

**MODELLING THE EFFECTS OF DEFAULTER TRACING ON RETENTION
IN HIV/AIDS CARE**

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**A Thesis Submitted to the Department of Mathematics and Statistics in Partial
Fulfilment of the Requirements for Award of the Degree of Master
of Science in Applied Mathematics (Mathematical, Modelling
and Computations) of Machakos University, Kenya**

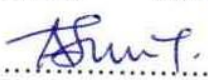
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DECLARATION

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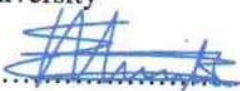
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DEDICATION

I dedicate this research thesis to Almighty God, my supervisors, my parents, brother, and sister. Also, to my wife, Beatrice, and daughter, Mitchell, who encouraged me through this work.

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My sincere appreciation goes to Almighty God for His wisdom, gift of life, direction, guidance, and His protection, which have led to the success of this work.

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LIST OF SYMBOLS

Symbol	Meaning
S	Susceptible
I	Infected
N	Total population
t	time
$N(0)$	Initial population
E_0	Disease-free equilibrium point
R_0	Reproduction number
DT_{eff}	Defaulter tracing effectiveness

LIST OF ABBREVIATIONS

AIDS	Acquired Immune-Deficiency Syndrome
ART	Anti-retroviral Treatment
GERMO	Generalized Removal Model for Open Population
HIV	Human Immunodeficiency virus
LTFU	Loss to Follow Up.
MSM	Men who have sex with men
ODE	Ordinary Differential Equations
PLHIV	People Living with HIV
PLWHIV	People Living with HIV
PMTCT	Prevention of Mother to Child Transmission.
PrEP	Pre-Exposure Prophylaxis
W.H.O.	World Health Organization

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ABSTRACT

Human Immunodeficiency Virus (HIV) has negatively affected the social lives of people in society. The economy has also been adversely affected; therefore, measures of control have been established. These measures include an uptake of anti-retroviral medication if infected, sex abstinence, use of condoms, and establishment of drop-in centers. Even with these measures some individuals default ARV medications. In this study a five compartmental model is developed to illustrate how HIV/AIDS medication defaulters are returned back to care and treatment to reduce HIV mortalities and further transmission of the virus. These compartments classify the human population as either Susceptible (S_p), Infectious (I_T), Infectious and on ARVs (I_{ARV}), Infectious and not on ARV (I_{NARV}), and the population under Defaulter tracing (D_{TR}). The R_0 is determined using the next generation matrix approach, as well as the local stability, endemic equilibrium points, bounded region, and positivity of solutions are obtained. The model equations are solved by applying Runge-Kutta methods within the MATLAB software. Scenarios explored (DT_{eff}) levels from 45% to 75% and retention rates (θ) from 65% to 85%. Simulation results demonstrated that increasing (DT_{eff}) significantly reduces the untreated infected population (I_{NARV}). At 600th day when $DT_{eff}=0.45$; $I_{ARV}=1.5$ million people and $DT_{eff}=0.75$; $I_{ARV}=1.65$ million. Indicating that defaulter tracing effectiveness increases the number of populations on ARV. However, when, ($\theta=0.65$); $I_{ARV}=1.55$ million and at ($\theta=0.85$); $I_{ARV}=1.7$ million. Showing that improving the retention rate (θ) showed a significant impact of reducing the need for tracing and the size of the untreated population, while substantially increasing ARV coverage. The findings highlight that while effective defaulter tracing is a vital component, particularly when retention is suboptimal, improving ARV retention is fundamental for long-term HIV/AIDS control. This study shows the need for integrated public health strategies that combine robust, proactive retention efforts with efficient defaulter tracing mechanisms to effectively manage the HIV/AIDS epidemic.

CHAPTER ONE

INTRODUCTION

1.0 Introduction

This chapter contains background information, definitions of terms used, Statement of the problem, significance of the study, limitations of the study objectives and significance of the study.

1.1 Background of the Study

The human immunodeficiency virus (HIV) is an infection that develops into acquired immunodeficiency syndrome (AIDS). It has been a very serious infectious disease within communities. It leads to expenditure of large amounts of money and resources in health care and disease control and it is deadly infection. The HIV/AIDS epidemic has presented as a quite pressing global health challenge in the recent past, with too much social, economic, and public health impacts. Since it was detected in the 1980s, HIV/AIDS has led to the loss of millions of lives and affected countless communities all over the world. According to the World Health Organization (WHO), about 38 million people were infected with the disease by 2019. Since the onset of the epidemic, almost 75 million people have been infected with HIV, and around 32 million have succumbed to AIDS-related illnesses. While HIV/AIDS affects people across the globe, certain regions have been afflicted with differentiated burdens. For instance, Sub-Saharan Africa remains adversely affected, with over two-thirds of the population living in this region being HIV/AIDS positive. The vast majority of new HIV/AIDS infections worldwide occur as a result of sexual contact, may also be induced during birth from mother to child and it also occurs through accidents. The

HIV/AIDS infection is transmitted through heterosexual contact due to the high number of infections in Africa, where this mode of transmission is dominant. Most new HIV diagnoses in most other regions of the world occur in men who have sex with men. (WHO. HIV Data and Statistics 2023.) In the United States, in 2021, 70% of all new infections were in men who have sex with men, whereas only 22% occurred through heterosexual contact. (CDC. Basic Statistics 2023.) However, regions such as parts of Asia, Eastern Europe, and Latin America also face several HIV/AIDS epidemics. This epidemic has adverse consequences beyond health, which include economic destabilization and social disruption. According to WHO “potential impact of funding cuts on the HIV response” 2025. A study published by the Burnet Institute and the WHO highlights the potential impact of international funding cuts on the global HIV response. The research underscores the urgent need for sustained financial support to prevent millions of new HIV infections and deaths in the coming years. This study put to consideration of data from 26 countries, and they found that if international support declines, an additional 4.43 to 10.75 million new HIV infections – including up to 880,000 in children – could occur by 2030. In the same period, 770,000 to 2.93 million more people could die from HIV-related causes, with up to 120,000 of these deaths affecting children. Low- and middle-income countries could be the most affected, particularly those in sub-Saharan Africa. This region has seen tremendous progress in HIV treatment coverage for people living with HIV, pregnant women, and children, and in prevention for populations at high risk of infection.

HIV/AIDS remains challenges even with significant progresses in prevention and treatment. According to Tegene L. D., *et al* (2024) in a study on experiences of people living with HIV in low- and middle-income countries and their perspectives in self-

management. Their results indicated that, numerous obstacles that limit their possibilities for efficient self-management and lower their quality of life are faced by PLWH in LIMICs. Misconceptions about the illness, low self-efficacy and self-management abilities, unfavorable social attitudes, and a non-patient-centered care approach that minimizes the participation of patients are the primary ones. Context (the condition itself, physical and environmental factors, individual and family factors) and process (knowledge and beliefs, relationship with the health care worker, self-regulation skills and abilities, and social facilitation) are the summaries of the experiences that influenced the ability to practice self-management. Context and procedure had a significant impact on patients' self-management habits and quality of life. These challenges affects social and environmental evolution of factors on HIV/AIDS transmission dynamics.

Therefore, HIV/AIDS testing and antiretroviral therapy (ART) are key components in the controlling and also mitigation of the spread of HIV/AIDS. To achieve viral suppression which is measured using a blood test called a nucleic acid amplification test (NAAT) or PCR test, timely detection of HIV is vital for initiating treatment and preventing further transmission. Blood tests, oral fluid tests, and rapid tests are the various available HIV testing methods. Testing is highly recommended for individuals who are sexually active, drug injectors, or have other higher risks of contracting the disease. Additionally, routine testing is advised for pregnant women to prevent mother-to-child transmission. Also, according to Kemnic, T.R., *et al* (2025), Antiretroviral Therapy (ART) involves the use of a combination of medications to suppress HIV and stop the progression of HIV/AIDS disease. Their results indicated that medications work by inhibiting different stages of the HIV/AIDS life cycle, preventing the virus

from replicating and reducing the viral load in the body. Also suggested that ARV typically consists of three or more drug component from at least two different classes of antiretroviral medications. They therefore concluded that viral suppression is therefore a goal of ARV treatment. When an individual consistently takes their ARV medications as prescribed, the HIV in their body is suppressed to undetectable levels. This means that the amount of virus in the blood is so low that it cannot be detected by standard laboratory tests. According to Digafe, H., *et al.*, “Viral Load Suppression and associated factors among HIV-infected patients on second-line antiretroviral therapy at public health facilities of West Guji, Guji and Borena zones, southern Ethiopia: facility based cross-sectional study”. The study revealed that the proportion of viral load suppression among HIV-infected patients on second-line antiretroviral therapy was 73.8% (95% CI, 68.0–79.1). Also indicated that to improve the health outcomes of people living with HIV/AIDS and reducing the risk of transmission to others, viral load suppression ha to be achieved.

Therefore testing, adherence to ARVs and ensuring viral load suppression are crucial interventions not only for enhancing individual well-being but also for the significant impact of viral suppression through antiretroviral therapy (ARV). Individuals with HIV who maintain an undetectable viral load are unable to sexually transmit the virus to their partners, encapsulated in the phrase "Undetectable = Untransmittable" (U=U). Therefore, timely HIV/AIDS testing, followed by the early initiation of ARV and strict adherence to treatment, are essential strategies for achieving viral suppression. This not only enhances the health and quality of life for those living with HIV/AIDS but also plays a significant role in preventing further virus transmission within communities. Mehdi, M. A., *et al* (2025) suggested insights into medication adherence among

HIV/AIDS-positive patients: the integrated change model. Results suggested that, ARV is the most effective strategy for preventing and treating HIV/AIDS, and good adherence to ARV is indirectly associated with suppressing viral load, increasing CD4 counts, preventing drug resistance, boosting immune system restoration, and delaying disease progression in HIV/AIDS patients, leading to a significant reduction in HIV-related illnesses and mortality. Furthermore, appropriate use of ARV improves the well-being of HIV patients, suppresses viral load, and reduces the risk of HIV transmission, thus serving as a key prevention strategy. Evidence suggests that early access to highly active antiretroviral therapy can potentially prevent 25% of HIV-related deaths.

According to Rachael, M. B., *et al* (2024) researched on reasons for disengagement from antiretroviral care in the era of “Treat All” in low- or middle-income countries: a systematic review. Results identified 21 studies which reported reasons for disengaging from ART care in the “Treat All” era, mostly in African countries: six studies in the general population of persons living with HIV/AIDS, nine in pregnant or postpartum women and six in selected populations (one each in people who use drugs, isolated indigenous communities, men, women, adolescents and men who have sex with men). Reasons reported were: side effects or other antiretroviral tablet issues (15 studies); lack of perceived benefit of ARV (13 studies); psychological, mental health or drug use (13 studies); concerns about stigma or confidentiality (14 studies); lack of social or family support (12 studies); socio-economic reasons (16 studies); health facility-related reasons (11 studies); and acute proximal events such as unexpected mobility (12 studies). The most common reasons for disengagement were unexpected events, socio-economic reasons, ART side effects or lack of perceived benefit of ART.

Discontinuing ARV medication allows HIV to multiply and rebound in the body, leading to an increase in viral load. According to <https://www.unaids.org/sites/default/files/2025-05/20250520>. After discontinuing ARV, individuals with previously suppressed HIV can experience a rapid increase in viral load, often reaching detectable levels within days to weeks. This increases the risk of HIV transmission, rendering individuals infectious shortly after stopping ARV. Higher the viral load is, the higher infections, particularly in sexual and vertical transmission (transmission from mother to child during pregnancy or through breastfeeding). HIV/AIDS weakens the immune system, making individuals more susceptible to infections and other HIV/AIDS-related complications if the affected individual fail to seek medication. Also, inadequate treatment adherence leads to the development of drug-resistant strains of HIV/AIDS, making future treatment options less effective. Individuals with higher levels of HIV/AIDS in their blood, increasing the risk of transmitting the virus to others are individuals who discontinue ARV and experience viral rebound. Therefore, efforts to address the underlying reasons for discontinued treatment and provide support for individuals to adhere to ARV are crucial in achieving optimal HIV treatment outcomes.

Controlling the spread of HIV/AIDS requires a detailed approach that addresses both prevention and treatment aspects, alongside addressing underlying social determinants of health. According to NSDCC “HIV estimates in Kenya”, 2024, Kenya has made significant moves in HIV prevention through the implementation of a comprehensive combination prevention approach that integrates behavioral, biomedical, and structural interventions. The government, in collaboration with international and community partners, has scaled up efforts, particularly among high-risk populations such as men

having sex with men, commercial sex workers. Increased condom distribution, expanded voluntary medical male circumcision (VMMC) services focusing on males aged 15-24 years, improved HIV testing services, and significant progress in Prevention of Mother-to-Child Transmission (PMTCT) were some key achievements according to these study. Coverage also increased upto 90.3% in 2023. Despite these progresses, long run oriented efforts are needed to achieve the global targets of ending the HIV/AIDS epidemic as a public health threat by 2030, as outlined in the Sustainable Development Goals (SDGs).

With a number of projects and programs, the Kenya Red Cross Society (KRCS) helps to prevent the spread of HIV/AIDS in Kenya. The Kenya Red Cross Society has contributed to a large-scale HIV/AIDS awareness and prevention campaign. Communities are more informed about HIV/AIDS transmission, preventative strategies, and the significance of testing and treatment thanks to these awareness campaigns. These efforts have frequently focused on women, young people (ages 15 to 24), and critical populations that are more susceptible to HIV infection. Additionally, the KRCS has offered HIV testing and counseling services via mobile clinics, community outreach initiatives, and permanent healthcare facilities.

Kenya Red Cross services have helped individuals to know their HIV status, an important step for early diagnosis that initiates treatment. Safe practices to prevent HIV transmission, such as the use of condoms, harm reduction strategies for people who inject drugs, and the promotion of safer sex practices have been encouraged by the KRCS has continually. These efforts equip individuals with the knowledge and tools to protect themselves and others from HIV infection. Services such as psychosocial support, adherence counseling, and assistance with accessing healthcare services and

treatment have also been offered by KRCS. These services help improve the quality of life for individuals living with HIV/AIDS and support them in adhering to antiretroviral therapy (ARV).

KRCS has advocated for policies and programs that support HIV prevention, treatment, care, and support at the national and local levels. By engaging with policymakers, stakeholders, and communities, the Kenya Red Cross has worked to ensure that HIV/AIDS remains a priority on the national health agenda and that allocation of resources is done effectively. The KRCS has been providing capacity building and training to healthcare workers, volunteers, and community members on HIV/AIDS prevention, treatment, care, and support. By building local capacity, the Red Cross strengthens community responses to HIV/AIDS and ensures sustainable interventions. KRCS has mobilized and engaged communities in HIV/AIDS prevention and control efforts through community dialogue sessions, peer education programs, and community-based initiatives. Kenya Red Cross Society has therefore played a pivotal role in the multi-sectoral response to HIV/AIDS in Kenya, working alongside government agencies, civil society organizations, and other stakeholders to control the spread of HIV and improve the health and well-being of communities affected by the epidemic.

Resuming antiretroviral medication (ART) after stopping it is crucial for HIV/AIDS management and averting additional health issues. By fostering a compassionate and encouraging healthcare environment that motivates patients to seek and follow ART, defaulters may be rehabilitated. Considering the study by, Patricia, S., *et al* (2025) on medication adherence and intervention strategies results indicated that medication adherence is critical for managing chronic diseases. The study suggested that, prompt

follow-up with patients who have discontinued treatment may help identify barriers to adherence and address them promptly.

The interest in studying HIV/AIDS transmission dynamics has become widespread in science fields such as mathematics and biology due to its increasing threats to humanity. Mathematical models have been used widely and differently in the research of the epidemiology of HIV/AIDS to help improve our understanding of the major factors leading to a given epidemic. The study by Omondi, E. O., *et al.* (2020) presents a mathematical model that explores HIV transmission dynamics between two high-risk groups: commercial sex workers and injection drug users. The findings are that, increase in the uptake of Pre-Exposure Prophylaxis (Pre-P) leads to a decline in the number of HIV patients receiving Antiretroviral Therapy (ART). According to this finding, Pre-P, taking medicine prior to possible HIV contact, can prevent infection. People who might have otherwise contracted the infection are less likely to require ART as a result of these practices. The study also indicated that ART and Pre-P uptake together would significantly slow the transmission of HIV. In addition to preventing new HIV infections, expanding access to Pre-P among high-risk groups can lessen the strain on healthcare systems by lowering the number of people in need of ART. A comprehensive strategy for HIV prevention and treatment that takes into account both primary prevention and secondary prevention among those who are already infected is represented by the combination of Pre-P and ART. HIV incidence might be significantly decreased and general public health outcomes could be improved by putting such combination tactics into practice.

Mukhtiar, K., *et al* (2025), discovered, using numerical analysis, a new fractal fractional mathematical model for HIV/AIDS transmission stability and sensitivity. The

findings demonstrated that in order to understand the complex dynamics of HIV/AIDS transmission, models that represent the trajectory and outcomes of treatments in the real world are required. With an emphasis on memory effects and nonlocal interactions that are crucial to the disease's transmission, this paper offers a novel mathematical framework for fractal-fractional calculus analysis of HIV/AIDS dynamics. The model represents important stages of infection and therapy by segmenting populations into four different compartments: susceptible individuals, infected individuals, individuals receiving treatment, and individuals in advanced stages of HIV/AIDS.

Oluwakemi et al. (2022) conducted a study that aimed to mathematically model the dynamics of HIV-HCV co-infection and investigate the effects of different parameters on the reproduction number (R_0), which is the average number of secondary infections caused by a single infectious person in a susceptible population. In epidemiology, the reproduction number (R_0) is a crucial indicator of disease transmission. To explain the patterns of HIV and HCV transmission within a community, the researchers created a mathematical model. In addition to include variables like transmission rates, treatment rates, and interactions between the two illnesses, this model comprises compartments that represent various groups, such as susceptible persons, HIV-infected individuals, and HCV-infected individuals. It sheds light on the likelihood that an infectious disease may proliferate within a community. In this study, the researchers investigated how changes in various parameters affected the reproduction number of the HIV-HCV co-infection model. Specifically, they found that the prevalence of HIV treatment in each compartment of the HIV model led to a reduction in the HIV in the treatment compartment. This suggests that increased access to HIV treatment is associated with a decrease in the number of HIV-infected individuals who are receiving treatment.

However, the other compartments of the model exhibited an increase in populations. This implies that while HIV treatment may reduce the number of individuals in the HIV on treatment compartment, it may also lead to increases in other compartments, potentially due to factors such as reduced mortality and increased longevity among treated individuals. These findings have important implications for public health interventions targeting HIV-HCV co-infection. Increased access to HIV treatment can lead to reductions in the number of HIV-infected individuals receiving treatment, which is a positive outcome in terms of improving individual health outcomes and reducing HIV transmission. However, the observed increases in other compartments highlight the need for comprehensive approaches to co-infection management that address both HIV and HCV, including prevention, treatment, and harm reduction strategies.

The systematic process of tracking down and re-engaging people who have missed or defaulted on appointments for HIV testing, treatment, or care services is known as "defaulter tracing" in HIV/AIDS management. The strategy entails locating people who have lost touch with healthcare services and working to reintegrate them into the care continuum. Because it guarantees that people living with HIV/AIDS continue to get critical healthcare services like antiretroviral medication (ARV), prompt assistance, and disease progression monitoring, defaulter tracking is vital. According to Azfar, D. H., *et al* (2022) on effectiveness of contact tracing in the control of infectious diseases. The study identified 9050 unique citations, of which 47 studies met the inclusion criteria: six were focused on COVID-19, 20 on tuberculosis, eight on HIV, 12 on curable sexually transmitted infections (STIs), and one on measles. More than 2 million index patients were included across a variety of settings (both urban and rural areas and low-resource and high-resource settings). Of the 47 studies, 29 (61.7%) used observational

designs, including all studies on COVID-19, and 18 (38.3%) were randomised controlled trials. Thus, defaulter tracing programs help in optimization of the limited healthcare resources allocation by rendering efforts towards individuals at higher risk of defaulting on HIV/AIDS care. Therefore, by focusing resources on those most in need, these programs can maximize the impact of HIV/AIDS prevention and treatment efforts.

The main 4 outcomes of tracing include:

- i. Return to care,
- ii. Transfer Out (to other health facility)
- iii. Dead,
- iv. Lost to follow up (untraceable)

Understanding the impacts of defaulter tracing on the spread of HIV/AIDS is crucial for several reasons, such as evaluating the effectiveness of defaulter tracing in HIV/AIDS management is essential for assessing the overall impact of HIV/AIDS control programs. Considering the study by, Hamid, T., *et al* (2025) researched on Cost-Effectiveness of HIV Prevention Strategies-A Systematic Review of Economic Evaluations. Results indicated that thirteen studies met the inclusion criteria, exhibiting diverse methodologies, target populations, and healthcare perspectives. The majority of studies reported that primary prevention methods—such as prenatal screening, harm reduction programs for drug users, and pre-exposure prophylaxis (PrEP) for high-risk groups—were more cost-effective than secondary or tertiary interventions. Study populations included pregnant women (38.4%), injection drug users (23.1%), men who have sex with men (23.1%), and general populations (15.4%). Overall, most studies demonstrated medium to high methodological quality. Understanding the impact of these interventions on transmission rates and health outcomes relative to their costs can

help program managers make informed decisions about resource allocation and prioritize interventions that yield the greatest benefits. Feng, R., et al, (2025) they developed a stochastic model that captures the dynamics of HIV infection, encompassing susceptible individuals, asymptomatic HIV-positive individuals, and those exhibiting symptoms. From an epidemiological viewpoint, their observations suggested that a decrease in environmental noise intensity results in a reduction of the oscillation amplitude in the disease dynamics. Conversely, an increase in noise intensity is associated with a lower mean of infectious individuals and a left-skewed distribution. Dongni, Z. and Tom, B. (2024) “An SEIR network epidemic model with manual and digital contact tracing allowing delays” results indicated that the decrease in the reproduction number serves as a numerical indicator of how well both contact tracing methods work. This demonstrates that the app-using proportion is crucial to the overall efficacy of contact tracing. If more of the transmission takes place on the network, the tracing delay is reduced, and the network degree distribution is heavy-tailed, the relative efficacy of manual tracing over digital tracing rises. In order for contact tracing to be successful in preventing large outbreaks, additional preventive actions are required to lower the reproduction number down to 1.2–1.4. For realistic values, the combined tracing case can cut by 20%–30%.

Mathematical models can be implemented while studying infectious diseases. The study by Ling, X., *et al* (2023) focuses on modeling the transmission dynamics of HIV infection in China and exploring optimal control strategies to mitigate its spread. The researchers developed a compartmental model to study the dynamics of HIV/AIDS transmission which divides the population into different compartments based on disease status (e.g., susceptible, infected, recovered) and model the flow of individuals between

these compartments over time. By using this method, the researchers were able to model the disease's progress and assess the effects of different interventions and control measures. Sexual behavior, injectable drug use, HIV/AIDS testing and diagnosis rates, treatment uptake, and other pertinent epidemiological statistics unique to China were all included in the model. Through the simulation of interactions between various population groups and HIV/AIDS transmission dynamics, the researchers evaluated the disease's spread and pinpointed important transmission factors. In addition to studying the natural dynamics of HIV/AIDS transmission, the researchers explored the effectiveness of various control strategies in reducing HIV/AIDS incidence and prevalence.

These control strategies included interventions such as promoting HIV/AIDS testing and early diagnosis, increasing access to antiretroviral therapy (ART), implementing harm reduction programs for injection drug users, and scaling up prevention measures like condom distribution and education campaigns. Taking resource limitations and other pragmatic factors into account, the researchers employed optimization tools to determine which combination of interventions would result in the largest reduction in HIV/AIDS transmission. The results shed light on how well various control measures work to slow the development of HIV/AIDS in China. This could entail figuring out which interventions are most effective at lowering HIV incidence and prevalence and evaluating how cost-effective they are. Based on their findings, the researchers also offered suggestions to public health officials and lawmakers, emphasizing the best approaches to HIV prevention in China.

Mathematical modelling results to be very crucial in studying dynamics of flow in many areas, Aslipah, T., *et al* (2025). Studied impacts and challenges of mathematical

modelling activities on students' learning development: A systematic literature review. Their research implied mathematical modelling to be essential in mathematics education, presenting real-world problems in mathematical terms.

The study by. Ayele, T.K., *et al.* (2021) focuses on mathematical modeling with optimal control strategies for HIV/AIDS, specifically within the context of Ethiopia. The researchers developed a mathematical model to simulate the transmission dynamics of HIV/AIDS within the Ethiopian population. This model incorporates various factors such as population demographics, sexual behavior, HIV testing and treatment rates, and other relevant epidemiological parameters specific to Ethiopia. Through mathematical equations and computational simulations, the model simulates how HIV spreads within the population over time and how different interventions impact the course of the epidemic. The study explores optimal control strategies aimed at reducing the spread of HIV/AIDS in Ethiopia. The researchers used mathematical optimization techniques to identify the combination of interventions that would achieve the greatest reduction in HIV transmission while considering cost-effectiveness and other practical constraints. The findings of the study suggest that a combination of optimal control strategies is a cost-effective measure to control the spread of HIV/AIDS in Ethiopia.

1.2 Definition of Key Words

In this section, we shall define the words that are relevant to the proposed study.

1.2.1. HIV/AIDS

According to <https://www.who.int/> (2025) Human immunodeficiency virus (HIV) is a virus that attacks the body's immune system. Acquired immunodeficiency syndrome

(AIDS) occurs at the most advanced stage of infection. HIV is a virus that compromises the immune system by specifically attacking CD4 cells, also known as T cells, which are essential for the body's defense against infections and diseases. The virus can be spread through exposure to specific body fluids, such as blood, semen, vaginal fluids, and breast milk. The disease can be transmitted through unprotected sexual activities, sharing needles or syringes that have been contaminated with HIV-infected blood, and from an HIV-positive mother to her child during childbirth or breastfeeding. If not treated, HIV can progressively deteriorate the immune system, increasing the risk of opportunistic infections and certain cancers. AIDS represents the most severe stage of HIV infection and is characterized by significant immune system impairment. A diagnosis of AIDS occurs when an individual with an HIV infection suffers considerable immune system damage. Individuals with AIDS face a higher risk of life-threatening infections and diseases, and without treatment, AIDS can be deadly.

1.2.2 Defaulter Tracing

According to <https://www.qld.gov.au/health/condition/infections-and-parasites/sexually-transmissible-infections/hiv-contact-tracing-client-responsibilities>.

“HIV contact tracing - client responsibilities” contact tracing is the process of contacting people who have been in contact with someone with an infectious condition and providing advice to protect their health and prevent further spread of the infection. Defaulter tracing is the procedure utilized in healthcare, especially concerning the management of epidemic conditions like HIV/AIDS, tuberculosis (TB), and various other infectious diseases.

The process of defaulter tracing consists of several steps; first, healthcare providers monitor patient attendance logs or adherence data to identify individuals who have not attended appointments or are not adhering to their prescribed treatment. This typically requires reviewing clinic records, electronic health records, or treatment databases. Next, once the defaulters are identified, healthcare workers start reaching out to them. This outreach can be conducted through phone calls, text messages, home visits, or community engagement efforts. This step aims to understand the reasons for non-adherence, address any barriers or concerns the individual may have, and motivate them to return to care. Throughout the follow-up process, healthcare workers offer education, counseling, and support to assist individuals in overcoming challenges to adherence. This includes addressing medication side effects, financial difficulties, transportation problems, stigma-related issues, or other psychosocial factors that may hinder treatment adherence.

The primary aim of defaulter tracing is to reintegrate individuals into care and ensure they follow their treatment regimens as advised by healthcare providers. This might entail scheduling new appointments, providing medication refills, offering transportation support, and even linking individuals to further assistance services as required.

1.2.3 Mathematical Model

A mathematical model is a representation of a real-world system or phenomenon using mathematical concepts and language. according to

https://en.wikipedia.org/wiki/Mathematical_model A mathematical model is an abstract description of a concrete system using mathematical concepts and language.

The process of developing a mathematical model is termed mathematical modeling. Mathematical models are used in many fields, including applied mathematics, natural sciences, and social sciences. Mathematical models range from simple equations to complex systems of equations incorporating variables, parameters, and constraints to simulate the outcomes of the real-world system under study.

1.2.4 Reproduction Number

One important epidemiological metric for characterizing the potential for infectious disease transmission within a population is the reproduction number, which is frequently represented by the symbol. It stands for the typical number of secondary infections that an infected person can infect a susceptible population during the course of their lifetime. It merely measures how contagious an illness is. If >1 , the sickness can spread exponentially across the community as an afflicted individual can infect more than one person. Conversely, if R_0 , is less than 1, the disease is expected to decline over time because each infected individual is, on average, infecting less than one other individual. It is a theoretical concept based on a population without immunity or interventions, and as a disease progresses, the effective reproduction number may become relevant, taking into account factors like immunity and control measures that may change over time. This epidemiological metric can be influenced by a number of factors, including the infectiousness of the pathogen, the duration of infectiousness, the contact rate between individuals, and the effectiveness of control measures like vaccination or social distancing.

1.2.5 Endemic Equilibrium

Endemic equilibrium refers to a stable state in an infectious disease system where the prevalence of the disease remains relatively constant over time within a population. In this state, the rate of new infections balances with the rate of recoveries and deaths, leading to a steady level of disease transmission. Endemic equilibrium is a concept commonly used in epidemiology to understand the long-term dynamics of infectious diseases within populations.

1.2.6 Disease-free Equilibrium

It occurs when the reproduction number is less than one, $R_0 < 1$, this is a state that implies that no one is suffering. The disease-free equilibrium (DFE) is a state in epidemiology where there are no infected individuals in the population, indicating the absence of the disease. The population, therefore, remains entirely susceptible to the infectious agent. According to Victor, H. K. (2020) “stability analysis of disease-free equilibrium state (E_0) for an endemic deterministic model for HIV/AIDS”. Disease-free indicators are, absence of infection, showing that there are no individuals currently infected with the disease within the population. The disease-free equilibrium serves as a baseline state in epidemiological models, providing insights into the potential impact of interventions and control measures on disease transmission dynamics. Also, maintaining the disease-free equilibrium often requires ongoing efforts, as reintroduction of the infectious agent or changes in population dynamics can lead to the reemergence of the disease

1.2.7 Numerical Simulation

Numerical simulation refers to the process of employing numerical techniques and computational methods to replicate mathematical systems to examine their LONG-TERM behavior, forecast outcomes, and comprehend intricate phenomena. According to Xhevdet Spahiu and Senad Orhani (2025) researched on the applications of numerical analysis in computer simulations. Results of the study indicated that numerical analysis is a crucial field of mathematics that is used for solving complex problems through approximation methods using algorithms and computers.

1.3 Statement of the Problem

In case of pandemics, organizations have put efforts together to prevent such calamities. Ronoh, M. C. (2021), mathematical modelled HIV/AIDS transmission dynamics coupled with awareness among adolescents and young adults in Kenya. The study suggested HIV/AIDS containment campaigns have brought substantial successes within the past decade, the disease still poses a big health concern to many developing countries, including Kenya. They developed deterministic models to study the effect of HIV/AIDS awareness in the disease transmission dynamics of adolescents aged 10 - 14 years and young adults aged 15-24 years in Kenya. However, individuals continue dropping from care and medication due to stigmatization, failure to know about the disease, lack of affection by the health service providers, among other factors. Our study therefore suggests incorporating defaulter tracing and retention a model, as measures to introduce back patients who opt out of care back to care.

1.4 Objectives

1.4.1 General Objectives

To model the effects of defaulter tracing on the retention in HIV/AIDS care.

1.4.2 Specific Objectives

- i. To develop an HIV/AIDS mathematical model incorporating defaulter tracing of infected individuals who have dropped off care and treatment.
- ii. To determine the impact of defaulter tracing as a control strategy to curb the spread of HIV and AIDS.
- iii. To graphically simulate the impact of defaulter tracing.

1.5 Justification of the Study

The research has concentrated on individuals who default on their HIV/AIDS medication. This group has been chosen because of the considerable effects the HIV/AIDS epidemic has on society. The research gathers information from individuals who are receiving care and treatment for HIV/AIDS at healthcare facilities. A mathematical modeling approach has been employed in the study to evaluate the effects of defaulter tracing on the transmission of HIV/AIDS.

1.6 Significance of the Study

The research findings on defaulter tracing in HIV/AIDS management have important implications that can enhance prevention and control strategies in various ways. For instance, demonstrating the effectiveness of defaulter tracing interventions can help re-engage individuals who have fallen out of HIV/AIDS care and treatment; these findings

provide a foundation for strategies aimed at improving care retention. This can result in improved health outcomes for those living with HIV/AIDS, as continuous participation in care is crucial for achieving viral suppression and minimizing disease progression. Additionally, research that emphasizes the effect of defaulter tracing on lowering HIV transmission rates can guide initiatives to control the virus's spread within communities. By locating and re-engaging individuals at risk of transmitting HIV due to treatment lapses or loss to follow-up, defaulter tracing interventions can aid in preventing secondary infections and contribute to a decrease in overall HIV incidence. Finally, by underscoring the significance of defaulter tracing in enhancing outcomes along the HIV/AIDS care continuum, research findings can help fortify health systems and improve the provision of comprehensive HIV/AIDS services. This comprises incorporating defaulter tracing activities into current healthcare delivery models, training healthcare professionals in defaulter tracing methods, and establishing processes to monitor and evaluate the effectiveness of these interventions over time. This will also assist to cushion financial situations for the infected and also the government in provision for medication.

1.7. Research Methods

This study considers generating system of Ordinary Differential equations (ODEs) derived from HIV/AIDS disease model. The model studied here comprises of total population (N) subdivided in several compartments,

$(N = S_p + I_T + I_{ARV} + I_{NARV} + D_{TR})$. The system of ODEs are in non-linear form, they are numerically solved using Ordinary differential equation 4th and 5th Rugge-kutta method and visualized using MATLAB software to obtain graphical solutions for the study.

CHAPTER TWO

LITERATURE REVIEW

The HIV/AIDS epidemic remains a global health challenge that is quite significant, thus requiring detailed strategies for prevention, treatment, and control. Defaulter tracing is an involving approach to re-engage individuals who have defaulted on HIV/AIDS treatment and care services, has emerged as a vital intervention to improve retention in care and reduction of transmission rates. This literature review examines existing research on mathematical modeling approaches to assess the impacts of defaulter tracing on the control of HIV/AIDS spread.

Mathematical modelling is widely spread in studying of fluids. Geena Taite and Joseph DiNapoli (2025), did perspectives on mathematical modeling education on conceptions and research. The study shows that mathematical modeling is a cyclical process such mathematics is used to represent, explore, and better understand real-world situations by mathematizing a problem and validating the results. Unlike traditional word problems, modeling tasks require learners to make assumptions, define quantities, apply mathematics, interpret results, and revise solutions within authentic contexts.

Understanding modelling has been very useful in areas of mathematics, according to Mathias Vogelsanger. H., *et al* (2025), mathematical modelling and self-efficacy- immediate and long-lasting effects of teaching mathematical modelling with a solution plan”. Both mathematical competences and skills are necessary for mathematical modeling, which is also impacted by motivational attitudes like self-efficacy. However, little research has examined whether self-efficacy leads to improvements in mathematical modeling or how teaching modeling through a solution plan affects

modeling competence and self-efficacy over the long run. In this study, we looked at (a) how teaching modeling affects modeling competence both immediately and over time, (b) how teaching modeling affects self-efficacy, and (c) how self-efficacy predicts modeling competence in students undergoing an intervention.

İbrahim, Ç., *et al* (2023), reviewed mathematical modeling research-a descriptive content analysis study. Using top research studies, this study sought to review the trends in the literature on mathematical modeling. This study examined the different kinds of studies that addressed modeling and were indexed in the Web of Science database between 2000 and 2021.

Mehmet Ali Kandemir and Nurullah Eryilmaz (2025), innovated approaches in mathematical modeling-harnessing technology for teaching second degree equations to Future Mathematics Educators in Türkiye. This qualitative study explores the mathematical modeling processes of eighty-seven pre-service mathematics teachers in Turkey, focusing on their approaches to real-world problem-solving and the integration of technology.

Olena, K., *et al* (2025), mathematically modeled Regional infectious disease dynamics based on extended compartmental models. This study presented an extended approach to compartmental modeling of infectious disease spread, it focused on regional heterogeneity within affected areas. Using classical SIS, SIR, and SEIR frameworks, the study simulated the dynamics of COVID-19 across two major regions of Ukraine—Dnipropetrovsk and Kharkiv—during the period 2020–2024.

Adel, T., *et al* (2025), applied the unsupervised stochastic neural network paradigm to the mathematical modeling of infectious disease dynamics According to these studies,

mathematical modeling was a crucial tool for assessing the possibility and severity of the illness and for controlling the coronavirus pandemic. This study used a unique stochastic neural network to propose and evaluate a deterministic six-compartment model.

Sweileh, Waleed M. (2022), Researched on mathematical modeling of the spread and management of 23 specific infectious disease outbreaks is being conducted worldwide. The paper claims that policymakers can comprehend and forecast the dynamics of an infectious disease under a variety of conditions by using mathematical analysis and modeling. Analyzing worldwide research on mathematical modeling of transmission and control of a number of infectious diseases with a documented history of severe outbreaks was the goal of the current study.

Mathematical models are very instrumental in the understanding of the dynamics of transmitting HIV within populations. Classic compartmental models, such as the Susceptible-Infectious-Removed (SIR) model, are adapted to simulate HIV transmission dynamics together with parameters such as transmission rates, treatment uptake, and viral load suppression. Mathematical modelling becomes an important approach in understanding and evaluating the spread and control of epidemics such as HIV and AIDS. Early testing followed by immediate treatment of HIV infection, as well as control of the viral load, remains a key intervention in reducing HIV infection.

Santoshi Misra (2024). Researched on mathematical modeling of infectious disease spread using the SIR model. It is an indication that mathematical modeling has become an essential tool for understanding and predicting epidemic changes, it enables the policymakers to design effective intervention strategies. This paper explored the

application of the classic SIR (Susceptible- Infectious-Recovered) model in simulating the spread of infectious diseases.

According to Houssine, Z., *et al* (2022) did a Mathematical Analysis, Forecasting, and Optimal Control of HIV/AIDS Spatiotemporal Transmission with a reaction-diffusion SICA Model. They proposed a mathematical spatiotemporal epidemic SICA model with a control strategy. The spatial behavior is modeled by adding a diffusion term with the Laplace operator, which is justified and interpreted both mathematically and physically. By applying semigroup theory to ordinary differential equations, they proved the existence and uniqueness of the global positive spatiotemporal solution for the system and some of its important characteristics. Some illustrative numerical simulations were carried out that motivated the researchers to consider optimal control theory. A suitable optimal control problem was posed and investigated. Using an effective method based on some properties within the weak topology, they proved the existence of an optimal control and developed an appropriate set of necessary optimality conditions to find the optimal control pair that minimizes the density of infected individuals and the cost of the treatment program.

Tim, B., *et al* (2024) studied the AIDS Epidemic Model 2023 for Estimating HIV Trends and Transmission Dynamics in Asian Epidemic Settings. In the study they used AIDS Epidemic Model (AEM) in Thailand, describing the outputs and uses in-country. AEM replicated observed epidemiological trends when given observed behavioral inputs. The strengths and limitations of AEM are presented and used to inform thoughts on future directions for global models.

The process of HIV diagnosis to viral suppression describes the HIV sequential stages in care. Mathematical models have been used to model the HIV sequential care stages to assess factors that influence retention in care, treatment adherence, and outcomes along the care procedures of HIV. However, gaps exist in modeling the impact of interventions, such as defaulter tracing, on care continuum outcomes. Dwomoh, D., *et al.* (2023) modelled HIV test positivity among female sex workers, men who have sex with men, people who inject drugs, transgender people, and prison inmates in Sierra Leone, 2021. They used Time Location Sampling, Respondent Driven Sampling (RDS), and Conventional cluster sampling designs to generate a representative sample of FSWs, MSM, TG, PI, and PWID. HIV prevalence and the corresponding 95% confidence intervals among each KP were estimated by adjusting for sampling weight using the logit-transformed confidence intervals. Results indicated HIV prevalence to be relatively high among FSWs, MSMs, PWID, and TGs as compared to the previous estimate of the general population. It indicated the need to improve and empower evidence-based HIV prevention interventions, such as Pre-Exposure Prophylaxis and needle and syringe exchange programs that target KPs, including prison inmates. The government should therefore improve both non-clinical and clinical routine HIV and STI testing and counseling services at the correctional center and drop-in centers for KPs screening and testing to meet the needs of the Key Population.

The study conducted by Ali, R., *et al.* in 2020 focused on modeling the impact of delay strategies on the transmission dynamics of HIV/AIDS. These delay strategies likely refer to interventions or policies aimed at delaying the transmission of the virus within a population. To analyze the stability of the proposed mathematical model, the researchers used tools such as the Routh-Hurwitz criterion, Volterra-Lyapunov

function, and the Lasalle invariance principle. These mathematical techniques were used in dynamical systems theory to assess the stability of equilibrium points and trajectories in mathematical models. Additionally, the study investigated the effects of delay tactics specifically within subpopulations. This aspect suggested that the model incorporated different compartments within the population, each representing distinct subpopulations such as high-risk individuals, low-risk individuals, or individuals with varying levels of access to healthcare services. By employing mathematical modeling and stability analysis techniques, along with considering delay strategies within subpopulations, the study provided insights into the potential effectiveness of different interventions in controlling the transmission dynamics of HIV/AIDS. Knowing how transmission delays impact the spread of the virus helps inform public health strategies and assists in the development of more efficient approaches for prevention and control of HIV/AIDS.

The study conducted by Zviiteyi, C., *et al* (2024) focused on analyzing an HIV model that incorporates control strategies and evaluates their cost-effectiveness. The study investigated various intervention methods for controlling the transmission and impact of HIV/AIDS within a population. The researchers developed a mathematical model to describe the transmission dynamics of HIV/AIDS within a population. Their model included compartments representing different compartments susceptible, infected, and treated, and also incorporated parameters that relate to disease transmission, progression, and treatment factors. Various control strategies aimed at reducing the transmission of HIV/AIDS were incorporated into the model. These strategies included HIV testing and counseling, antiretroviral therapy (ART), pre-exposure prophylaxis (Pre-P), condom distribution, and education campaigns. The study evaluated the cost-

effectiveness of different control strategies in terms of their ability to reduce HIV transmission and associated costs compared to their implementation costs. Cost-effectiveness analysis is quite critical in decision-making since it prioritizes interventions that offer the greatest health benefits for the limited resources invested. They employed optimization techniques to identify optimal sequences of interventions that would maximize health benefits while minimizing resource utilization. Therefore, the study contributed to the understanding of how different control strategies impact the transmission dynamics and economic burden of HIV/AIDS, thus providing valuable insights for policymakers and public health practitioners in designing effective and efficient prevention and control programs for HIV/AIDS.

More modelling work includes the study by Nsanzimana, S., *et al* (2020) studied on the prevalence and incidence of HIV among female sex workers and their clients, modelling the potential impacts in Rwanda. They developed a model to estimate the impacts of targeted strategies to FSWs on HIV prevalence in Rwanda from 2017 to 2027. They considered three subpopulations, that is, FSWs, Sex clients, and the general population. The results indicated that neglected usage of condoms as a preventative measure would lead to the overall number of infected people significantly rising from 344,971 to 402,451 by the year 2027. HIV incidence will also decrease from 1.36 to 1.20 in each 100 persons per year. Therefore, if condom usage is improved among FSWs would result in a reduction of HIV prevalence among the FSWs, Sex clients, and the general population by 7.86%, 5.97% and 0.17% respectively, by 2027. Also, introduction of Pre-P to FSWs in 2019 reduced the HIV incidence by 1.28% among FSWs.

The research conducted by Levy, Correia, C., *et al.* (2021) modelled the effects of HIV/AIDS stigma on the dynamics of HIV infection in Kenya. The study addresses the HIV/AIDS stigma and its impact on HIV transmission dynamics in Kenya. Stigma and discrimination associated with HIV/AIDS can have profound effects on individuals' behaviors, healthcare-seeking practices, and overall well-being. It further explains that understanding how stigma influences HIV transmission dynamics is important when developing effective interventions and policies to combat the epidemic. The researchers developed a mathematical model to simulate the transmission dynamics of HIV within the Kenyan population. Sexual behavior, HIV testing and treatment uptake, healthcare access, and the impact of stigma on risk behaviors and HIV preventive and care service engagement were all included in this model. Including HIV/AIDS stigma in the study's mathematical model is a crucial component. Stigmatization can take several forms, such as fear of revelation, discrimination, and social exclusion. In order to evaluate the impact of stigma on HIV transmission rates, illness progression, and the overall course of the epidemic in Kenya, our model took these dynamics into account. In order to inform and validate the model, the researchers have used epidemiological data from Kenya, such as HIV prevalence rates, behavioral surveys, and qualitative research on stigma experiences. By relating the model to real-world data, the study provided more accurate predictions and insights into the dynamics of HIV transmission and stigma within Kenya. The findings presented key implications for HIV/AIDS prevention and control efforts in Kenya. By quantifying the impact of stigma on HIV transmission dynamics, the research therefore informs the development of stigma reduction interventions, community-based education programs, and policies aimed at promoting HIV testing, treatment adherence, and supportive environments for people living with HIV/AIDS.

Lu, Z., *et al* (2020) did a mathematical model for HIV prevention and control among men who have sex with men in China. To be able to assess the efficiency of ART in controlling HIV/AIDS infection among MSM, they developed a compartmental model for the annually reported HIV/AIDS MSM from 2007 to 2019 in the Zhejiang Province of China. R_0 was 2.3946 (95% CI (2.2961–2.4881)). The results of the paper indicated that effective consumption of ART largely controlled the spread of the disease, even in the presence of drug resistance. Therefore, behavioral and biological interventions proved to be the most effective interventions to control the HIV/AIDS epidemic among MSM.

Kumama, R., *et al* (2021) studied on Bifurcation and Stability Analysis of HIV Transmission Model with Optimal Control. Researchers used MATLAB to run numerical simulations. The numerical results by simulation showed that the number of individuals at the AIDS stage and the number of newly infected HIV individuals decreased as a result of taking control measures. These cost-effective studies demonstrated that when the preventative and treatment control measures are combined and used, the disease is curbed.

Numerous areas of study have also focused on modeling the impact of contact tracing programs for epidemics like COVID-19, for instance, Nosyk, B., *et al* (2020), conducted a study on contact tracing for COVID-19. Which was an opportunity to reduce health disparities and end the HIV/AIDS epidemic in the United States. Their results indicated that testing to promote health allows for stigma-free messaging and broad acceptance. Testing and contact tracing for COVID-19 will provide an entry into social networks in communities where risk factors for conditions like HIV or non-communicable diseases may be shared.

Viet, L. B., et al, (2024) who researched on agent-based modelling of mycobacterium tuberculosis transmission. Results indicated that traditional epidemiological models tend to oversimplify the transmission dynamics of Mycobacterium tuberculosis (M.tb) to replicate observed tuberculosis (TB) epidemic patterns. This has led to growing interest in advanced methodologies like agent-based modelling (ABM), which can more accurately represent the complex heterogeneity of TB transmission.

Researchers have explored mathematical modeling approaches to evaluate the impacts of defaulter tracing on HIV/AIDS control. These models simulate the effects of defaulter tracing interventions on transmission rates, viral load suppression, and retention in care, providing insights into the potential population-level impact of these interventions. The study conducted by Etoori, D., *et al.* in (2020) focused on examining the challenges associated with tracing patients on antiretroviral therapy (ART) who are late for clinic appointments in rural South Africa. The study addressed the critical issue of retention in HIV care and treatment programs, particularly among individuals who are late for clinic appointments. Maintaining regular clinic attendance is essential for ensuring optimal health outcomes among people living with HIV/AIDS and receiving ART. The research also identified various challenges associated with tracing patients who are late for clinic appointments, such as difficulty reaching patients due to incorrect contact information, transportation barriers, fear of stigma or discrimination, competing priorities, and socioeconomic constraints. These challenges lead to poor retention in care and may ultimately impact treatment outcomes and the effectiveness of HIV/AIDS programs. Based on their findings, the study provided recommendations for improving patient tracing and retention in care practices in rural South Africa. These recommendations included strengthening communication and outreach strategies,

improving data management systems to ensure accurate patient information, addressing transportation barriers, providing community-based support services, and implementing patient-centered approaches to care. The study contributes valuable insights into the challenges of tracing patients on ART who are late for clinic appointments in rural South Africa.

De Angeles, K., (2024) investigated the impact of interactive text messaging and regular tracing of defaulters on engagement in PMTCT care in western Kenya, as well as the interplay between these interventions and existing social and health system practices. A mixed-methods strategy was adopted, merging a longitudinal cohort study with qualitative research that was integrated into the WelTel-PMTCT randomized control trial conducted across six healthcare facilities from July 2016 to February 2019. The initial study focused on a cohort of 299 women who received weekly interactive text messages for a duration of 24 months. Information was collected through questionnaires, logbooks, and data from the intervention platform. Descriptive statistics, multivariable-adjusted logistic regression, and negative binomial models were employed to examine the connections between sociodemographic factors and adherence to the intervention. A combination of narrative analysis and an intersectionality lens was utilized to investigate the elements that influenced these women's participation in PMTCT care. Thematic network analysis was conducted, informed by maintenance and repair theory. Out of the total 31,638 text messages sent as part of the intervention, women replied to 49% of them, with 48% expressing no concerns ("okay" responses) and 1% reporting problems. Younger women (ages 18-24) were less likely to respond to more than 50% of the messages compared to older

women. Defaulter tracing interventions seek to reconnect individuals who have missed HIV/AIDS care and treatment services.

While research has shown that defaulter tracing can effectively enhance retention in care and adherence to treatment, relatively few mathematical models have explicitly included defaulter tracing as a mechanism for controlling the spread of HIV/AIDS within systems of equations. Difficulties in modeling defaulter tracing include challenges in parameter estimation, data availability, and the complexity of the model. Nonetheless, mathematical modeling presents opportunities to evaluate the cost-effectiveness of defaulter tracing interventions, optimize resource distribution, and guide policy decisions in HIV/AIDS control efforts. Thus, mathematical modeling plays an essential role in understanding the impact of defaulter tracing interventions on HIV/AIDS spread control. By merging empirical evidence with mathematical frameworks, researchers can assess the effectiveness of defaulter tracing, refine intervention strategies, and aid in creating evidence-based policies for controlling HIV/AIDS.

According to CDC “basic statistics” (2023), the World Health Organization (WHO) has set ambitious targets to combat HIV, aiming for 95% of all people living with HIV to know their status, 95% of those diagnosed to receive sustained antiretroviral therapy (ART), and 95% of those on ART to achieve viral suppression by 2025. This "95-95-95" strategy is designed to significantly reduce HIV-related morbidity, mortality, and transmission. Recent data indicate substantial progress toward these goals. Globally, new HIV infections have decreased by almost 22% between 2010 and 2021, and HIV-related deaths have fallen nearly 40% in the same period. Notably, sub-Saharan Africa experienced a 60% reduction in the risk of HIV infection from 1995 to 2021. However,

challenges persist. In 2022, only 65% of people diagnosed with HIV in the United States had achieved viral suppression, underscoring the need for enhanced efforts to reach the 95% target. To address these disparities, WHO emphasizes the importance of integrating viral load testing into routine HIV/AIDS care. This approach ensures that individuals on ART are effectively monitored, and those not achieving viral suppression receive timely interventions. By promoting adherence to ART and regular monitoring, WHO aims to enhance the quality of life for people living with HIV and reduce transmission rates globally. Achieving the 95-95-95 targets requires sustained global commitment, resource allocation, and the implementation of structured evidence-based strategies to diverse populations and regions. This means that all newly traced HIV infected individuals are linked with immediate effect to treatment and retained in the system through regular testing.

Mathematical modelling is very key in understanding dynamics of life and its components. Jia, R., et al (2024) did a study on MODELS-a six-step framework for developing an infectious disease model. Since the COVID-19 pandemic began, a plethora of modeling studies related to COVID-19 have been released. While some models stand out due to their innovative approaches, others are flawed in their methodology. To assist novices, frontline healthcare workers, and public health policymakers in navigating the complex landscape of these models, we introduced a structured framework named MODELS. This framework is designed to detail the essential steps and considerations for creating a dependable epidemic model, offering direction to researchers engaged in epidemic modeling endeavors.

Lili H., *et al* (2025), researched on transmission dynamics and stability analysis of fractional HIV and AIDS epidemic model with antiretroviral therapy. To establish the

existence and uniqueness of solutions, qualitatively examined the model via fixed-point theory. Apart from that, a new numerical technique for simulations focused on the predictor-corrector strategy is implemented and MATLAB is used to verify the results.

Numerous models have been suggested to address certain epidemics, Ronoh, M. C., *et al.* (2021), mathematical modeled HIV/AIDS transmission dynamics coupled with awareness among adolescents and young adults in Kenya. They developed deterministic models to study the effect of HIV/AIDS awareness in the disease transmission dynamics of adolescents aged 10 - 14 years and young adults aged 15-24 years in Kenya.

Semra, A., *et al* (2022) did a study of a Susceptible–Infectious (SI) model with two infective stages and an endemic equilibrium. They employed mathematical computer related Simulation to obtain their results. This study used a model that assumed that susceptible individuals have access to Pre-p to prevent themselves from HIV. Such individuals became exposed to HIV once they stopped taking oral Prep. In this study, intensified defaulter tracing systems were involved to intensify the number of infected individuals accessing the services.

Wandera, O., *et al* (2024).” Mathematical modelling of non-pharmaceutical interventions to control infectious diseases: application to COVID-19 in Kenya”. They applied a deterministic mathematical model to simulate the dynamics of COVID-19 transmission in Kenya. Using baseline data, they estimated transmission and recovery rates and proposed a mathematical model of how NPIs affect disease transmission rates. The model extends to interventions that yield an increase in disease transmission, unlike

previous models that were limited to a decrease in transmission. They computed the mitigation and relaxation fractions and hence deduced the impact of the interventions.

Additional research is necessary to improve modeling techniques, tackle methodological issues, and enhance the relevance of mathematical models in guiding public health practices. Motivated by the above work, this study will consider an HIV/AIDS epidemic model incorporating defaulter tracing and retention in care in the analysis and control of the disease. In this study, we employed a mathematical model to illustrate and describe the transmission dynamics of HIV, the impact of defaulter tracing, testing, and treatment on the disease transmission. Here, our model considered contact tracing data secondary obtained to describe the spread of HIV/AIDS. The model also considered the basic compartments for the population (SI).

CHAPTER THREE

METHODOLOGY

MODEL FORMULATION AND ANALYSIS

3.1 Introduction

The methodology section outlines the approach used to develop and implement a mathematical model to assess the impacts of defaulter tracing interventions on the control of HIV/AIDS spread. This section describes the model structure, parameterization process, simulation techniques, and data sources used in the study. The mathematical model is based on compartmental modeling frameworks, such as the Susceptible-Infectious-Removed (SIR) model adapted for HIV/AIDS transmission dynamics. The model includes compartments representing different population groups based on HIV status (susceptible, infected, and treated) and engagement in care (engaged, defaulting, lost to follow-up). Defaulter tracing interventions are incorporated as control mechanisms within the model, with parameters representing the effectiveness and coverage of defaulter tracing activities.

Model parameters are derived from a combination of sources, including empirical data from HIV/AIDS surveillance systems, programmatic data from healthcare facilities, and literature reviews. Key parameters include transmission rates, treatment uptake rates, defaulter tracing effectiveness, and population demographics. The solutions for the modelled ordinary differential equations have been obtained using an inbuilt function in MATLAB.

3.2 Model Description and Formulation

The model of this study has the following compartments: susceptible individuals, S_p individuals who are infected, (I_T) individuals who are infected and under the ARV-program, (I_{ARV}) individuals who are infected and not under any ARV-program (I_{NARV}) and individuals under the defaulter tracing program (D_{TR}) .

The $(S_p, I_T, I_{ARV}, I_{NARV}, D_{TR})$ model will be studied and is an improvement of the (SI) model by adding extra compartments. The R_0 (Reproduction number) has been calculated using the next generation matrix and defaulter tracing adjusted regarding the reproduction number.

Susceptible Population (S_p) : This compartment represents individuals who have chances to HIV/AIDS infection and have not yet been infected. Susceptible individuals may engage in behaviors that put them at risk of HIV transmission, such as unprotected sexual activity, drug injector sharing needles.

Infected Population (I_T) : The infected population comprises individuals who have contracted HIV and are infectious to others. This includes both newly infected individuals and those who have progressed from the susceptible compartment due to HIV transmission.

Infected and Not under Antiretroviral Therapy (I_{NARV}) : It is a compartment that represents individuals who have been diagnosed with HIV but are not currently receiving antiretroviral therapy (ART). These individuals may be aware of their HIV

status but have not initiated treatment, either due to barriers to accessing care or their reasons.

Infected under Antiretroviral Therapy (I_{ARV}): Individuals in this compartment are HIV-positive and receiving antiretroviral therapy (ART) for HIV/AIDS treatment. ART suppresses viral multiplication, reducing the viral load in the bloodstream and the risk of transmitting HIV to others.

Infected and under Defaulter Tracing (D_{TR}): This compartment includes individuals who were initially receiving ART for HIV/AIDS treatment but have defaulted on their treatment or missed scheduled appointments. Defaulter tracing interventions target individuals in this compartment to re-engage them in HIV/AIDS care and treatment services, thereby reducing the risk of treatment interruption and disease progression. These compartments collectively represent the population dynamics of HIV/AIDS transmission, treatment, and defaulter tracing within the model.

Susceptible-Infectious (S-I) model is employed in this study to consider the significance of defaulter tracing on the reduction of HIV mortality rates. Numerous mathematical equations have been extracted from the S-I model developed. The model includes parameters that affect population progression rate from a compartment to another. Population compartments explaining the composition and influence of factors on each compartment are as follows. These factors include;

- i) Rate of disease transmission from one compartment to another.
- ii) Death rate due to disease-related illnesses.

- iii) Rate of disease control using the preferred measures, such as ARVs (ART-methods), condom usage, treatment, and creation of awareness.
- iv) Rate of tracing the infected individuals who are not under any treatment or disease control program.

Basic Defaulter Tracing strategy is implemented, involving periodic follow-up of patients who have missed scheduled clinic appointments. Parameters such as the defaulter tracing effects, and the proportion of traced defaulters re-engaged in care are varied to assess their impact. The Defaulter tracing interventions are integrated into compartmental mathematical models representing HIV/AIDS transmission dynamics. A separate compartment for defaulters has been added to the model, with individuals transitioning from the defaulting state back to active treatment following successful tracing efforts. These movements are governed by the parameters reflecting the effectiveness of tracing efforts, such as tracing frequency, coverage, and success rate.

The model assumptions for this study are;

- i) The population size N is constant, meaning births and deaths (except disease-related deaths) balance each other.
- ii) Individuals mix randomly with others, leading to uniform exposure risks.
- iii) The infection spreads through contact between susceptible and infected individuals.
- iv) The force of infection depends on the number of infectious individuals.
- v) The model incorporates (ARV) (Antiretroviral Therapy) and (N_{NARV}) non-ART compartments, suggesting treatment strategies.

- vi) There is a differential effect of tracing (DT_{eff}) for transitions from compartment to another.
- vii) The transition rates between compartments are constant.
- viii) Some infected individuals receive ART while others do not.
- ix) Natural death rates (μ) are included in different compartments
- x) The model allowed for individuals to be taken back to care after successful tracing and initial treatment. Some transitions depend on treatment effectiveness and other factors.
- xi) HIV/AIDS related deaths (δ) only occur to the population not in any medication program.

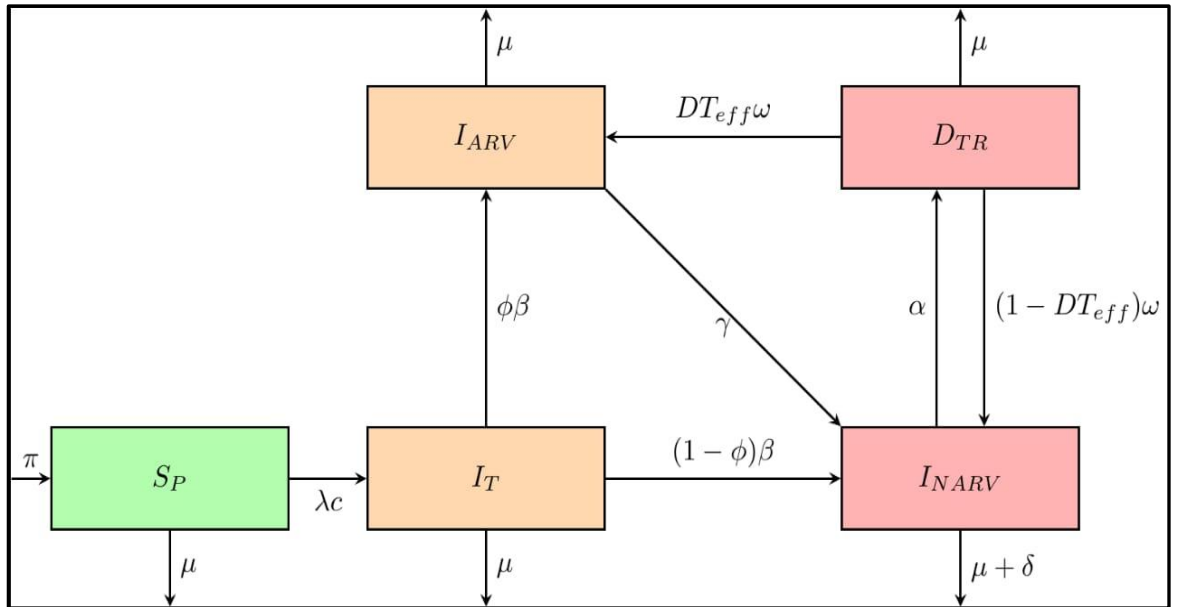


Figure 1: Flow diagram of the HIV/AIDS model with defaulter tracing.

Arrows indicate the transition of individuals between compartments S_p (Susceptible), I_T (Infected/Initial), I_{ARV} (Infected on ART), I_{NARV} (Infected not on ART), D_{TR} (Defaulters under tracing). Parameters governing the transitions are shown alongside the arrows. The flow of individual between these compartments is depicted in Figure

1. New individuals enter the susceptible population at a rate of πN . Susceptible individuals become infected at a rate λc (where λ represents the force of infection while c represents the contact rate). Infected population I_T may either start ART or proceed to I_{ARV} at a rate of $\phi\beta$, or fail to enroll/default early and move to I_{NARV} at a rate of $(1-\phi)\beta$. Likewise individuals on ARV, I_{ARV} may abandon treatment and proceed to I_{NARV} at a rate γ where $\gamma = (1-\phi)\theta\beta$. Individuals not on ARV I_{NARV} can be successfully traced at a rate α , to D_{TR} compartment. Individuals under tracing D_{TR} can successfully return to ART I_{ARV} at a rate proportional to tracing effectiveness DT_{eff} or fail to get into care at a rate $(1-DT_{eff})$. Natural death occurs in all compartments at a rate μ , and an additional HIV-related death rate of δ for individuals not virally suppressed I_{NARV} .

From the description above, the dynamics of the given system are explained by the following system of ordinary differential equations (ODEs), derived from the flow diagram in Figure 1.

$$\left[\begin{aligned} \frac{dS_p}{dt} &= \pi - \frac{\lambda c S_p I_T}{N} - \mu S_p \\ \frac{dI_T}{dt} &= \frac{\lambda c S_p I_T}{N} - (\phi\beta + \mu + (1-\phi)\beta) I_T \\ \frac{dI_{ARV}}{dt} &= \phi\beta I_T - (\gamma + \mu) I_{ARV} + DT_{eff} \omega D_{TR} \\ \frac{dI_{NARV}}{dt} &= (1-\phi)\beta I_T + \gamma I_{ARV} - (\alpha + \mu + \delta) I_{NARV} + (1-DT_{eff}) \omega D_{TR} \\ \frac{dD_{TR}}{dt} &= \alpha I_{NARV} - (\omega + \mu) D_{TR} \end{aligned} \right] \quad (3.1)$$

Table 1: Model Parameters

The parameters below represent various epidemiological and intervention rates.

Parameter	Description
π	Recruitment rate by birth and immigration
μ	Natural per capita death rate
λ	Rate of infection of the susceptible population.
c	Contact rate of the infected with the susceptible population
β	Testing rate from the Infectious population to the Infected population under ARV treatment.
ϕ	Proportion of HIV/AIDS-infected individuals who fail to enroll in any program and thus proceed to the region under no support program.
α	Defaulter tracing rate of HIV/AIDS-infected population not under ARVs.
γ	The rate at which the infected population under ARVs abandons medication
ω	The rate at which the infected population not under the ARV program listens to awareness campaigns and responds by proceeding to ARV treatment
D_{Teff}	Defaulter tracing effectiveness
θ	Rate of retention on the ARV disease suppression program
δ	Death rate due to HIV-related complications

3.3 Model Analysis

3.3.1 Positivity Invariance

Considering model (3.1) describes the human population, and hence it is important to prove that the solutions to model (3.1) with positive initial conditions will remain positive for all $t \geq 0$

Proposition 3.1: *If the initial conditions of the model (3.1) are non-negative, then the solution set is non-negative for future time $t \geq 0$*

Proof: To prove the existence of a non-negativity of solution to model (3.1), given that all the model parameters are positive, we proceed as follows;

The first equation in the model (3.1) is written as follows;

$$\frac{dS_p}{dt} = \pi - \frac{\lambda c S_p I_T}{N} - \mu S_p \quad (3.2)$$

Since π is positive, then

$$\frac{dS_p}{dt} \geq -\frac{\lambda c S_p I_T}{N} - \mu S_p \quad (3.3)$$

Solving (3.3) by separation of variables and integrating from 0 to t for τ , we proceed as follows;

$$\int_0^t \frac{dS_p}{S_p} d\tau \geq \int_0^t -\left(\frac{\lambda c I_T}{N} + \mu\right) d\tau$$
$$\ln S_p(t) - \ln S_p(0) \geq -\left(\frac{\lambda c I_T}{N} + \mu\right)t$$

$$\ln \left| \frac{S_p(t)}{S_p(0)} \right| \geq - \left(\int_0^t \frac{\lambda c I_T}{N} + \mu \right) t \quad (3.4)$$

Introducing exponential to both sides of (3.4), we rewrite as follows:

$$\begin{aligned} \frac{S_p(t)}{S_p(0)} &\geq e^{-\left(\int_0^t \frac{\lambda c I_T}{N} + \mu \right) t} \\ S_p(t) &\geq S_p(0) e^{-\left(\int_0^t \frac{\lambda c I_T}{N} + \mu \right) t} \end{aligned} \quad (3.5)$$

From equation (3.5), we notice that $S_p \geq 0$ for all the values of t .

The set of model equations can be solved similarly.

$$I_T(t) \geq I_T(0) e^{-\left(\int_0^t \beta + \mu \right) t} \quad (3.6)$$

$$I_{ARV}(t) \geq I_{ARV}(0) e^{-\left(\int_0^t \gamma + \mu \right) t} \quad (3.7)$$

$$I_{NARV}(t) \geq I_{NARV}(0) e^{-\left(\int_0^t \alpha + \mu + \delta \right) t} \quad (3.8)$$

$$D_{TR}(t) \geq D_{TR}(0) e^{-\left(\int_0^t \omega + \mu \right) t} \quad (3.9)$$

Implying that the initial conditions are, $S_p \geq 0; I_T \geq 0; I_{ARV} \geq 0; I_{NARV} \geq 0; D_{TR} \geq 0$

Thus, all the solutions of the model (3.1) with non-negative initial conditions will remain positive for all time $t \geq 0$

3.3.2 Boundedness of Solutions

The epidemiological HIV/AIDS model above depicts the human population in different compartments.

Proposition 3.2 (invariant region). *Let the feasible region φ be defined by;*

$$\varphi = \left\{ (S_p, I_T, I_{ARV}, I_{NARV}, D_{TR}) \in R_+^5 : N \leq \frac{\pi}{\mu} \right\} \quad (3.10)$$

The above are positively invariant for all $t \geq 0$.

Proof: The total population at any time t is given by

$$N(t) = S_p(t) + I_T(t) + I_{ARV} + I_{NARV} + D_{TR} \text{ Adding the model equations (3.1), we obtain;}$$

$$\begin{aligned} \frac{dN}{dt} &= \frac{dS_p}{dt} + \frac{dI_T}{dt} + \frac{dI_{ARV}}{dt} + \frac{dI_{NARV}}{dt} + \frac{dD_{TR}}{dt} \\ &= \pi - \mu(S_p + I_T + I_{ARV} + I_{NARV} + D_{TR}) - \alpha I_{NARV} \end{aligned} \quad (3.11)$$

Now, since $N_t = S_p + I_T + I_{ARV} + I_{NARV} + D_{TR}$ (3.11) becomes;

$$= \pi - \mu N - \alpha I_{NARV} \quad (3.12)$$

Considering α to be positive, we then write;

$$\frac{dN(t)}{dt} \leq \pi - \mu N \quad (3.13)$$

Rearranging equation (3.13). we get

$$\frac{dN}{dt} + N\mu \leq \pi \quad (3.14)$$

Solving (3.14) using the integrating factor method, we obtain;

$$N \cdot \exp^{\mu t} \leq \frac{\pi e^{\mu t}}{\mu} + c \quad (3.15)$$

Dividing by $e^{\mu t}$ (3.15) results in;

$$N(t) \leq \frac{\pi}{\mu} + \frac{C}{e^{\mu t}} \quad (3.16)$$

At $t = 0$ (3.17) reduces to;

$$N(0) \leq \frac{\pi}{\mu} + \frac{C}{e^0} \quad (3.17)$$

Thus, the value of C from (3.17) can be written as;

$$C \leq \left(N(0) - \frac{\pi}{\mu} \right) e^0 \quad (3.18)$$

Replacing the value C from (3.19) in equation (3.17);

$$N(t) \leq \frac{\pi}{\mu} + \left(N(0) - \frac{\pi}{\mu} \right) e^{-\mu t} \quad (3.19)$$

When the value of t approaches infinity, then $e^{-\mu t}$ tends to zero and therefore (3.19) can be expressed as;

$$N(t) \leq \frac{\pi}{\mu} \quad (3.20)$$

3.3.3. Disease-Free Equilibrium (D.F.E)

The DFE occurs when there are no infected individuals in the population. Assuming that the community has not yet experienced an HIV infection, then it is expected to remain free from the disease. This shows that the entire community is considered susceptible to the infection.

Thus, all the disease variables reduce to zero, that is;

$$I_T = 0, I_{ARV} = 0, I_{NARV} = 0, D_{TR} = 0 \quad (3.21)$$

To evaluate disease-free equilibrium, we choose the infected population model equation from (3.1) and replace the value of I_T since all the disease variables reduce to zero, we therefore have;

$$\pi - \frac{\lambda c S_p I_T}{N} - (\mu) S_p = \frac{dS_p}{dt} \quad (3.22)$$

Then (3.22) reduces to

$$\pi - \left[\frac{\lambda c I_T}{N} - \mu \right] S_p = \frac{dS_p}{dt} \quad (3.23)$$

Now that $I_T = 0$ the above equation (3.23) simplifies and also since at equilibrium

$\frac{dS_p}{dt} = 0$, therefore;

$$[\pi - \mu S_p] = \frac{dS_p}{dt} = 0 \quad (3.24)$$

Implying that;

$$S_p = \frac{\pi}{\mu} \quad (3.25)$$

Indicating that in the absence of these diseases;

$$E_0 = \left[\frac{\pi}{\mu}, 0, 0, 0, 0 \right] \quad (3.26)$$

Implying that in the absence of the disease, the susceptible population stabilizes at

$$S_p = \frac{\pi}{\mu} \text{ and there are no infected individuals in the population } I_T = 0.$$

3.3.4. Reproduction number.

According to Yao-Hsuan, C., *et al* (2022) estimated the HIV effective reproduction number in the United States and evaluating HIV elimination strategies. Their research highlighted that reproduction number is a fundamental epidemiologic concept used to assess the potential spread of infectious diseases and whether they can be eliminated. Therefore, the basic reproduction number refers to the average number of new infections generated by a single infected individual in a completely susceptible population. We therefore use the next-generation matrix method as defined by Abiodun, O.E., *et al* (2022), such that the matrices of the new infections evaluated at the disease-free equilibrium are given as below. The basic reproduction number is given by the spectral radius of FV^{-1} , and it is denoted by R_0 .

Let $X' = (I_T, I_{ARV}, I_{NARV}, D_{TR})$ represent the disease compartments. Then from the model equations we can write;

$$X' = \frac{dX}{dt} = F(X) - V(X) \quad (3.27)$$

Where $F(X)$ gives the rate of appearance of the new infections in a compartment, while

$V(X)$ gives the transfer of individuals, that is

$$F(X) = \begin{bmatrix} \lambda c \\ 0 \\ 0 \\ 0 \end{bmatrix} \quad (3.28)$$

$$V(X) = \begin{bmatrix} -(\beta + \mu)I_T \\ \phi\beta I_T - (\gamma + \mu)I_{ARV} + DT_{eff}\omega D_{TR} \\ (1 - \phi)I_T + \gamma I_{ARV} - (\alpha + \mu + \delta)I_{NARV} + (1 - DT_{eff})\omega D_{tr} \\ \alpha I_{NARV} - [\omega + \mu]D_{TR} \end{bmatrix} \quad (3.29)$$

Therefore letting $F = F(I_T, I_{ARV}, I_{NARV}, D_{TR})$ and $V = V(I_T, I_{ARV}, I_{NARV}, D_{TR})$

From F, we obtain the Jacobian matrix;

$$F = \begin{bmatrix} \frac{\partial f_1}{\partial I_T} & \frac{\partial f_1}{\partial I_{ARV}} & \frac{\partial f_1}{\partial I_{NARV}} & \frac{\partial f_1}{\partial D_{TR}} \\ \frac{\partial f_2}{\partial I_T} & \frac{\partial f_2}{\partial I_{ARV}} & \frac{\partial f_2}{\partial I_{NARV}} & \frac{\partial f_2}{\partial D_{TR}} \\ \frac{\partial f_3}{\partial I_T} & \frac{\partial f_3}{\partial I_{ARV}} & \frac{\partial f_3}{\partial I_{NARV}} & \frac{\partial f_3}{\partial D_{TR}} \\ \frac{\partial f_4}{\partial I_T} & \frac{\partial f_4}{\partial I_{ARV}} & \frac{\partial f_4}{\partial I_{NARV}} & \frac{\partial f_4}{\partial D_{TR}} \end{bmatrix} \quad (3.30)$$

Obtaining the partial derivatives from the above matrix f, we get F;

$$F = \begin{bmatrix} \frac{\lambda c S_P}{N} & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix} \quad (3.31)$$

Since from (3.26) $S_p = \frac{\pi}{\mu}$ therefore $F =$

$$\begin{bmatrix} \frac{\lambda c \pi}{\mu} & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix} \quad (3.32)$$

Similarly, from $V(x)$ we obtain the Jacobian matrix v ;

$$V = \begin{bmatrix} \frac{\partial v_1}{\partial I_T} & \frac{\partial v_1}{\partial I_{ARV}} & \frac{\partial v_1}{\partial I_{NARV}} & \frac{\partial v_1}{\partial D_{TR}} \\ \frac{\partial v_2}{\partial I_T} & \frac{\partial v_2}{\partial I_{ARV}} & \frac{\partial v_2}{\partial I_{NARV}} & \frac{\partial v_2}{\partial D_{TR}} \\ \frac{\partial v_3}{\partial I_T} & \frac{\partial v_3}{\partial I_{ARV}} & \frac{\partial v_3}{\partial I_{NARV}} & \frac{\partial v_3}{\partial D_{TR}} \\ \frac{\partial v_4}{\partial I_T} & \frac{\partial v_4}{\partial I_{ARV}} & \frac{\partial v_4}{\partial I_{NARV}} & \frac{\partial v_4}{\partial D_{TR}} \end{bmatrix} \quad (3.33)$$

Solving v above, we obtain the partial derivatives as V ;

$$V = \begin{bmatrix} -(\beta + \mu) & 0 & 0 & 0 \\ \phi\beta & -(\gamma + \mu) & 0 & DT_{eff}\omega \\ (1-\phi) & \gamma & -(\alpha + \mu + \delta) & (1-DT_{eff})\omega \\ 0 & 0 & \alpha & -(\omega + \mu) \end{bmatrix} \quad (3.34)$$

Let: $a_1 = (\beta + \mu)\mu$, $a_2 = \gamma + \mu$, $a_3 = \alpha + \mu + \delta$, $a_4 = \omega + \mu$

The inverse of V becomes;

$$V^{-1} = \begin{bmatrix} \frac{-(\beta + \mu)}{a_1} & 0 & 0 & 0 \\ \frac{\phi\beta}{a_1 a_2} & \frac{-(\gamma + \mu)}{a_2} & 0 & \frac{DT_{eff}\omega}{a_2 a_4} \\ \frac{1-\phi}{a_1 a_3} + \frac{\gamma\phi\beta}{a_1 a_2 a_3} & \frac{\gamma}{a_2 a_3} & \frac{-(\alpha + \mu + \delta)}{a_2 a_3} & \frac{(1-DT_{eff})\omega}{a_3 a_4} \\ 0 & 0 & \frac{\alpha}{a_3 a_4} & \frac{-(\omega + \mu)}{a_4} \end{bmatrix} \quad (3.36)$$

The basic reproduction number $R_0 = \rho(FV^{-1})$ is the spectral radius of the product FV^{-1} ; hence, for this model, we get;

$$FV^{-1} = \begin{bmatrix} \frac{-\lambda c \pi}{\mu(\mu + \beta) - \alpha \omega (1 - DT_{eff})} & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{bmatrix} \quad (3.37)$$

Therefore, we have;

$$R_e = \left[\frac{\lambda c \pi}{\mu(\mu + \beta) - \alpha \omega (1 - DT_{eff})} \right] \quad (3.38)$$

When $\alpha = 0$ and $\omega = 0$ the behavior of the basic reproduction number is analyzed as follows;

Setting $\alpha = 0$ in the equation (3.38) implies that any terms containing α will vanish and the equation reduces to;

$$R_e = \frac{\lambda c \pi}{\mu[(\mu + \beta)]} \text{ since } \alpha = 0 \text{ then } R_e = R_0 \quad (3.39)$$

This is interpreted as follows;

- (i) If $\alpha > 0$, shows that there are interventions that reduce the value of R_e
- (ii) When $\alpha = 0$ the model relates to a traditional HIV model, where $R_e = R_0$ is dictated by the transmission rate and progression dynamics only.

Therefore, setting $\alpha = 0$ removes the impacts of defaulter tracing and awareness creation, making $R_e = R_0$ to be higher and similar to standard HIV models without any behavioral adaptation.

3.3.5 Endemic Equilibrium.

At the endemic equilibrium state, all the variables in the dynamic system, that is, the Infectious population, the Infectious population under medication, Infectious population not under medication are taken into consideration. Here, the system is a steady state, and all-time derivatives are related to zero.

At the endemic equilibrium, the system is a steady state, implying that time derivatives are equal to zero;

$$\text{Thus, } \frac{dS_P}{dt} = 0 \quad \frac{dI_T}{dt} = 0 \quad \frac{dI_{ARV}}{dt} = 0 \quad \frac{dI_{NARV}}{dt} = 0 \quad \frac{dD_{TR}}{dt} = 0$$

$$\text{The EE is given by } EE = (S_P^*, I_T^*, I_{ARV}^*, I_{NARV}^*, D_{TR}^*) \quad (3.39)$$

From the system of model equations (3.1), we notice that the second equation reduces as follows;

$$\frac{dI_T}{dt} = \left(\frac{\lambda c S_P}{N} - (\beta + \mu) \right) I_T$$

$$\frac{dI_T}{dt} = \left(\frac{\lambda c}{N} \cdot \frac{\pi}{\mu} N - (\beta + \mu) \right) I_T$$

$$\frac{dI_T}{dt} = (R_0 - 1)I_T \quad \text{when } R_0 > 1 \quad \frac{dI_T}{dt} \geq 0 \quad (3.40)$$

At the endemic equilibrium setting $\frac{dI_T}{dt} = 0$ and since $I_T^* \neq 0$ then (3.40) simplifies to;

$$0 = \left(\frac{\lambda c S_p}{N} \right) - (\beta + \mu) \quad (3.41)$$

Which follows that;

$$\left(\frac{\lambda c S_p^*}{N} \right) = (\beta + \mu) \quad (3.42)$$

Rearranging the above equation (3.42) results in;

$$S_p^* = \frac{(\mu + \beta)}{\lambda c} N \quad (3.43)$$

Now, considering the first equation of model (3.1)

$$\frac{dS_p}{dt} = \pi - \frac{\lambda c S_p I_T}{N} - \mu S_p$$

When $\frac{dS_p}{dt} = 0$ the above equation at the endemic equilibrium is expressed as;

$$0 = \pi - \frac{\lambda c S_p^* I_T^*}{N} - \mu S_p^* \quad (3.44)$$

Above equation (3.44) simplifies to;

$$\pi = \frac{(\lambda c I_T^* + \mu)}{N} S_p^* \quad (3.45)$$

Now, replacing the value of $S_p^* = \frac{(\mu + \beta)}{\lambda c} N$ in the above equation, we get and

simplifying it to make I_T^* the subject of the formula, we have

$$\begin{aligned}
I_T^* &= \frac{\pi N}{\mu + \beta} - \left(\frac{\mu}{\lambda c} \right) \\
I_T^* &= \frac{\mu}{\lambda c} \left(\frac{\pi \lambda c}{\mu(\mu + \beta)} - 1 \right) \\
&= \frac{\mu}{\lambda c} (R_0 - 1) \text{ therefore, } R_0 > 1
\end{aligned} \tag{3.46}$$

For an endemic equilibrium to exist with a positive number of infected individuals,

$I_T^* > 0$ we require:

$$\pi - \frac{\mu(\beta + \mu)}{\lambda c} > 0 \text{ Implying that, } \frac{\lambda c \pi}{\mu(\beta + \mu)} > 1$$

This condition relates to the basic reproduction number $R_0 > 1$.

Similarly,

$$D_{TR}^* = \frac{\alpha \left[(1 - \phi) \beta \left(\frac{\pi}{\mu + \beta} - \frac{\mu}{\lambda c} \right) + \gamma \phi \beta \left(\frac{\pi}{\mu + \beta} - \frac{\mu}{\lambda c} \right) \right]}{[(\omega - \mu)(\alpha + \mu + \delta) - (\gamma \omega D T_{eff} + 1 - D T_{eff} \omega)]} \tag{3.47}$$

$$\text{But, } I_T^* = \frac{\pi}{\mu + \beta} - \left(\frac{\mu}{\lambda c} \right) \text{ but } I_T^* = \frac{\mu}{\lambda c} (R_0 - 1)$$

Thus (3.47) becomes

$$D_{TR}^* = \frac{\alpha \beta \frac{\mu}{\lambda c} (R_0 - 1) [(1 - \phi) + \gamma \phi]}{[(\omega - \mu)(\alpha + \mu + \delta) - (\gamma \omega D T_{eff} + 1 - D T_{eff} \omega)]} \tag{3.48}$$

Similarly, the other equations from model (3.1) at the endemic equilibrium simplify as follows;

$$I_{ARV}^* = \frac{\phi\beta \frac{\mu}{\lambda c} (R_0 - 1) + DT_{eff} \omega D_{TR}^*}{\gamma + \mu} \quad (3.49)$$

$$I_{NARV}^* = \left(\frac{\omega - \mu}{\alpha} \right) \left[\frac{\alpha\beta \frac{\mu}{\lambda c} (R_0 - 1) [(1 - \phi) + \gamma\phi]}{[(\omega - \mu)(\alpha + \mu + \delta) - (\gamma\omega DT_{eff} + 1 - DT_{eff} \omega)]} \right] \quad (3.50)$$

The above is interpreted as;

Even in the presence of other control mechanisms such as ARVs and PrEP but in the absence of defaulter tracing, the defaulter population will remain entirely infected and not detected by any measure. Also, the population under ARV-treatment will not be contributed to by any measure to enable control and curb the spread of the disease, nor will it be monitored by any parameter. Therefore, the entire population will remain at risk of contracting and spreading the disease.

Mathematically, an endemic equilibrium exists only when $R_0 > 1$. These suggests that introducing an infected individual to the existing population and causing no new infection, the disease will die out.

3.3.6 Stability Analysis.

3.3.6.1 Stability Analysis of the Disease-free Equilibrium

The local stability of the DFE (Disease-Free Equilibrium) is defined by obtaining the eigenvalues of the model (3.1). To calculate the local stability of the Disease-Free Equilibrium (DFE), we need to derive the Jacobian matrix and analyze its eigenvalues.

lemma 3.1 *Disease-free equilibrium becomes locally asymptotically stable if $R_0 < 1$ and becomes unstable if $R_0 > 1$.*

Proof: To determine the local stability of the disease-free equilibrium, we construct a Jacobian matrix (J) from the model equations (3.1) at the disease-free equilibrium as follows;

At the DFE, the Eigenvalues for each equation in the system for the Jacobian matrix are obtained for the state variables $S_p, I_t, I_{Arv}, I_{NArv}, D_{tr}$ as below;

$$J(E^*) = \begin{bmatrix} \frac{\partial S_p}{\partial S_p} & \frac{\partial S_p}{\partial I_t} & \frac{\partial S_p}{\partial I_{Arv}} & \frac{\partial S_p}{\partial I_{NArv}} & \frac{\partial S_p}{\partial D_{tr}} \\ \frac{\partial S_p}{\partial I_t} & \frac{\partial I_t}{\partial I_t} & \frac{\partial I_t}{\partial I_{Arv}} & \frac{\partial I_t}{\partial I_{NArv}} & \frac{\partial I_t}{\partial D_{tr}} \\ \frac{\partial I_{Arv}}{\partial S_p} & \frac{\partial I_{Arv}}{\partial I_t} & \frac{\partial I_{Arv}}{\partial I_{Arv}} & \frac{\partial I_{Arv}}{\partial I_{NArv}} & \frac{\partial I_{Arv}}{\partial D_{tr}} \\ \frac{\partial I_{NArv}}{\partial S_p} & \frac{\partial I_{NArv}}{\partial I_t} & \frac{\partial I_{NArv}}{\partial I_{Arv}} & \frac{\partial I_{NArv}}{\partial I_{NArv}} & \frac{\partial I_{NArv}}{\partial D_{tr}} \\ \frac{\partial D_{tr}}{\partial S_p} & \frac{\partial D_{tr}}{\partial I_t} & \frac{\partial D_{tr}}{\partial I_{Arv}} & \frac{\partial D_{tr}}{\partial I_{NArv}} & \frac{\partial D_{tr}}{\partial D_{tr}} \end{bmatrix} \quad (3.51)$$

$$\text{At disease disease-free equilibrium, } E_0^* \left(\frac{\pi}{\mu}, 0, 0, 0, 0 \right) \quad (3.52)$$

Therefore;

$$J_{E_0} = \begin{bmatrix} -\mu & 0 & 0 & 0 & 0 \\ 0 & -(\mu + \beta) + \lambda c \frac{\pi}{\mu} & 0 & 0 & 0 \\ 0 & \phi\beta & -(\gamma + \mu) & 0 & DT_{eff} \omega \\ 0 & (1 - \phi)\beta & \gamma & -(\alpha + \mu + \delta) & (1 - DT_{eff}) \omega \\ 0 & 0 & 0 & \alpha & -(\omega + \mu) \end{bmatrix} \quad (3.53)$$

The DFE will be stable if the eigenvalues of the above matrix J_{E_0} are less than zero.

The eigenvalues are $-(\mu)$ which represents natural death, $-(\mu + \beta) + \lambda c \frac{\pi}{\mu}$ which represents infection rate, $-(\gamma + \mu)$ indicating progression from one stage of infection, $-(\alpha + \mu + \delta)$ which is a transition rate, and $-(\omega + \mu)$ representing the decay term. Since all the eigenvalues from the Jacobian matrix (3.53) are negative, DFE is locally asymptotically stable whenever $R_0 > 1$.

3.3.7 Sensitivity Analysis.

In order to decide the most sensitive parameters, it is necessary to know the relative importance of the different factors responsible for its transmission. Honar, J. H., *et al* (2024), modelled analysis for an HIV infectious disease using elasticity and sensitivity techniques. They discovered that sensitivity analysis is conducted to determine which model parameters have the greatest impact on the spread of HIV. We therefore calculate the sensitivity indices around R_0 of the different parameters in the model. These indices tell us how key each parameter is to the disease transmission.

Here, we used the normalized forward sensitivity index of a variable, u , which depends continuously on parameters used in the study denoted by P , and is defined as;

$$S_P^u = \frac{\partial u}{\partial P} \cdot \frac{P}{u} \quad (3.54)$$

We therefore evaluate the parametric values $(\pi, \lambda, \mu, \beta, \phi, \gamma, c, \delta, \alpha, DT_{eff})$ using the general formula (3.56) of the sensitivity index for parameters as follows;

$$S_\lambda = 1 \quad (3.55)$$

$$S_c = 1 \quad (3.56)$$

$$S_\pi = 1 \quad (3.57)$$

$$S_\gamma = -\frac{\gamma(DT_{\text{eff}}\alpha\omega)(\beta+\mu)+(\mu+\omega)(\alpha+\delta+\mu)}{DT_{\text{eff}}\alpha\gamma\omega(\beta+\mu)+\alpha\omega(DT_{\text{eff}}-1)+(\gamma+\mu)(\mu+\omega)(\alpha+\delta+\mu)} < 0 \quad (3.58)$$

$$S_\mu = -\frac{\mu(DT_{\text{eff}}\alpha\gamma\omega+(\gamma+\mu)(\mu+\omega))+(\gamma+\mu)(\alpha+\delta+\mu)+(\mu+\omega)(\alpha+\mu+\delta)}{DT_{\text{eff}}\alpha\gamma\omega(\beta+\mu)+\alpha\omega(DT_{\text{eff}}-1)+(\gamma+\mu)(\mu+\omega)(\alpha+\delta+\mu)} < 0 \quad (3.59)$$

$$S_\alpha = -\frac{\alpha(DT_{\text{eff}}\alpha\gamma\omega(\beta+\mu)+\omega(DT_{\text{eff}}-1)+(\gamma+\mu)(\mu+\omega))}{DT_{\text{eff}}\alpha\gamma\omega(\beta+\mu)+\alpha\omega(DT_{\text{eff}}-1)+(\gamma+\mu)(\mu+\omega)(\alpha+\delta+\mu)} < 0 \quad (3.60)$$

$$S_\delta = -\frac{\delta((\gamma+\mu)(\mu+\omega))}{DT_{\text{eff}}\alpha\gamma\omega(\beta+\mu)+\alpha\omega(DT_{\text{eff}}-1)+(\gamma+\mu)(\mu+\omega)(\alpha+\delta+\mu)} < 0 \quad (3.61)$$

$$S_{DT_{\text{eff}}} = -\frac{DT_{\text{eff}}\alpha\omega(\gamma(\beta+\mu)+1)}{DT_{\text{eff}}\alpha\gamma\omega(\beta+\mu)+\alpha\omega(DT_{\text{eff}}-1)+(\gamma+\mu)(\mu+\omega)(\alpha+\delta+\mu)} < 0 \quad (3.62)$$

$$S_D = -\frac{DT_{\text{eff}}\alpha\omega(\gamma(\beta+\mu)+1)}{DT_{\text{eff}}\alpha\gamma\omega(\beta+\mu)+\alpha\omega(DT_{\text{eff}}-1)+(\gamma+\mu)(\mu+\omega)(\alpha+\delta+\mu)} < 0 \quad (3.63)$$

$$S_{\beta} = -\frac{DT_{eff}\alpha\omega\beta\gamma}{DT_{eff}\alpha\gamma\omega(\beta + \mu) + \alpha(1(DT_{eff} - 1) + (\gamma + \mu)(\mu + \omega)(\alpha + \delta + \mu))} < 0$$

(3.64)

$$S_{\omega} = -\frac{\omega(DT_{eff}\alpha\gamma(\beta + \mu) + \alpha(DT_{eff} - 1) + (\gamma + \mu)(\alpha + \delta + \mu))}{DT_{eff}\alpha\gamma\omega(\beta + \mu) + \alpha\omega(DT_{eff} - 1) + (\gamma + \mu)(\mu + \omega)(\alpha + \delta + \mu)} < 0$$

(3.65)

We therefore notice that parameters with positive values increase the rate of the disease spread, while those resulting in negative values decrease the spread of the disease. The sensitivity indices for λ , c , and π are >1 while DT_{eff} and α are <1 , indicating that these parameters have a direct proportional and indirect effect on R_e respectively. The indices for other parameters are negative, meaning that an increase in these parameters leads to a decrease in R_e . Parameters like μ , γ , δ , ω , and β have complex expressions showing their intricate influence on R_e .

CHAPTER FOUR

NUMERICAL SIMULATION AND DISCUSSION

4.1 Numerical Method

The Runge-Kutta-Fehlberg (RKF) method is a numerical technique for solving ordinary differential equations (ODEs). According to Noar, N. A. Z. M., Apandi, N. I. A., & Rosli, N. (2024, March). Who did a comparative study of Taylor method, fourth order Runge-Kutta method and Runge-Kutta Fehlberg method to solve ordinary differential equations. The paper mainly presented the Taylor method, Runge-Kutta fourth-order (RK4) method for solving initial value problem (IVP) for ordinary differential equations (ODE). The method is therefore useful for problems where adaptive step size control is desired, as is often the case in modeling the dynamics of HIV/AIDS. It uses a combination of two Runge-Kutta formulas of different orders to estimate the solution and its error at each step. By comparing the estimates, it dynamically adjusts the step size to control the error within a specified tolerance.

Let y_n be the numerical approximation of the solution at time t_n and h be the step size.

The RK5 formula for advancing from t_n to $t_{n+1} = t_n + h$ is given by:

$$K_1 = hf(t_n, y_n) \quad 4.1$$

$$K_2 = hf\left(t_n + \frac{1}{4}h, y_n + \frac{1}{4}K_1\right) \quad 4.2$$

$$K_3 = hf\left(t_n + \frac{3}{8}h, y_n + \frac{3}{32}K_1 + \frac{9}{32}K_2\right) \quad 4.3$$

$$K_4 = hf \left(t_n + \frac{12}{13}h, y_n + \frac{1933}{2197}K_1 - \frac{7200}{2197}K_2 + \frac{7296}{2197}K_3 \right) \quad 4.4$$

$$K_5 = hf \left(t_n + h, y_n + \frac{439}{216}K_1 - 8K_2 + \frac{3680}{513}K_3 - \frac{845}{4104}K_4 \right) \quad 4.5$$

$$K_6 = hf \left(t_n + \frac{1}{2}h, y_n - \frac{8}{27}K_1 + 2K_2 - \frac{3544}{2565}K_3 + \frac{1859}{4104}K_4 - \frac{11}{40}K_5 \right) \quad 4.6$$

$$y_{n+1} = y_n + \frac{25}{216}K_1 + \frac{1408}{2565}K_3 + \frac{2197}{4104}K_4 - \frac{1}{5}K_5 \quad 4.7$$

$$z_{n+1} = y_n + \frac{16}{135}K_1 + \frac{6656}{12825}K_3 + \frac{28561}{56430}K_4 - \frac{9}{50}K_5 + \frac{2}{55}K_6 \quad 4.8$$

Here z_{n+1} is the RK4 approximation of the solution at t_{n+1} , and y_{n+1} is the RK5 approximation.

The error estimate is given by $|y_{n+1} - z_{n+1}|$, and the step size is adjusted based on this error to maintain a specified tolerance level.

The step size h is typically adjusted based on the error estimate to ensure that the desired accuracy is maintained. If the error is within the specified tolerance, the step size can be kept the same or adjusted to optimize efficiency. By implementing the RKF method with appropriate step size control, researchers can numerically solve the differential equations involved in modeling the control of HIV/AIDS while ensuring accuracy and efficiency in the simulations.

4.2 Numerical Simulations for the Population

To initialize the simulations, we utilized the currently available statistics of the various populations considered within this study. According to <https://analytics.nsdcc.go.ke>, the population at risk in Kenya at the age of 15-64 years is 52 million of the total Kenyan population. That is $S_p(0) = 52m$. According to NSDCC “HIV situation in 2025 and Young, P.W., *et al.*, (2023), who researched on HIV Incidence, Recent HIV Infection, and Associated Factors in Kenya, their results indicated that 53% of this population are PLHIV between 15-64 years, i.e. $I_T(0) = 1.6m$. Out of this population, a total of 1.338 million are on ART, implying that $I_{ARV}(0) = 1.388m$. This therefore shows that $I_{NARV}(0) = I_T(0) - I_{ARV}(0)$ i.e. $I_{NARV}(0) = 0.16m$. In this study, we assume that defaulter tracing is currently ineffective, as according to Etoori, D., *et al* (2020), who researched on challenges facing tracing patients on antiretroviral therapy who are late for clinic appointments in rural South Africa and recommendations for future practice. This therefore suggests that $D_{TR}(0) = 0$. The values of various parameters in the model are given in Table 2. The simulation's time is estimated to be 5 years (equivalent to 1800 days).

Table 2. Baseline Sensitivity Parametric Values used for this Numerical Simulation

Parameter	Description	Value	Source
π	The rate of population recruitment to the susceptible population	5250	World Bank website
β	The rate at which the infected population engages the ARTs program	0.0015	Assumed
α	Tracing the rate of infected people who have defaulted on the medication program	0.0055	Assumed
δ	Death rate due to HIV related complications	3.45×10^{-5}	HIV estimates report 2018
ϕ	The rate at which infected persons default on medication	0.75	HIV estimates report 2018
μ	Natural death rates	3.56×10^{-4}	World Bank website
λ	The probability rate at which susceptible persons become infected	3.72×10^{-1}	Assumed
C	The contact rate of infection for the disease.	2.00×10^{-4}	Assumed
γ	Proportion of the infected population that defaults medication program	3.76×10^{-4}	P. Wekesa (2022)
θ	The rate of retention on the ARV program in the suppression program	[0.65 – 0.85]	Assumed
DT_{eff}	Effect of defaulter tracing on positive suppression of the disease	[0.45 – 0.75]	Assumed
ω	Awareness campaigns for ART uptake	0.005	Assumed

The proportion of the infected population that defaults medication is given as $\gamma = \beta(1-\theta)\phi$, whereby, γ is the proportion of the infected population under the ARV-program that defaults medication, ϕ is the rate at which infected persons default medication, and β is the rate at which the infected population uses medication.

Numerically, the sensitivity parameters are given below. For the basic reproduction number R_0

$$R_e = \left[\frac{\lambda c \pi}{(\gamma + \mu)[(\alpha + \mu + \delta)(1 + \mu) - \alpha(1 - DT_{eff})] + (\beta + \mu)DT_{eff} 1\gamma\alpha} \right]$$

Substituting the values as given in the above table, for $DT_{eff} = 0.45$

$$R_0 = \left[\frac{(0.373)(0.0002)(5250)}{(3.76 \times 10^{-4} + 3.56 \times 10^{-4})(0.0055 + 3.56 \times 10^{-4} + 3.45 \times 10^{-5})(1 + 3.56 \times 10^{-4}) - (0.0055)(1 - 0.45)} \right] \quad (4.5)$$

Now for, $DT_{eff} = 0.45$

$$R_0 = \left[\frac{(0.373)(0.0002)(5250)}{(3.76 \times 10^{-4} + 3.56 \times 10^{-4})(0.0055 + 3.56 \times 10^{-4} + 3.45 \times 10^{-5})(1 + 3.56 \times 10^{-4}) - (0.0055)(1 - 0.75)} \right] \quad (4.6)$$

Therefore, the basic reproduction number R_0 is;

$$R_0 < 0 \text{ when } DT_{eff} = 0.45$$

$$R_0 < 0 \text{ when } DT_{eff} = 0.75$$

The other sensitivity parameters are computed as below in Table 3;

Table 3: Updated Sensitivity Indices (Using Given Numerical Values from Table 2)

Parameter	Description	Sensitivity Index
π	Recruitment by natural births and immigrations	1.0000
β	Rate of using ARVs when infected	4.62×10^{-7}
α	Defaulter tracing rate	-1.0001
δ	HIV/AIDS related death rates	8.36×10^{-6}
ϕ	Rate at which patients on ARV default medication	0.0000
μ	Natural death rate	7.81×10^{-4}
λ	Probability of infection	1.0000
c	Contact rate of infection	1.0000
ω	Rate of return of defaulters by awareness campaigns	0.0000
γ	Proportion of defaulting medication	7.34×10^{-4}

Based on the numerical values presented in Table 3, the parameters with a sensitivity index magnitude of 1 (π, λ, c, α) appear to be more influential on the computed R_0 . The

positive indices for recruitment and transmission parameters $(\pi, \lambda, c,)$ show their role in driving the epidemic. The large negative index for the tracing initiation rate (α) suggests that under the assumptions leading to these results, increasing the rate at which non-ART individuals are identified for tracing significantly reduces R_0 . The other parameters, such as ART initiation rate (β) , mortality rates (δ, μ) , and ART drop-out rate (γ) , show very small indices in this numerical evaluation.

Therefore, these numerical results together with the model equation (3.1) realize the following graphical representations, which analyze the impacts of defaulter tracing towards the control of the spread of the pandemic.

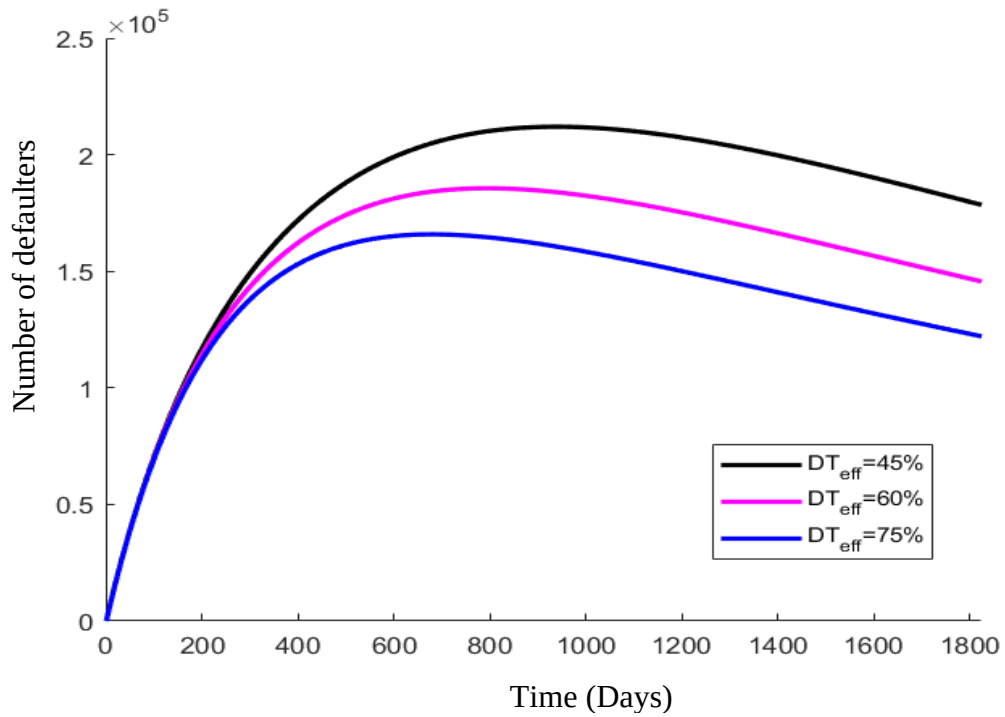


Figure 2: Influence of Defaulter tracing towards return to the ART population

The graph illustrates a sharp rise in D_{TR} , reflecting an increasing number of defaulters being located as ART programs expand. A lower DT_{eff} of 45% leads to a higher peak, as more defaulters build up due to inefficient tracing efforts. Conversely, a higher DT_{eff}

of 75% results in a reduced peak, indicating that defaulters are effectively returned to ART earlier after being identified. The rate of decline is notably quicker when DT_{eff} is 75%, signifying that more individuals are being reintegrated into ART programs and fewer stay in the defaulter category. In comparison, with a DT_{eff} of 45%, the decline occurs at a slower pace since defaulters stay untraced for an extended period, leading to increased accumulation. On the 800th day when DT_{eff} is at 45% number of defaulters is at 2.0×10^5 while at DT_{eff} is at 75% defaulters are at 1.5×10^5 . Therefore, when tracing effectiveness is high (at $DT_{eff} = 75\%$), fewer people remain in the defaulter group, showcasing a successful reintegration into ART. On the other hand, reduced tracing effectiveness (at $DT_{eff} = 45\%$) means that more individuals linger in the defaulter pool for longer periods, which heightens the risk of HIV progression and transmission.

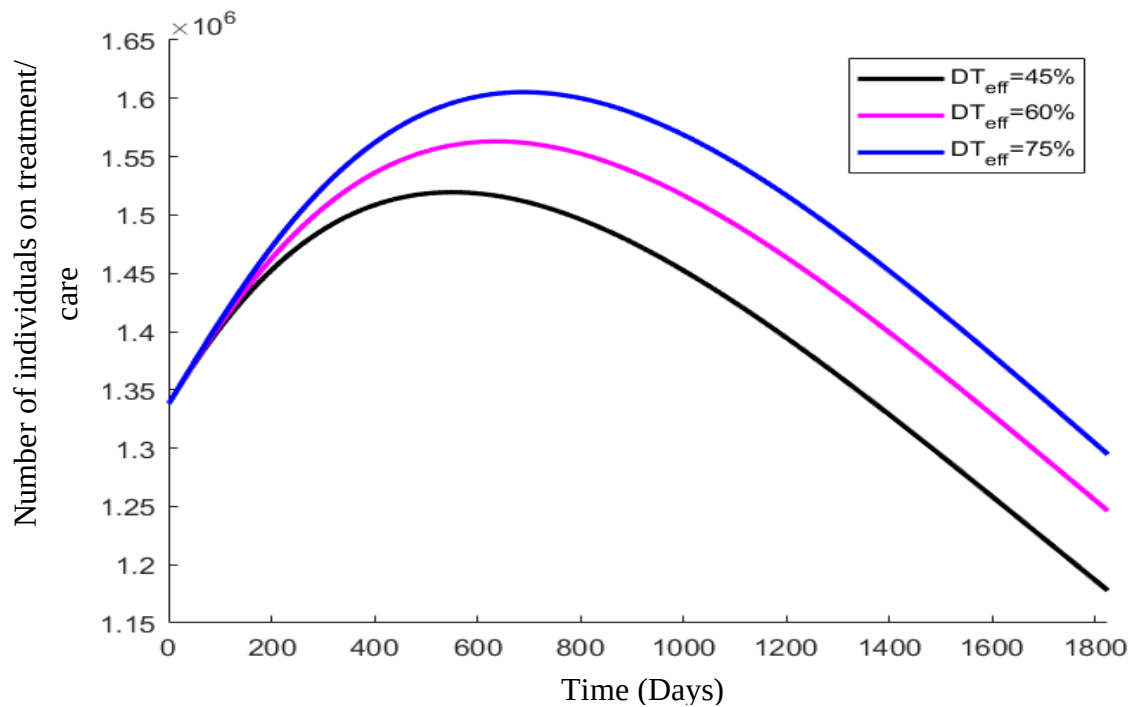


Figure 3: Influence of DT_{eff} on the Population under ARVs

Defaulter tracing has a notable effect on retention rates in long-term medication regimens. With a tracing rate of 45% (DT_{eff}), retention steadily declines. Numerous patients who miss their appointments may not receive timely contact, resulting in an increased dropout rate. Over 1800 days, a significant percentage of the population may stop their medication due to insufficient follow-up assistance. A moderate tracing rate of 60% (DT_{eff}) offers better retention compared to 45%, as more patients are re-engaged, leading to fewer treatment disruptions. Nonetheless, a considerable loss to follow-up remains, particularly among patients who encounter structural obstacles like transportation issues or stigma. An elevated level of defaulter tracing ($DT_{\text{eff}} = 75\%$) ensures that most patients who miss their doses are reached out to and guided back into care. Consequently, this results in improved long-term retention, decreasing treatment failures, and enhancing health outcomes. On the 600th $DT_{\text{eff}} = 45\%$ individuals on treatment are 1.5×10^6 while at $DT_{\text{eff}} = 75\%$, individuals on treatment are 1.6×10^6 . Increased tracing rates correlate with a larger number of individuals participating in HIV care, aiding in the management of HIV transmission within the population receiving ARV treatment.

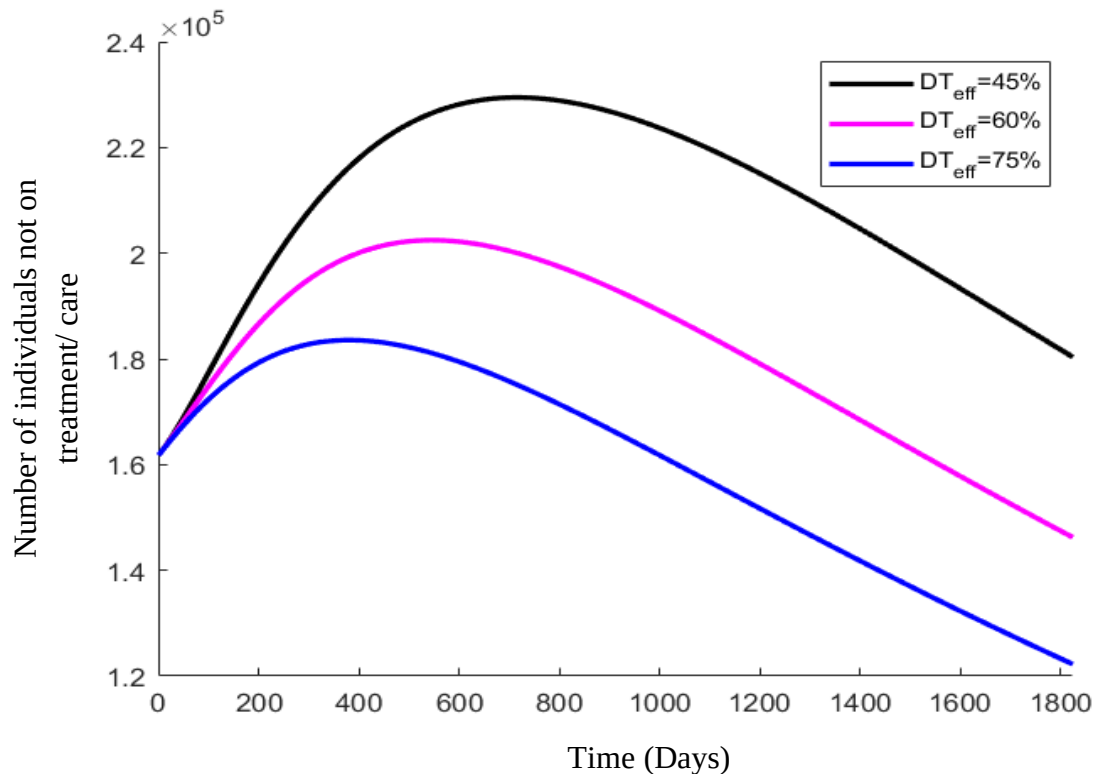


Figure 4: Impacts of Defaulter Tracing on Population Not under ARVs

Initially, all curves show an increase, indicating that the number of individuals infected with HIV who are not receiving treatment rises over time. The curves eventually reach a peak and then begin to fall, suggesting that after a certain duration, more individuals either seek treatment or succumb to the illness. A higher tracing effectiveness ($DT_{eff} = 75\%$) leads to a lower peak and a quicker decline in the number of untreated HIV cases. This indicates that when more defaulters are identified and returned to care, the count of untreated cases decreases more swiftly. Conversely, a lower tracing effectiveness ($DT_{eff} = 45\%$) results in a higher peak and a slower decrease. If fewer individuals return to antiretroviral therapy (ART), the population of untreated HIV cases remains elevated for a longer time, increasing the likelihood of complications and disease transmission. Consequently, improving the tracing and reintegration of defaulters into ART programs significantly decreases the number of untreated individuals over time. On the 600th

$DT_{\text{eff}}=45\%$ individuals on treatment are 2.2×10^5 while at $DT_{\text{eff}}=75\%$, individuals on treatment are 1.8×10^5 . This highlights the necessity of enhancing healthcare systems to track, inform, and re-engage defaulters in HIV care initiatives.

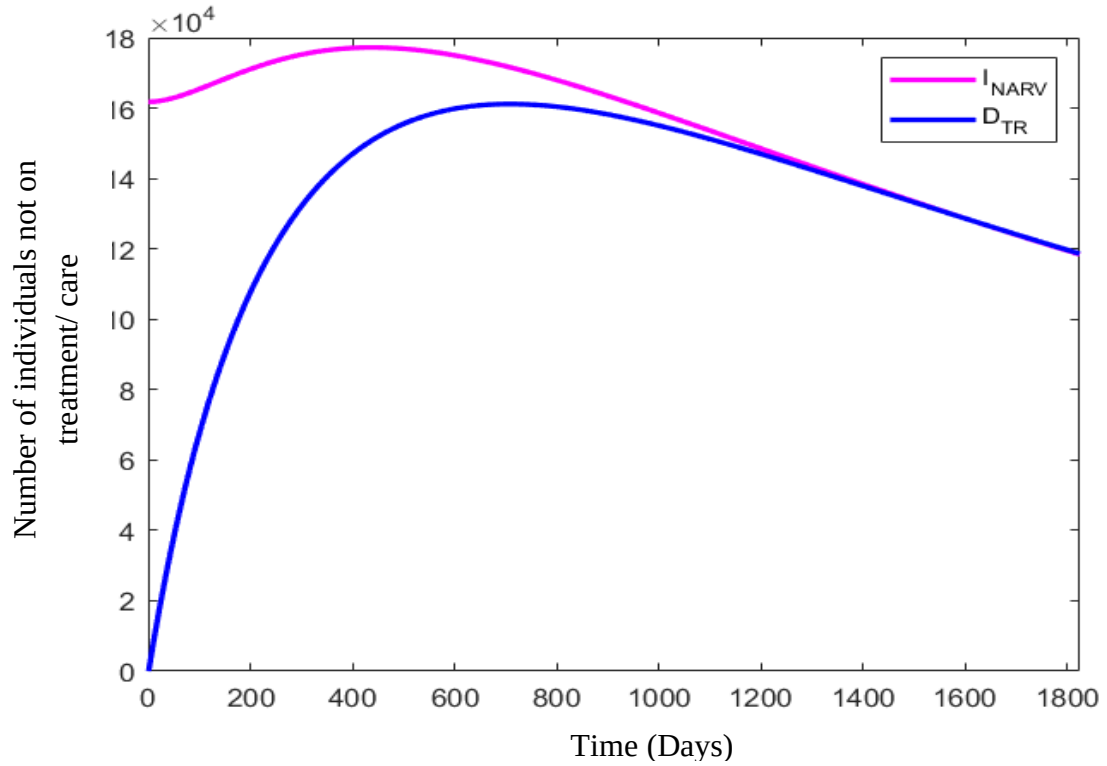


Figure 5: Relation between the Population not under ARV and to population being traced over time for $DT_{\text{eff}}=0.75$

Initially, both the untreated population (I_{NARV}) and the tracked defaulters (D_{TR}) show an upward trend. Before tracing is initiated (defaulters=0) while individuals not on treatment being (1.6×10^4). After 400 days of defaulter tracing (defaulters= 1.8×10^4) while individuals not on treatment being (1.4×10^4). This indicates that, at first, the number of individuals either defaulting on treatment or not seeking it is increasing, resulting in a growing need for tracing initiatives. The (I_{NARV}) curve reaches its highest point and then starts to gradually fall. Meanwhile, the (D_{TR}) curve rises steeply before it stabilizes and subsequently declines. This suggests that as tracing efforts improve and

become more effective, a greater number of defaulters are returning to treatment, which reduces the untreated HIV population. After a certain period (approximately 1400 days), both curves converge to similar values (defaulters=individuals not on treatment= (1.4×10^4)), implying that a considerable number of untreated individuals are being effectively traced. As the count of traced individuals (D_{TR}) rises, the untreated HIV population (I_{NARV}) decreases over time and converges, indicating that the defaulter population is successfully being re-engaged in care. If tracing efforts were inadequate or delayed, the (I_{NARV}) curve would remain elevated, resulting in a heightened risk of HIV transmission and disease progression. After a particular time, the number of traced individuals (D_{TR}) starts to decline, likely due to fewer new defaulters or enhanced retention in ART programs. Thus, government and health agencies should focus on and enhance tracing mechanisms for defaulters to ensure that individuals who discontinue treatment are re-engaged as quickly as possible. It is also important to recognize that a delayed response to tracing leads to more individuals living with untreated HIV, heightening the risk of transmission. Therefore, as the tracing of the untreated HIV population diminishes, ongoing monitoring and interventions are essential to sustain ART adherence and avert future defaults.

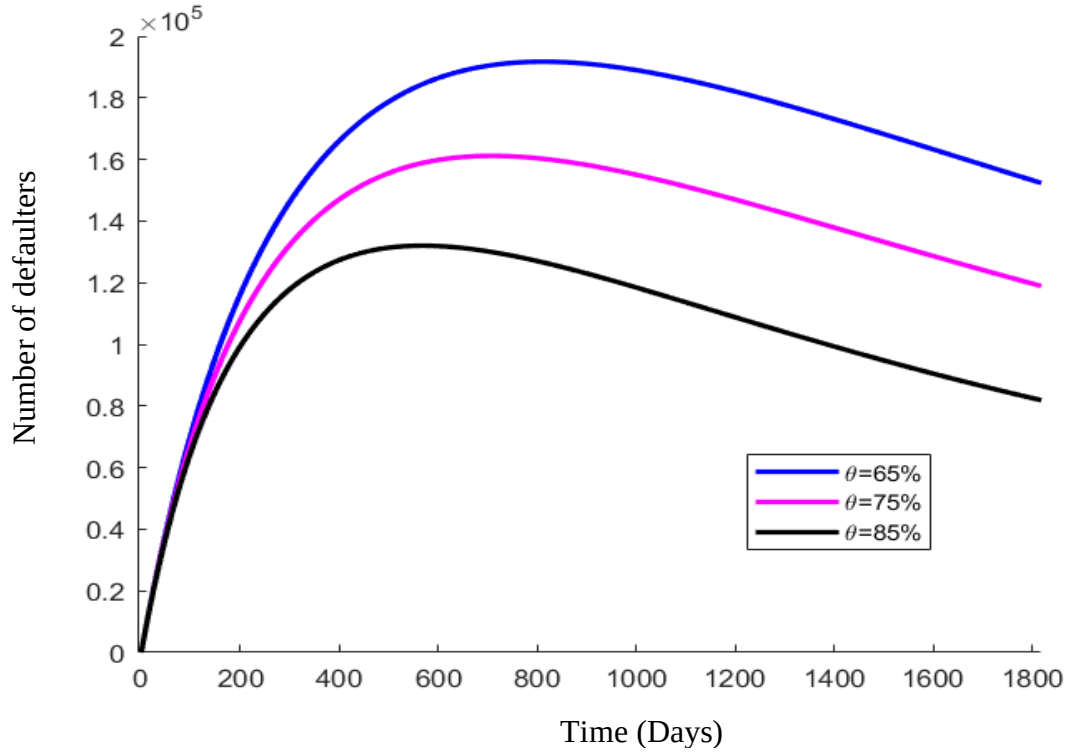


Figure 6 Defaulter Traced Population over time, Considering Varying Retention Rate

At a retention rate of 60%, a significant number of people discontinue ART, resulting in a large population of defaulters that require tracing. This accounts for the sharp initial increase in D_{TR} , as tracing initiatives aim to re-engage the substantial number of ART dropouts. However, due to low retention, many of those who are reengaged may default again, resulting in a persistent need for tracing over time. When retention improves to 85%, the majority of individuals remain in ART programs without discontinuing treatment. Consequently, the number of defaulters needing tracing (D_{TR}) remains low, reaching a peak early on but then experiencing a steady decline. On the 600th day from as retention rates are 60%, defaulters= (1.8×10^5) while at 75% defaulters= 1.6×10^5 and at 85% defaulters= 1.2×10^5 , there is a significant reduction in the number of individuals who default and require tracing. With only a 60% retention rate, tracing

efforts are high, making it challenging and resource-intensive to manage HIV control, implying that more frequent tracing may be necessary, thus increasing the burden on healthcare systems. In contrast, with 85% retention, the urgency for tracing lessens, enabling the redirection of resources towards prevention, early diagnosis, and programs aimed at supporting retention. Therefore, long-term adherence to ART decreases the number of defaulters and aids in achieving the objectives for HIV epidemic control. Enhancing ART adherence initiatives (such as counseling, support groups, and community-based ART) helps to prevent defaults and decreases reliance on tracing efforts. As retention rates enhance, tracing should be focused more selectively on high-risk populations, like mobile individuals or those facing stigma. Thus, at lower retention rates, tracing plays a critical role in re-engaging individuals in ART. However, over time, transitioning the focus from tracing to retention strategies becomes a more sustainable approach.

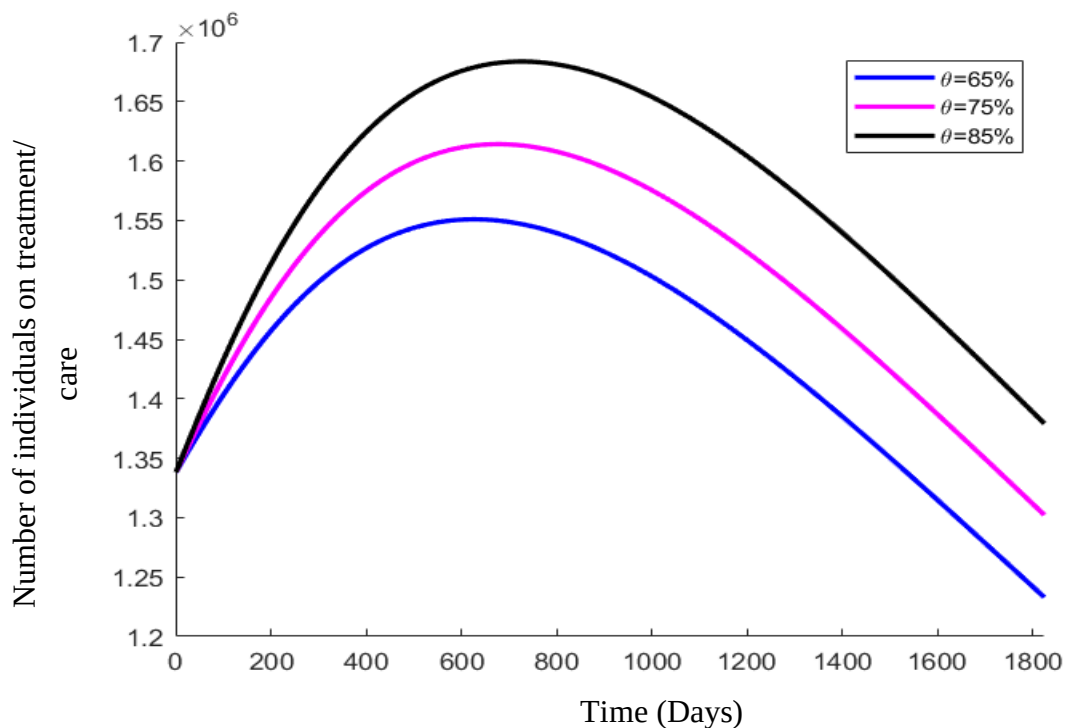


Figure 7: Retention rate relation to the ART program

Retention rate is a vital element in the ongoing success of HIV treatment and epidemic management. It indicates the percentage of individuals who continue their antiretroviral therapy (ART) without interruption. A higher retention rate enhances the stability and efficacy of the ART program. The retention rate directly influences the number of participants remaining on ART, which in turn affects treatment access, the progression of the disease, and rates of transmission. When the retention rate is low at 65%, many patients discontinue ART shortly after beginning treatment. Despite efforts to trace these individuals, some may not return or might default again. Initially, the number of people on ART rises, but it eventually fluctuates and declines due to ongoing dropouts. On the 600th day individuals on treatment at retention rate of 65% = 1.7×10^6 , while individuals on treatment at retention rate of 75% = 1.6×10^6 and at individuals on treatment at retention rate of 85% = 1.55×10^6 . As a result, HIV transmission remains elevated, given that many infected individuals are not achieving viral suppression. When the retention rate improves to 75%, a greater number of individuals continue with ART, resulting in a more consistent growth of the ART population. Although some individuals still default, tracing efforts are more successful in returning these defaulters to treatment. Consequently, the overall ART population expands, leading to a decrease in HIV transmission rates over time. The decline following the peak indicates that while defaulting has lessened, it still occurs. When the retention rate reaches a high of 85%, the majority of individuals adhere to ART, ensuring consistently high ART coverage. Tracing efforts become less necessary at this rate, as few individuals disengage from treatment. Additionally, increased adherence to ART promotes better viral suppression and reduces the risk of HIV transmission. Despite varying retention rates, the ART population tends to decrease after attaining a peak. This decrease is largely due to higher

mortality rates among individuals living with HIV compared to the general population. Over time, some patients may die from HIV-related complications or other health issues, which leads to a reduction in the ART population. Thus, at lower retention rates, a significant number of individuals discontinue ART over time. Even when retention rates are higher, some degree of loss to follow-up remains, contributing to a gradual decline in ART coverage. The influx of new individuals starting ART may not be adequate to offset those who exit due to death or discontinuation. For example, if enrollment in ART slows down, the overall ART population will diminish after reaching its peak. Certain individuals on ART might face treatment failure or progress to advanced stages of HIV, which can result in elevated mortality or necessitate a switch to different treatment options. Therefore, it is crucial to ensure that patients remain on ART for their entire lives to maintain high ART coverage. Improved early diagnosis, treatment optimization, and enhanced access to healthcare also contribute to a decline in HIV-related deaths. Finally, increasing HIV testing and ensuring linkage to care are essential to prevent reductions in the ART population.

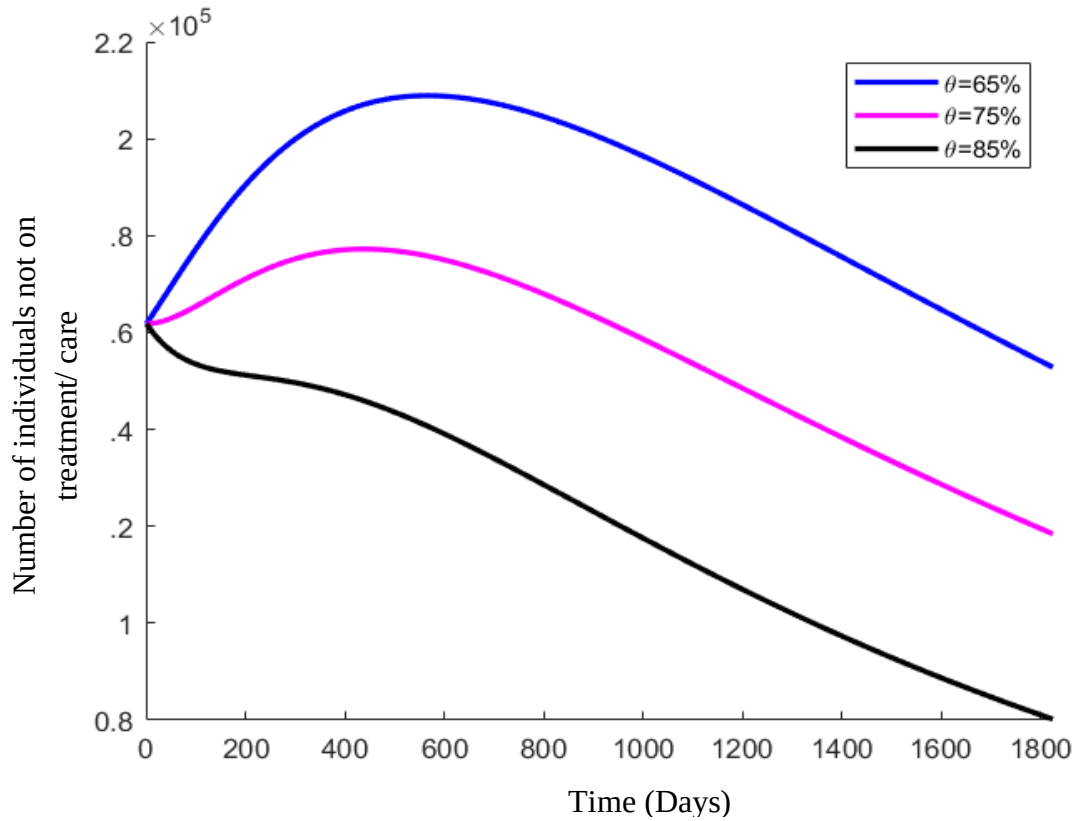


Figure 8: Retention rate relation to Population Not under ARV program

The curve at ($\theta = 65\%$) displays an initial rise in I_{NARV} , reaching a peak before gradually decreasing. This indicates that at 65% retention, a substantial number of infected individuals exit ART, thereby increasing the population of uncontrolled HIV-positive persons. Similarly, a greater number of individuals default or fail to stay in care, which contributes to an uptick in HIV transmission. The gradual decline observed in the later stages suggests that treatment programs are not effectively keeping individuals engaged, thus undermining the success of HIV suppression initiatives. At a higher ART coverage of ($\theta = 75\%$, on the 400th day individuals not on treatment= 1.7×10^5), the graph peaks at a lower level compared to the ($\theta = 65\%$, on the 400th day individuals not on treatment= 2.2×10^5) curve, signifying that fewer individuals are left untreated, as more are on ART and achieving viral suppression. Over time, I_{NARV} decreases at a

quicker rate compared to the 65% retention scenario due to enhanced HIV control and suppression. The difference between the 65% and 75% retention curves highlights the significance of boosting retention rates in HIV treatment initiatives. When ($\theta = 85\%$, on the 400th day individuals not on treatment= 1.42×10^5) is reached, the curve does not display a notable peak; instead, it begins to decline almost immediately. This indicates that when 85% of individuals adhere to ART, very few remain untreated, leading to a swift reduction in the population of HIV-positive individuals without ART. This illustrates the most pronounced effect of HIV suppression, as a high retention rate ensures sustained ART adherence, preventing HIV transmission and alleviating disease burden. The steep decline shown in I_{NARV} signifies effective linkage to care and adherence to treatment, resulting in fewer individuals remaining without ART. This implies that as retention rates improve from 65% to 85%, the number of individuals not receiving ART decreases more rapidly, thereby lowering the spread of HIV. It is also important to note that at 65% retention, numerous individuals struggle to remain in treatment, resulting in a higher peak in I_{NARV} , indicating that more individuals are not virally suppressed. Retention Rate is thus crucial for Sustained Epidemic Control, as a higher retention rate correlates with a quicker decline in I_{NARV} , meaning more individuals will maintain ART, thus preventing transmission and achieving viral suppression. However, even at a retention rate of 85%, there are still individuals who exit ART programs, which is why I_{NARV} does not reach zero immediately. This suggests that achieving 100% retention is nearly unattainable, but maximizing retention as much as possible is vital for controlling the epidemic.

CHAPTER FIVE

DISCUSSION AND CONCLUSION

5.1 Analysis Conclusion

This study presented the formulation and mathematical analysis of a compartmental model for HIV/AIDS transmission, incorporating the dynamics of antiretroviral therapy (ART) and defaulter tracing. The analysis provides theoretical insights into the conditions governing the spread and persistence of the disease within this framework. The confirmation of positivity and boundedness of solutions ensures that the model is epidemiologically meaningful, as population sizes remain non-negative and do not grow infinitely, confined within the feasible region Ω . This establishes the mathematical well-posedness of the system. The analysis identified two key equilibrium states: The Disease-Free Equilibrium (DFE) and the Endemic Equilibrium (EE). The DFE, where the population is entirely free of infection, always exists. Its local stability is governed by the basic reproduction number, R_0 . Our analysis, using the standard next-generation matrix method applied to the derived model equations, yielded the R_0 . The condition for DFE stability is $R_0 < 1$. This result aligns with epidemiological theory, indicating that the disease cannot successfully invade the population if each primary infected individual generates, on average, less than one new infection during their initial infectious period (before treatment initiation or death). The parameters influencing the spread within the population are; contact rate (λc), the recruitment rate (π), the natural death rate (μ), and the rate of progression out of the initial infectious state (β). Conversely, when $R_0 > 1$, the DFE becomes unstable, and the analysis indicates the existence of an Endemic Equilibrium (EE), where the

infection persists within the population. The existence of the EE signifies that HIV transmission can be sustained over the long term, with the levels of infection in different compartments ($I_T^*, I_{ARV}^*, I_{NARV}^*, D_{TR}^*$) determined by the balance between new infections, treatment dynamics, defaulting, tracing, and mortality, as shown in the complex expressions derived implies the necessity of interventions to control the disease burden. The sensitivity analysis offers insights into potential control levers. Parameters related to transmission (λ, c) and population turnover (π) showed a positive and proportional impact on R_0 , highlighting the importance of prevention measures (reducing λ, c) for controlling the epidemic threshold. Parameters related to treatment initiation (β), ART abandonment (γ), tracing initiation (α), tracing effectiveness (DT_{eff}), and mortality (μ, δ) were found to have a negative impact on the R_0 . This suggests that, according to that formulation, improving treatment uptake and retention, as well as enhancing defaulter tracing efforts, theoretically contributed to reducing R_0 and controlling the epidemic. The magnitude of these indices, if numerically evaluated, would rank the relative effectiveness of targeting each parameter. The primary contribution of this mathematical analysis is the rigorous establishment of the model's basic properties and the threshold condition ($R_0 < 1$) for disease elimination, based on standard epidemiological methods applied to the formulated system. This theoretical foundation supports further investigation, such as numerical simulations, to quantify the impact of different tracing and retention strategies on the long-term dynamics of HIV.

5.2 Key Findings and Numerical Conclusion.

This section provides the significant results from the mathematical modeling analysis that examined the impact of defaulter tracing on controlling the spread of HIV/AIDS in

a population. The research utilized mathematical techniques to assess how the tracing and re-engagement of individuals who disengage from ARV programs influence disease management. As a result, our initiative focused on decreasing HIV/AIDS transmission among a susceptible population by implementing defaulter tracing as the primary control method. Through meticulous planning, effective execution, and continuous evaluation, we have made substantial strides toward our objectives. Our project advocated for community engagement and support, which were vital for our successes. The findings discussed under numerical simulation and discussion indicated that successful tracing of defaulters significantly diminishes the number of HIV-positive individuals not receiving ARV (I_{NARV}). When activities aimed at tracing defaulters are intensified, a larger portion of individuals return to treatment, thus improving disease control. Defaulter tracing has proven to be a key component in our approach to addressing the spread of HIV/AIDS. The data represented in Figure 2 shows that defaulter tracing is especially crucial during the early stages of ART dropouts, but gradually loses its importance as retention rates increase. Sustainable HIV control methods should integrate tracing efforts with proactive retention strategies to reduce defaulting and foster long-term ART compliance. By swiftly locating and re-engaging individuals who have defaulted on their treatment, we effectively mitigated the risk of transmission and improved treatment adherence within the population.

Simulation results demonstrated that increasing (DT_{eff}) significantly reduces the untreated infected population (I_{NARV}). At 600th day when $DT_{\text{eff}}=0.45$; $I_{\text{ARV}}=1.5$ million people and $DT_{\text{eff}}=0.75$; $I_{\text{ARV}}=1.65$ million. Indicating that defaulter tracing effectiveness increases the number of populations on ARV. However, when, ($\theta=0.65$); $I_{\text{ARV}}=1.55$ million and at ($\theta=0.85$); $I_{\text{ARV}}=1.7$ million. Showing that improving the

retention rate (θ) showed a significant impact of reducing the need for tracing and the size of the untreated population, while substantially increasing ARV coverage. Also, within the first 400 days of defaulter tracing (defaulters= 1.8×10^4) while individuals not on treatment being (1.4×10^4). This indicates that, at first, the number of individuals either defaulting on treatment or not seeking it is increasing, resulting in a growing need for tracing initiatives. The (I_{NARV}) curve reaches its highest point and then starts to gradually fall. After a certain period (approximately 1400 days), both curves converge to similar values (defaulters=individuals not on treatment= (1.4×10^4)), implying that a considerable number of untreated individuals are being effectively traced. As the count of traced individuals (D_{TR}) rises, the untreated HIV population (I_{NARV}) decreases over time and converges, indicating that the defaulter population is successfully being re-engaged in care. The findings highlight that while effective defaulter tracing is a vital component, particularly when retention is suboptimal, improving ARV retention is fundamental for long-term HIV/AIDS control. This study shows the need for integrated public health strategies that combine robust, proactive retention efforts with efficient defaulter tracing mechanisms to effectively manage the HIV/AIDS epidemic.

Moreover, increased retention and tracing rates result in quicker HIV suppression; specifically, enhancing defaulter tracing efficiency alongside improved retention (from 65% to 85%) led to a more pronounced decrease in untreated HIV cases over time. This finding suggests that a well-organized tracing program can effectively support ART retention initiatives, minimizing the spread of HIV. Additionally, defaulter tracing has the effect of delaying the peak and lowering long-term prevalence. The simulations revealed that, without defaulter tracing, the number of untreated cases peaks at a higher level and remains in the population for a more extended period. Thus, tracing reduces

the peak of untreated cases and stimulates the decline of the infected population, contributing to long-term control. By focusing on individuals at risk of defaulting on their treatment, we were able to interrupt transmission chains and avert new infections. Defaulter tracing not only aided in managing the spread of HIV/AIDS but also facilitated improved treatment adherence among those living with the virus. This study shows the need for integrated public health strategies that combine robust, proactive retention efforts with efficient defaulter tracing mechanisms to effectively manage the HIV/AIDS epidemic.

5.3 Recommendations of the Research

The research emphasizes several crucial recommendations for aiming at controlling HIV/AIDS. First, enhancing essential Defaulter Tracing Programs, health systems that focuses on implementing proactive tracing strategies such as utilizing community health workers, digital reminders, and mobile health (m-Health) solutions. Improving Retention Strategies through counseling, support networks, and financial incentives, which can further minimize defaulter rates and enhance adherence to ART. Additionally, Integrating Data-Driven Decision Making. Applying mathematical models and real-time data to help optimize resource distribution and prioritize defaulter tracing for high-risk populations. Finally, through Community Engagement and Education. Addressing stigma and misinformation around ART thus decreasing the chances of individuals defaulting. Involving healthcare providers and other relevant stakeholders, can help establish a supportive infrastructure that may enable the effectiveness of initiatives to curb and control the spread of HIV/AIDS within the society. If defaulter tracing programs are encouraged, significant reduction in transmission rates within the susceptible population can be achieved. By also inclusion

of offering support, counseling, and availing resources to individuals who infected, return to care of defaulters may be encouraged and ensure they continue to access the necessary medication to effectively manage their condition.

5.4 Suggestions Future Research

Although the study offers significant insights, certain limitations must be outlined, such as the assumption of constant tracing efficiency. This model presumes that tracing success rates remain unchanged, but in practice, various logistical difficulties, societal stigma, and mobility issues can influence the effectiveness of tracing. Future research should include dynamic tracing probabilities informed by real-world data. Socio-economic and behavioral factors. Our model fails to fully consider social determinants like poverty, education level, and mental health, which all play a role in ART adherence. Additional studies should integrate behavioral dynamics into mathematical frameworks. The effects of drug resistance and reinfection. Furthermore, the study does not take into account the risks of drug resistance and reinfection linked to inconsistent ART adherence. Subsequent work should enhance the model to evaluate the long-term effects of ART resistance on HIV management.

Based on the findings of this study, several critical recommendations can be presented for policymakers, healthcare providers, and researchers. First, make Defaulter Tracing a National Focus. Governments should incorporate defaulter tracing into national HIV/AIDS management plans, ensuring consistent funding and implementation. Utilizing digital health tools (such as SMS notifications, mobile health applications, and geolocation tracking) can aid in the prompt monitoring and intervention of defaulters. Additionally, enhancing Community Health Worker (CHW)-led tracing

programs could improve patient follow-up and reduce the burden on healthcare systems. Strengthening financial support for Defaulters may have a significant impact. Many individuals default due to financial constraints, transportation issues, and stigma. Providing financial incentives, food assistance, and mental health services can enhance adherence to ART. Finally, decentralizing ART distribution, extending prescription refill intervals, and employing differentiated service delivery (DSD) methods can improve retention and decrease default rates. If these suggestions are implemented, HIV/AIDS control efforts can boost ART adherence, lower transmission rates, and advance towards epidemic management.

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APPENDICES

Appendix I: Matlab Code

```
function HIV_DefaulterTrace()

clear all;clc;

popKE=50000000;popKE_risk=0.59*popKE;%% 59pct of kenyans are aged 15-64;

PLHIV=1400000;onART=1160000;newInf=41500;

%% =====PARAMETER VALUES =====

%recruitment rate

P=1500;

%rate of progression from Sp to It

lambda=newInf/popKE_risk

%natural per capital death rate

miu=0.001;

%screening rate of It to Iarv

scale=PLHIV/popKE_risk

%%Mwangi et al. BMC Public Health (2022) 22:643 https://doi.org/10.1186/s12889-022-12928-0

beta=scale*0.87;

%rate of progression from It to Inarv

phi=scale-beta;

%rate of progression from Iarv to Inarv (dropout from care)

%%Asiimwe et al. BMC Infectious Diseases (2016) 16:43 DOI 10.1186/s12879-016-1392-7

varphi=0.27;

%proportion of those who enroll for ARV,after advertisement/campaigns awareness
```

```

omega=0.85;

%defaulter tracing rate of HIV infected population

scale2=1;%onART/PLHIV

alpha=scale2*0.85;

%death rate due to HIV-related complications

delta=0.00044;

%% =====SPECIFICATION OF INITIAL CONDITIONS=====

%% SOURCE: https://www.unaids.org/en/regionscountries/countries/kenya

prev=4.3/100; % HIV prevalence in Kenya in 2022

Sp0=popKE_risk; It0=PLHIV; Iarv0=onART; Inarv0=It0-Iarv0; Dtr0=0;

%% =====MODEL EQUATIONS SOLVER=====

solinit=[Sp0 It0 Iarv0 Inarv0 Dtr0]; tspan=1:365*8;

options=odeset('RelTol', 1e-4,'AbsTol',[1e-4 1e-4 1e-4 1e-4 1e-4]);

[T,Y]=ode45(@(t,y) HIVmodel(t,y),tspan,solinit, options);

%% =====OUTPUT OF SOLUTIONS=====

figure(1);plot(T,Y(:,1),'b','linewidth',2);

xlabel('Date'); ylabel('S_p');

figure(4);plot(T,Y(:,2),'r',T,Y(:,3),'k',T,Y(:,4),'m',T,Y(:,5),'b','linewidth',2);

xlabel('Date'); ylabel('Infectious');legend('I_t','I_{arv}','I_{narv}','D_{tr}')

figure(3);hold on

plot(T,Y(:,2),'k','linewidth',2);

xlabel('Date'); ylabel('Infectious');hold off

%% =====SPECIFICATION OF THE MODEL EQUATIONS=====

function dy=HIVmodel(t,y)

```

```

%y(1)=Sp, y(2)=It, y(3)=Iarv, y(4)=Inarv, y(5)=Dtr

dy = zeros(5,1);

dy(1)=P-lambda*y(1)-miu*y(1);

dy(2)=lambda*y(1)-(beta+miu+phi)*y(2);

dy(3)=beta*y(2)-(varphi+miu)*y(3)+omega*y(5);

dy(4)=phi*y(2)+varphi*y(3)-(alpha+miu+delta)*y(4)+(1-omega)*y(5);

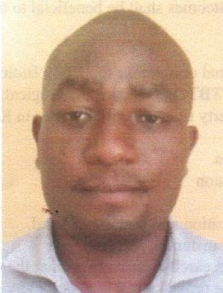
dy(5)=alpha*y(4)-(omega+1-omega)*y(5)-miu*y(5);

end

end

```

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Appendix IV: Plagiarism Report



Page 1 of 96 - Cover Page

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Our system's algorithms look deeply at a document for any inconsistencies that would set it apart from a normal submission. If we notice something strange, we flag it for you to review.

A Flag is not necessarily an indicator of a problem. However, we'd recommend you focus your attention there for further review.

Match Groups

- **43 Not Cited or Quoted 2%**
Matches with neither in-text citation nor quotation marks
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- 1 Publication
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