Model for HIV/AIDS Incorporating Pre- and Post-Exposure Treatments & Reproduction Number Derivation

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Abstract

Given the emergence of Pre-Exposure Prophylaxis (PrEP) as a preventative method for HIV, analyzing its potential impact has been a major area of research recently. When taken at the prescribed level, PrEP has been shown to be remarkably effective at preventing HIV, especially in high risk individuals.

We propose a robust compartmental model incorporating both Pre- and Post-Exposure treatment methods. We derive the basic, control, and effective control reproduction numbers for the HIV epidemic in the presence of treatment measures by formulating the next generation matrix of our model. We subsequently prove the stability criteria of the model in terms of these reproduction numbers.

Large cost savings can be achieved by increasing uptake of PrEP and thereby decreasing the value of the effective control reproduction number. The ratio between transfer rates in our compartmental model has great implications — our research indicates that it possible for HIV prevalence to be greatly reduced in the near future by increasing uptake into the two care states.

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1 Introduction

1.1 HIV Background

Human Immunodeficiency Virus (HIV) has been regarded as an epidemic for decades, and while new treatments and prevention measures have arisen, it still presents a great burden on communities and social systems. HIV is transmitted through bodily fluids, and the most common ways in which this disease is spread is through sharing needles and unprotected sex. Historically, incidences of HIV has been the highest among men who have sex with men. It is important to note that Acquired Immunodeficiency Syndrome (AIDS) is the most extreme infection phase of HIV. Therefore, in this paper HIV and AIDS are used interchangeably as preventing HIV also prevents AIDS.

Recently, it has been seen that the incidence of HIV/AIDS has not significantly decreased [2]. While there is no cure for this virus, the emergence of improved post-exposure treatment combinations has increased the overall life expectancy of individuals living with HIV to more than 32 years from the time of diagnosis. This treatment method is known as Antiretroviral Therapy (ART), a cocktail of various drugs that the patients must take on a strict schedule. An unintended consequence of this remarkably effective treatment is that people living with HIV must take these medications for the rest of their lives, with lifetime costs rising to \$375,000 or more [12].

The importance of preventative measures is clear from both medical and economic perspectives. One of the most promising preventative strategies is Pre-Exposure Prophylaxis (tenofovir and emtricitabine), a daily pill taken before potential exposure to HIV. Taking the pill with the prescribed adherence has been shown to tremendously reduce the risk of contracting HIV [5]. With usage of PrEP growing in popularity, we would like to analyze the mathematical implications of introducing such an effective prevention measure.

1.2 Modeling Background

We model the system dynamics of the HIV epidemic by extending existing compartmental models [8] [11]. The classical compartmental model for representing disease dynamics is the Kermack-McKendrick model, which divides a population into mutually exclusive groups that relate to specific disease states. The population is broken up into three main groups: Susceptible (S), Infected (I), and Recovered (R) to form the SIR model. An individual can either be removed from a state or they can join a state, and it is the interaction of these two processes that determine the system dynamics.

The literature of mathematical epidemiology is well established and diverse in scope [3]. Compartmental models have long been applied to biological systems, and their mathematical properties are well formulated [4]. Previous modelling approaches similar to this one have been used to characterize the stability of a variety of diseases [14], including HIV/AIDS in the presence of post-exposure treatments [11] [7]. We will follow the procedure of these studies in our investigation of HIV/AIDS in the presence of PrEP to derive a novel formulation of the reproduction numbers of the system.

1.3 Goals and Objectives

In this paper, we first present our model for HIV in the presence of treatment methods. Next, we derive the reproduction number and explore the stability of our model. We finish with a discussion of the results and directives for future research.

Our goals for this project are twofold. First, we set out to create a model representing the dynamics of the HIV/AIDS epidemic to include recently developed prevention methods. Second, we sought to understand our model's theoretical stability by deriving its reproduction numbers.

2 Compartmental Model Formulation

We begin our modelling efforts with a modified Kermack-McKendrick compartmental model. There is no recovered state for HIV, but we will include states for both Pre-Exposure and Post-Exposure treatment methods (PrEP and ART respectively). The state variables of our system are S, P, I, A which correspond to the Susceptible, on PrEP, Infected, and on ART states. The infected states of our model are those individuals in the Infected state and those in the ART state. To be clear, the individuals in the Infected state are those infected and not taking the antiretroviral therapy treatment, while the individuals in the ART state are those infected and taking the treatment. The total population of the system is defined as N [4].

The model is proposed as follows:

$$
\begin{aligned}
&\frac{dS}{dt} = \beta N + \phi_p P - (\lambda I + \epsilon_a \lambda A + \tau_p + \mu_s) S \\
&\frac{dP}{dt} = \tau_p S - (\mu_p + \phi_p + \epsilon_p \lambda I + \epsilon_p \epsilon_a \lambda A) P \\
&\frac{dI}{dt} = \phi_a A + \lambda (IS + \epsilon_a AS + \epsilon_p IP + \epsilon_a \epsilon_p AP) - (\mu_i + \tau_a) I \\
&\frac{dA}{dt} = \tau_a I - (\phi_a + \mu_a) A \\
&N = S + P + I + A
\end{aligned}
$$

N	Total Population Size
β	Recruitment Rate
λ	Contact Rate
τ_p	Entering PrEP
τ_a	Entering ART
μ_*	Death Rate
ϕ_p	Exiting PrEP (dropping out of care)
ϕ_a	Exiting ART (dropping out of care)
ϵ_*	reduced infectiousness (effect of treatment)

Table 1: HIV model formulation including PrEP and ART

This model consists of a series of four first order, nonlinear ordinary differential equations. The first equation corresponds to the rate of change in the number of the susceptible population. Individuals can enter the susceptible state through recruitment or dropping out of PrEP treatment and thereby becoming susceptible again. When modelling, one must be careful to define his or her susceptible population appropriately. In this case, sexually active individuals are the susceptible population. Individuals can leave the susceptible state by no longer being sexually active, becoming infected from someone who themself is infected. However, the likelihood of becoming infected from an individual who is infected and on ART is lower than becoming infected from someone who is infected and not on ART [1]. People can also leave the susceptible state by entering PrEP. The second equation relates to the rate of change of people on PrEP. Individuals can enter the PrEP state by being prescribed and taking the preventative drugs at the proper dosage. Individuals can exit the PrEP state by dying, dropping out of care, or becoming infected. It should be noted that the chance of becoming infected while on PrEP is extremely low, and $\epsilon_p \to 0$. The third equation relates to the rate of change in the infected population. People can enter the infected state if they are already infected and exit the ART state or by becoming infected with the virus. There are four ways the disease can be transmitted in this model: a susceptible person is infected by someone in the infected state, a susceptible person is infected by someone in the ART state, an individual on PrEP is infected by someone in the infected state, or an

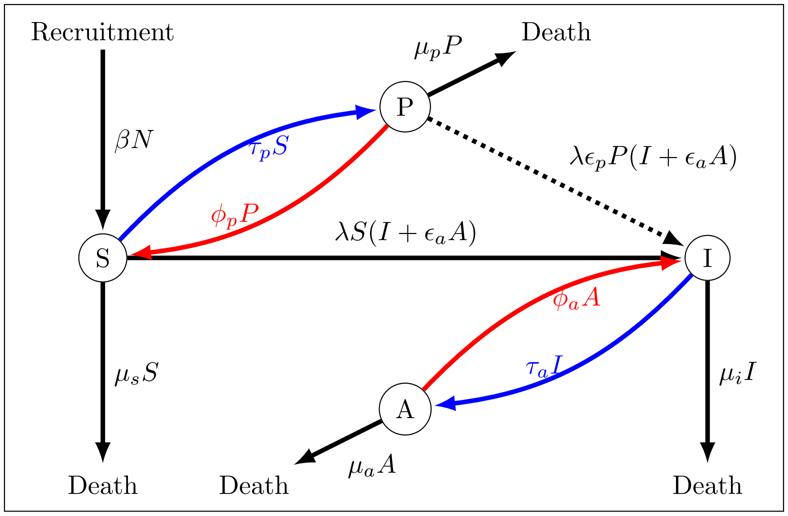

Figure 1: State flow graph of compartmental model depicting transitions between states

individual on PrEP is infected by someone in the ART state. It should be noted that the first way is the most likely out of all of these as the probabilities of other modes of transmission are reduced by the effects of the treatment methods. Meanwhile, people can exit the infected state by dying or starting Antiretroviral Therapy. A person can enter this state by beginning antiretroviral treatment and taking their prescribed pills. A person can exit the ART state by dying or dropping out of treatment through no longer taking their medication. The transfers between states can be seen in Figure 1 where blue arrows correspond to entrance into a care state and red arrows correspond to dropping out of care.

2.1 Derivation of Basic and Effective Control Reproduction Number

From this formulation, we follow the methods outlined by Driessche et al. [4] and propose that the model can be rewritten in the form $\frac{d}{dt}(\vec{x}) = \mathbb{F}(\vec{x}) - \mathbb{V}(\vec{x})$. We define the vector $\vec{x} = (I, A, S, P)^t$. In this formulation, $\mathbb{F}$ represents the transmission matrix (new infections in the system) and $\mathbb{V}$ represents the transition matrix (transfers between the states). Therefore we have:

$$\mathbb{F}(\vec{x}) = \begin{bmatrix} \lambda(IS + \epsilon_a AS + \epsilon_p IP + \epsilon_a \epsilon_p AP) \\ 0 \\ 0 \\ 0 \end{bmatrix} \tag{1}$$

$$\mathbb{V}(\vec{x}) = \begin{bmatrix} I(\mu_i + \tau_a) - A\phi_a \\ A(\mu_a + \phi_a) - I\tau_a \\ S(\mu_s + \tau_p) - \beta N - P\phi_p + S\lambda(I + A\epsilon_a) \\ P(\mu_p + \phi_p) - S\tau_p + P\epsilon_p\lambda(I + A\epsilon_a) \end{bmatrix} \tag{2}$$

Continuing, we calculate the Disease Free Equilibrium (DFE), the equilibrium point where there is no change in the states of the model and the number of infected individuals is 0. For this calculation, we set the rate of change of the system equal to 0 and solve for the values of equilibrium points S^* and P^*. In this calculation, we let the recruitment into the system βN to be a constant B. This is a generally safe as $\frac{dN}{dt} \approx 0$ as the total population of the system can seen to be relatively stable [2]. Thus we calculate DFE as follows:

$$\begin{aligned} 0 &= P\phi_p + B - S(\mu_s + \tau_p) \\ 0 &= S\tau_p - P(\mu_p + \phi_p) \end{aligned} \tag{3}$$

Thus when solved, this system yields $S^* = \dfrac{B(\mu_p + \phi_p)}{\mu_p\mu_s + \mu_s\phi_p + \mu_p\tau_p}$; $P^* = \dfrac{B\tau_p}{\mu_p\mu_s + \mu_s\phi_p + \mu_p\tau_p}$

Subsequently, we calculate the Jacobian Matrices $D\mathbb{F}$ and $D\mathbb{V}$ linearized about DFE $\vec{x_0} = (S^*, P^*, 0, 0)$ as follows:

$$D\mathbb{F}(\vec{x_0}) = \begin{bmatrix} \lambda(S^* + P^*\epsilon_p) & \lambda(S^*\epsilon_a + P^*\epsilon_a\epsilon_p) & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix} \tag{4}$$

$$D\mathbb{V}(\vec{x_0}) = \begin{bmatrix} \mu_i + \tau_a & -\phi_a & 0 & 0 \\ -\tau_a & \mu_a + \phi_a & 0 & 0 \\ S^*\lambda & S^*\epsilon_a\lambda & \mu_s + \tau_p & -\phi_p \\ P^*\epsilon_p\lambda & P^*\epsilon_a\epsilon_p\lambda & -\tau_p & \mu_p + \phi_p \end{bmatrix} \tag{5}$$

At this point it is worth noting that because the reproduction numbers of an epidemic signify the number of secondary infections caused by an initially infected individual, only the infected states are relevant to their derivation [3]. Therefore, we can partition the Jacobian matrices (4) and (5) as follows to isolate submatrices

F and V as they encode the infected states, I and A.

$$D\mathbb{F}(\vec{x_0}) = \begin{pmatrix} F & 0 \\ 0 & 0 \end{pmatrix}; D\mathbb{V}(\vec{x_0}) = \begin{pmatrix} V & 0 \\ J_1 & J_2 \end{pmatrix}$$

We can now calculate the spectral radius ρ of the Next Generation matrix FV^{-1}. The significance of this value is explored at length in Driessche et al [4]. We will take this as our control reproduction number, R_c. Thus we have:

$$FV^{-1} = \begin{bmatrix} \frac{\lambda(S^*\mu_a+S^*\phi_a+P^*\epsilon_p\mu_a+P^*\epsilon_p\phi_a+S^*\epsilon_a\tau_a+P^*\epsilon_a\epsilon_p\tau_a)}{(\mu_a\mu_i+\mu_i\phi_a+\mu_a\tau_a)} & \frac{\lambda(S^*\phi_a+P^*\epsilon_p\phi_a+S^*\epsilon_a\mu_i+S^*\epsilon_a\tau_a+P^*\epsilon_a\epsilon_p\mu_i+P^*\epsilon_a\epsilon_p\tau_a)}{\mu_a\mu_i+\mu_i\phi_a+\mu_a\tau_a} \\ 0 & 0 \end{bmatrix} \tag{6}$$

$$\begin{aligned} R_c = \rho(FV^{-1}) = \frac{\lambda(S^* + \epsilon_p P^*)(\mu_a + \phi_a + \epsilon_a\tau_a)}{\mu_a\mu_i + \mu_i\phi_a + \mu_a\tau_a} = \frac{\lambda(\mu_a + \phi_a + \epsilon_a\tau_a)}{\mu_a\mu_i + \mu_i\phi_a + \mu_a\tau_a}(S^* + \epsilon_p P^*) \\ = \frac{\lambda B(\mu_a + \phi_a + \epsilon_a\tau_a)}{(\mu_p\mu_s + \mu_s\phi_p + \mu_p\tau_p)(\mu_a\mu_i + \mu_i\phi_a + \mu_a\tau_a)}(\mu_p + \phi_p + \epsilon_p\tau_p) \end{aligned} \tag{7}$$

To clarify, the subtle distinction between the control reproduction number R_c and the basic reproduction number R_0 is that R_c includes the entrance into treatment measures where R_0 is defined as the number of individuals an initially infected individual will infect in a susceptible population. If we eliminate the treatment measures by setting $\tau_a = \tau_p = 0$ we achieve our basic reproduction number given by

$$R_0 = \frac{\lambda B(\mu_a + \phi_a)}{(\mu_p\mu_s + \mu_s\phi_p)(\mu_a\mu_i + \mu_i\phi_a)}(\mu_p + \phi_p) \tag{8}$$

From available data, We can make the assumption that the death rates across all states are relatively the same [2]. Therefore we have that $\mu_a = \mu_i = \mu_p = \mu_s = \mu$ and if we operate at DFE, we know that the recruitment into the system must equal the exit from the system such that $\beta = \mu$. Our reproduction numbers simplify to:

$$R_0 = \frac{\lambda N}{\mu} \tag{9}$$

$$R_c = \frac{\lambda N}{\mu} \cdot \frac{(\mu + \phi_a + \epsilon_a\tau_a)(\mu + \phi_p + \epsilon_p\tau_p)}{(\mu + \phi_p + \tau_p)(\mu + \phi_a + \tau_a)} = R_0 \cdot \frac{(\mu + \phi_a + \epsilon_a\tau_a)(\mu + \phi_p + \epsilon_p\tau_p)}{(\mu + \phi_p + \tau_p)(\mu + \phi_a + \tau_a)} \tag{10}$$

It is worth noting that our proposed basic reproduction number is exactly as formulated in previous research, thereby confirming our procedure. Finally, we drive $\epsilon_a = \epsilon_p \to 0$, meaning that ART and PrEP are completely effective at preventing transmission when taken at the prescribed adherence [2]. In other words, individuals taking ART are completely virally suppressed, and individuals taking PrEP have no risk for contracting the disease. With this we formulate R_{ce}, the effective control reproduction number. We take R_{ce} to represent the discounted control reproduction number, only taking those individuals truly susceptible to the disease into account. Thus we posit

$$R_{ce} = R_0 \cdot \frac{(\mu + \phi_a)(\mu + \phi_p)}{(\mu + \phi_p + \tau_p)(\mu + \phi_a + \tau_a)} \tag{11}$$

2.2 Stability Criteria

The stability of this system can be investigated in terms of the basic reproduction numbers. We make the following substitution for brevity: $f_1 = \dfrac{dS(t)}{dt}$, $f_2 = \dfrac{dP(t)}{dt}$, $f_3 = \dfrac{dI(t)}{dt}$, $f_4 = \dfrac{dA(t)}{dt}$. Thus we formulate the Jacobian of this system as follows:

$$J = \begin{bmatrix} \frac{\partial f_1}{\partial S} & \frac{\partial f_1}{\partial P} & \frac{\partial f_1}{\partial I} & \frac{\partial f_1}{\partial A} \\ \vdots & \vdots & \vdots & \vdots \\ \frac{\partial f_4}{\partial S} & \frac{\partial f_4}{\partial P} & \frac{\partial f_4}{\partial I} & \frac{\partial f_4}{\partial A} \end{bmatrix}$$

If we continue with the assumptions made above that the recruitment and death rates are equal across all states at the equilibrium point, and that $\epsilon_a = \epsilon_p = 0$ Our Jacobian linearized about DFE $(S^*, P^*, 0, 0)^t$ becomes:

$$J = \begin{bmatrix} -\mu - \tau_p & \phi_p & -\lambda S^* & 0 \\ \tau_p & -\mu - \phi_p & 0 & 0 \\ 0 & 0 & \lambda S^* - \tau_a - \mu & \phi_a \\ 0 & 0 & \tau_a & \mu - \phi_a \end{bmatrix} \tag{12}$$

Since (12) is a Linearly Time Invariant (LTI) matrix, showing that that the real parts of the eigenvalues of the Jacobian are negative is sufficient to establish that this is a stable system. By solving the characteristic equation of (12), we find the eigenvalues of this system to be:

$$
\begin{aligned}
e_1 &= -\mu \\
e_2 &= -\mu - \phi_p - \tau_p \\
e_3 &= \frac{\lambda S^* - \phi_a - \tau_a - 2\mu - \sqrt{(\lambda S^* + \tau_a + \phi_a)^2 - 6S^*\lambda\tau_a}}{2} \\
e_4 &= \frac{\lambda S^* - \phi_a - \tau_a - 2\mu + \sqrt{(\lambda S^* + \tau_a + \phi_a)^2 - 6S^*\lambda\tau_a}}{2}
\end{aligned} \tag{13}
$$

Where it is trivial to see that $e_1, e_2 < 0$ as the parameters in our model are positive. The real part of e_3 simplifies to $-\mu$ which is the same as e_1. When similarly simplifying the real part of e_4 we have the relation $\mathrm{Re}(e_4) = \lambda S^* - \mu$. To make this negative we must have $\mu > \lambda S^*$, where we have the value of $S^* = \dfrac{N(\mu + \phi_p)}{(\phi_p + \tau_p + \mu)}$. Thus we have,

$$
\begin{aligned}
\frac{\lambda N(\mu + \phi_p)}{(\phi_p + \tau_p + \mu)} &< \mu \\
Re(e_4) = R_0 \frac{\mu + \phi_p}{\mu + \phi_p + \tau_p} &< 1
\end{aligned} \tag{14}
$$

It can be seen that the above expression of $\mathrm{Re}(e_4)$ is the Disease-Free formulation of R_{ce}. Meaning, if we have no infected individuals and drive $(\tau_a, \phi_a) \to 0$, this expression is exactly our effective control reproduction number, $\mathrm{Re}(e_4) = R_{ce}$. Thus, in an infection free state, driving R_{ce} below 1 yields a stable system.

Extending this procedure to the endemic equilibrium state $(S^*, P^*, I^*, A^*)^t$, we must satisfy the relation

$$
R_0 \cdot \frac{\mu + \phi_p}{\mu + \phi_p + \tau_p} \cdot \frac{(\mu + \phi_a)}{(\mu + \phi_a + \tau_a)} < 1 \tag{15}
$$

in order for the real parts of the eigenvalues to be negative. Thus, if we satisfy $R_{ce} < 1$ the real parts of the eigenvalues of the linearized Jacobian are negative and the system is stable.

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3 Discussion

3.1 Epidemiological Interpretation

In this section we hope to offer meaning to important concepts in our mathematical abstraction of the biological system. One can interpret our formulation of DFE as the number of individuals in the susceptible vs PrEP states at the point where there are no more infected individuals. The ratio of $\frac{S^*}{P^*} = \frac{\mu + \phi_p}{\tau_p}$ makes intuitive sense as the DFE susceptible population should be proportional to the DFE PrEP population by a ratio of individuals exiting vs. entering PrEP.

The elements (i,j) of the next generation matrix FV^{-1} signify the number of new cases in state i generated by an individual recruited into state j [3]. This may be less readily apparent from the formulation given in equation (5), but it is clear that individuals cannot initially start in the ART state (i.e. they must first transfer from the Infected State). Therefore the elements corresponding to generation into the ART state are 0.

The various reproduction numbers are the most important derivation in this report, so their epidemiological meaning deserves close attention. The basic reproduction number represents the number of secondary infections that will be produced by a single initially infected case in a population of susceptible individuals. With $R_0 > 1$, we see the number of cases of the disease increase over time. Derived from R_0 is R_c (9) which takes into account a more realistic population, including individuals who are not only susceptible. Finally, we consider R_{ce} (10), which eliminates those individuals who are taking PrEP from the susceptible population. Therefore, R_{ce} is the most epidemiologically interesting for us to consider as it reflects the current state of the system. As shown above, the effective control reproduction number is the basic reproduction number multiplied by a factor that accounts for the two treatment options for individuals in the system. Since we are in a positively invariant space and the values of the parameters are all positive, we can see that $R_{ce} < R_0$. This critical observation confirms that the treatment options reduce the burden of the disease.

The value of R_{ce} is driven down by increasing the values of its denominator— we see that as we increase the uptake rates into treatment (τ_p and τ_a) relative to the drop out rates and mortailty rates R_{ce} decreases, which as proven in Section 4.2, yields stability of the model.

3.2 Numerical Evaluation of Compartmental Model

In order to minimize R_{ce}, we need to maximize the value of its denominator. By inspecting equation (11) we may be tempted to assume that τ_p and τ_a have similar effects on reducing R_{ce}. However, we would expect that the drop-out rate of individuals on ART ϕ_a would be relatively low, much lower than that of PrEP ϕ_p, because ART is a life saving drug. Those individuals in the A state are highly incentivized to stay in care. As such, we can reason that $\phi_a \ll \phi_p$. Therefore, a larger change in τ_p is required to decrease R_{ce} than is required from τ_a.

We approximated the values of the some parameters of the model given existing figures. The likelihood of a HIV+ individual to be virally suppressed on ART, τ_a, is approximated to be 0.49 [9] [13]. The value of the basic reproduction number of HIV is estimated to be approximately 4.0 [13]. The remaining parameter values are not readily available in the literature, so we substitute reasonable values to illustrate the effect of varying τ_p. We achieved the sensitivity response displayed in Figure 2.

This figure shows that a rate of uptake of PrEP among the susceptible population greater than 0.015 will decrease the simulated value of R_{ce} below 1. At the current rate of ART uptake, and assuming that the treatment methods are effective, a small fraction of susceptible individuals must be enrolled on PrEP to control the HIV epidemic.

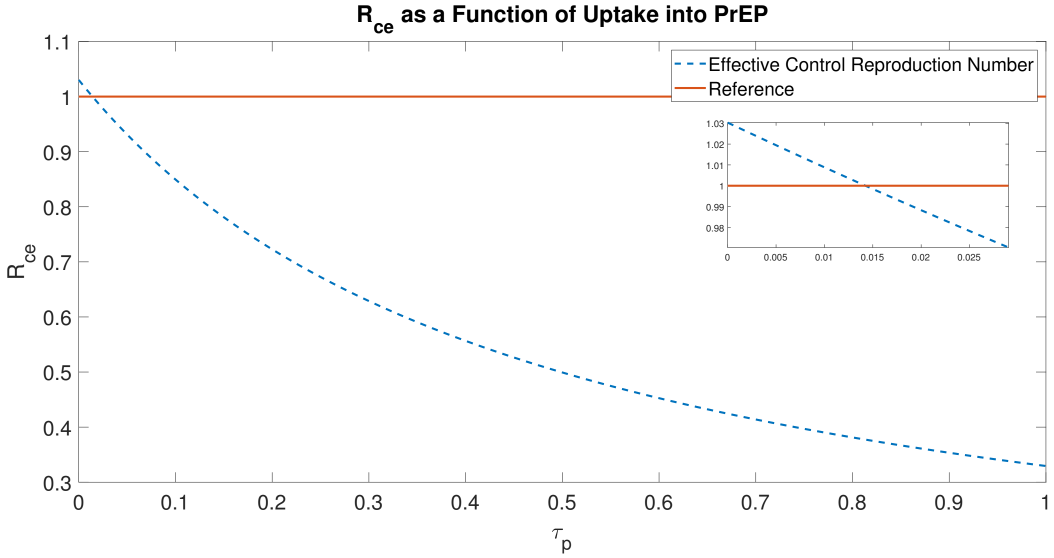
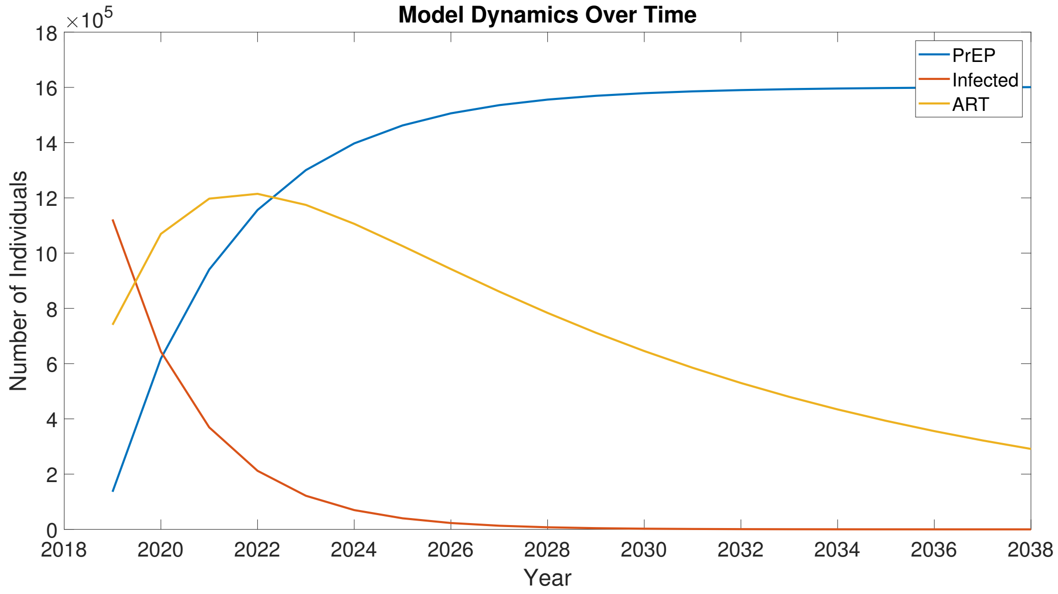
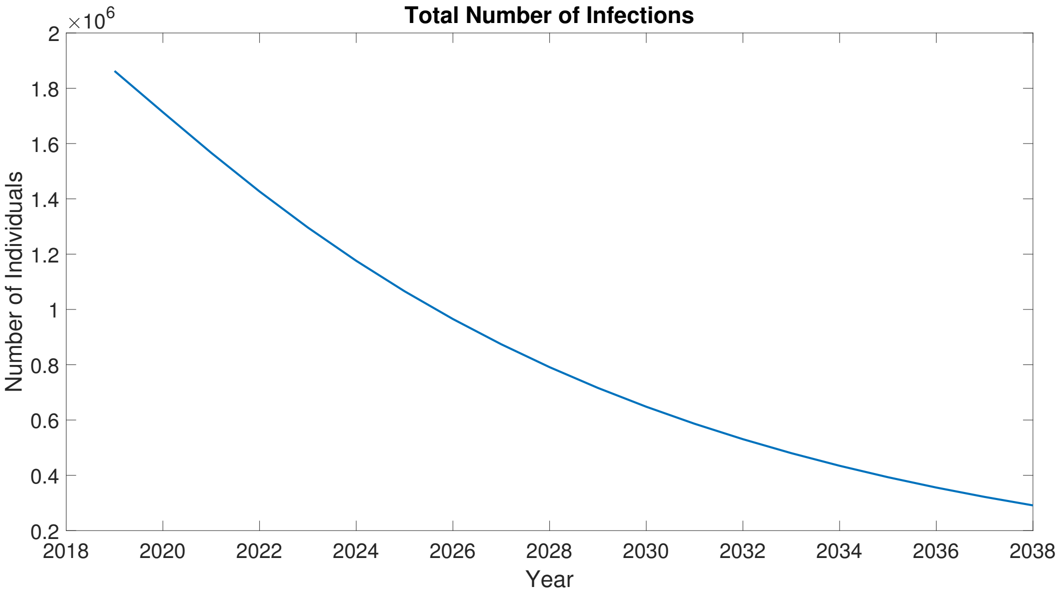

R_{ce} as a Function of Uptake into PrEP

Figure 2: Sensitivity of R_{ce} to τ_p
We evaluated R_{ce} with the parameters $(R_0 = 4.0, \mu = 0.17, \phi_a = 0, \phi_p = 0.3, \tau_a = 0.49)$

We extend the model over a time horizon to visualize the effects of these treatment methods an HIV epidemic. In the presence of these treatment methods, the total number of infections decreases over time as shown in Figure 3.



(a) Forward Looking Model Dynamics



(b) Forward Looking Number of Infections

Figure 3: HIV Epidemic Model Extended 50 years
Parameters: $(\beta = 0.12, \lambda = 2.6994 \times 10^{-10}, \tau_p = 0.015, \mu_s = 0.1, \phi_p = 0.3, \mu_p = 0.1, \phi_a = 0, \mu_i = 0.1, \tau_a = 0.49, \mu_a = 0.1)$

3.3 Cost/Benefit Discussion

The economic costs of both PrEP and ART are of real concern not only to patients, but also to governments and healthcare institutions that provide these drugs. As was discussed in the introduction, the cost of ART can be quite high for patients who have to take it throughout their lives. The cost of a years worth of treatment of ART is around \$26,000 dollars [2]. Meanwhile, the current price of PrEP is approximately \$18,000 dollars a year [10]. According to CDC guidelines, a "prevention intervention is deemed cost-saving if its CE ratio is less than \$379,668 per infection averted" [6]. Adjusted to 2019 dollars, this amounts to \$433,000 per new case averted.

3.4 Directives for Future Research

We hope that applying mathematical modeling to investigate the impact of PrEP on the HIV epidemic can continue through further research. Some key potential areas of further research in this field of study would be to subdivide the infected stage n states of infectedness as done by Otunga [11]. Another area for future research would be to make the model more robust by adding time dependency into the recruitment and death rate parameters. Adding a non-constant infectivity parameter into the existing model we created could be another avenue to more accurately represent the system dynamics of HIV. Additionally, we can further compartmentalize the susceptible population by considering various socioeconomic factors such as race, income, and risk factor (i.e. MSM). This modification would allow for a more optimal calculation of the critical threshold of uptake into PrEP.

It should be noted that this potential for cost savings can be dramatically increased if we were to focus our efforts on individuals at a high risk for HIV, such as young men who have sex with men (MSM). When modelling this population special attention should be given to the contact parameter, λ, is necessary to reflect the fact that MSM are at a much greater risk of developing HIV over their lifetime than otherwise.

Further, we suggest fitting the proposed model to available data in order to run meaningful numerical simulations of the epidemic. The need for and implications of a rigorous numerical simulation are clear—demonstrating the cost effectiveness of PrEP can influence policy decisions and increase accessibility to the drug. We suggest a rigorous parameter search through carefully fitting the proposed model to appropriate data.

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4 Conclusion

In this project we first mathematically model the HIV/AIDS epidemic, including both available treatment methods, PrEP and ART. With this model, we are able to formulate the next generation matrix. Second, we derive the spectral radius of this matrix as the control reproduction number. With completely effective treatment methods, the control reproduction number becomes our effective control reproduction number. We also find that driving these relations below 1 satisfies the stability requirements of our model. We also provide numerical simulation of this model.

With the effective control reproduction number of this epidemic, we are able to provide a relation to optimize to control the HIV epidemic. These efforts are significant because the reproduction numbers of this model have great epidemiological implications as the HIV epidemic presents great sociological and economic burdens on society. The effective control reproduction number for the HIV epidemic in the presence of PrEP has not been previously formulated, and provides new insight into potential control measures.

Acknowledgements

The author would like to thank Dr. Michael Otunga of Marshall University and Dr. Pauline Driessche of the University of Victoria for their advice. The author also like to thank Dr. Jason Trobaugh, Dr. Rupa Patel, and Dr. Zach Feinstein for their mentorship.

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