

A Semi Analytical Solution to Two Strains Covid-19 Model with Vaccination and Awareness Program

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Abstract

Awareness and vaccination are important considerations in modelling the transmission dynamics of multiple COVID-19 strains. This study developed and analysed a deterministic model of two-strain COVID-19 transmission incorporating awareness and vaccination. The model comprised seven nonlinear differential equations describing transitions between epidemiological compartments. Positivity and boundedness of the model solutions were established. The disease-free equilibrium and the endemic equilibria associated with each strain were examined, and the conditions for the existence of the strain-specific endemic equilibria were derived analytically. Using available data, semi-analytical solutions were constructed through the Adomian Decomposition Method (ADM), yielding convergent series representations of the state variables as functions of time. Numerical simulations indicated that awareness reduced infections and increased vaccination rates within the model. The ADM solutions agreed with those obtained using the classical fourth-order Runge–Kutta method, supporting the numerical accuracy of the semi-analytical approximations. These findings demonstrate the utility of ADM for solving the proposed nonlinear transmission model and highlight the potential contribution of awareness to reducing infections and increasing vaccination rates in a two-strain setting.

Keywords: COVID-19 Modelling; Adomian Decomposition Method; Semi-Analytical Solutions; Disease Awareness; Vaccination

INTRODUCTION

Mathematical modeling has become a very useful and applicable tool used to assess the transmission dynamics of infectious diseases such as Ebola Virus, HIV/AIDs, Malaria, Lassa fever, the novel SARS-CoV-2 and lots more. It has been used to analyse multiple characteristics of diseases and can provide the tools to predict the trends of transmission dynamics of a contagious disease. There are many mathematical models for infectious diseases, including compartmental models, starting from the classical SIR to more sophisticated models. Such models play important roles in helping to quantify possible infectious disease control and mitigation strategies (Ndairou et.al 2020).

Most mathematical models for infectious disease dynamics are generally written as systems of non-linear differential equations, in which their exact solutions are usually difficult to solve analytically. To compute the solutions of these models, numerical and semi-analytical methods are often employed (He, 2004). Some common Numerical methods include Euler method, Euler Improved method, Runge-Kutta method, e.t.c. (Chakraverty, 2019). However, the most popular numerical solution method is the Runge-Kutta method which was developed by Runge and Kutta (Kutta 1901; Runge 1895) used to find the solution to the differential equation in the field of atomic spectra.

The Semi-analytical method has become an important tool in mathematical modeling. Some Common semi-analytical method of solving model equations are the Adomian Decomposition method (ADM), Homotopy Perturbation Method (HPM), Homotopy Analysis Method (HAM), Optimised Decomposition Method (ODM), e.t.c. (Hussain & Arora, 2024).

The Adomian Decomposition Method (ADM) is a semi-analytical method which can be applied in solving a wide range of linear and nonlinear ordinary differential equations, partial differential equations, algebraic equations, difference equations, integral equations and integro-differential equations. It was first developed and used by an American mathematician, George Adomian was the first to develop and apply the Adomian decomposition method in solving mathematical problems (Adomian, 1994). The ADM exhibits rapid solution convergence and offers a number of significant advantages. Additionally, it approaches the problem directly, without the use of linearization, perturbation, or any other restrictive presumptions that might alter the model physical behavior (Adomian, Cherruault & Abbaoui, 1996).

Coronavirus 2019 (COVID-19) is a highly infectious disease caused by the SARS-Cov-2 virus. It was a devastating disease that spread to most parts of the world. The pandemic started in December 2019 in Wuhan, China and the disease was spread to other parts of the world by people traveling to or through China during their new year (WHO1). The virus spreads through small liquid particles expelled from an infected person's mouth or nose when they cough, sneeze, speak, sing or breathe. The particles emitted ranges from larger respiratory droplets to smaller aerosols (WHO2). The common symptoms of the disease are; dry cough, shortness of breath and fatigue. It may also cause other symptoms such as sore throat, headache, chills, congestion, nausea and diarrhea. In more extreme cases, it can prompt pneumonia, numerous organ failure and even death (Gumel et.al 2021).

Since the discovery of the ADM, many authors have used it to find semi-analytical solutions to differential and integral problems in epidemiology, fluid mechanics and many more (Ibrahim 2016, Jiya & Ojubu, 2015). The main advantage of using the ADM is that it can significantly minimize the amount of computational work without compromising the precision of the numerical results. It also provides extremely precise solutions that are close to the starting points (Adomian, 2013).

Abioye et al. (2020) used the ADM to analyse a malaria model. The result obtained using the Adomian Decomposition Method (ADM) was compared to that obtained using the Fourth order Runge-Kutta (R-K 4) method in-built in Maple 18. The results were almost the same. Thus validating the efficacy of the ADM. Makinde (2007) also used the ADM on an SIR model epidemic with constant Vaccination. The result was validated by the Maple software which was used to compute some quantitative results and graphical analysis.

Agarwal et al. (2022) also applied the ADM to estimate the Covid-19 pandemic in India, where a semi-analytic ADM was used without considering any discretization to perform the first-order differential equations related to COVID-19 cases. Somma et al. (2021) used the Adomian Decomposition Method (ADM) to solve the mathematical model of measles and the solution was validated with the Runge-Kutta built in Maple software.

As a result of the emergence of multiple strains of the Covid-19 disease, there is the need to study the interaction between two or more strains existing in a society at a particular time. This study provide such platform. This work also provide a semi-analytical method of solution that can be used to solve similar system of equations.

The rest of the paper is organized as follows: section 2 discuss the model formulation and equation, section 3 present the positivity and boundedness, section 4 present the equilibriums, section 5 presents the Adomian Decomposition Method. In section 6 we present the conclusion.

Model formulation

This model consist of seven mutually exclusive compartments (i.e. an individual can only belong to one compartment at any given time). The compartments include the susceptible un-aware population S_u , the susceptible aware population S_a , the vaccinated population V , those infected with the first strain of the virus I_1 , those infected with the second strain of the virus I_2 , the hospitalized population H and the recovered population R .

The unaware population include all those individuals who have no knowledge about the disease or do not believe in the danger posed by the disease. This group of individuals will thus not take any or adequate measures against contacting the virus. This class has a recruitment rate of Λ either through birth or migration or both. As the population gain awareness θ , they move into S_a . The S_a class consist of individuals who are aware of the disease and take precautionary measures including vaccination V at the rate ω . The S_a class also consist of those individuals who recovered from the disease as they have also gained some awareness about it.

The I_1 class consist of individuals who are infected with the first strain from both the S_u class and the S_a class. The I_2 class consist of those infected with the second strain from the S_u and S_a classes. This class also consist of those who lose their immunity from the vaccinated class.

Individuals who are infected with I_1 or I_2 are either hospitalized H , or they die from the first and second strains at the rates d_1 and d_2 respectively, or they move to the recovery class R due to natural immunity. The R class also consist of those from the H class. The saturating infection functions are given by $\frac{\alpha_1 I_1}{1+\theta I_1}$ and $\frac{\alpha_2 I_2}{1+\theta I_2}$ for the first and second strains respectively. Also, all the compartments contain individuals who die naturally at the rate μ .

Model equations

The following are the differential equations of the model:

$$\frac{dS_u}{dt} = \Lambda - (\alpha_1 I_1 + \alpha_2 I_2 + \theta + \mu) S_u, \quad (1)$$

$$\frac{dS_a}{dt} = \theta S_u + \gamma R - \left(\frac{\alpha_1 I_1}{1+\theta I_1} + \frac{\alpha_2 I_2}{1+\theta I_2} + \omega + \mu \right) S_a, \quad (2)$$

$$\frac{dV}{dt} = \omega S_a - (\tau + \mu) V, \quad (3)$$

$$\frac{dI_1}{dt} = \frac{\alpha_1 I_1}{1+\theta I_1} S_a + \alpha_1 I_1 S_u - (\delta_1 + \beta_1 + d_1 + \mu) I_1, \dots \quad (4)$$

$$\frac{dI_2}{dt} = \tau V + \frac{\alpha_2 I_2}{1+\theta I_2} S_a + \alpha_2 I_2 S_u - (\delta_2 + \beta_2 + d_2 + \mu) I_2, \quad (5)$$

$$\frac{dH}{dt} = \delta_1 I_1 + \delta_2 I_2 - (\phi + d_3 + \mu) H, \quad (6)$$

$$\frac{dR}{dt} = \beta_1 I_1 + \beta_2 I_2 + \phi H - (\gamma + \mu) R \quad (7)$$

Positivity and Boundedness of the Solution

In this section we shall determine the mathematical properties that shows that the model is meaningful.

Positivity: For the model to be epidemiologically and mathematically meaningful, it is necessary to prove that all the state variables are non-negative for all $t > 0$. This will be done by using the following theorem:

Theorem 3.2.1 Let $S_u(0) > 0, S_a \geq 0, V \geq 0, I_1 \geq 0, I_2 \geq 0, H(0) \geq 0, R(0) \geq 0 \in \Gamma$

Then the solution $S_u(t), S_a(t), V(t), I_1(t), I_2(t), H(t), R(t)$ of the model system equation are positive for all $t > 0$.

Proof: To prove that $S_u(t) > 0$, we note from equation (1) that

$$\frac{dS_u}{dt} \geq -(\alpha_1 I_1 + \alpha_2 I_2 + \theta + \mu) S_u$$

$$\ln S_u \geq -[\alpha_1 I_1 + \alpha_2 I_2 + \theta + \mu]t + k$$

Taking the exponential of both sides yield

$$S_u(t) \geq e^{[\alpha_1 I_1 + \alpha_2 I_2 + \theta + \mu]t + k}$$

Now at $t = 0$, we obtain $S_u(0) > k$

Thus our general solution becomes

$$S_u(t) \geq S_u(0)e^{-[\alpha_1 I_1 + \alpha_2 I_2 + \theta + \mu]t}$$

Notice that $e^k > 0$ and $e^{-[\alpha_1 I_1 + \alpha_2 I_2 + \theta + \mu]t} > 0$ ensures that their product is also positive i.e.

$$S_u(0)e^{-[\alpha_1 I_1 + \alpha_2 I_2 + \theta + \mu]t} > 0,$$

$$\text{Implies } S_u(t) > 0 \dots \quad (8)$$

Same prove for equations (2)-(7). Thus we conclude that all the state variables are positive.

Boundedness of the Solution: In order to show that the model solutions do not grow without bound as time progresses, we need to show that it is bounded. This will be done by proving the following theorem.

Theorem 1: The model system is bounded in

$$\Omega = \{S_u, S_a, V, I_1, I_2, H, R \in \mathbb{R}_+ : N \leq \frac{\Lambda}{\mu} + (N(0) - \frac{\Lambda}{\mu})e^{-\mu t}\}$$

Proof: The total population $N(t) = S_u(t) + S_a(t) + V(t) + I_1(t) + I_2(t) + H(t) + R(t)$
...

$$\text{Differentiating w.r.t } t, \text{ we've } \frac{dN}{dt} = \frac{dS_u}{dt} + \frac{dS_a}{dt} + \frac{dV}{dt} + \frac{dI_1}{dt} + \frac{dI_2}{dt} + \frac{dH}{dt} + \frac{dR}{dt} \dots \quad (9)$$

Substitute (1)-(7) into (9), we have

$$\frac{dN}{dt} = \Lambda - \mu S_u - \mu S_a - \mu V - (\mu + d_1)I_1 - (\mu + d_2)I_2 - (\mu + d_3)H - \mu R$$

$$\frac{dN}{dt} = \Lambda - \mu(S_u + S_a + V + I_1 + I_2 + H + R) - d_1 I_1 - d_2 I_2 - d_3 H$$

$$\frac{dN}{dt} = \Lambda - \mu N - d_1 I_1 - d_2 I_2 - d_3 H \leq \Lambda - \mu N$$

$$\text{Implies that } \frac{dN}{dt} \leq \Lambda - \mu N \quad (10)$$

In order to find the solution set, we first solve the differential equation $\frac{dN}{dt} = \Lambda - \mu N$ which has integrating factor $e^{\int \mu dt} = e^{\mu t}$

Thus we have the solution set to (10) as,

$$N(t) \leq \frac{\Lambda}{\mu} + \left(N(0) - \frac{\Lambda}{\mu}\right) e^{-\mu t}$$

Taking the limit as $t \rightarrow \infty$, we have $\lim_{t \rightarrow \infty} N(t) \leq \frac{\Lambda}{\mu}$

Thus,

$$0 \leq \frac{dN}{dt} \leq \left(N(0) - \frac{\Lambda}{\mu}\right) e^{-\mu t}$$

Also, taking the *limsup* we have

$$\lim_{t \rightarrow \infty} \sup (S_u(t) + S_a(t) + V(t) + I_1(t) + I_2(t) + H(t) + R(t))$$

Hence the feasible region for the system

$$\Omega = \left\{ S_u(t) > 0, S_a(t) \geq 0, V(t) \geq 0, I_1(t) \geq 0, I_2(t) \geq 0, H(t) \geq 0, R(t) \geq 0 \text{ and } N(t) \leq \frac{\Lambda}{\mu} \right\}$$

We conclude that the system is bounded in Ω .

Equilibriums

In order to gain insights into the fundamental behaviour of this system and predict its future states, we shall determine the Disease Free and Disease Endemic equilibriums.

We know that at equilibrium point(s) we have,

$$\frac{dN}{dt} = \frac{dS_u}{dt} = \frac{dS_a}{dt} = \frac{dV}{dt} = \frac{dI_1}{dt} = \frac{dI_2}{dt} = \frac{dH}{dt} = \frac{dR}{dt} = 0$$

Disease Free Equilibrium DFE

$$\text{At DFE, } I_1(t) = I_2(t) = 0.$$

$$\text{Thus we have } H(t) = R(t) = 0, \text{ while } S_u(t) \neq 0, S_a(t) \neq 0, V(t) \neq 0$$

$$\text{Thus DFE, } E^0 = \{S_u^0, S_a^0, V^0, 0, 0, 0, 0\}.$$

Now we solve (1)-(3) for S_u^0 , S_a^0 and V^0

$$E^0 = \left(\frac{\Lambda}{\theta + \mu}, \frac{\Lambda\theta}{(\theta + \mu)(\omega + \mu)}, \frac{\omega\theta\mu}{(\tau + \mu)(\theta + \mu)(\omega + \mu)}, 0, 0, 0, 0 \right)$$

Strain 1 Disease Endemic Equilibrium (DEE 1)

For strain1 DEE, $I_1 \neq 0, I_2 = 0$

The strain 1 DEE is given as $E^* = \{S_u^*, S_a^*, V^*, I_1^*, 0, H^*, R^*\}$

Next we solve (1)-(7) analytically while substituting $I_2 = 0$. We express the state variables in terms of I_1^* and the parameters and find a general solution to I_1^* in terms of the parameters.

Thus, we have a quadratic equation in I_1^* which can be expressed as

$$P_1(I_1^*)^2 + P_2(I_1^*) + P_3 = 0 \dots$$

$$P_1 = A_1 \alpha_1^2 = \alpha_1^2 (\delta_1 + \beta_1 + d_1 + \mu)$$

$$P_2 = a_1 [(\delta_1 + \beta_1 + d_1 + \mu)[(\omega + \mu) - \gamma(\theta + \mu) - \Lambda(\omega + \theta + \mu)]],$$

$$P_3 = \alpha_1 (\delta_1 + \beta_1 + d_1 + \mu)[(\omega + \mu) - \gamma(\theta + \mu) - \Lambda(\omega + \theta + \mu)].$$

Thus the general solution to be given by

$$I_1^* = \frac{-P_2 \pm \sqrt{(P_2^2 - 4P_1P_3)}}{2P_1}$$

This solutions are
$$I_{1,1}^* = \frac{-P_2 + \sqrt{(P_2^2 - 4P_1P_3)}}{2P_1}, I_{1,2}^* = \frac{-P_2 - \sqrt{(P_2^2 - 4P_1P_3)}}{2a} < 0$$

Observe that $I_{1,2}^*$ is not biologically feasible as the value will always negative

For $I_{1,1}^*$ to be biologically feasible, $\sqrt{P_2^2 - 4P_1P_3} > -P_2$

$$\text{Implies} \quad 4P_1P_3 < 0$$

Thus, strain 1 disease endemic equilibrium is attained if the terms in $P_1 < 0$ or $P_3 < 0$, where P_1, P_2 and P_3 are functions of the parameters as described above.

Strain 2 Disease Endemic Equilibrium

For Strain 2 DEE occurs when $I_2 \neq 0, I_1 = 0$. It is given by

$$E^{**} = (S_u^{**}, S_a^{**}, V^{**}, I_1^{**}, 0, H^{**}, Q^{**})$$

Solving equations (1) - (7) for I_2^{**} , we have cubic equation

$$B_{20}(I_2^{**})^3 + B_{21}(I_2^{**})^2 + B_{22}(I_2^{**}) + B_{23} = 0$$

Where

$$\begin{aligned} B_{20} &= \alpha_2^2 \theta (\delta_2 + \beta_2 + d_2 + \mu) (\eta + \mu) (\omega + \mu) \\ B_{21} &= \frac{\gamma \alpha_2 [(\tau + \mu) \beta_2 + \phi + \delta_2] \tau \omega + \gamma (\tau + \mu) [\tau + \mu] \beta_2 + \phi \delta_2}{(\gamma + \mu) (\tau + \mu)} \\ B_{22} &= (\theta + \mu) \left[\frac{\tau \omega \gamma (\tau + \mu + \phi \delta_2)}{(\gamma + \mu) (\tau + \mu)} + \theta \Lambda (\tau \omega \theta + (\tau + \mu) (\delta_2 + \beta_2 + d_2 + \mu)) \right] + (\tau + \mu) (\omega + \mu) [\delta_2 + \beta_2 + d_2 + \mu + \alpha_2 \Lambda] \\ B_{23} &= \theta \Lambda \tau \omega - (\tau + \mu) (\theta + \mu) (\delta_2 + \beta_2 + d_2 + \mu) (\alpha_2 + \theta_2 (\omega + \mu)) \end{aligned}$$

In order to obtain the general solution of (41), we apply the Cardan's formula for cubic equation (Burton, 2007). This done as follows;

Step 1: we reduce the coefficient of $(I_2^{**})^3$ to unity to obtain

$$(I_2^{**})^3 + C_1 (I_2^{**})^2 + C_2 (I_2^{**}) + C_3 = 0 \dots \dots$$

$$\text{Where } C_1 = \frac{B_{21}}{B_{20}}, C_2 = \frac{B_{22}}{B_{20}}, C_3 = \frac{B_{23}}{B_{20}}$$

Step 2: We express in the standard Cardian equation;

$$(I_2^{**})^3 + m I_2^{**} = n$$

$$\text{Where } m = C_2 - \frac{C_1^2}{3}, n = -\left(\frac{2C_1^3}{27} - \frac{C_1 C_2}{3} + C_3\right)$$

The solution to the cardian equation is given as

$$I_2^{**} = \sqrt[3]{\frac{n}{2} + \sqrt{\frac{n^2}{4} + \frac{m^3}{27}}} - \sqrt[3]{\frac{-n}{2} + \sqrt{\frac{n^2}{4} + \frac{m^3}{27}}}$$

For the equation to be biologically feasible, $\frac{n^2}{4} \geq \frac{m^3}{27}$

Thus, strain 2 endemic equilibrium is attained if $\frac{n^2}{4} \geq \frac{m^3}{27}$

Adomian Solution of our model equation

In order to determine the solution to the model equation using the ADM, the following steps shall be taken:

Step 1: The equation under investigation is separated into linear and nonlinear portions,

Step 2: The linear operator representing the linear portion of the equation is inverted, and then the inverse operator is applied to the equation. Any given conditions are taken into consideration,

Step 3: The nonlinear portion is decomposed into a series of Adomian polynomials,

Step 4: This method generates a solution in the form of a series whose terms are determined by a **recursive** relationship using these Adomian polynomials.

The **non-linear** terms in (1) to (7) are; $I_1 S_u, I_2 S_u, \frac{I_1 S_a}{1+\theta I_1}, \frac{I_2 S_a}{1+\theta I_2}$ while other terms of the equations are linear.

The Adomian solution to the model equations, where L^{-1} is the **inverse operator**, are

$$S_u(t) - S_u(0) = L^{-1}(\Lambda) - L^{-1}[(\alpha_1 I_1 + \alpha_2 I_2 + \theta + \mu)S_u]$$

$$S_a(t) - S_a(0) = L^{-1}(\theta S_u) + L^{-1}(\gamma R) - L^{-1}\left[\left(\frac{\alpha_1 I_1}{1+\theta I_1} + \frac{\alpha_2 I_2}{1+\theta I_2} + \omega + \mu\right)S_a\right]$$

$$V(t) - V(0) = L^{-1}(\omega S_a) - L^{-1}[(\tau + \mu)V]$$

$$I_1(t) - I_1(0) = L^{-1}\left(\frac{\alpha_1 I_1}{1+\theta I_1} S_a\right) + L^{-1}(\alpha_1 I_1 S_u) - L^{-1}[(\delta_1 + \beta_1 + d_1 + \mu)I_1]$$

$$I_2(t) - I_2(0) = L^{-1}(\tau V) + L^{-1}\left(\frac{\alpha_2 I_2}{1+\theta I_2} S_a\right) + L^{-1}(\alpha_2 I_2 S_u) - L^{-1}[(\delta_2 + \beta_2 + d_2 + \mu)I_2]$$

$$H(t) - H(0) = L^{-1}(\delta_1 I_1) + L^{-1}(\delta_2 I_2) - L^{-1}[(\phi + d_3 + \mu)H]$$

$$R(t) - R(0) = L^{-1}(\beta_1 I_1) + L^{-1}(\beta_2 I_2) + L^{-1}(\phi H) - L^{-1}[(\gamma + \mu)R]$$

The **Adomian polynomials** A_n, B_n, C_n, M_n of the non-linear terms are defined respectively as follows;

$$A_n = \frac{1}{n!} \frac{d^n}{d\lambda^n} \left[\sum_{k=0}^n S_{u,k} \lambda^k \cdot \sum_{k=0}^n I_{1,k} \lambda^k \right]_{\lambda=0}, B_n = \frac{1}{n!} \frac{d^n}{d\lambda^n} \left[\sum_{k=0}^n S_{u,k} \lambda^k \cdot \sum_{k=0}^n I_{2,k} \lambda^k \right]_{\lambda=0}$$

$$C_n = \frac{1}{n!} \frac{d^n}{d\lambda^n} \left[\frac{\sum_{k=0}^n S_{a,k} \lambda^k \cdot \sum_{k=0}^n I_{1,k} \lambda^k}{1+\theta \sum_{k=0}^n I_{1,k} \lambda^k} \right]_{\lambda=0}, M_n = \frac{1}{n!} \frac{d^n}{d\lambda^n} \left[\frac{\sum_{k=0}^n S_{a,k} \lambda^k \cdot \sum_{k=0}^n I_{2,k} \lambda^k}{1+\theta \sum_{k=0}^n I_{2,k} \lambda^k} \right]_{\lambda=0}$$

The solutions at time t are given as

$$S_u(t) = S_u(0) + \Lambda - \alpha_1 \int_0^t \left(\sum_{n=0}^{\infty} I_{1,n} S_{u,n} \right) dt - \alpha_2 \int_0^t \left(\sum_{n=0}^{\infty} I_{2,n} S_{u,n} \right) dt - (\theta + \mu) \int_0^t \left(\sum_{n=0}^{\infty} S_{u,n} \right) dt$$

Same for $S_a(t), V, I_1(t), I_2(t), H(t)$ and $R(t)$

for $n = 1, 2, 3, \dots$

The initial stages are given as

$$S_{u,0}(t) = S_u(0) + \Lambda t, \quad S_{a,0}(t) = S_a(0), \quad V_0(t) = V(0), \quad I_{1,0}(t) = I_1(0), \quad I_{2,0}(t) = I_2(0), \quad H_0(t) = H(0), \quad R_0(t) = R(0)$$

The **Recursive formulae** are given as

$$S_{u,n+1}(t) = -\alpha_1 \int_0^t (\sum_{n=0}^{\infty} A_n) dt - \alpha_2 \int_0^t (\sum_{n=0}^{\infty} B_n) dt - (\theta + \mu) - \alpha_1 \int_0^t (\sum_{n=0}^{\infty} S_{u,n}) dt$$

$$S_{a,n+1}(t) = \theta \int_0^t \left(\sum_{n=0}^{\infty} S_{u,n} \right) dt + \gamma \int_0^t \left(\sum_{n=0}^{\infty} R_n \right) dt - (\theta + \mu) - \alpha_1 \int_0^t \left(\sum_{n=0}^{\infty} C_n \right) dt - \alpha_2 \int_0^t \left(\sum_{n=0}^{\infty} M_n \right) dt - (\omega + \mu) \int_0^t \left(\sum_{n=0}^{\infty} S_{a,n} \right) dt$$

$$V_{n+1}(t) = \omega \int_0^t (\sum_{n=0}^{\infty} S_{a,n}) dt - (\tau + \mu) \int_0^t (\sum_{n=0}^{\infty} V_n) dt$$

$$I_{1,n+1}(t) = \alpha_1 \int_0^t (\sum_{n=0}^{\infty} C_n) dt - \alpha_1 \int_0^t (\sum_{n=0}^{\infty} A_n) dt - (\delta_1 + \beta_1 + d_1 + \mu) \int_0^t (\sum_{n=0}^{\infty} I_{1,n}) dt$$

$$I_{2,n+1}(t) = \tau \int_0^t \left(\sum_{n=0}^{\infty} V_n \right) dt + \alpha_2 \int_0^t \left(\sum_{n=0}^{\infty} M_n \right) dt + \alpha_2 \int_0^t \left(\sum_{n=0}^{\infty} B_n \right) dt - (\delta_2 + \beta_2 + d_2 + \mu) \int_0^t \left(\sum_{n=0}^{\infty} I_{2,n} \right) dt$$

$$H_{n+1}(t) = \delta_1 \int_0^t \left(\sum_{n=0}^{\infty} I_{1,n} \right) dt - \delta_2 \int_0^t \left(\sum_{n=0}^{\infty} I_{2,n} \right) dt - (\phi + d_3 + \mu) \int_0^t \left(\sum_{n=0}^{\infty} H_n \right) dt$$

$$R_{n+1}(t) = \beta_1 \int_0^t \left(\sum_{n=0}^{\infty} I_{1,n} \right) dt + \beta_2 \int_0^t \left(\sum_{n=0}^{\infty} I_{2,n} \right) dt + \phi \int_0^t \left(\sum_{n=0}^{\infty} H_n \right) dt - (\gamma + \mu) \int_0^t \left(\sum_{n=0}^{\infty} R_n \right) dt$$

Solution using Variable and Parameter numerical values

In this section, we shall use some data obtained from NCDC (2022), Eegunjobi & Makinde (2022), Akinwade et al (2022) serve as the initial values. Note that the accuracy of this method does not depend on the initial data.

$$\begin{aligned} \text{Data: } S_u(0) &= 2045882, & S_a(0) &= 3068821, V(0) = 734768, I_1(0) = \\ &245802, I_2(0) = 1000, H(0) = 207481, R(0) = 249936 \quad \Lambda = 6/\text{day}, \alpha_1 = 0.05, \alpha_2 = \\ &0.07, \omega = 0.18, \beta_1 = 0.97, \beta_2 = 0.97, \tau = 0.01, \delta_1 = 0.33, \delta_2 = 0.5, \gamma = 0.99, & \phi = \\ &0.98, \mu = 0.011, d_1 = 0.01229, d_2 = 0.02, \theta = 0.6 \end{aligned}$$

Using the recursive formula computed above, the solution is obtained as

$$S_u(t) = S_{u,0}(0) + S_{u,1}(t) + S_{u,2}(t) + S_{u,3}(t) + \dots$$

Same for $S_a(t), V, I_1(t), I_2(t), H(t)$ and $R(t)$

Using MAPLE 18 software on the recursive formulae, we obtained the following solutions

$$S_u(t) = -8.388427500 \times 10^2 t^6 - 1.578377375 \times 10^9 t^5 - 9.382508271 \times 10^{14} t^4 - 1.737738453 \times 10^{20} t^3 - 2.280062484 \times 10^{15} t^2 - 2.528855614 \times 10^{10} t + 2045882$$

$$S_a(t) = -4.266651738 \times 10^{-8} t^6 - 1.336500672 \times 10^3 t^5 - 2.186800263 \times 10^9 t^4 - 9.110261347 \times 10^{14} t^3 - 1.525861672 \times 10^{10} t^2 + 2.756542853 \times 10^5 t + 3068821$$

$$V(t) = -2.013765718 \times 10^3 t^4 + 2.746551815 \times 10^9 t^3 + 3.834165889 \times 10^4 t^2 + 5.36957736 \times 10^5 t + 734768$$

$$I_1(t) = 8.295817500 \times 10^2 t^6 + 1.560399520 \times 10^9 t^5 + 9.269831646 \times 10^{14} t^4 + 1.714946821 \times 10^{20} t^3 + 2.261253235 \times 10^{15} t^2 + 2.514402484 \times 10^{10} t + 245802$$

$$I_2(t) = 9.261000043 t^6 + 1.797479757 \times 10^7 t^5 + 1.126265889 \times 10^{13} t^4 + 2.277078783 \times 10^{18} t^3 + 1.879129942 \times 10^{13} t^2 + 1.435750200 \times 10^8 t + 1000$$

$$H(t) = 1.081817910 \times 10^3 t^5 + 1.769788719 \times 10^9 t^4 + 7.368095004 \times 10^{14} t^3 + 8.225875453 \times 10^9 t^2 - 1.316985725 \times 10^5 t + 207481$$

$$R(t) = 3.244443390 \times 10^3 t^5 + 5.309190628 \times 10^9 t^4 + 2.211626706 \times 10^{15} t^3 + 2.452865006 \times 10^{10} t^2 + 1.92543384 \times 10^5 t + 249936$$

Simulation and Interpretation

In this section we show the effect of awareness on the model and we also show a comparison between our ADM solutions and the MAPLE RK-4 solution

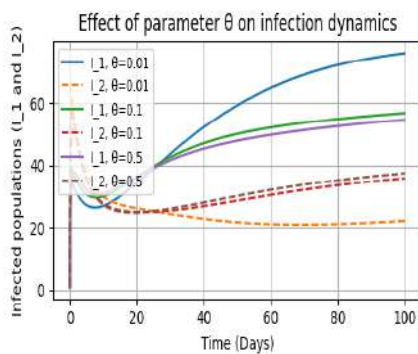


Figure 1: Effect of θ on the infectious classes

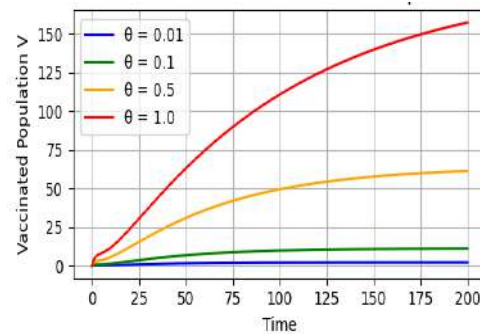


Figure2: Effect of awareness on vaccination

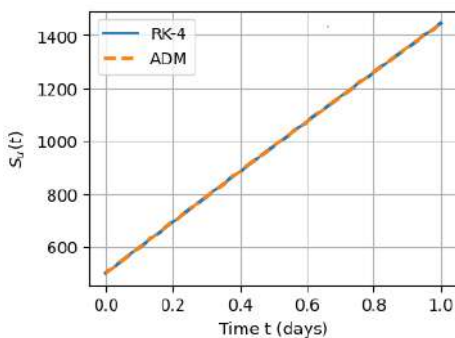


Figure3: ADM Vs RK-4 solution for S_u class

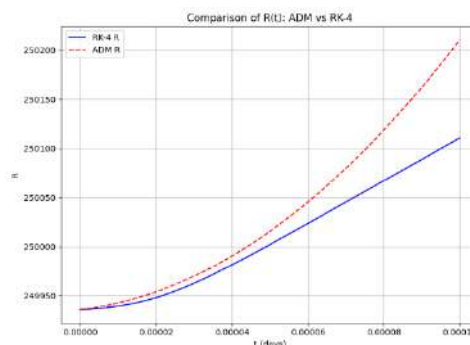


Figure 4: ADM vs RK-4 solutions for R class

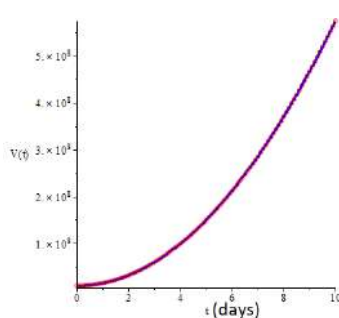


Fig 5: ADM Vs RK-4 solution for S_u class

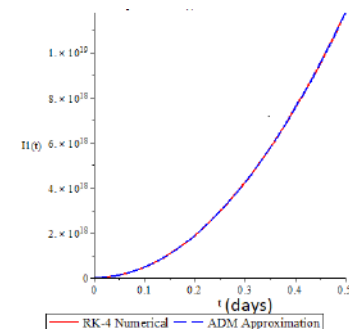


Fig 6: ADM Vs RK-4 solution for I_1 class

Interpretation: Figures 1 and 2 shows the effect of awareness on infection and vaccination respectively. While awareness flattened the curve (reduces) infection of strain 2, the number of those infected with strain 1 continue to grow with time. This is because those infected with the second strain are aware of the disease. Also, as awareness increases so is the vaccination rate as observed in figure 2. Figures 3, 4, 5 and 6 shows a strong agreement between the ADM solution and the Runge-Kutta RK-4 solution.

CONCLUSION

The deterministic model obtained was shown to be mathematically and epidemiologically meaningful from the positivity and boundedness analyses. Three equilibriums were also analysed for the disease free, disease endemic for strain 1 and disease endemic for strain 2. The general solutions to the equations for I_1 and I_2 were analysed using the traditional quadratic and cubic equations formulae. A semi analytical solution of the model was presented and compared with the RK-4 solution. The result validates the fact that the ADM is also an efficient and accurate method of finding the solution to our model.

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