J. DIFERENSIAL/E-ISSN:2775-9644
Vol.6(1),2024, 65–77
doi:https://doi.org/10.35508/jd.v6i1.12293

RESEARCH ARTICLE

On the Numerical Simulation of the Effect of Disease Transmission Coefficient on SEIR Epidemic Model Using Hybrid Block Method

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Received: 08 August 2023; Revised: 30 August 2023; Accepted: 16 October 2023; Published:09 February 2024.

Abstract: This work contains the study, analysis, and solution of a SEIR epidemic model. An effective hybrid block method was used in the solution of the system of linear differential equations to investigate the effect of transmission coefficient on the SEIR model with a permanent immunity. Numerical simulation of the included control parameters are carried out. The obtained results and outcomes are presented graphically.

Keywords: Epidemic Model, Basic Reproduction Number, Local Stability, Global Stability, Disease Transmission Coefficient, Hybrid Block Method.

1. Introduction

In recent times, the attention of scientists has been drawn to the SEIR model due to their naturally occurrence and repeatedly in physical models. The most important concepts of epidemic models can be demonstrated using the SEIR model by [1]. The model considered is formulated by Olayiwola & Kolawole (2019) to induce and as a good strategic cure for total eradication of the disease. The set of individuals who are vaccinated do not move to the infected mode. Dynamically, modeling of human and its daily challenges over time in all areas of social, cultural, physical, science, and engineering can be formulated with mathematical equation in [2]. Several vaccination strategies for infectious disease has been formulated by modelers across board to proffer solutions to infectious diseases based on the population understudy in [3]. Models are subjected to fractals as susceptible $S(t)$ individuals, exposed $E(t)$ individuals, infected individuals and population of those that have recovered $R(t)$. An SEIR model can represent human infectious disease such as Marburg, smallpox, typhoid, measles, and cholera by [4]. A generic model of SEIR focusing on immunity from the infectious disease under focus. Saturation term takes a vital role in determining the course of spread of a disease, the threshold which governs the model formulated take a junk of the disease trajectory. The focus of our research is an optimal control proposed by [5]. Several researchers have worked on the impact of saturation term as a tool to controlling the spread and eradication of disease, as studied by considering saturation term for susceptible individuals of an SEIR epidemic model analysing the impact of saturation term on the incidence rate whose result revealed that it's a proper and effective

strategy to eradicate the infectious disease by [6]. The infection of human by vectors and human to adhere to restricted domains are crucial to avoid the rapid spread of the disease solely to evaluate the impact of each factors of spread of covid-19 through sensitization by health professionals. Their research reveals that saturation term helps in reducing the prevalence of malaria in [7–9]. To solve an EIAV infection, their results revealed how prominent the method of resolving double fractal nonlinear differential equations by [10]. SEIR varying time-population said to analyze and determine the equilibrium points and its correspondence stability at equilibrium points by [11–14]. The subclass of and SIR model focus on the implementation that the delay in the latency time rate which is the time required for an infected individual to migrate to being infectious in [15]. The research of an SVEIR, they explore the spontaneous predator-host disease with a saturated treatment function, which is the proper and effective control measure to eradicate the disease in [16]. Effects of saturation term on corona virus SIR model with the law of mass action in its application as a control was studied in [10]. This paper explore the effect of saturation term as a control policy to proffer total immunity against typhoid disease, the numerical simulation result reveals that plays a vital role in the eradication of the disease.

2. Materials and method

2.1. Description and model formulation

A set of an ordinary differential equations illustrating proposed mathematical model by Olayiwola et al :
Existing model

$$\begin{aligned} S^* &= \Lambda - \frac{\beta SI}{1+m_1S+m_2I} - \mu S + \delta R \\ E^* &= \frac{\beta SI}{1+m_1S+m_2I} - (\mu+\epsilon)E \\ I^* &= \epsilon E - (\mu+\gamma+\delta)I \\ R^* &= \gamma I - (\mu+\delta)R \end{aligned} \tag{2.1}$$

Subjected to $\delta = 0$ and $d = 0$ gives the proposed model in Equation 2.2.
Modified Model
A compartmental based mathematical model for analyzing the spontaneity of an epidemic disease to investigate the effect of transmission coefficient on the SEIR model with a permanent immunity. Total population of $N(t)$, subclass of susceptible $S(t)$, exposed $E(t)$, infected $I(t)$, and the recovered individuals $R(t)$. Govern model expressed with the state variables and study parameters as illustrated below:

$$\begin{aligned} S^* &= \Lambda - \frac{\beta SI}{1+m_1S+m_2I} - \mu S \\ E^* &= \frac{\beta SI}{1+m_1S+m_2I} - (\mu+\epsilon)E \\ I^* &= \epsilon E - (\mu+\gamma)I \\ R^* &= \gamma I - \mu R \end{aligned} \tag{2.2}$$

Subject to the following initial conditions $S(0) = S_0, E(0) = e_0, I(0) = i_0, R(0) = r_0$.

2.2. Existence Model

Consider the compartment of model formulation as obtained, we have;

$$\Gamma = \left\{ S(t), E(t), I(t), R(t) \in \mathcal{R}_+^4 : N \leq \frac{\Lambda}{\mu} \right\} \tag{2.3}$$

The derivative is obtained as;

$$\begin{aligned}
N^* &= \frac{d}{dt}(S(t)+E(t)+I(t)+R(t)) \\
N^* &= (S^*+E^*+I^*+R^*) \\
N^* &= [\Delta - \frac{\beta SI}{1+m_1S+m_2I} - \mu S + \frac{\beta SI}{1+m_1S+m_2I} - (\mu+\epsilon)E + \epsilon E - (\mu+\gamma)I + \gamma I - \mu R] \\
N^* &= \Delta - \mu(S+E+I+R) \\
N^* &\leq \Lambda - \mu N \\
N(t)l^{\mu t} &= \frac{\Lambda}{\mu}l^{\mu t} + C, \text{ as } C \text{ is a constant of integration} \\
N(t) &= \frac{\Lambda}{\mu} + Cl^{-\mu t}, \text{ by the initial condition at } t=0 \\
C &\leq N(0) - \frac{\Lambda}{\mu}
\end{aligned} \tag{2.4}$$

Taking the initial t and $N(t)$ such that;

$$\lim_{t\to\infty} N(t) \leq \lim_{t\to\infty}\left[\frac{\Delta}{\mu} + \left(N(0) - \frac{\Lambda}{\mu}\right)l^{-\mu t}\right] = \frac{\Lambda}{\mu} \tag{2.5}$$

If $N(0) \leq \frac{\Lambda}{\mu}$, then $N(t) \leq \frac{\Lambda}{\mu}$. It is hereby concluded that considering the dynamics of the model in the domain $\mathcal{R}^4_+$. It can be considered to be well posed. However, the non-negativity the model formulation migrates to be feasible region, Γ which is a positively invariant set.

2.3. Positivity of the Model

Theorem 2.1. *If $\Psi = \{S,E,I,R \in \mathcal{R}^4_+ : S_0 > 0, E_0 > 0, I_0 > 0, R_0 > 0\}$ at $t > 0$ the solutions of (S,E,I,R) is positively invariant.*

Proof.

$$\begin{aligned}
S^* &= \Lambda - \frac{\beta SI}{1+m_1S+m_2I} - \mu S(t) \\
S^* &\geq -\mu S(t) \\
\int \frac{S^*}{S(t)} &\geq -\mu \int dt \\
S(t) &\geq S_0 e^{-\mu t} > 0
\end{aligned} \tag{2.6}$$

$$\begin{aligned}
E^* &= \frac{\beta SI}{1+m_1S+m_2I} - (\mu+\epsilon)E(t) \\
E^* &\geq -(\mu+\epsilon)E(t) \\
\int \frac{E^*}{E(t)} &\geq (\mu+\epsilon)\int dt \\
E(t) &\geq E_0 e^{-(\mu+\epsilon)t} > 0
\end{aligned} \tag{2.7}$$

$$\begin{aligned}
I^* &= \epsilon E - (\mu+\gamma)I \\
I^* &\geq -(\mu+\gamma)I(t) \\
\int \frac{I^*}{I(t)} &\geq -(\mu+\gamma)\int dt \\
I(t) &\geq I_0 e^{-(\mu+\gamma)t} > 0
\end{aligned} \tag{2.8}$$

$$\begin{aligned} R^* &= \gamma I - \mu R(t) \\ R^* &\geq -\mu R(t) \\ int\frac{R^*}{R(t)} &\geq -\mu \int dt \\ R(t) &\geq R_0 e^{-\mu t} > 0 \end{aligned} \tag{2.9}$$

□

The partial derivatives of these functions exist and are continuous and bounded, therefore, Equation 3.10 exists and has a unique solution, therefore is well-posed in $\mathcal{R}^4$.

3. Model Analysis

3.1. Existence of disease free equilibrium state

At disease free equilibrium point, there is no outbreak of disease.

$$S^* = E^* = I^* = R^* = 0$$

As obtained, $\Lambda - \frac{\beta SI}{1+m_1S+m_2I} - \mu S = 0$, $\Lambda = \mu S$, $S_0 = \frac{\Lambda}{\mu}$. The Disease Free Equilibrium (DFE) $E_1 = (S_0, E_0, I_0, R_0)$ where $S_0 \neq 0, I = 0$ is

$$E_1 = \left(\frac{\Lambda}{\mu}, 0, 0, 0\right) \tag{3.10}$$

3.2. Endemic equilibrium point

Let $E_e = (S^*, E^*, I^*, R^*)$ as endemic equilibrium where $I \neq 0$. Model Equation 2.1 at equilibrium point as:

$$\begin{aligned} \Lambda - \frac{\beta S^* I^*}{1 + m_1 S^* + m_2 I^*} - \mu S^* &= 0 \\ \frac{\beta S^* I^*}{1 + m_1 S^* + m_2 I^*} - (\mu + \epsilon) E^* &= 0 \\ \epsilon E^* - (\mu + \gamma) I^* &= 0 \\ \gamma I^* - \sum R^* &= 0 \end{aligned} \tag{3.11}$$

$$\begin{aligned} \Lambda - \mu S^* &= (\mu + \epsilon) E^* \\ I^* &= \frac{\epsilon E^*}{\mu + \gamma} \end{aligned} \tag{3.12}$$

Also from the Equation 2.4, we obtain that $\beta S^* I^* = \lfloor 1 + m_1 S^* + m_2 I^* \rfloor (\mu + \epsilon) E^*$

$$\begin{aligned} \frac{\beta S^* E^* \epsilon}{(\mu + \gamma)} &= \left[1 + m_1 S^* + m_2 \frac{\epsilon E^*}{(\mu + \gamma}\right] (\mu + \epsilon) E^* \\ \beta S^* \epsilon &= (\mu + \epsilon)(\mu + \gamma) \left[1 + m_1 S^* + m_2 \frac{\epsilon E^*}{(\mu + \gamma}\right] \\ \beta S^* \epsilon &= (\mu + \epsilon)(\mu + \gamma) + (\mu + \epsilon)(\mu + \gamma) m_1 S^* + m_2 \epsilon E^* (\mu + \epsilon) \\ S^* \left[\beta\epsilon - (\mu + \epsilon)(\mu + \gamma) m_1\right] &= (\mu + \epsilon)(\mu + \gamma) + m_2 \epsilon E^* (\mu + \epsilon) \\ S^* &= \frac{(\mu + \epsilon)((\mu + \gamma) + m_2 \epsilon E^*)}{[\beta\epsilon - (\mu + \epsilon)(\mu + \gamma) m_1]} \end{aligned} \tag{3.13}$$

$$
\begin{aligned}
E^* &= \frac{\Lambda - \mu S^*}{\mu + \epsilon} \\
R^* &= \frac{\epsilon\gamma E^*}{\mu(\mu+\gamma)} \\
R^* &= \frac{\gamma\epsilon}{\mu(\mu+\gamma)}\left[\frac{\Lambda - \mu(\mu+\epsilon)(\mu+\gamma+m_2\epsilon E^*)}{(\mu+\epsilon)(\beta\epsilon)(\beta\epsilon - m_1(\mu+\epsilon)(\mu+\gamma))}\right]
\end{aligned} \tag{3.14}
$$

3.3. The basic reproductive ratio

The spread of the disease is tantamount to an infectious individual who communicate this within the populace. The threshold as the govern factor for its spread R_0 . This is obtained considering its feasibility via next generation as the transmission and transition matrix of the model formulation is resolved.

$$
\begin{aligned}
E^* &= \frac{\beta SI}{1 + m_1 S + m_2 I} - (\mu+\epsilon)E \\
I^* &= \epsilon E - (\mu+\gamma)I
\end{aligned} \tag{3.15}
$$

$R_0 = G = \rho(F \times V^{-1})$, from equilibrium $S_0 = \frac{\Lambda}{\mu}$, transition & transmission matrix obtained from the partial derivatives with respect to the disease classes evaluated at the disease free equilibrium E_1.

$$
F_i = \left(\frac{\partial f_i(x_i)}{\partial x_j}\right), V_i = \left(\frac{\partial v_i(x_i)}{\partial x_j}\right), i, j = 1, 2, \ldots, n, \ \forall n < \infty \tag{3.16}
$$

$$
\begin{aligned}
f &= \begin{pmatrix} \frac{betaSI}{1+m_1S+m_2I} \\ 0 \end{pmatrix}, v = \begin{pmatrix} (\mu+\epsilon)E \\ -\epsilon E` + (\mu+\gamma)I \end{pmatrix} \\
F &= \begin{pmatrix} \frac{\beta S_0}{m_2} & 0 \\ 0 & 0 \end{pmatrix}, V = \begin{pmatrix} (\mu+\epsilon) & 0 \\ -\epsilon & (\mu+\gamma) \end{pmatrix}
\end{aligned} \tag{3.17}
$$

As $\det(V) = (\mu+\epsilon)(\mu+\gamma)$, $V^{-1} = \begin{pmatrix} \frac{1}{(\mu+\epsilon)} & \frac{\epsilon}{(\mu+\epsilon)(\mu+\gamma)} \\ 0 & \frac{1}{(\mu+\gamma)} \end{pmatrix}$. Since $R_0 = G = \rho(F \times V^{-1})$

$$
R_0 = \begin{pmatrix} \frac{\beta S_0}{m_2} & 0 \\ 0 & 0 \end{pmatrix} \begin{pmatrix} \frac{1}{(\mu+\epsilon)} & \frac{epsilon}{(\mu+\epsilon)(\mu+\gamma)} \\ 0 & \frac{1}{(\mu+\gamma)} \end{pmatrix} \tag{3.18}
$$

The dominant Eigenvalue is the Basic Reproduction Number.

4. Stability of Disease Free Equilibrium

4.1. Local stability

The model representation for typhoid as above locally asymptotically stable if $R_o < 1$, vice versa whenever $R_o > 1$. at equilibrium $E_1 = \left(\frac{\Lambda}{\mu}, 0, 0, 0, 0\right)$ taking Jacobian matrix with the characteristic equation of $|J_{E_1} - \gamma_i I| = 0$ as γ_1 and I are the Eigenvalues and identity matrix respectively. Where $i = 1, 2, 3, 4$.
Therefore:

$$
J_{E_1} = \begin{vmatrix} -\nu & 0 & -\frac{\beta S_0}{m_2} & 0 \\ 0 & -(\nu+\epsilon) & \frac{\beta S_0}{m_2} & 0 \\ 0 & \epsilon & -(\nu+\gamma & 0 \\ 0 & 0 & \gamma & -\nu \end{vmatrix}
$$

$$J_{E_1} = \begin{vmatrix} -\nu & 0 & -\frac{\beta\lambda}{\mu m_2} & 0 \\ 0 & -(\nu+\epsilon) & \frac{\beta\lambda}{\mu m_2} & 0 \\ 0 & \epsilon & -(\nu+\gamma & 0 \\ 0 & 0 & \gamma & -\nu \end{vmatrix} \tag{4.19}$$

then, determining the eigenvalues,
$|J_{E_1} - \lambda_i I| = 0$

$$\begin{vmatrix} -\nu-\lambda 1 & 0 & -\frac{\beta\Lambda}{\nu m_2} & 0 \\ 0 & -(\nu+\epsilon)-\lambda_2 & \frac{\beta\Lambda}{\nu m_2} & 0 \\ 0 & \epsilon & -(\nu+\lambda-\lambda_3 & 0 \\ 0 & 0 & \lambda & -\nu-\lambda 4 \end{vmatrix} = 0 \tag{4.20}$$

$\lambda_1 = -\mu, \lambda_4 = -\mu$

$$\begin{vmatrix} -(\mu+\varepsilon)-\lambda & \frac{\beta\Lambda}{\mu m_2} \\ \varepsilon & (\mu+\nu)-\lambda \end{vmatrix}$$

$\lambda^2 - [(\mu+\nu)(\mu+\varepsilon]\lambda + \left|\lambda+\varepsilon)(\mu+\nu)\frac{\beta\Lambda}{\mu m_2}\right| = 0$

By Descartes rule of sign, the non-negative roots obtained which are negatively invariant; therefore they are locally asymptotically stable.

4.2. Stability of Endemic Equilibrium Point.

At equilibrium of the proposed model is said to be locally asymptotically stable if $R_0 < 1$.
Let $S = a + S*, E = b + E*, I = c + I*, R = d +^R *$. From system of equation below,

$$\begin{aligned} S^*\Lambda - \frac{\beta SI}{1+m_1S+m_2I} - (\mu\varepsilon) \\ E^* = \frac{\beta SI}{1+m_1S+m_2I} - (\mu+\varepsilon)E \\ I^* = \varepsilon E - (\mu+\lambda)I \\ R^* = \lambda I - \mu R \end{aligned} \tag{4.21}$$

By linearization, substituting to the above equation;

$$\begin{aligned} a^* &= \Lambda - \beta(a+S^*)(c+I^*)[1+m_1(a+S^*)+m_2(c+I^*)]^{-1} - \mu(a+S^*) \\ b^* &= \beta(a+S^*)(c+I^*)[1+m_1(a+S^*)+m_2(c+I^*)]^* - (\mu+\varepsilon)(b+E^*) \\ c^* &= \varepsilon(b+E^*) - (\mu+\gamma)(c+I^* \\ d^* &= \gamma(c+I^*) - \mu(d+R^*) \end{aligned} \tag{4.22}$$

Therefore,

$$\begin{aligned} a^* &= \beta az[1+m_1x+m_2z]^{-1} - \mu a + higherorder + non-linear \\ b^* &= \beta az[a+m_1a+m_2z]^{-1} - (\mu+\varepsilon)b + higherorder + non-linear \\ c^* &= \varepsilon b - (\mu+\gamma)x + higherorder + non-linear \\ d^* &= \gamma c - \mu d + higherorder + non-linear \end{aligned} \tag{4.23}$$

$$\begin{vmatrix} -\frac{\beta c+\mu}{m_1} & 0 & -\frac{\beta a}{m_2} & 0 \\ \frac{\beta c+\mu}{m_1} & -(\mu+\varepsilon) & \frac{\beta a}{m_2} & 0 \\ 0 & \varepsilon & -(\mu+\gamma) & 0 \\ 0 & 0 & \gamma & -\mu \end{vmatrix} \tag{4.24}$$

Characteristic equation of $|J_{E_1} - \lambda_i I| = 0$

$$\begin{vmatrix} -\frac{(\beta z+\mu}{m_1} - \lambda & 0 & -\frac{\beta x}{m_2} & 0 \\ \frac{(\beta z+\mu}{m_1} & -(\mu+\epsilon) - \lambda & \frac{\beta x}{m_2} & 0 \\ 0 & \epsilon & -(\mu+\gamma) - \lambda & 0 \\ 0 & 0 & \gamma & -\mu - \lambda \end{vmatrix} \tag{4.25}$$

The resulting Eigen-value become,

$$(\frac{(\beta z+\mu)}{m_1} - \lambda)(-(\mu+\epsilon-\lambda)(-(\mu+\gamma) - \lambda)(-\mu - \lambda = 0 \tag{4.26}$$

Let $u = -\frac{(\beta z+\mu}{m_1}, v = -(\mu+\epsilon), w = -(\mu+\gamma), x = -\mu$
$(u-\lambda)(v-\lambda)(w-\lambda)(x-\lambda) = 0$

$$\lambda^4 - [(u+v) = (w+x]\lambda^3 + [(u+v)(w+x) + uv + wx]\lambda^2 - [uv(w+x) + wx(u+v)]\lambda + uvwx = 0 \tag{4.27}$$

Therefore, they are Locally Asymptotically Stable.

4.3. Global stability

Consider that Lyapunov function in the neighborhood of zero. However, $v(x_1, x_2) = v > 0, \forall x_1, x_2 > 0$, ,global asymptotic stability of the proposed model in the region $\Re^2$, with respect to time, at equilibrium state via Lyapunov algorithm is obtained;

$$\omega = \{E(t), I(t), \in \Re^2; N \leq \frac{\Lambda}{\mu}\} \tag{4.28}$$

$V(t, E, I) = C_1 I_1 + C_2 I_2$
$\frac{dV}{dt} = C_1 I_1^* + C_2 I_2^*$
$V^* = C_1 \left[\frac{\beta S_0 I_2}{1+m_1 S_0+m_2 I_2} - \mu + \epsilon)I_1\right] + C_2[\epsilon I_1 - (\mu+\gamma)I_2]$
$= C_1 \frac{\beta S_0 I_2}{1+m_1 S_0+m_2 I_2} - C_1 - \mu + \epsilon)I_1 + C_2\epsilon I_1 - C_2(\mu+\gamma)I_2$

$$V^* \leq [C_2\epsilon - C_1(\mu+\epsilon)]I_1 + \left[C - 1\frac{\beta S_0}{1+m_1 S_0+m_2} - C_2(\mu+\gamma\right] I \tag{4.29}$$

$V^* \leq [C_2\epsilon - C_1(\mu+\epsilon)]I_1 + \left[C - 1\frac{\beta S_0}{1+m_1 S_0+m_2} - C_2(\mu+\gamma\right] I_2 \leq N, S$

$$As\ \ 1 + m_1 S_0 \leq S_0 = \frac{\Lambda}{\mu},\ \ Let\ \ C_1 = \frac{1}{\mu+\epsilon}, C_2 = \frac{\beta\Lambda}{\mu m_2(\mu+\epsilon)(\mu+\gamma)}) \tag{4.30}$$

$\leq \left[\frac{\beta\epsilon\Lambda}{\mu m_2 9(\mu+\epsilon)(\mu+\gamma} - \frac{(\mu+\epsilon)}{\mu+\epsilon}\right] I_1 + \left[\frac{\beta\Lambda}{\mu m_2(\mu+\epsilon)} - \frac{\beta\Lambda(\mu+\gamma)}{\mu m_2(\mu+\epsilon)(\mu+\gamma)}\right] I_2$
$v^* \leq \left[\frac{\beta\epsilon\Lambda}{\mu m_2(\mu+\epsilon)(\mu+\gamma)}\right] I_1$

$$V^* \leq [R_0 - 1]I \tag{4.31}$$

Imperatively to note that $V^* = 0$ only at any outbreak of infection beyond the domain, at equilibrium and at $t \to \infty$. As postulated by LaSalle's invariance whenever $E_0 = 0$ is said to be globally asymptotically stable whenever $R_0 > 1$.

4.4. Sensitivity Analysis on R_o

The sensitivity indices of R_o is obtained via partial differentiating with respect to all the parameters in R_o. The normalized forward sensitivity index is defined: As $R_0 = \frac{\beta\epsilon\Lambda}{\nu m_2(\nu+\epsilon)(\nu+\gamma)}$

$$\begin{aligned}
\frac{\partial R_0}{\partial \mu} &= \frac{\beta\epsilon\Lambda}{m_2\epsilon\gamma}.\frac{\mu\mu m_2(\mu+\epsilon)(\mu+\gamma)}{\beta\epsilon\Lambda} = \frac{\mu^2(\mu+\epsilon)(\mu+\gamma)}{\epsilon\gamma} \\
\frac{\partial R_0}{\partial \beta} &= \frac{\epsilon\Lambda}{\mu m_2(\mu+\epsilon)(\mu+\gamma)}.\frac{\beta\mu_2(\mu+\epsilon)(\mu+\gamma}{\Lambda\epsilon\beta} = 1 \\
\frac{\partial R_0}{\partial \Lambda} &= \frac{\beta\epsilon}{\mu m_2(\mu+\epsilon)(\mu+\gamma)}.\frac{\Lambda\mu_2(\mu+\epsilon)(\mu+\gamma)}{\Lambda\epsilon\beta} = 1 \\
\frac{\partial R_0}{\partial \epsilon} &= \frac{\beta\Lambda}{\mu^2 m_2(\mu+\gamma)}.\frac{\epsilon\mu_2(\mu+\epsilon)(\mu+\gamma)}{\Lambda\epsilon\beta} = \frac{(\mu+\epsilon)}{\mu} \\
\frac{\partial R_0}{\partial \gamma} &= \frac{\beta\epsilon\Lambda}{\mu^2 m_2(\mu+\gamma)}.\frac{\gamma\mu_2(\mu+\epsilon)(\mu+\gamma)}{\Lambda\epsilon\beta} = \frac{\gamma(\mu+\gamma)}{\mu} \\
\frac{\partial R_0}{\partial m_2} &= \frac{\beta\epsilon\Lambda}{\mu(\mu+\epsilon)(\mu+\gamma)}.\frac{\mu(m_2)^2(\mu+\epsilon)(\mu\gamma}{\Lambda\epsilon\beta} = m_2^2
\end{aligned} \tag{4.32}$$

The parameter and indices of sensitivity analysis is deduced from the initial values of the said parameters

Table 4.1: Description, symbols, values, and sources

Parameters and description	**Symbol**	**Values**	**Sources**
$S(t)$ Time-dependent number of susceptible humans	$S_0(t)$	15	Assumed
$E(t)$ Time-dependent number of exposed humans	$E_0(t)$	10	Assumed
$I(t)$ Time-dependent number of infected humans	$I_0(t)$	13	Assumed
$R(t)$ Time-dependent number of recovered humans	$R_0(t)$	11	Assumed
Rate of migration to susceptible	ϵ	0.25	Assumed
Natural death rate	μ	0.3	Assumed
Recruitment rate of individuals	Λ	49	Assumed
Recovery rate from infected individuals	γ	0.1	Assumed
Recovery rate to Susceptible class	m_1	0.1	Assumed
Recovery rate from Infected class	m_2	0.2	Assumed
Successful contact rate	β	1.0	Assumed

Parameter values of the model result,

Table 4.2: Sensitivity Indices on R_0

S/N	**Parameters**	**Sensitivity Indices**
$\frac{\partial R_0}{\partial \mu}$	$\frac{\mu^2(\mu+\epsilon)(\mu+\gamma)}{\epsilon\gamma}$	0.79200
$\frac{\partial R_0}{\partial \beta}$	1	1.00000
$\frac{\partial R_0}{\partial \Lambda}$	1	1.00000
$\frac{\partial R_0}{\partial \gamma}$	$\frac{\gamma(\mu+\gamma)}{\mu}$	0.13333
$\frac{\partial R_0}{\partial \epsilon}$	$\frac{(\mu+\epsilon)}{\mu}$	1.83333
$\frac{\partial R_0}{\partial m_2}$	m_2^2	0.04000

5. Numerical simulation

In numerical analysis, numerical block methods are a class of algorithms used to approximate solutions to differential equations (DEs). The term "block" refers to the idea of combining two or more methods to solving a problem. These set of methods work as a unit method which are essentially useful when the equations are complex or when traditional numerical techniques like explicit or implicit methods become computationally expensive or unstable. The combination of these methods gives rise to a computationally stable and efficient method. The term hybrid refers to the division of the region of the problem into sub-regions, thereby creating an instance in which the fractional (hybrid) step points are considered. This also improves the accuracy of the method. The basic concept of numerical block methods involves the following steps:

Problem Decomposition: The first step is to decompose the original problem into a set of smaller sub-problems or blocks. These blocks can be either spatial or temporal regions, depending on the nature of the problem.

Selection of Numerical Methods: Once the blocks are defined, different numerical methods can be selected to solve each block efficiently. The choice of methods can vary depending on the characteristics of the specific block and the overall problem.

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Coupling Strategy: After solving each block independently, a coupling strategy is used to integrate the solutions and ensure consistency across the entire problem domain. This step is essential as it determines how the solutions from different blocks interact and influence each other.

Stability and Accuracy Analysis: Like any numerical method, stability and accuracy are crucial considerations. The stability of the method depends on the stability properties of the chosen numerical methods for each block, as well as the coupling strategy used. The overall accuracy of the method is affected by the accuracy of individual block solutions and the coupling scheme.

Implementation and Efficiency: Once the numerical hybrid block method is designed, it needs to be implemented using appropriate programming techniques to solve the original problem effectively. Efficiency and computational cost are also essential factors to consider.

Numerical hybrid block methods can be particularly advantageous in problems where the equations have distinct features or behaviors in different regions of the domain, as they allow for specialized treatment in each block. They can lead to faster computations and increased stability, especially for large-scale problems.

The method for solving the problem in differential equation defined by;

$$\frac{dy(t)}{dt} = f(t,y), \qquad y(x_0) = y_0 \tag{5.33}$$

and its related system

$$\frac{dY(t)}{dt} = f(t,Y), \qquad Y(x_0) = Y_0 \tag{5.34}$$

$f(t,y)$ is said to be continuous on f and y^{th} differentiable in the neighbourhood of $y(x_0) = y_0$, was derived by assuming a continuous approximate for $u_n(t)$ of a multi-step and multi-derivative for fourth order differentials having its form as:

$$u_n(t) = a_n(t)y_n + \Sigma_{i=1}^{l} h^i \left(\beta_{i,0(t)f_n^{i-1}} + \beta_{i,v}(t)f_{n+v}^{(i-1)} + \Sigma_{j=1}^{k}\beta_{i,k}(t)f_{n+j}^{(i_1)}\right) \approx y(t) \tag{5.35}$$

Where k is the fold obtained,l is order of derivatives, $v \in (0,k)$ is an out of boundary point achieved and j is the order of derivative for $f(t,y)$. Moreover, the continuous coefficients $\beta_{i,j}(t), i = 0, v, k, j = 1(1)k$ is determined and obtained via approximation of the exact solution $y(t)$ by evaluating the function:

$$u(t) = \Sigma_{j=0}^{r+ls-1} r_j t^j \tag{5.36}$$

Where $r_j, (j = 0, 1, ..., r + ls - 1)$ are coefficients determined, t^j are the basis functions of degree $r + ls - 1, l, r$ and s is the order of derivatives, interpolating and collocations points respectively. While ensuring that the function corresponds with the analytical solution at the end point t_n, the following conditions were imposed on $u(t)$ and its derivatives $u^{(k)}(t)$ to get the coefficients of the desired methods:

$$\begin{aligned}
&u\left(t_{n+j}\right) = y_{n+j}, && j = 0\\
&u'\left(t_{n+j}\right) = f_{n+j}, && j \in [0, ..., k]\\
&u'\left(t_{n+j}\right) = f_{n+j}, && j \in [0, ..., k]\\
&u"\left(t_{n+j}\right) = f'_{n+j} = g_{n+j}, && j \in [0, ..., k]\\
&u"\left(t_{n+j}\right) = f"_{n+j} = h_{n+j}, && j \in [0, ..., k]\\
&.\\
&.\\
&.\\
&u^{(k)}\left(t_{n+j}\right) = f_{n+j}^{(k-1)}, && j \in [0, ..., k]
\end{aligned} \tag{5.37}$$

The coefficients obtained were substituted into (6) to obtain the continuous coefficients in (6) which were then evaluated at t_{n+k} to obtain the desired methods.

5.1. One-step, derivative of first order and two off-step method

For $k = 1$, $l = 1$, and $v = \frac{1}{7}$ and $\frac{2}{7}$, the one-step, first derivative and two off-grid points method in block form as follows:

$$\begin{aligned}
y_{n+1} &= y_n + \frac{h}{24}\left(19f_n - 49f_{n+\frac{1}{7}} + 49f_{n+\frac{2}{7}} + 5f_{n+1}\right)\\
y_{n+\frac{1}{7}} &= y_n + \frac{h}{5880}\left(335f_n - 595f_{n+\frac{1}{7}} - 91f_{n+\frac{2}{7}} + f_{n+1}\right)\\
y_{n+\frac{2}{7}} &= y_n + \frac{h}{21}\left(f_n + 4f_{n+\frac{1}{7}} + f_{n+\frac{2}{7}}\right)
\end{aligned} \tag{5.38}$$

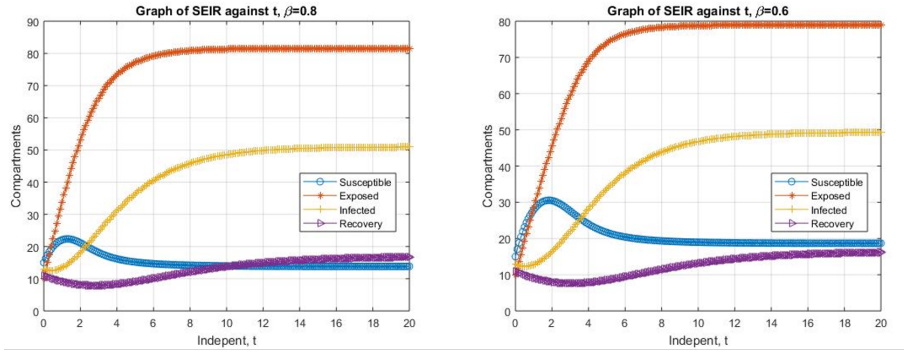
Appling Equation 5.34 to system of equations obtained in Equation 5.35, we have

$$\begin{aligned} Y_{n+1} &= Y_n + \frac{h}{24}\left(19f_n - 49f_{n+\frac{1}{7}} + 49f_{n+\frac{2}{7}} + 5f_{n+1}\right) \\ Y_{n+\frac{1}{7}} &= Y_n + \frac{h}{5880}\left(335f_n - 595f_{n+\frac{1}{7}} - 91f_{n+\frac{2}{7}} + f_{n+1}\right) \\ Y_{n+\frac{2}{7}} &= Y_n + \frac{h}{21}\left(f_n + 4f_{n+\frac{1}{7}} + f_{n+\frac{2}{7}}\right) \end{aligned} \tag{5.39}$$

The application of the numerical results on the SEIR model, brings about a non-linear algebraic equations whose solutions were obtained using the Newton Krylov's formula.

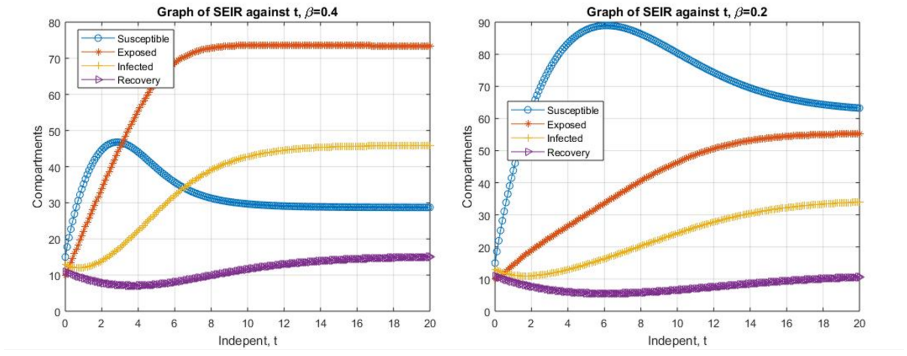
5.2. Numerical Results and Simulating Graphs

Numerical result obtained via the Hybrid block algorithm clearly illustrate the rapid convergence of the derivatives of the differential equations of the model formulation which enhance the desired iteration. The numerical results obtained are presented graphically.



(a) (b)

Figure 5.1: SEIR simulation graph at (a.) $\beta = 0,8$ and (b.) $\beta = 0,6$



(a) (b)

Figure 5.2: SEIR simulation graph at (a.) $\beta = 0,4$ and (b.) $\beta = 0,2$

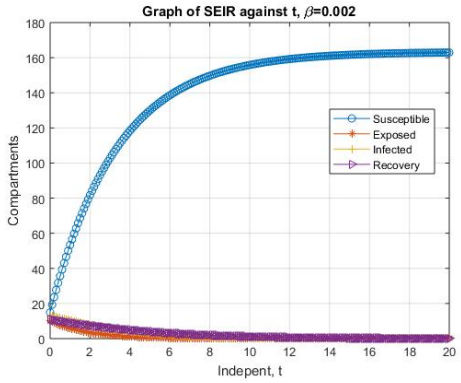


Figure 5.3: SEIR simulation graph at $\beta = 0,002$

6. Discussion of Results and Conclusion

Figure 5.1 (a.) displays the simulating result when $\beta = 0,8$, clearly shows that as exposed class decreases with infected class, the susceptible and recovered class are on the increase. Figure 5.1 (b.) shows the simulation at $\beta = 0,6$ and it was observed that the exposed class reduces rapidly with an increase in the susceptible, relatively with the recovered class. Figures 5.2 and Figure 5.3 reveals drastic changes in susceptible class. It is therefore concluded that the lower the value of β , the better the stability of the disease free equilibrium. In conclusion, the presence of a permanent immunity, β plays a vital role in disease eradication and as an adequate control measure to flatten the curve of typhoid with time.

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Citation IEEE Format:
M. K. Kolawole, "*On the Numerical Simulation of the Effect of Disease Transmission Coefficient on SEIR Epidemic Model Using Hybrid Block Method*", *Jurnal Diferensial*, vol. 6(1), pp. 65-77, 2024.