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ORIGINAL RESEARCH

Mathematical Modeling of Hepatitis C Virus: Transmission and Control

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Abstract

The Hepatitis C virus (HCV) is the global burden and becomes one of the pandemic affecting about 71 million in chronic infected individuals. We constructed a HCV transmission dynamics model and used it to assess control strategies. We have included the factors that affect the transmission of HCV including those who are susceptible, latent, acute infected chronic infected, inpatients and recovered as shown. Conventional approaches, such as testing, treatment and harm reduction have only marginally reduced the spread of HCV. This paper analyses shortcomings of a deterministic compartmental model as it captures HCV epidemiology considering literature and country data. We check for the positivity of the model at all times t ≥ 0. The analysis reveals that the virus can be eradicated in all epidemiological compartments apart from susceptible individuals. The model's reproductive number (R_0) confirm global stability and the eventual extinction of Hepatitis C through targeted governmental action. Sensitivity analysis identifies injection drug use and poor healthcare infection control as primary transmission drivers. By balancing transmission reduction (50%) with increased recovery coverage (80%), simulations demonstrate that this optimal control strategy can reduce chronic infections by 55% over 40 months.

Keywords: Endemic, Equilibrium, Sensitivity analysis, Basic reproduction number.

1. Introduction

Cancer of the liver, cirrhosis, and chronic liver disease are the primary consequences of the viral infection termed hepatitis C. Worldwide, approximately 71 million individuals are afflicted with chronic HCV infection, resulting in significant morbidity and mortality rates. The World Health Organization estimates that 175 million people globally, or more than 3% of the population, are infected with the hepatitis C virus (HCV), resulting in around 400,000 deaths annually due to HCV-related illnesses, Wiessing et al. (2021). The principal mechanism of transmission occurs by blood-to-blood contact, including blood transfusions, needle sharing among intravenous drug users, hazardous medical practices, transfusions with contaminated blood, unprotected sexual intercourse, and vertical transfer from mother to child during birth. Dontwin et al. (2010). The World Health Organization (WHO) reports that the most impacted areas are the WHO Eastern Mediterranean Region and the WHO European Region, with estimated prevalences in 2015 of 2.3% and 1.5%, respectively (WHO, 2017). The incubation period for the hepatitis C virus varies from 2 weeks to 6 months. The virus can be identified between 14 to 180 days post-infection and may remain, potentially evolving into chronic hepatitis C (WHO, 2022).

Scientific visualization and mathematical modeling aid in problem characterization, information understanding, comprehension teaching and assessment, and outcome prediction. It is possible to investigate aspects of viral transmission and its regulation among the different susceptible and infected

population subgroups by using a deterministic compartmental model. Hence, a deterministic compartmental model is a research tool for the creation of epidemiological data. In epidemiology, the "energy of contamination" is a very relevant metric. This is the typical rate of infection for vulnerable individuals. The energy of contamination can be ascertained in an open population where individuals are monitored following their initial HCV infection and once, they develop chronic illness. Many mathematicians have studied numerical models on the spread and management of hepatitis C virus during the past 20 years. Several numerical models have been used by Dontwi et al. (2010), Nowak et al. (1996), and Hickman (2000) to evaluate and manage the spread of hepatitis C infection. In order to comprehend the dynamics of transmission and create efficient control measures, mathematical modeling of infectious diseases has grown in significance in recent years. Such modeling efforts have focused on the worldwide burden and public health consequences of hepatitis C virus (HCV) infection in particular.

Mathematical modeling provides a framework for understanding the complex interplay of factors that contribute to the spread of HCV, such as risk behaviors, healthcare access, and the use of harm reduction strategies. Models can also evaluate the potential impact of interventions, such as treatment scale-up, needle exchange programs, and screening initiatives, on the trajectory of HCV transmission and disease burden.

A study by Hellard *et al*. (2014) highlighted the value of mathematical modeling in understanding the impact of various interventions on HCV transmission dynamics, particularly in the context of injecting drug use. The study emphasized the importance of combining prevention and treatment strategies to effectively control the spread of HCV among people who inject drugs.

Similarly, Martin *et al*. (2013) utilized mathematical modeling to assess the long-term impact of different treatment and screening strategies for HCV, emphasizing the potential benefits of early diagnosis and treatment in reducing the overall disease burden and healthcare costs. These studies and others have underscored the significance of mathematical modeling in elucidating the spread and control of HCV, as well as in guiding policy and resource allocation for HCV prevention and treatment efforts.

2. Related Works

2.1. Mathematical Modelling of HCV Spread

Mathematics-based models have been employed to examine the transmission trends of HCV within human populations. These models take into account the widespread distribution of HCV, transmission modalities, and the effects of therapies. Hamed et al. (2020) conducted a study that created a model to evaluate the effects of harm reduction methods on HCV transmission in individuals who inject drugs.

Hsieh et al. (2018) developed a mathematical model to investigate the impact of screening and treatment on the spread of Hepatitis C virus in a population. The model suggested that increasing the coverage of screening and treatment could significantly reduce the burden of Hepatitis C virus in the population.

Hashim et al. (2021) proposed a mathematical fractional order model for the analysis and numerical investigation of the propagation of the hepatitis C virus (HCV). The model is an expansion of the classical model of fractional order. Based on the Lagrange polynomial interpolation, the numerical findings showed that the fractional order model's solution behavior was identical to that of the current integer order model.

Sunday et al. (2023) formulated and examined a mathematical model for hepatitis C virus transmission utilizing ordinary differential equations and a Susceptible-Infected-Removed framework with a segmented population based on disease risk indicators. The model's feasible region was validated, and the positivity of the solutions was established. Either infectious and disease-free equilibria were achieved.

The local and global stability of both the disease-free and endemic equilibria were established, with the calculation and analysis of the model's basic reproduction numbers. The model was implemented and validated by simulation across several demographic segments. The results indicate that the stability conditions for the endemic equilibrium were determined, and the disease-free equilibrium remained stable. The model's infectious and disease-free equilibrium is classified as endemic or unstable when $R_0 > 1$, and is both globally and locally asymptotically stable when $R_0 < 1$. The model's numerical simulations indicate that if adequate education, awareness, and intensive treatment are administered promptly during the initial stages of the disease outbreak, along with the proposed model interventions, the hepatitis C virus could be eradicated or significantly diminished within the targeted population.

2.2 Control Strategies

Another important aspect of mathematical modelling in the context of Hepatitis C virus is the evaluation of different treatment strategies. Scott et al. (2016) used a mathematical model to compare the cost-effectiveness of different treatment strategies for Hepatitis C virus, including interferon-based therapies and direct-acting antiviral drugs. The results of the study suggested that direct-acting antiviral drugs were not only more effective in reducing the spread of Hepatitis C virus, but also more cost-effective compared to interferon-based therapies. In another development Scott et al. (2016) underlined the importance of incorporating real-world data into mathematical models, emphasizing the need for accurate parameter estimation and validation to ensure the reliability of model projections.

Various control strategies have been proposed to reduce the burden of HCV. Mathematical models have been used to evaluate the effectiveness of these strategies and inform public health policies. A study by de Oliveira et al. (2019) used a mathematical model to estimate the impact of increasing treatment rates on HCV incidence and prevalence.

One of the significant challenges in combating HCV is the complex dynamics of transmission, which involves various risk factors including injection drug use, healthcare-associated exposures, and vertical transmission. A study by Razavi et al. (2014) emphasized the role of mathematical modelling in capturing these intricate transmission pathways and projecting the potential impact of interventions. The authors highlighted the utility of modelling in estimating the future disease burden and evaluating the effectiveness of different control measures, such as screening, treatment, and harm reduction programs.

In addition, the field of HCV treatment has changed with the advent of direct-acting antiviral (DAA) medications. The impact of DAA introduction and scale-up at the population level has been evaluated using mathematical models. The possibility of DAA treatment to lower HCV transmission among injecting drug users was examined by Martin et al. (2018), who emphasized the value of modeling in assessing the long-term impacts of treatment expansion on disease incidence and prevalence.

In addition to treatment, mathematical modelling has been employed to evaluate preventive measures and control strategies for HCV transmission. A study by Hellard et al. (2014) utilized modelling to assess the impact of needle and syringe exchange programs on HCV prevalence among people who inject drugs, providing evidence to support the implementation and expansion of harm reduction initiatives.

By integrating epidemiological and clinical data, these models provide valuable insights into the efficacy of interventions and the long-term impact of public health interventions.

3. Methodology

This study categorizes the whole population $N(t)$ into the following epidemiological classes: susceptible class $S(t)$, latent class $L(t)$, acutely infected class A(t), chronically infected class $C(t)$,

hospitalized class $H(t)$, and recovered class $R(t)$. This facilitates the development and analysis of a mathematical model for the dynamics of Hepatitis C viral transmission.

The susceptible class is the group of people in the general population who have not yet contracted the disease; the latent class is the period of time between the onset of the disease and the first exposure; and the hospitalized class is the group of people who, voluntarily or involuntarily, report or admit themselves to the hospital after exhibiting some of the disease's symptoms. Acutely infected people are those who have the disease but are not very contagious; chronically infected people are those who have the disease but are highly contagious or infectious; and recovered people are those who have responded to treatment and are cured or recovered.

The total population $N(t)s$ is given by

$$N(t) = S(t) + L(t) + H(t) + A(t) + C(t) + R(t).$$

whereby a steady rate of π is used to attract susceptible individuals into the population through migration and birth. When a susceptible person comes into touch with an infected person, they are exposed to the HCV and are moved to the latent stage at a rate of βI. where βI is the product of the probability of each contact with an infected individual and the effective contact rate. At the rate μ, a vulnerable person may pass away from a reason unrelated to HCV. After some time, those who were first exposed but did not exhibit any symptoms may develop symptoms and switch to the acutely infected class at rate ψ, while others who were hospitalized at rate ρ and others whose immune systems were deemed chronically infected at rate θ. Individual in this class can die naturally at a constant rate μ. Individual in the chronic infected and symptomatic class will either die of the disease at the rate ∝ or die naturally at the rate μ or get treated and recover from the disease at the rate ϕ and move to the recovered class. Patients who are admitted to the hospital receive treatment, recover at a rate of τ, and then enter the recovered class, where they may have a natural death rate of μ. Acutely infected people can be treated and progress to the recovered class at a rate of ∝. In this scenario, they may pass away naturally at a rate of μ. It goes without saying that interaction with infected individuals can cause the recovered class to transition to the acutely infected class at rate δ, and that such individuals may also naturally pass away at rate μ.

The following system of ordinary differential equations can be used to represent the associated mathematical equations of the schematic diagram below:

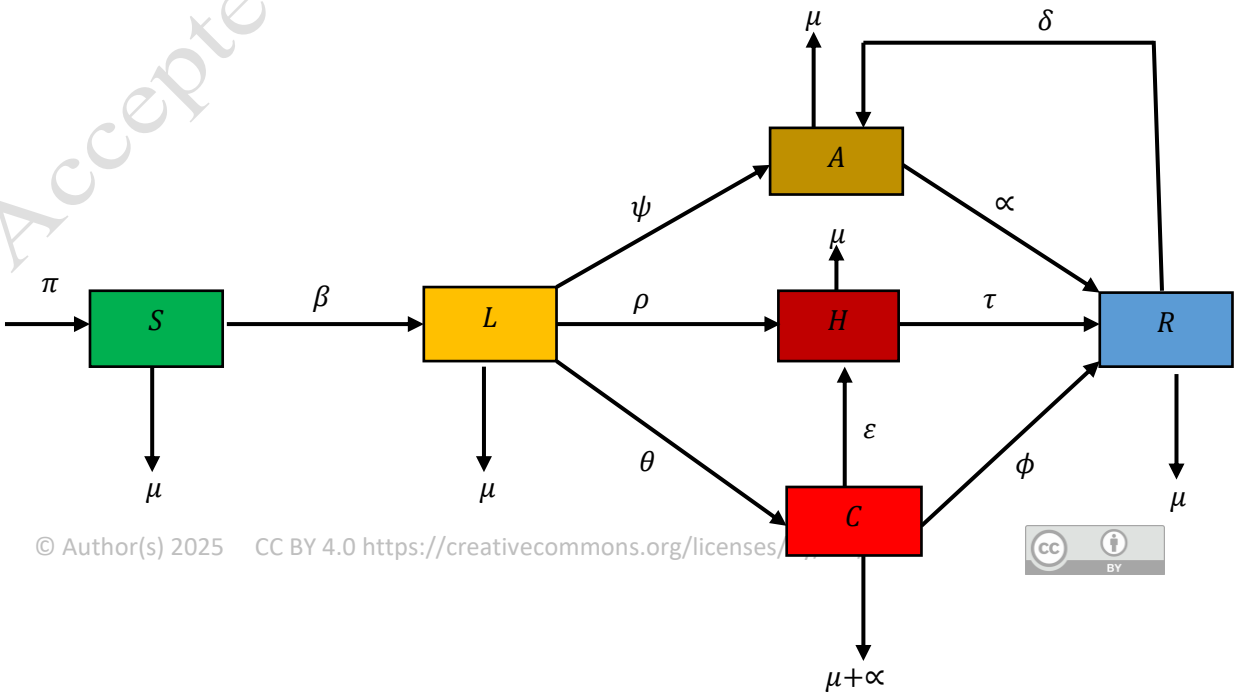

Figure 1: The flow chart

3.1. ***The Model Equation***

Based on the assumptions and interactions between the compartments shown in Figure 1 above, the following system of ordinary differential equations simulates how vaccination affects the hepatitis C virus's epidemiology.

;

$$\left.\begin{aligned}
\frac{dS}{dt} &= \pi - \beta IS - \mu S = \pi - (\beta I + \mu)S \\
\frac{dL}{dt} &= \beta SI - (\psi + \rho + \theta + \mu)L \\
\frac{dA}{dt} &= \psi L + \delta R - (\mu + \propto)A \\
\frac{dC}{dt} &= \theta L - (\varepsilon + \phi + \mu + \propto)C \\
\frac{dH}{dt} &= \rho L + \varepsilon C - (\mu + \tau)H \\
\frac{dR}{dt} &= \propto A + \tau H + \phi C - (\mu + \delta)R
\end{aligned}\right\} \quad (1)$$

Table 1: Notation and definition of Variables

Variables	Description
$\boldsymbol{S(t)}$	Susceptible individuals at time t
$\boldsymbol{L(t)}$	Latent individuals at time t
$\boldsymbol{H(t)}$	Hospitalized individuals at time t
$\boldsymbol{A(t)}$	Acutely infected individuals at time t
$\boldsymbol{C(t)}$	Chronically infected individual at time t
$\boldsymbol{R(t)}$	Recovered individuals at time t
$\boldsymbol{N(t)}$	Total population at time t

Table 2: Notation and definition of Parameters

Parameters	Description
$\boldsymbol{\pi}$	Constant recruitment rate
$\boldsymbol{\beta}$	Constant rate at which susceptible becomes infected
$\boldsymbol{\mu}$	Natural death rate
$\boldsymbol{\alpha}$	Death rate due to HCV
$\boldsymbol{\theta}$	The rate at which Latent becomes chronic
$\boldsymbol{\rho}$	The rate at which Latent becomes chronic
$\boldsymbol{\phi}$	Treatment rate for Chronic infected
$\boldsymbol{\psi}$	The rate at which Latent becomes acutely infected
$\boldsymbol{\epsilon}$	The rate at which Chronically infected are hospitalized
$\boldsymbol{\tau}$	Treatment rate for Hospitalized individuals
$\boldsymbol{\delta}$	Treatment rate for Acutely infected

4. Analysis of the Model Equations

4.1. Positivity and Boundedness of the Solution for the Model

Theorem 1. We let $t_0 > 0, S(0) >, L(0) > 0, H(0) > 0, A(0) > 0, C(0) > 0, R(0) > 0$ then the solutions $S(t), L(t), H(t), A(t), C(t)$ and $R(t)$ of the model equations in (1) are positive for every $t \geq 0$

Proof:

We will prove $S(t), L(t), H(t), A(t), C(t)$ and $R(t)$ are positive in $\Re_+^6$ for all $[0, t_0]$.

Note that every model parameter is positive. Equation (1) indicates that

$$\frac{dS}{dt} = \pi - \beta IS - \mu S \geq -(\beta I + \mu)S \tag{2}$$

So that we have

$$s(t) \geq s(0)e^{-\int(\beta I - \mu)dt} \geq 0 \tag{3}$$

Also, we can show from equation (1) that is

$$\frac{dL}{dt} = \beta SI - (\psi + \rho + \theta + \mu)L \geq -(\psi + \rho + \theta + \mu)L \tag{4}$$

So that

$$L(t) = L(0)e^{-\int(\psi+\rho+\theta+\mu)dt} \geq 0 \tag{5}$$

Similarly, since $e^{(t)} > 0 \forall \omega \epsilon \mathbb{R}$, it can be said that the remaining equations are positive for any $t \geq 0$.

Theorem 2 (Invariant Region).

Equation (1) shows the biologically viable region of the model.

$$\Omega = (S, L, H, A, C, R)\epsilon\Re_+^6 : S(t) + L(t) + H(t) + A(t) + C(t) + R(t) \leq \frac{\pi}{\mu} \tag{6}$$

is positively invariant.

Proof.

Adding all the equations model in (1), we have

$$\frac{dN}{dt} = \frac{dS}{dt} + \frac{dL}{dt} + \frac{dA}{dt} + \frac{dC}{dt} + \frac{dH}{dt} + \frac{dR}{dt} \tag{7}$$

$$\frac{dN}{dt} = \pi - (S + L + A + C + H + R)\mu - \alpha C \tag{8}$$

So that

$$\frac{dN}{dt} \leq \pi - \mu(N) \tag{9}$$

It follows from the Gronwall Inequality

$$N(t) \leq N(0)e^{-\mu(t)} + \frac{\pi}{\mu}\left(1 - e^{-\mu(t)}\right) \tag{10}$$

Hence $N(t) \leq \frac{\pi}{\mu}$ if $N(0) \leq \frac{\pi}{\mu}$ (11)

Thus Ω is positively invariant; therefore, the model equation in (1) is both epidemiologically and mathematically well posed.

4.2. Disease-Free Equilibrium State

The disease-free equilibrium of the model in (1) is obtained by setting

$$\frac{dS}{dt} = \frac{dL}{dt} = \frac{dH}{dt} = \frac{dA}{dt} = \frac{dC}{dt} = \frac{dR}{dt} = 0 \quad (12)$$

In these cases, there is no disease if $L = H = A = C = R = 0$, Hence, the DFE of our equation is given by:

$$\boldsymbol{E^0} = (S^0, L^0, H^0, A^0, C^0, R^0) = \left(\frac{\pi}{\mu}, 0, 0, 0, 0, 0\right) \quad (13)$$

4.3. Basic Reproduction Number

The Basic Reproduction Number (R_0) denotes the average number of secondary infections produced by an infectious individual over their lifespan, as articulated by Diekman et al. (2010). Employing the advanced operator method articulated by Diekmann and Heesterbeek (2000), we calculated the Basic Reproduction Number, R_0, of the model in Equations (7), defined as the spectral radius (ρ) of the next generation matrix, K, so that $R_0 = \rho(K)$, where $K = FV^{-1}$. We define F as the matrix representing the rate of new infections, and V as the matrix indicating the rate of transitions among various sections and the infected sections.

The matrices F, denoting the new infection terms, and V, indicating the transition terms, are formulated based on the infected classes (i.e., L, H, A and C) at HCV-free equilibrium.

where

$$k_0 = (\beta I - \mu)$$

$$K_1 = (\psi + \rho + \theta + \mu)$$

$$K_2 = (\mu + \propto)$$

$$K_3 = (\varepsilon + \phi + \mu + \propto)$$

$$K_4 = (\mu + \tau)$$

$$K_5 = (\mu + \delta)$$

Setting (f_1, f_2, f_3, f_4) as the infected classes of equation (1), and differentiating partially with respect to (*L*,*H*,*A*,*C*) respectively yields F as given below

$$F = \begin{bmatrix} \beta S^0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix} \quad (14)$$

$$V = \begin{bmatrix} K_1 & 0 & 0 & 0 \\ \psi & -K_2 & 0 & 0 \\ 0 & 0 & K_3 & 0 \\ \rho & 0 & \epsilon & -K_4 \end{bmatrix} \quad (15)$$

With

$$V^{-1} = \begin{bmatrix} \frac{1}{K_1} & 0 & 0 & 0 \\ \frac{\psi}{K_1 K_2} & -\frac{1}{K_2} & 0 & 0 \\ -\frac{\theta}{K_1 K_3} & 0 & \frac{1}{K_3} & 0 \\ \frac{\alpha\rho+\epsilon\rho-\epsilon\theta+\mu\rho+\phi\rho}{K_1 K_3 K_4} & 0 & \frac{\epsilon}{K_3 K_4} & -\frac{1}{K_4} \end{bmatrix} \quad (16)$$

multiplying equation (14) and equation (16), thus we have

$$K = FV^{-1} = \begin{bmatrix} \frac{\beta S^0}{K_1} & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix} \quad (17)$$

To get the highest eigenvalue (ρ), we find the characteristic polynomial of K

$$\begin{bmatrix} \frac{\beta S^0}{K_1} - \lambda_1 & 0 & 0 & 0 \\ 0 & 0 - \lambda_2 & 0 & 0 \\ 0 & 0 & 0 - \lambda_3 & 0 \\ 0 & 0 & 0 & 0 - \lambda_4 \end{bmatrix}$$

Therefore, the Basic Reproduction Number is $R_0 = \rho(FV^{-1}) =$ Spectral Radius of FV^{-1} and hence

Consequently, the Basic Reproduction Number is defined as $R_0 = \rho(FV^{-1})$, which corresponds to the Spectral Radius of FV^{-1}. Thus,

$$R_0 = \frac{\beta S^0}{K_1} \quad (18)$$

4.4. Local Stability Analysis of Disease-Free Equilibrium State

Theorem 3:

The disease-free equilibrium, E^*, is locally asymptotically stable in D if $R_0 < 1$ and unstable if $R_0 > 1$.

Proof

We will perform the local asymptotic analysis of the disease-free equilibrium using Jacobian stability techniques.

Jacobian Matrix of the system of equations at disease disease-free equilibrium is at DFE point $\boldsymbol{E^0} = (S^0, 0, 0, 0, 0, 0)$, then we have

$$\boldsymbol{J}=\begin{bmatrix}\beta S^0-K_1 & 0 & 0 & 0 & 0 & 0\\ \psi & -K_2 & 0 & 0 & 0 & 0\\ \theta & 0 & K_3 & 0 & 0 & 0\\ \rho & 0 & \varepsilon & -K_4 & 0 & 0\\ 0 & 0 & 0 & 0 & K_6 & 0\\ 0 & \alpha & \theta & \tau & 0 & -K_5\end{bmatrix} \tag{19}$$

Next applying Gaussian elimination with a series of elementary row operation on matrix J we obtain the row equivalent matrix.

$$\boldsymbol{J}=\begin{bmatrix}\beta S^0+K_1 & 0 & 0 & 0 & 0 & 0\\ 0 & -K_2 & 0 & 0 & 0 & 0\\ 0 & 0 & K_3 & 0 & 0 & 0\\ 0 & 0 & 0 & -K_4 & 0 & 0\\ 0 & 0 & 0 & 0 & K_6 & 0\\ 0 & 0 & 0 & 0 & 0 & K_5+\frac{\alpha\delta}{K_2}\end{bmatrix} \tag{20}$$

Determinant gives

Therefore $\lambda_1 < 0$ if and only if $\beta S^0 - K_1 < 0$. This yield

$$\frac{\beta S^0}{K_1} < \frac{K_1}{K_1}$$

$$\frac{\beta S^0}{K_1} < 1 \tag{21}$$

But

$$R_0 = \frac{\beta S^0}{K_1}$$

The fact that we obtained $R_0 < 1$ and that every single eigenvalue was negative indicates that the disease-free equilibrium is locally asymptotically stable.

4.5. Global Stability of the Disease-Free Equilibrium

Theorem 4:

$R_0 \leq 1$ indicates that the HCV-Free equilibrium (DFE) is globally asymptotically stable.

Proof

Creating a Lyapunov Function to prove this theorem is a popular method for researching the global asymptotic stability of the DFE.

Consider the Lyapunov function

$$L_1 = \psi L + K_1 A \tag{22}$$

Then, taking the derivative along with the solution of the model equation, we have

$$L_1^* = \psi L^* + K_1 A^*$$

$$= \psi(\beta S I - K_1 L) + K_1(\psi L + \delta R - K_2 A)$$

$$= \psi\beta SI - \psi K_1 L + \psi K_1 L + K_1\delta R - K_1 K_2 A$$

$$L_1^* = \psi\beta SI + K_1\delta R - K_1 K_2 A \quad (23)$$

$$= \psi K_1\left[\frac{\beta S^0}{K_1} + \frac{\delta R}{\psi} - \frac{K_2}{\psi}\right]$$

But since $S^0 > S$

$$L_1^* \leq \psi K_1\left[\frac{\beta}{K_1} + \frac{\delta R}{\psi} - \frac{K_2}{\psi}\right]$$

$$\leq \left[R_0 + \frac{\delta R}{\psi} - \frac{K_2}{\psi}\right] \quad (24)$$

The non-negativity of every model parameter indicates that $R_0 \leq 1$, $L_1^* \leq 0$.. This additionally suggests that the Inequality $L_1^* = 0$ is valid when $R_0 = 1$. Thus, this substantiates the theorem and demonstrates that HCV will be managed well.

4.6. Existence of Endemic Equilibrium Point in Terms of Force of Infection

$E^* = (S^*, L^*, A^*, C^*, H^*, R^*) \neq (0,0,0,0,0,0)$. To obtain the endemic equilibra, we see that

From equation (1)

$$S^* = \frac{\pi}{\kappa_0} \quad (25)$$

From equation (2)

$$L^* = \frac{\beta SI}{\kappa_1} \quad (26)$$

Substitute S^* in L^*

$$L^* = \frac{\pi\beta I}{\kappa_0\kappa} \quad (27)$$

Substitute L^* in equation (4)

$$C^* = \frac{\beta I\pi\theta}{\kappa_0\kappa_1\kappa_3} \quad (28)$$

Substitute L^* and C^* in equation (5)

$$H^* = \frac{\beta I\pi\rho K_3 + (\beta I\pi\theta\epsilon)}{\kappa_0\kappa_1\kappa_2\kappa_3} \quad (29)$$

From equation (3)

$$\delta R^* = \kappa_2 A^* - \frac{\psi\beta I\pi}{\kappa_0\kappa_1}$$

From equation (6)

$$A^* = \frac{K_5 R^*}{\alpha} - \frac{\beta I\pi\rho\tau\kappa_3 + \beta\pi\theta\epsilon\tau}{\alpha K_0 K_1 K_3 K_4} - \frac{\beta\pi\theta\phi}{\alpha K_0 K_1 K_3} \quad (30)$$

Substitute A^* in δE^*

$$\delta R^* = K_2\left(\frac{K_5 R^*}{\alpha} - \frac{\beta I\pi\rho\tau\kappa_3 + \beta\pi\theta\epsilon\tau}{\alpha K_0 K_1 K_3 K_4} - \frac{\beta\pi\theta\phi}{\alpha K_0 K_1 K_3}\right) - \frac{\psi\beta I\pi}{K_0 K_1}$$

Hence, we have

$$R^* = \frac{\beta\pi\kappa_2(I\rho\tau\kappa_3+\theta\psi\kappa_2\kappa_4)-\beta I\pi\psi\alpha\kappa_3\kappa_4}{\kappa_0\kappa_1\kappa_3\kappa_4(\delta\alpha-\kappa_2\kappa_5)} \quad (31)$$

Substitute R^* in A^* we have

$$A^* = \frac{\beta\pi\kappa_2\kappa_5(2I\rho\tau\kappa_3+2\theta\epsilon+\theta\psi\kappa_2\kappa_4)-\beta\pi\alpha(I\psi\kappa_3\kappa_4\kappa_5+\delta\tau I\rho\kappa_3+\delta\tau\theta\epsilon+\theta\phi\delta\kappa_4)}{\alpha\kappa_0\kappa_1\kappa_3\kappa_4(\delta\alpha-\kappa_2\kappa_5)} \quad (32)$$

5. **Numerical Simulation**

Owing to the difficulties of acquiring reliable data on disease transmission, we derived certain parameter values from data presently available from the World Health Organization (WHO) and reputable literature. The β variable values designated as "Estimated" in Table 3 were modified to account for disease transmission in relation to treatment rates. They were chosen to precisely reflect the differences in disease transmission risk among demographic categories. Table 4 presents the selected parameter values for disease dynamics.

The numerical computations were performed at 40-month intervals. Considering that the shift from acute to chronic infection often requires three to six months and that direct-acting antiviral treatment spans 12 weeks, a duration of 40 months sufficed to illustrate the disease dynamics.

Table 3: Table for parameters and Value for the Sensitivity index

Parameters	Values	Reference	Sensitivity Sign
β	1	Estimated	+
ψ	0.3025	Estimated	−
ρ	0.3445	Estimated	−
θ	0.3151	Estimated	−
μ	0.0378	Estimated	−

Table 4: Table of population parameter

Parameters and values	Value	Source Estimated
β	0.100	Estimated
ϵ	0.03	WHO (2017)
δ	0.45	WHO (2017)
τ	0.071	Estimated
ψ	0.072	Estimated
ϕ	0.600	WHO (2017)
ρ	0.082	Estimated
θ	0.075	Estimated

μ	0.009	Estimated
α	0.10	Estimated
I	0.1	Estimated

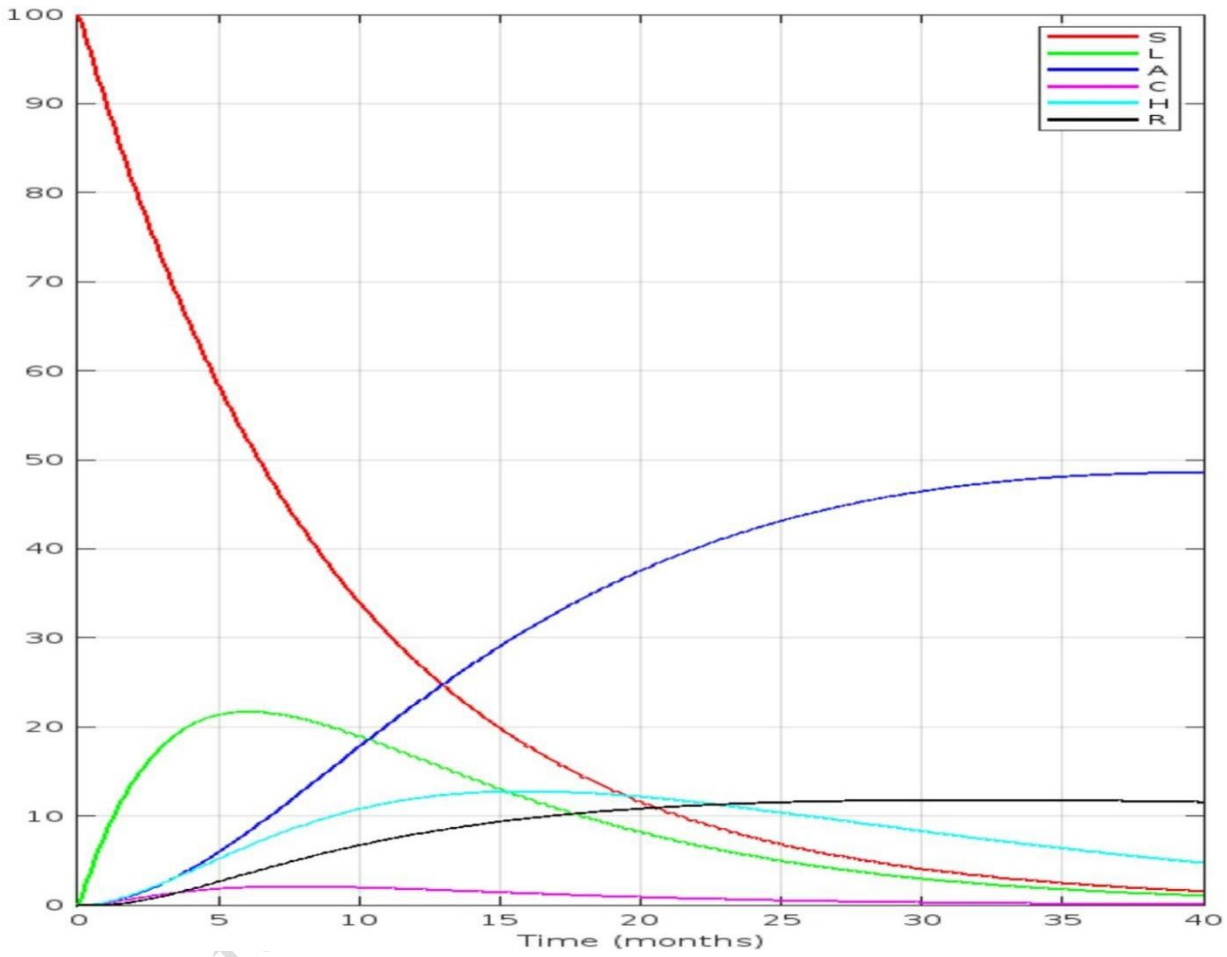

Figure 2: Simulation of HCV model showing the populations of the variables

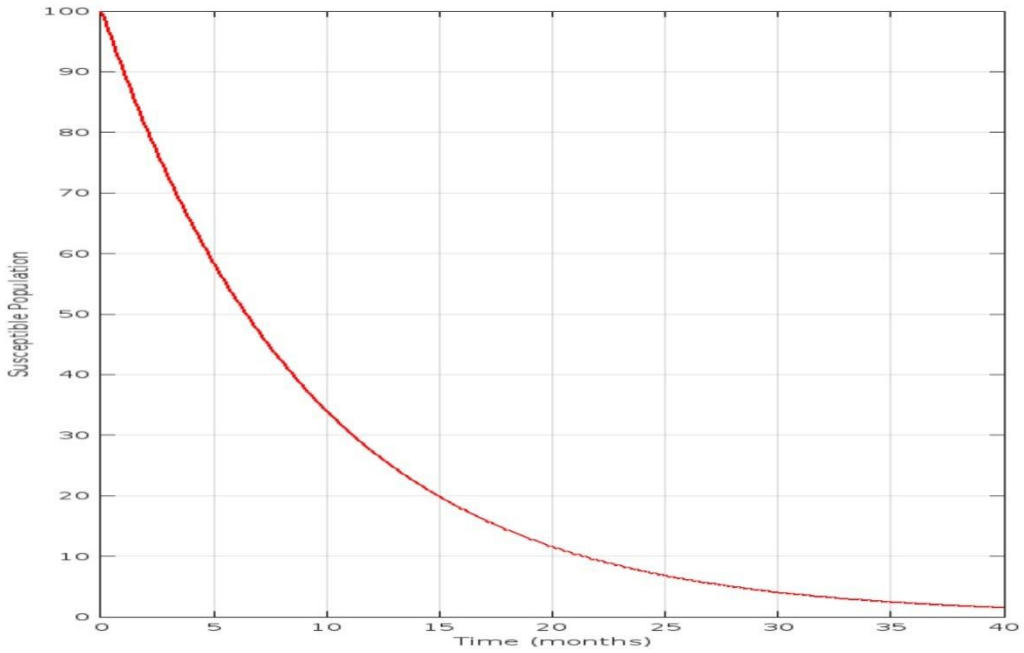

Figure 3: Graph demonstrating the decreased in the susceptible class due to the infection

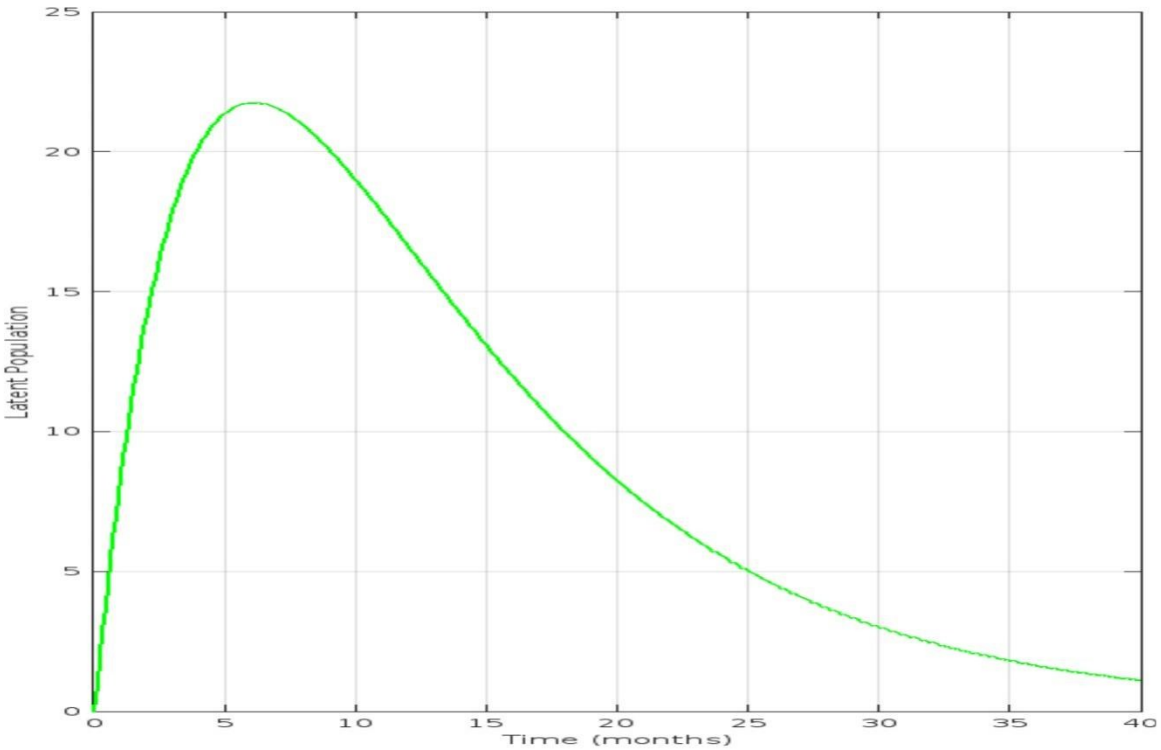

Figure 4: Graph demonstrating the Latent class as they are exposed to the disease

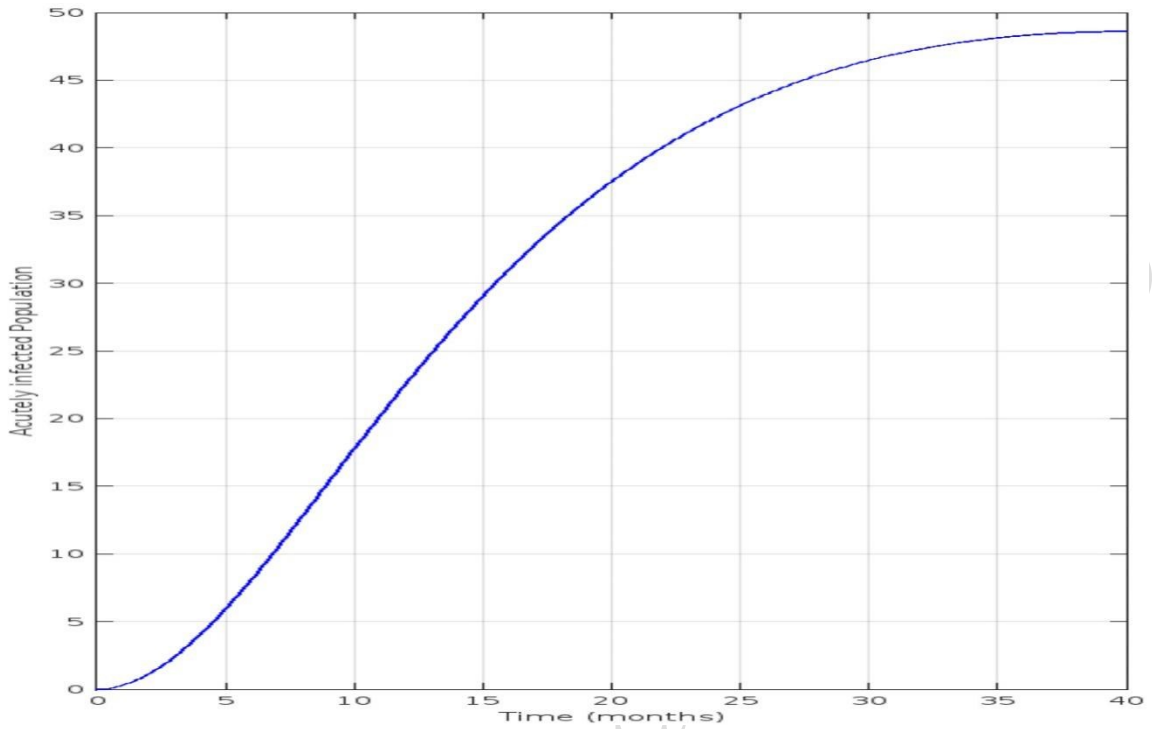

Figure 5: Graph demonstrating the growth of Acutely infected individuals

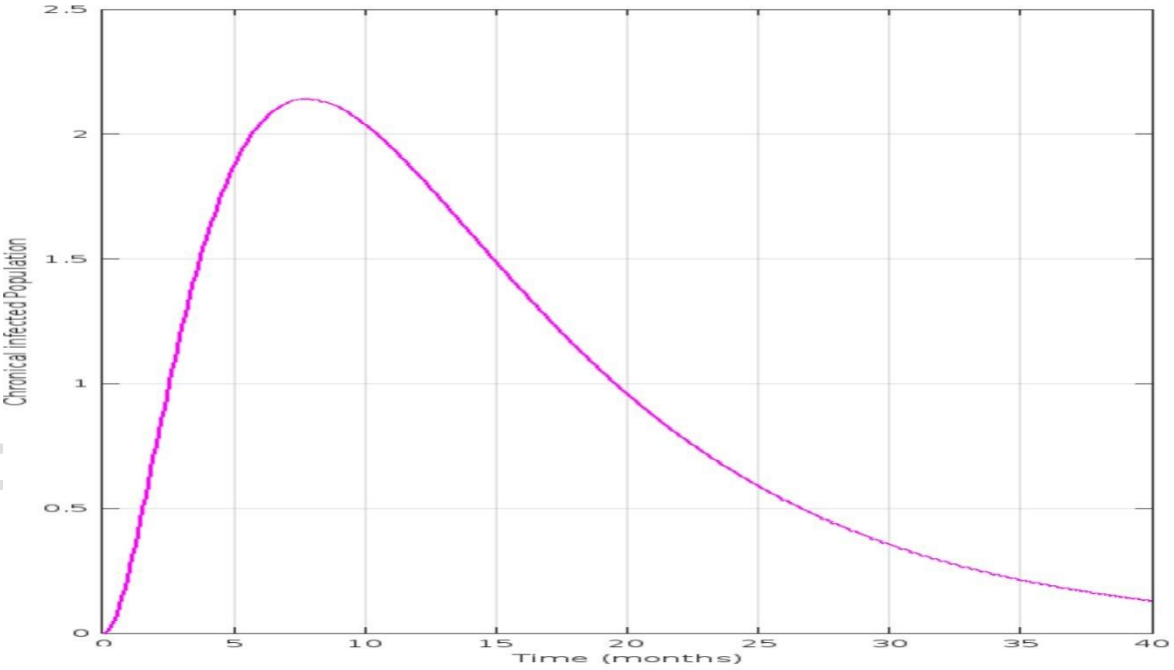

Figure 6: Graph demonstrating the effect of control measures on the Chronically infected class

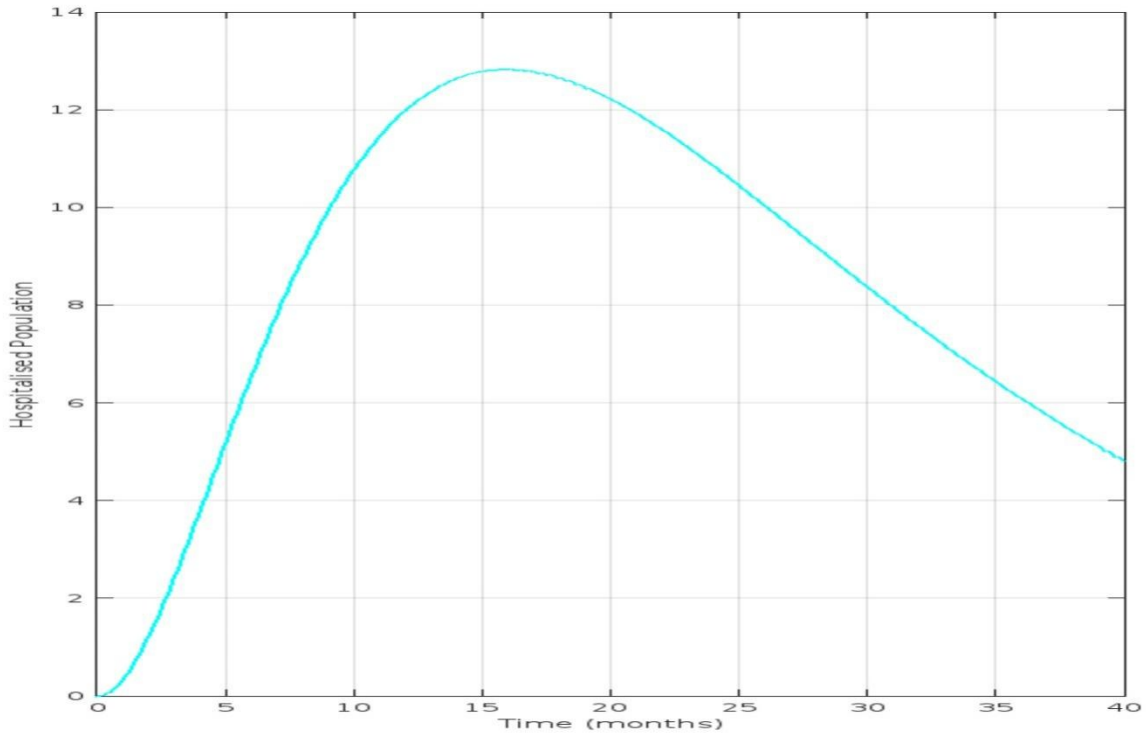

Figure 7: Graph demonstrating the population of individuals who willingly or unwillingly goesto the hospital

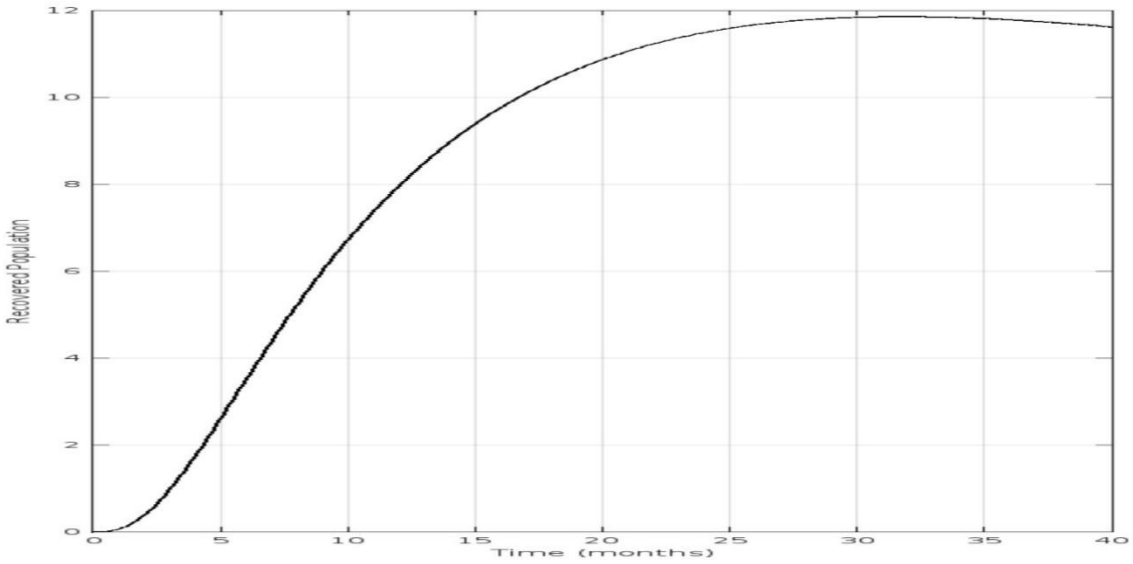

Figure 8: Graph demonstrating the recovery rate of individuals after taking control measures

5.1. Optimal Control

The goal is to minimize the number of infected individuals (both acute and chronic) while considering the cost of implementing measures. We introduce control variables $\mu_1(t)$ and $\mu_2(t)$, representing the efforts to reduce the transmission rate (β) and to increase the recovering rate (α), respectively.
The objective functional is defined as:

$$J(\mu_1, \mu_2) = \int_0^T \left(C_1 A(t) + C_2 C + \frac{1}{2}\left(B_1 \mu_1^2(t) + B_2 \mu_2^2(t)\right)\right) dt$$

where C_1 and C_2 are the weights on the infected populations, and B_1 and B_2 are the weights on the control efforts.
The state equations with the controls incorporated are:

$$\frac{dS}{dt} = \pi + (\beta(1-\mu_1)I - \mu)S \quad (33)$$

$$\frac{dL}{dt} = \beta(1-\mu_1)SI - (\psi + \rho + \theta + \mu)L \quad (34)$$

$$\frac{dA}{dt} = \psi L + \delta R - \left(\mu + \alpha(1-\mu_2)\right)A \quad (35)$$

$$\frac{dC}{dt} = \theta L - \left(\epsilon + \phi + \mu + (1-\mu_2)\right)C \quad (36)$$

$$\frac{dH}{dt} = \rho L + \epsilon C - (\mu + \tau)H \quad (37)$$

$$\frac{dR}{dt} = \alpha(1-\mu_2)A + \tau H + \phi C + (\mu + \delta)R \quad (38)$$

The Hamiltonian H for this control problem is:

$$H = C_1 A(t) + C_2 C(t) + \frac{1}{2}(B_1 \mu_1^2(t) + B_2 \mu_1^2(t) + \lambda s(\pi + (\beta(1-\mu_1)I - \mu)S) + \lambda_L(\beta(1-\mu_1)SI - (\psi + \rho + \theta + \mu)L + \lambda_A(\psi L + \delta R - \left(\mu + \alpha\left((1-\mu_2)\right)A\right) + \lambda_C(\theta L - \left(\epsilon + \phi + \mu + \alpha\left((1-\mu_2)\right)C\right) + \lambda_H(\rho L + \epsilon C - (\mu + \tau)H) + \lambda_R(\alpha(1-\mu_2)A + \tau H + \phi C + (\mu + \delta)R) \quad (39)$$

Where λ_i are the adjoint variables.
The necessary condition for optimality includes:

1. $\frac{\partial H}{\partial \mu_1} = 0$
2. $\frac{\partial H}{\partial \mu_2} = 0$
3. The adjoint equations, derived from $\frac{d\lambda_i}{dt} = -\frac{\partial H}{\partial x_i}$

We employ Pontryagin's Maximum Principle for the optimal control problem. The state and adjoint equations can be solved concurrently with the transversality condition $\lambda_i(T) = 0$ to obtain the optimal controls μ_1^* and μ_2^*.

The optimal controls are given by:

$$\mu_1^*(t) = \min\left\{\max\left\{0, \frac{\beta SI(\lambda_S - \lambda_L)}{B_1}\right\}, 1\right\} \quad (40)$$

$$\mu_2^*(t) = \min\left\{\max\left\{0, \frac{\alpha A(\lambda_A - \lambda_R) + \alpha C(\lambda_C - \lambda_R}{B_2}\right\}, 1\right\} \quad (41)$$

5.2. Numerical Simulation for Optimal Control

To illustrate the application of the optimal control strategy, a numerical simulation can be performed. The forward-backward sweep method is typically used for such simulations, which involves:

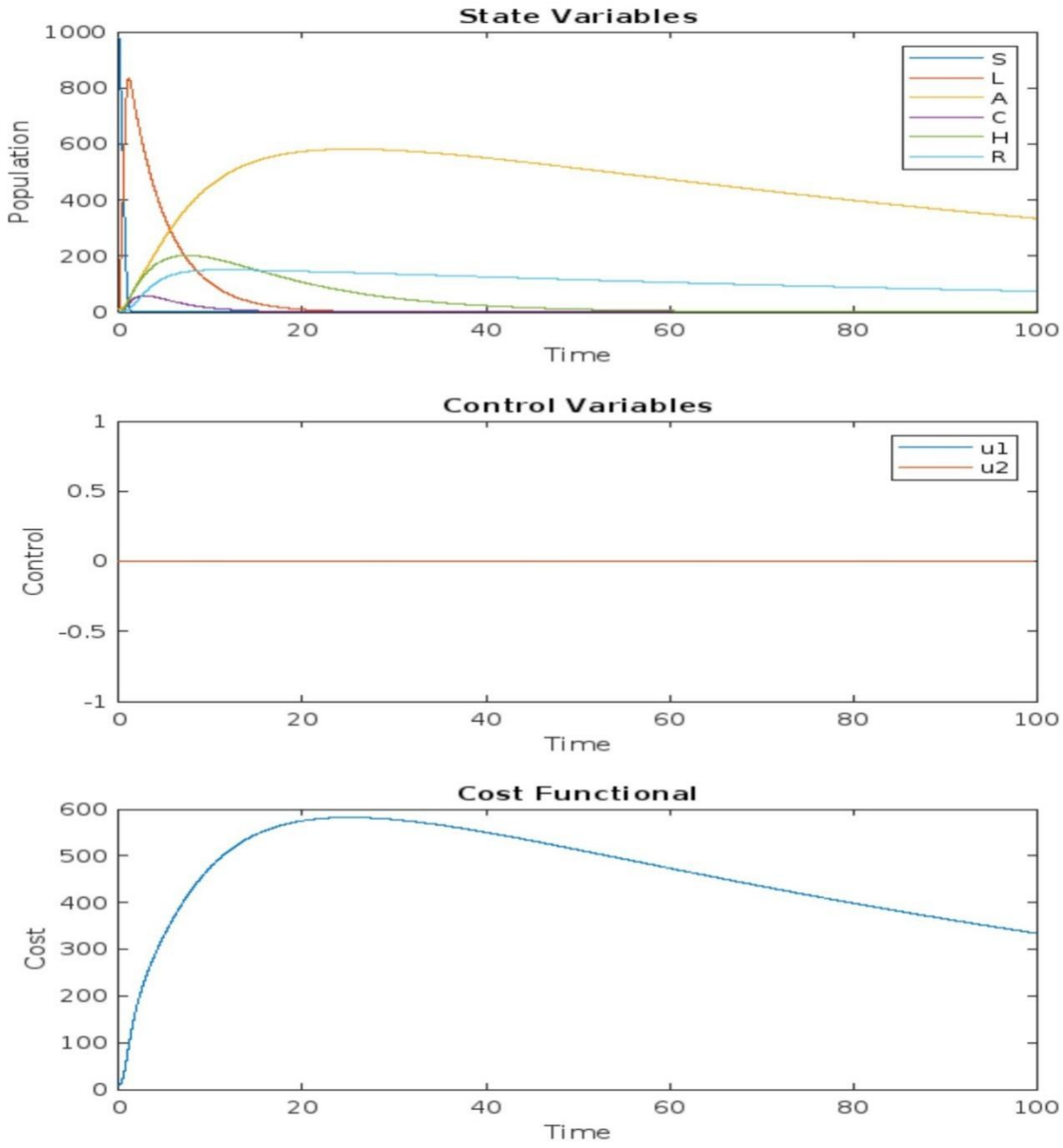

Figure 9: Plot of Optimal Control

By examining these graphs, we can assess the dynamics of the Hepatitis C epidemic under the optimal control strategy. The state variables subplot reveals how the disease progresses and responds to control measures. The control variables subplots indicate the level of effort applied to control the disease over time. Finally, the cost functional subplot demonstrates the effectiveness of these control measures in reducing the number of infected individuals, balancing public health outcomes with the associated costs.

The optimal control strategy for Hepatitis C involves balancing the efforts to reduce the transmission and increase recovery. By implementing the controls U_1 and U_2, it is possible to minimize the number of acutely and chronically infected individuals while considering the costs associated with the control

measures. The numerical simulations demonstrate the effectiveness of the optimal control strategy in managing Hepatitis C.

6. **Discussion**

The effect of increasing the treatment rate and executing specific control procedures is illustrated in the graphs of Figures 2–9. When a government policy is implemented, public awareness is heightened, and proper education on drug usage and condom utilization is delivered to avoid STDs. As it can be seen from Figure 2. The susceptible class curve shows a rapid decline in the susceptible population. This suggests that most individuals are either getting infected or transitioning to another compartment.

The latent class curve shows an initial rise in the latent population, peaking around 8months and then declining. This indicates that many individuals become latent (exposed but not yet infectious) early on, but the number of latent individuals decreases over time as they progress to other stages (e.g., acute infection or recovery).

The acutely infected population rises steadily, peaking around 25 months, suggesting that as individuals move from latency, they enter the acute infection phase, leading to an increase in cases.

The chronically infected population is very small compared to others, peaking around 10 months. This suggests that only a small fraction of the population moves into the chronic infection state.

The hospitalized population peaks around 12-15months, after which it begins to decline. This reflects a trend where acute cases are severe enough or require hospitalization, but the number of hospitalized individuals decreases as the epidemic winds down. The recovered population increases gradually and stabilizes after about 15months. This indicates that after infection or hospitalization, individuals eventually recover, and the numbers stabilize over time.

In Figure 3 at the start of the timeline, the susceptible population is at its highest, close to 100. This implies that almost all individuals in the population are vulnerable to infection at the onset of the epidemic. By the 40-month mark, the susceptible population is almost zero. This indicates that the vast majority of individuals have either been infected and moved to another category (e.g., latent, acutely infected, or recovered) or possibly vaccinated or immune, leaving very few people still at risk of infection.

In figure 4 the latent population increases rapidly at the start, reaching its peak around 5months.This suggests that during the initial phase of the epidemic, a significant portion of the population is entering the latent stage of the infection. These individuals are infected but not yet actively spreading the disease or showing severe symptoms. After the peak, the number of latent individuals steadily declines. This could be due to the transition of these individuals from the latent phase to either becoming acutely infected, showing symptoms, or recovering. The steady decline continues throughout the 40months, indicating that fewer people are remaining in the latent stage as the disease progresses.

In figure 5 the curve starts with a gradual increase in the acutely infected population, indicating that the infection begins slowly but gains momentum over time. During this phase, the infection rate might still be relatively low, and only a small portion of the population is affected. Around 35 to 40months, the graph begins to plateau, suggesting that the number of new acute infections is stabilizing. The infection is no longer spreading as quickly, likely due to factors such as containment measures, increased immunity, or saturation of susceptible individuals.

In figure 6 The number of chronically infected individuals rises quickly at the start, reaching a peak around 5 months. This suggests that some individuals develop chronic conditions early in the disease progression, likely due to long-term effects of the infection that aren't resolved immediately. After reaching

the peak, the graph steadily declines, indicating a reduction in the number of chronically infected individuals. This could be due to either successful treatment, recovery, or other outcomes that reduce the number of long-term cases over time. The decline continues over the 40month period without leveling off, suggesting the chronic infections are gradually being resolved.

In figure 7 at the start, the number of hospitalized individuals increases rapidly. This suggests a growing outbreak or disease spread, where more people are becoming severely affected and requiring hospitalization. After the peak, the curve shows a steady decline, suggesting that the number of hospitalized individuals decreases over time. This is due to recovery, better treatment, or containment of the outbreak, leading to fewer people requiring hospitalization.

In figure 8 at the start, the curve shows a rapid increase in the number of recovered individuals. This could represent a scenario where recovery starts slowly at first but accelerates as more individuals start recovering, possibly due to increasing medical interventions or natural recovery processes. After about 25months, the curve begins to level off, reaching a plateau. This indicates that there covering rate slows down, and eventually, no significant increase in the recovered population occurs. This is typical when the maximum recovery potential is reached, and most of the affected population has recovered.

6.1. Concluding Remarks

This study utilized a set of first-order ordinary differential equations to enhance and assess a mathematical model for the spread and control of hepatitis C virus infection. The constructed model was assessed by analyzing the different transmission routes of the disease, integrating treatment and additional control strategies. After calculating the model's basic or effective reproduction number, the equilibrium states were identified, and their stability concerning the effective reproduction number was examined. The findings demonstrate that the stability criteria for the endemic equilibrium were established, whereas the disease-free equilibrium persisted in a stable state. The model's equilibria, whether infectious or disease-free, are endemic or unstable when $R_0 > 1$, and are locally and globally asymptotically stable when $R_0 < 1$. The model's numerical simulations indicate that if adequate education, awareness, and public consciousness are implemented promptly at the onset of the disease outbreak, alongside the model's recommended interventions, the hepatitis C virus can be eradicated or diminished to the lowest feasible level within the targeted population. In conclusion, individuals are more inclined to seek medical care at hospitals when there is sufficient knowledge, effective government policy, public education, information on drug use, promotion of condom usage, suitable facilities, and high-quality treatment available. This will assist in managing and averting the dissemination of HCV.

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