q individuals
23	γ_3	Recovery of P individuals due to treatment
24	ξ	Progression Rate from I_a to I_s

6.2 Disease Free Equilibrium (DFE)

The disease-free equilibrium of model system (105) – (116) is obtained by setting

$$\frac{dS}{dt}=\frac{dV_1}{dt}=\frac{dV_2}{dt}=\frac{dL}{dt}=\frac{dQ}{dt}=\frac{dI_a}{dt}=\frac{dI_s}{dt}=\frac{dP}{dt}=\frac{dR}{dt}=0, \tag{118}$$

and in the absence of disease, $L=Q=I_a=I_s=P=0$ and further simplification gives: $DFE(E_0)=(S^0,V_1^0,V_2^0,L^0,Q^0,I_a^0,I_s^0,P^0,R^0)=$

$$\left(\frac{\Lambda k_2}{k_1k_2-\rho_1\omega},\frac{\Lambda\rho_1}{k_1k_2-\rho_1\omega},\frac{\Lambda\rho_1\rho_2}{k_3(k_1k_2-\rho_1\omega)},0,0,0,0,\frac{\Lambda\rho_1\rho_2\rho_3}{\mu k_3(k_1k_2-\rho_1\omega)}\right) \tag{119}$$

where,

$$k_1=\rho_1+\mu,\quad k_2=\omega+\rho_2+\mu,\quad k_3=\rho_3+\mu$$

6.3 Computation of the Basic Reproduction Number, $\Re_0$

Since the infection components in this model are L, Q, I_a, I_s and P, then from (105) –(116)

$$F_i=\begin{pmatrix}\frac{c(1-\varepsilon\varphi)(I_a+\eta I_s)(\tau_1S+\tau_2V_1)}{N}\\0\\0\\0\\0\end{pmatrix} \tag{120}$$

Partial differentiation of F_i with respect to L, Q, I_a, I_s and P gives the new infection matrix

$$F = \begin{pmatrix} 0 & 0 & \frac{c(1-\varepsilon\varphi)(\tau_1 S^0 + \tau_2 V_1^0)}{N^0} & \frac{c(1-\varepsilon\varphi)\eta(\tau_1 S^0 + \tau_2 V_1^0)}{N^0} & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \end{pmatrix} \tag{121}$$

On the other hand,

$$V_i = \begin{pmatrix} (\sigma + \theta + \gamma_1 + \mu)L \\ -\theta L + (\phi_1 + \gamma_2 + \mu)Q \\ -\sigma(1-\psi)L + (\phi_2 + \xi + \mu)I_a \\ -\sigma\psi L - \xi I_a + (\phi_3 + \delta_1 + \mu)I_s \\ -\phi_1 Q - \phi_2 I_a - \phi_3 I_s + (\gamma_3 + \delta_2 + \mu)P \end{pmatrix} \tag{122}$$

Partial differentiation of V_i with respect to L, Q, I_a, I_s and P gives the transition matrix

$$V = \begin{pmatrix} k_4 & 0 & 0 & 0 & 0 \\ -\theta & k_5 & 0 & 0 & 0 \\ -\sigma(1-\psi) & 0 & k_6 & 0 & 0 \\ -\sigma\psi & 0 & -\xi & k_7 & 0 \\ 0 & -\phi_1 & -\phi_2 & -\phi_3 & k_8 \end{pmatrix} \tag{123}$$

It follows that

$$V^{-1} = \begin{pmatrix} \frac{1}{k_4} & 0 & 0 & 0 & 0 \\ A_3 & \frac{1}{k_5} & 0 & 0 & 0 \\ -A_4 & 0 & \frac{1}{k_6} & 0 & 0 \\ -A_5 & 0 & A_7 & \frac{1}{k_7} & 0 \\ -A_6 & A_8 & A_9 & A_{10} & \frac{1}{k_8} \end{pmatrix} \tag{124}$$

It follows that the next generation matrix is given by

$$FV^{-1} = \begin{pmatrix} -A_1A_4 - A_2A_5 & 0 & \frac{A_1}{k_6} + A_2A_7 & \frac{A_2}{k_7} & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \end{pmatrix} \tag{125}$$

Where,

$$k_4 = \sigma + \theta + \gamma_1 + \mu, \quad k_5 = \phi_1 + \gamma_2 + \mu, \quad k_6 = \phi_2 + \xi + \mu, \quad k_7 = \phi_3 + \delta_1 + \mu, \quad k_8 = \gamma_3 + \delta_2 + \mu$$

$$A_1 = \frac{c(1-\varepsilon\varphi)(\tau_1 S^0 + \tau_2 V_1^0)}{N^0}, \quad A_2 = \frac{c(1-\varepsilon\varphi)\eta(\tau_1 S^0 + \tau_2 V_1^0)}{N^0}, \quad A_3 = \frac{\theta}{k_4 k_5}, \quad A_4 = \frac{\sigma(\psi - 1)}{k_4 k_6},$$

$$A_5 = \frac{\sigma(\xi\psi - \psi k_6 - \xi)}{k_4 k_6 k_7}, \; A_6 = \frac{(\sigma\psi\xi k_5\phi_3 - \sigma\psi k_5 k_6\phi_3 + \sigma\psi k_5 k_7\phi_2 - \sigma\xi k_5\phi_3 - \sigma k_5 k_7\phi_2 - \theta k_6 k_7\phi_1)}{k_4 k_5 k_6 k_7 k_8},$$

$$A_7 = \frac{\xi}{k_6 k_7}, \qquad A_8 = \frac{\phi_1}{k_5 k_8}, \qquad A_9 = \frac{\phi_3\xi + \phi_2 k_7}{k_6 k_7 k_8}, \qquad A_{10} = \frac{\phi_3}{k_7 k_8}$$

The spectral radius for FV^{-1} gives the effective reproduction number (basic reproduction number with controls) denoted by $\Re_0^c$ which is given by

$$\Re_0^c = -A_1A_4 - A_2A_5 = \frac{c(1-\varepsilon\varphi)(\sigma k_7(1-\psi) + \sigma\eta(\xi(1-\psi) + k_6\psi))(\tau_1 S^0 + \tau_2 V_1^0)}{k_4 k_6 k_7 N^0} = \frac{c(1-\varepsilon\varphi)\sigma\mu(k_7(1-\psi) + \eta(\xi(1-\psi) + k_6\psi))(\tau_1 k_2 + \tau_2\rho_1)}{k_4 k_6 k_7(\mu(k_2 + \rho_1) + \rho_1\rho_2)} \tag{126}$$

which provides a measurement for the disease risk during COVID-19 transmission.

6.4 Local Asymptotic Stability of DFE

Theorem 4: The DFE, E_0 of the model equations (105) – (116) is locally asymptotically stable if R_0.

Proof: The stability of E_0 is established from the roots of the characteristic polynomial, which says that the equilibrium is stable if the roots of the characteristic polynomial are all negative. The Jacobian Matrix of equations (105) to (116) is given as:

$$J=\begin{bmatrix} -\lambda_1-k_1 & \omega & 0 & 0 & 0 & \frac{B_1S}{N} & \frac{B_2S}{N} & 0 & 0 \\ \rho_1 & -\lambda_2-k_2 & 0 & 0 & 0 & \frac{B_3V_1}{N} & \frac{B_4V_1}{N} & 0 & 0 \\ 0 & \rho_2 & -k_3 & 0 & 0 & 0 & 0 & 0 & 0 \\ \lambda_1 & \lambda_2 & 0 & -k_4 & 0 & \frac{B_1S}{N}+\frac{B_3V_1}{N} & \frac{B_2S}{N}+\frac{B_4V_1}{N} & 0 & 0 \\ 0 & 0 & 0 & \theta & -k_5 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & \sigma(1-\psi) & 0 & -k_6 & 0 & 0 & 0 \\ 0 & 0 & 0 & \sigma\psi & 0 & \xi & -k_7 & 0 & 0 \\ 0 & 0 & 0 & 0 & \phi_1 & \phi_2 & \phi_3 & -k_8 & 0 \\ 0 & 0 & \rho_2 & \gamma_1 & \gamma_2 & 0 & 0 & \gamma_3 & -\mu \end{bmatrix} \quad (127)$$

At DFE (127) becomes,

$$J(E_0)=\begin{bmatrix} -k_1 & \omega & 0 & 0 & 0 & B_1B_5 & B_2B_5 & 0 & 0 \\ \rho_1 & -k_2 & 0 & 0 & 0 & B_3B_6 & B_4B_6 & 0 & 0 \\ 0 & \rho_2 & -k_3 & 0 & 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & -k_4 & 0 & B_7 & B_8 & 0 & 0 \\ 0 & 0 & 0 & \theta & -k_5 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & \sigma(1-\psi) & 0 & -k_6 & 0 & 0 & 0 \\ 0 & 0 & 0 & \sigma\psi & 0 & \xi & -k_7 & 0 & 0 \\ 0 & 0 & 0 & 0 & \phi_1 & \phi_2 & \phi_3 & -k_8 & 0 \\ 0 & 0 & \rho_2 & \gamma_1 & \gamma_2 & 0 & 0 & \gamma_3 & -\mu \end{bmatrix} \quad (128)$$

Applying elementary row operation on (128) gives

$$\begin{bmatrix} -k_1 & \omega & 0 & 0 & 0 & B_1B_5 & B_2B_5 & 0 & 0 \\ 0 & B_9 & 0 & 0 & 0 & B_{10} & B_{11} & 0 & 0 \\ 0 & 0 & -k_3 & 0 & 0 & -B_{12} & -B_{13} & 0 & 0 \\ 0 & 0 & 0 & -k_4 & 0 & B_7 & B_8 & 0 & 0 \\ 0 & 0 & 0 & 0 & -k_5 & \dfrac{\theta B_7}{k_4} & \dfrac{\theta B_8}{k_4} & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & -B_{14} & \dfrac{\sigma(1-\psi)B_8}{k_4} & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & B_{15} & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & -k_8 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & -\mu \end{bmatrix} \tag{129}$$

where,

$$\left.\begin{aligned} &B_1 = \tau_1 c(1-\varepsilon\varphi), \quad B_2 = \tau_1 c\eta(1-\varepsilon\varphi), \quad B_3 = \tau_2 c(1-\varepsilon\varphi), \quad B_4 = \tau_2 c\eta(1-\varepsilon\varphi), \\ &N^0 = \frac{\Lambda k_2}{k_1k_2-\rho_1\omega} + \frac{\Lambda\rho_1}{k_1k_2-\rho_1\omega} + \frac{\Lambda\rho_1\rho_2}{k_3(k_1k_2-\rho_1\omega)} + \frac{\Lambda\rho_1\rho_2\rho_3}{\mu k_3(k_1k_2-\rho_1\omega)} = \frac{\Lambda(\mu A_{10}+\rho_1\rho_2)}{\mu(k_1k_2-\rho_1\omega)}, \\ &A_{10} = k_2+\rho_1, \quad B_5 = \frac{S^0}{N^0} = \frac{\mu k_2}{\mu A_{10}+\rho_1\rho_2}, \quad B_6 = \frac{V_1^0}{N^0} = \frac{\mu\rho_1}{\mu A_{10}+\rho_1\rho_2} \\ &B_7 = B_1B_5+B_3B_6, \quad B_8 = B_2B_5+B_4B_6, \quad B_9 = \frac{\rho_1\omega-k_1k_2}{k_1}, \quad B_{10} = \frac{k_1B_3B_6+\rho_1B_1B_5}{k_1}, \\ &B_{11} = \frac{k_1B_4B_6-\rho_1B_2B_5}{k_1}, \quad B_{12} = \frac{\rho_2(k_1B_3B_6+\rho_1B_1B_5)}{\rho_1\omega-k_1k_2}, \quad B_{13} = \frac{\rho_2(k_1B_4B_6-\rho_1B_2B_5)}{\rho_1\omega-k_1k_2}, \\ &B_{14} = \frac{k_4k_6-\sigma(1-\psi)B_7}{k_4}, \quad B_{15} = \frac{\xi\sigma(1-\psi)B_8+\sigma\psi k_6B_8-k_4k_6k_7+\sigma(1-\psi)k_7B_7}{k_4k_6-\sigma(1-\psi)B_7} \end{aligned}\right\} \tag{130}$$

The characteristic equation of (130) is given as

$$\begin{vmatrix} -k_1-\lambda & \omega & 0 & 0 & 0 & B_1B_5 & B_2B_5 & 0 & 0 \\ 0 & B_9-\lambda & 0 & 0 & 0 & B_{10} & B_{11} & 0 & 0 \\ 0 & 0 & -k_3-\lambda & 0 & 0 & -B_{12} & -B_{13} & 0 & 0 \\ 0 & 0 & 0 & -k_4-\lambda & 0 & B_7 & B_8 & 0 & 0 \\ 0 & 0 & 0 & 0 & -k_5-\lambda & \frac{\theta B_7}{k_4} & \frac{\theta B_8}{k_4} & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & -B_{14}-\lambda & \frac{\sigma(1-\psi)B_8}{k_4} & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & B_{15}-\lambda & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & -k_8-\lambda & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & -\mu-\lambda \end{vmatrix} = 0 \quad (131)$$

$$(-k_1-\lambda)(B_9-\lambda)(-k_3-\lambda)(-k_4-\lambda)(-k_5-\lambda)(-B_{14}-\lambda)(B_{15}-\lambda)(-k_8-\lambda)(-\mu-\lambda)=0 \quad (132)$$

$$\lambda_1=-k_1,\ \lambda_2=B_9,\lambda_3=-k_3,\ \lambda_4=-k_4,\ \lambda_5=-k_5,\ \lambda_6=-B_{14},\ \lambda_7=B_{15},\ \lambda_8=-k_8,\ \lambda_9=-\mu \quad (133)$$

It is observed from equation (133) that for the DFE to be stable λ_2 and λ_7 must be less than zero ($\lambda_2<0$ and $\lambda_7<0$) ;

This implies that,

$$\left.\begin{array}{l} \lambda_2<0 \\ B_9<0 \\ \dfrac{\rho_1\omega-k_1k_2}{k_1}<0 \\ \rho_1\omega-k_1k_2<0 \\ \rho_1\omega<k_1k_2 \\ \rho_1<\dfrac{k_1k_2}{\omega} \end{array}\right\} \quad (134)$$

From equation (134) the DFE will be stable if $\rho_1<\dfrac{\mu k_2}{\omega-k_2}$

$$\left.\begin{array}{l} \lambda_7<0 \\ B_{15}<0 \\ \dfrac{\xi\sigma(1-\psi)B_8+\sigma\psi k_6B_8-k_4k_6k_7+\sigma(1-\psi)k_7B_7}{k_4k_6-\sigma(1-\psi)B_7}<0 \\ \xi\sigma(1-\psi)B_8+\sigma\psi k_6B_8-k_4k_6k_7+\sigma(1-\psi)k_7B_7<0 \\ \xi\sigma(1-\psi)B_8+\sigma\psi k_6B_8+\sigma(1-\psi)k_7B_7<k_4k_6k_7 \end{array}\right\} \quad (135)$$

Divide (135.5.28) $k_4k_6k_7$ gives

$$\frac{\xi\sigma(1-\psi)B_8+\sigma\psi k_6B_8+\sigma(1-\psi)k_7B_7}{k_4k_6k_7}<1 \tag{136}$$

The Left Hand Side of (134) is equivalent to the Right Hand Side of (127). Hence,

$$R_0<1 \tag{137}$$

Therefore, the DFE is locally asymptotically stable if $\rho_1<\frac{\mu k_2}{\omega-k_2}$ and $R_0<1$.

7.0 Concluding Remarks

We have presented a discourse on the methods of computation of basic reproduction number which is one of the fundamental concepts in mathematical biology that is used to analyze the stability of Disease Free Equilibrium state. The note will be of great assistance to researchers in epidemiological modelling.

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