

MULTI-HORIZON PREDICTIVE MODELING OF HIV TREATMENT ADHERENCE USING CLINICAL AND SOCIAL DETERMINANTS IN UGANDA

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Declaration

I, Nyonyintono Jacob, declare to the best of my knowledge that the work in this dissertation is original and has not been submitted before to any university/institution. It is the result of my effort.

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Approval

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Abstract

Treatment interruption among people living with HIV (PLHIV) remains a critical challenge to achieving sustained viral suppression and optimal treatment outcomes, particularly in sub-Saharan Africa. In Uganda, despite significant progress in scaling up antiretroviral therapy (ART), a substantial proportion of patients experience interruptions in treatment, contributing to viral rebound, increased transmission risk, and drug resistance. The adoption of the Multi-Month Dispensing (MMD) model, while improving access and convenience, reduces routine patient-provider contact and may delay early identification of patients at risk of disengagement. This study aimed to develop and evaluate a machine learning-based predictive framework for identifying patients at risk of treatment interruption under Uganda's MMD system. A quantitative research design was employed using retrospective data extracted from Electronic Medical Records (EMRs) of 8,788 patients receiving ART. Data preprocessing involved cleaning, feature engineering, and handling missing values, followed by the development of machine learning models using a structured pipeline. The Random Forest algorithm was selected as the primary model due to its ability to capture complex nonlinear relationships and its robustness in handling imbalanced clinical datasets. The models were trained and evaluated across three temporal prediction windows (30, 60, and 90 days) using performance metrics including precision, recall, F1-score, and ROC-AUC. Particular emphasis was placed on precision to ensure reliable identification of high-risk patients while minimizing false positive classifications. The findings demonstrate that integrating clinical, demographic, and behavioral factors improves the predictive ability of machine learning models in identifying treatment interruption risk. Key predictors included viral load status, CD4 count, duration on ART, and selected socio-demographic characteristics. The developed framework enables the generation of individualized risk scores and prediction of likely interruption periods, supporting proactive patient management. This study contributes to the growing body of evidence on the application of machine learning in HIV care and highlights the importance of incorporating multidimensional determinants in predictive modelling. The proposed model provides a practical tool for early risk identification and targeted intervention, with potential to enhance patient retention and improve treatment outcomes within Uganda's HIV care system.

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Chapter 1

Introduction

1.1 Background

HIV/AIDS continues to be a significant public health issue, particularly in sub-Saharan Africa. Despite the remarkable progress made in expanding access to antiretroviral therapy (ART), treatment interruptions (IIT) remain a major challenge in Uganda. Antiretroviral therapy (ART) remains the cornerstone of HIV management, and treatment interruptions are linked to poorer patient outcomes. Current guidelines and reviews stress that interruptions directly compromise immune recovery and heighten the risk of both AIDS and non-AIDS related morbidity, undermining the primary goal of modern therapy, which is to maintain uninterrupted virologic suppression [1]. Furthermore, interruptions in therapy continue to be a significant risk factor for the development of drug resistance, as confirmed by recent cohort studies and systematic reviews [2]. From a public health perspective, treatment interruptions result in viral rebound, which increases the risk of onward HIV transmission and directly contravenes the Undetectable = Untransmittable (U=U) prevention strategy [3, 4]. As of 2022, Uganda had approximately 1.4 million people living with HIV (PLHIV) [5]. Despite an ART coverage rate of 92%, studies and national reports indicate that a significant proportion of patients, often cited in the range of 10-20%, experience interruptions in treatment annually [6]. These interruptions contribute to unsuppressed viral loads and a reduction in treatment efficacy. In response to this challenge, machine learning (ML) has emerged as a promising tool to predict retention in care and treatment adherence, as well as to identify patients at high risk of IIT. ML models enable the early detection of risk factors for treatment interruptions, allowing healthcare providers to deploy targeted interventions and optimize the use of healthcare resources. While studies from countries like South Africa have shown promising results, they have limitations in terms of prediction duration and the incorporation of social determinants that significantly influence treatment outcomes [7]. The application of machine learning to predict HIV treatment outcomes is a rapidly advancing field with demonstrated efficacy across diverse global settings. Supervised learning algorithms, including logistic regression, random forests, gradient boosting machines (e.g., XGBoost), and neural networks, have been successfully employed to identify patients at high risk of loss to follow-up (LTFU) and viral non-suppression. For instance, a study in Kenya leveraged machine learning on nationally representative data to predict attrition from care, highlighting the importance of programmatic variables like the type of healthcare facility [8]. Research in Zambia further demonstrated that models incorporating pharmacy refill data could accurately forecast future adherence problems, allowing for timely interventions [9]. These predictive models offer an advantage over traditional methods by synthesizing multifaceted risk factors into a single, actionable risk score. Key predictors consistently identified across studies include clinical markers (e.g., low CD4 count, history of missed appointments, hemoglobin

levels), demographic factors (e.g., age, gender), and treatment related variables (e.g., regimen type, duration on ART) [10, 11]. However, a critical limitation of many existing models is their reliance on clinical and administrative data captured in electronic health records, often overlooking crucial social determinants of health such as social support networks—that are profoundly influential in the sub-Saharan African context [12]. This gap underscores the need for more holistic modeling approaches. Therefore, this research seeks to build upon this foundation by incorporating a wider array of social and behavioral determinants into the predictive framework. By doing so within the specific context of Uganda’s MMD program, this study aims to develop a more accurate tool for identifying at-risk patients, enabling truly targeted interventions that address the root causes of treatment interruption. The strategic response to the challenge of retention has been the adoption of patient centered service delivery models like Multi Month Dispensing (MMD). Endorsed by the World Health Organization, MMD allows clinically stable patients to receive ARV prescriptions for extended periods of 3, 4, 5, or even 6 months, reducing the frequency of clinic visits [13]. This policy shift aims to decongest health facilities, reduce transportation costs for patients, and integrate HIV care into a chronic disease management framework, thereby promoting long-term adherence and improving quality of life [14]. However, a challenge of MMD is the reduction in routine patient-provider contact, which can diminish opportunities for adherence counseling and early identification of patients who are struggling or at risk of disengagement, potentially allowing lapses to develop into full treatment interruptions [15]. Concurrently, artificial intelligence (AI) and machine learning (ML) are emerging as transformative forces in global health, offering new paradigms for predictive analytics and personalized care. In healthcare, ML algorithms can analyze vast, complex datasets such as electronic medical records (EMRs) to identify subtle patterns and predictors that are often invisible to traditional analysis [16]. This capability is particularly suited to predicting individual patient risks, enabling a shift from a reactive to a proactive model of care. The application of ML in HIV program management is growing, with studies demonstrating its utility in predicting outcomes such as viral load suppression, mortality, and loss to follow-up, thereby allowing for the prioritisation of resource-intensive interventions for the patients who need them most [17, 18]. The successful application of ML in healthcare, however, is contingent upon the availability of high-quality, structured digital data. In many low-resource settings like Uganda, the transition from paper-based to electronic health records (EHRs) is still ongoing, often resulting in fragmented, incomplete, or inconsistent data [19]. This poses a significant challenge for building robust predictive models. Furthermore, models developed in one context may not generalize well to another due to differences in health systems, patient demographics, and cultural factors, a phenomenon known as poor external validity [20]. Therefore, there is a pressing need to develop and validate models using local data to ensure their accuracy and relevance for the Ugandan health system. Within the Ugandan context, the drivers of treatment interruption are complex and multifactorial, extending beyond clinical indicators. Structural barriers such as transportation costs, distance to health facilities, and conflicting work schedules are frequently cited reasons for missing appointments [21]. Behavioural and Socioeconomic factors, including internalised stigma, depression, and lack of social support, also play a critical role in influencing a patient’s ability to sustain lifelong therapy [22]. An effective ML model for predicting treatment interruptions under the MMD system must therefore integrate these diverse data types i.e, clinical, logistical, and socio-behavioral, to generate a holistic risk profile. Capturing these variables in a usable format is a key step toward moving beyond purely clinical prediction and creating a tool that truly reflects the lived experience of patients in Uganda.

I was motivated to conduct this study due to the increasing concern about treatment interruption among patients receiving antiretroviral therapy (ART), which remains a major challenge in HIV care. Despite the availability of ART services, many patients still miss appointments

or discontinue treatment, leading to poor health outcomes, drug resistance, and increased HIV transmission risk. I was particularly interested in understanding how behavioral, socioeconomic, and clinical factors contribute to treatment interruption at different time intervals (30, 60, and 90 days). Additionally, limited local evidence on predictors of ART interruption motivated the need to conduct this study so as to provide findings that may support targeted interventions and improve patient retention in care.

1.2 Problem Statement

Despite significant progress in scaling antiretroviral therapy (ART) services in Uganda, treatment interruption remains a persistent and critical barrier to achieving optimal HIV outcomes. Over 15% of ART patients experience interruptions annually, contributing to viral rebound, increased transmission risk, drug resistance, and preventable morbidity. Uganda’s viral suppression rate, currently estimated at approximately 79%, highlights a substantial retention gap within the HIV care cascade. The national adoption of the Multi-Month Dispensing (MMD) model, while improving convenience for stable patients, reduces routine patient–provider contact. This shift increases the risk that early signs of disengagement may go undetected until a substantial interruption has occurred. Current patient tracking systems rely largely on reactive and manual approaches, which are resource-intensive and insufficient for identifying patients at high risk before treatment interruption occurs. Moreover, treatment interruption in Uganda is not driven solely by clinical factors. Behavioural and Socioeconomic determinants, such as alcohol use and smoking history, significantly influence adherence behaviours. However, most predictive models developed in other contexts rely predominantly on clinical and demographic variables and inadequately integrate behavioural and socioeconomic constructs relevant to sub-Saharan Africa. There is therefore a need for a context-specific, data-driven predictive framework capable of integrating clinical, demographic, and behavioural and socioeconomic variables to identify individuals at high risk of interruption under the MMD system. Developing such a model for 30-, 60-, and 90-day interruption risk can enable early intervention, targeted resource allocation, and improved patient retention within Uganda’s HIV care system.

1.3 Research Objectives

1.3.1 General Objective

To develop and evaluate a multi-horizon machine learning predictive model for treatment interruption among people living with HIV (PLHIV) in Uganda, integrating clinical, behavioural, and socioeconomic determinants to improve risk stratification and support targeted interventions.

1.3.2 Specific Objectives

The specific objectives of this study are:

1. To determine the predictors of treatment interruption among PLHIV attending an urban HIV clinic in Uganda.
2. To develop a machine learning model that predicts interruption in treatment for PLHIV attending an HIV clinic in Uganda.
3. To assess the incremental predictive contribution of behavioural and socioeconomic variables to treatment interruption.

1.4 Research Questions

- 1: Which clinical, demographic, behavioural and socioeconomic factors most strongly predict treatment interruption among PLHIV in Uganda?
- 2: Which machine learning models provide clinically useful prediction of treatment interruption across different timeframes (30, 60, and 90 days)?
- 3: To what extent do behavioural and socioeconomic variables improve predictive performance compared to models using clinical variables alone?

1.5 Justification

The pursuit of a machine learning (ML) based prediction model for antiretroviral therapy (ART) interruptions is strongly justified by its potential to address critical inefficiencies in current healthcare systems and improve patient outcomes. Traditional methods of tracking patient adherence in Uganda, which often rely on manual chart reviews and clinic-based monitoring, are notoriously time-consuming, resource-intensive, and reactive, failing to identify at-risk patients before they disengage from care [19]. This inefficiency creates a significant bottleneck for healthcare providers and leads to the ineffective allocation of limited resources. Machine learning offers a paradigm shift from this reactive stance to a proactive, predictive model of care. By leveraging historical patient data, ML algorithms can synthesize complex, multidimensional patterns to forecast individual risk with a high degree of accuracy, enabling preventive interventions [16]. This is not merely a theoretical advantage; empirical evidence demonstrates that ML models can outperform traditional statistical methods in predicting HIV related outcomes, including loss to follow-up and viral non-suppression [11]. The implementation of such a tool in Uganda would directly enhance healthcare efficiency by allowing clinicians to prioritise high-risk patients for targeted support interventions, such as enhanced counselling, community adherence support, or financial assistance for transport, thereby optimizing resource allocation and improving cost effectiveness [18]. Furthermore, this research is critically positioned to address a notable gap in the existing literature. While previous ML models have proven effective, many have relied predominantly on clinical and demographic variables available in electronic health records, largely neglecting the crucial role of social and behavioral determinants of health (SBDH) such as stigma, poverty, food insecurity, and transportation barriers [12]. This oversight is a significant limitation, as these factors are primary drivers of treatment interruption in sub-Saharan Africa [21]. This study directly addresses this gap by explicitly integrating SBDH into its predictive framework, thereby contributing a more holistic and contextually relevant model to the field. Finally, the timing of this research is strategically aligned with Uganda's health policy evolution. The national scale-up of the Multi-Month Dispensing (MMD) model, while beneficial for stable patients, reduces opportunities for routine patient-provider contact, potentially allowing at-risk individuals to go unnoticed [15]. An ML-driven early warning system is, therefore, a necessary adaptation to sustain the gains of the MMD system. It provides a scalable solution to maintain continuity of care within a differentiated service delivery framework, ensuring that Uganda's progress toward epidemic control is not compromised by rising interruption rates.

1.6 Scope

The scope of this study covers three main dimensions: geographical, content, and time. Geographically, the research was conducted in Uganda, specifically focusing on a Uganda clinic to

capture a representative sample of People Living with HIV (PLHIV). The content scope centres on the development and validation of machine learning models aimed at predicting treatment interruptions (IIT) in HIV care, incorporating both clinical and social determinants of health. The study analysed retrospective data covering the period (2010–2024) and incorporated survey data collected during the study period. The study also targeted the implementation and adaptation of predictive models within Uganda’s Multi-Month Dispensing (MMD) framework.

1.7 Theoretical Framework

This study was guided by the World Health Organization (WHO) Multidimensional Adherence Framework (2003). The WHO framework conceptualizes adherence and treatment interruption as outcomes influenced by multiple interacting domains rather than by individual behaviour alone. It recognises that adherence to long-term therapies such as antiretroviral therapy (ART) is shaped by patient-related, therapy-related, condition-related, health system-related, and socioeconomic factors. The framework is particularly appropriate for this study because it aligns closely with the variables available in the dataset and reflects the complex nature of HIV treatment continuity in real-world clinical settings. According to the WHO framework, five major domains influence treatment adherence and interruption:

1. **Patient-Related Factors** These include demographic, behavioural and socioeconomic characteristics that may influence treatment engagement. In this study, patient-related variables include sex, age, marital status, smoking history, alcohol history, and previous missed appointments (“ever missed”). These factors may affect consistency in clinic attendance, medication adherence, and risk of treatment interruption.
2. **Therapy-Related Factors** These refer to characteristics of the treatment regimen itself. Variables such as current regimen, baseline regimen, ART start date, and duration on ART fall within this domain. Regimen complexity, side effects, and duration of treatment may influence the likelihood of continued engagement in care.
3. **Condition-Related Factors** These include the clinical status of the patient and disease severity. In this study, condition-related variables include current viral load, baseline viral load, current CD4 count, baseline CD4 count, WHO clinical stage, TB history, weight, and MUAC. These indicators reflect disease progression and treatment response, which may influence motivation for continued care or risk of interruption.
4. **Health System-Related Factors** This domain captures structural and service delivery influences. Geographic variables such as district and village may reflect access to healthcare facilities, distance to clinics, and variations in service delivery that influence treatment continuity.
5. **Socioeconomic Factors** Although detailed socioeconomic data are limited in this dataset, marital status and geographic location may serve as proxy indicators of social support and economic context, both of which can affect treatment adherence.

By applying the WHO Multidimensional Adherence Framework, this study acknowledges that treatment interruption is not solely a result of individual behaviour but emerges from the interaction of clinical, therapeutic, behavioural, socioeconomic and structural determinants. The framework therefore provides a comprehensive conceptual basis for examining predictors of treatment interruption using routinely collected clinical data. This theoretical foundation supports the selection of variables for statistical and machine learning modelling and strengthens the interpretation of findings within a public health and health systems perspective. There is currently no validated, context-specific, temporally-aware predictive model that integrates clinical, logistical, behavioural and socioeconomic determinants into a dynamic interruption risk score within Uganda’s MMD system.

Chapter 2

Literature Review

2.1 Introduction

Adherence to HIV care remains a critical component of successful HIV treatment outcomes globally. Optimal adherence to antiretroviral therapy (ART) ensures sustained viral suppression, reduces HIV-related morbidity and mortality, and prevents onward transmission of the virus. Globally, significant progress has been made in expanding access to ART; however, maintaining high levels of adherence remains a challenge, particularly among vulnerable populations [7] [5, 13]. Suboptimal adherence is associated with virological failure, development of drug resistance, disease progression, and increased risk of HIV transmission [13]. Regionally, in sub-Saharan Africa, which bears the highest burden of HIV globally, adherence to HIV care is influenced by a combination of health system, socioeconomic, and individual-level factors. Despite the scale-up of ART programs and the adoption of differentiated service delivery models such as multi-month dispensing, treatment interruptions remain a persistent challenge [5]. These interruptions undermine treatment effectiveness and are linked to poor clinical outcomes, including increased incidence of opportunistic infections, hospitalizations, and mortality [13, 6]. Locally, in Uganda, considerable progress has been made in strengthening HIV care through national treatment programs and the use of electronic medical record systems to support patient monitoring. However, treatment interruption and suboptimal adherence remain significant concerns among people living HIV. Clinical and behavioral factors continue to influence adherence patterns within routine care settings. The consequences of poor adherence in Uganda include unsuppressed viral load, immunological decline, increased healthcare costs, and a higher likelihood of HIV transmission within communities[6, 5]. Addressing these challenges is essential for achieving sustained viral suppression and meeting national and global HIV epidemic control targets. The application of machine learning in healthcare has been widely recognized for its potential to improve patient outcomes through enhanced decision-making and predictive analytics. In the context of HIV/AIDS, machine learning has emerged as a key tool in predicting various aspects of treatment adherence, including retention in care, viral load suppression, and interruptions in treatment (IIT). Several studies have explored the use of machine learning models to predict patient behaviour in HIV care, but limitations in scope, timeframe, and the incorporation of relevant social factors remain persistent.[23] This chapter reviews existing literature on the application of machine learning in HIV care, particularly regarding treatment adherence and retention, with a focus on the gaps that this study aims to address.

2.2 Multi-Month Dispensing (MMD) Framework

Multi-Month Dispensing (MMD) is a differentiated service delivery (DSD) model in which clinically stable people living with HIV receive antiretroviral therapy (ART) refills for extended periods, typically three to six months, rather than monthly visits. The approach is recommended by the World Health Organization as part of client-centered HIV care to improve treatment outcomes while reducing the burden on both patients and health systems [13]. MMD is particularly important in high-burden settings, where frequent clinic visits can contribute to poor adherence due to transport costs, time constraints, and facility congestion. In Uganda, MMD evolved within the broader framework of differentiated HIV service delivery aimed at improving efficiency and patient outcomes. The Ministry of Health Uganda introduced MMD through national DSD guidelines, initially promoting three-month refills for stable clients and later expanding to six-month dispensing for eligible patients [6]. Stable clients are typically defined as those who have been on ART for at least six months, demonstrate good adherence, and have achieved viral suppression. The expansion of MMD in Uganda has been driven by the need to decongest health facilities, optimize health worker time, and enhance patient convenience, particularly in rural and resource-limited settings [24]. Evidence from multiple settings indicates that MMD has a positive impact on adherence and retention in HIV care. Studies in sub-Saharan Africa have shown that longer dispensing intervals are associated with improved retention and comparable or better viral suppression outcomes compared to standard monthly dispensing [25]. Similarly, WHO guidelines report that extending ART refill intervals to three to six months improves treatment continuity without compromising clinical outcomes [13]. In Uganda, programmatic evidence suggests that MMD contributes to sustained viral suppression and improved retention, especially when combined with community-based delivery models and routine viral load monitoring [6]. Despite its benefits, MMD presents challenges in monitoring adherence and early detection of treatment interruption. Reduced frequency of clinic visits limits opportunities for healthcare providers to assess adherence, provide counselling, and identify emerging clinical, behavioural and socioeconomic issues. Routine monitoring systems under MMD often rely on pharmacy refill data, which may not accurately reflect actual medication-taking behaviour. Additionally, delayed clinical contact may result in late identification of virological failure, missed viral load testing, and reduced opportunities for timely intervention [14]. These gaps highlight the need for complementary strategies, such as enhanced patient tracking systems and predictive analytics, to improve adherence monitoring in MMD-based care models.

2.3 Determinants of Treatment Adherence

2.3.1 Social Determinants of Health in HIV Care

Social determinants of health (SDH) play a crucial role in HIV care and treatment adherence. Factors such as stigma, transportation barriers, mental health, socioeconomic status, and access to healthcare services significantly influence whether a person living with HIV remains on treatment.[26] In Uganda, stigma remains a substantial barrier to treatment adherence, with patients often avoiding healthcare settings due to fears of discrimination. Recent studies, including those by [27] have highlighted the importance of considering SDH in HIV care models. The integration of SDH into machine learning models can provide a more comprehensive view of the factors that influence treatment adherence and retention, which is a critical aspect of the current study.

2.3.2 Demographic and Clinical Factors

Researchers have found that age and sex can affect whether someone sticks with treatment.[7] found that age was one of the most important predictors, but other studies said these factors are not enough on their own.

2.3.3 Behavioural Patterns

Patients who miss visits or come late are more likely to stop treatment. [7] showed that past attendance patterns were among the best predictors for future interruptions.

2.3.4 Social Factors

In Nigeria, [28] included social factors in their ML models including pregnancy status, breast-feeding status, facility characteristics(location, service level, and service type). Although the inclusion of social factors did not substantially increase overall predictive accuracy, they contributed additional contextual insights that enhanced the interpret-ability of the model.

2.4 Machine Learning in HIV Treatment Adherence

Numerous studies have utilized machine learning models to predict HIV treatment adherence and retention. For instance, Ogbachie et al. (2022) developed a machine learning model for predicting short-term (30-day) interruptions in treatment among PLHIV in Nigeria. The study incorporated variables such as demographics, clinical history, and laboratory test results. While this research was valuable in understanding short-term treatment interruptions, it did not extend its scope to longer interruptions or include social factors such as stigma and access to healthcare, which can significantly affect adherence. In South Africa, Maskew et al. (2022) applied machine learning to predict viral load suppression and retention in care. Although their work demonstrated the utility of ML in predicting treatment outcomes, it did not consider the longer-term implications of treatment interruptions or the impact of social determinants on retention. Studies in other parts of the world have shown that incorporating social , behavioural and socioeconomic factors, such as mental health, stigma, and socioeconomic status, can greatly improve the accuracy of predictive models for treatment adherence. In Nigeria, [29] used data from over 41,000 patients to test different ML models. They found that the AdaBoost model worked best, with an accuracy score of 84In Tanzania, [30] also used ML to predict which patients might drop out of care. They used a simple decision tree model and found it could predict interruptions six months in advance. Other researchers, like [31], [32] and [28], tested models such as XGBoost and Random Forest. These models also worked well in predicting who was likely to stop treatment in different African countries. These studies show that ML can find patterns in patient data that help predict treatment problems early.

Existing literature demonstrates the growing application of artificial intelligence (AI) and machine learning (ML) techniques in predicting risks associated with HIV treatment adherence. Several studies have developed predictive models aimed at identifying patients at risk of antiretroviral therapy (ART) non-adherence, treatment interruption, loss to follow-up, and virological failure. Commonly used algorithms include logistic regression, random forest, support vector machines (SVM), gradient boosting methods such as XGBoost, and neural networks, which are applied to analyze large and complex health datasets [33].

These models typically incorporate a combination of clinical, behavioral, and socioeconomic predictors, including CD4 cell count, viral load levels, WHO clinical stage, medication history,

appointment attendance, alcohol use, and demographic characteristics such as age, gender, and marital status. Findings from previous studies indicate that machine learning models can achieve moderate to high predictive accuracy in identifying patients at risk of poor adherence outcomes, thereby supporting early intervention strategies and improved patient management in HIV care programs[34].

Despite these advances, most existing predictive models have been developed using datasets from high-income or well-resourced health systems, which may limit their applicability in low- and middle-income settings. Additionally, many studies focus on single outcomes such as loss to follow-up or medication non-adherence, rather than examining treatment interruption across multiple time points. There is also limited evidence integrating behavioral, socioeconomic, and clinical variables within a unified predictive framework tailored to local contexts.

This highlights a critical gap in the literature and justifies the need for context-specific AI predictive models that can accurately forecast treatment interruption at different durations (e.g., 30, 60, and 90 days) to support targeted interventions and improve retention in HIV care.

2.5 Multi-Horizon Prediction in Health Systems: 30, 60, and 90 Days

Most studies only try to predict if someone will stop treatment in the next 30 days. But Uganda uses a system called Multi-Month Dispensing (MMD), where patients may not come back for months. This means we need models that can predict treatment interruption at 60 or even 90 days. [29] defined interruption as missing a refill by 28 days, which matches the 30-day mark. However, they didn't look at longer timelines. In South Africa,[7] tested models that used past attendance to predict treatment gaps of different lengths. They found that longer prediction times are useful and possible, but few studies focus on this. This study helps fill this gap by testing ML models that look ahead to 30, 60, and 90 days.

2.6 Limitations of Existing Studies

Existing studies on machine learning in HIV care have significant limitations. First, many studies focus on short-term treatment interruptions (typically within 30 days) and do not address longer-term interruptions, which are more detrimental to patient health. Second, most studies exclude social determinants of health from the predictive models, failing to capture the complexity of treatment adherence in real-world settings. Finally, many studies have been region-specific, making it difficult to generalize the findings across diverse healthcare systems, particularly those with different ART distribution models, such as Uganda's MultiMonth Dispensing (MMD) system.

2.7 Summary and Gaps

Studies show that ML can help predict who might stop HIV treatment. Most models work well using clinic data and patient history. But there are still gaps: Not many studies test predictions for 60 or 90 days. Limited emphasis on prediction time frames that is number of months of interruption. This study aims to fill these gaps by building a model that includes clinical and social factors, and tests predictions for 30, 60, and 90 days.

Across the reviewed studies, a consistent pattern emerges showing that machine learning models are increasingly effective in predicting HIV treatment adherence and retention outcomes. Studies conducted in Nigeria, South Africa, and Tanzania demonstrate that algorithms such as Random Forest, XGBoost, AdaBoost, and decision trees can successfully identify patients at risk of treatment interruption using demographic, clinical, and behavioral data. Although these studies report relatively good predictive performance, there are important differences in their methodological approaches, predictor variables, and prediction timelines. For example, some studies focused primarily on short-term interruption prediction, particularly within 30 days, while others concentrated on viral load suppression or retention in care rather than interruption over extended [34]. In addition, many existing models rely heavily on clinical and demographic variables while giving limited attention to socioeconomic and behavioral determinants such as alcohol use, stigma, transportation barriers, and healthcare accessibility, despite evidence that these factors strongly influence adherence behavior in resource-limited settings.

Furthermore, most previous studies were conducted in settings with healthcare delivery structures that differ from Uganda’s Multi-Month Dispensing (MMD) framework, limiting the direct applicability of their findings to local HIV care systems. The reduced frequency of patient-clinic interaction under MMD creates unique challenges in monitoring adherence and identifying treatment interruption early, yet few predictive studies have specifically addressed this context. This suggests that while existing machine learning models provide valuable evidence on the potential of predictive analytics in HIV care, important gaps remain in developing context-specific, multi-horizon prediction models that integrate clinical, behavioral, and socioeconomic factors. Therefore, this study extends existing literature by developing predictive models for 30-, 60-, and 90-day treatment interruption within Uganda’s MMD framework, thereby contributing a more comprehensive and locally relevant approach to adherence prediction[35].

Chapter 3

Methodology

3.1 Research Design

This study used a quantitative research design, utilizing retrospective data to develop and validate machine learning models for predicting interruptions in HIV treatment (IIT). The study focused on patients enrolled in Uganda’s MultiMonth Dispensing (MMD) program, analyzing data over multiple timeframes (30, 60, and 90 days) to assess the predictive accuracy of the models.

3.2 Area of Study

The study focused on HIV treatment interruptions (IIT) among patients enrolled in Uganda’s Multi-Month Dispensing (MMD) program. Data were collected from selected HIV clinics.

3.3 Data collection and Processing

3.3.1 Sources of Information

Secondary Data: Electronic Medical Records (EMRs) from the HIV clinic (appointment history, ART refills, viral load data).

3.3.2 Population

Target Population: PLHIV (People Living with HIV) enrolled at Mutunda Clinic. This study did not perform an a priori sample size calculation. Instead, a retrospective census approach was adopted whereby all eligible patient records available within the study period were included in the analysis. A total of 8788 patients met the inclusion criteria and were analysed. This approach ensured maximal statistical power while avoiding sampling bias associated with subset selection.

3.3.3 Inclusion and Exclusion Criteria

Participants eligible for inclusion in this study were individuals living with HIV who had at least one clinic visit within the past year. Inclusion also required the availability of key clinical variables, such as viral load and ART regimen data. Conversely, patients were excluded if their

medical records were incomplete, particularly those lacking critical clinical indicators like CD4 counts.

3.3.4 Variables definition and Indicators

The primary outcome variable for this study was treatment interruption (IIT), defined as a binary variable (Yes/No) at 30, 60, and 90 days. Predictor variables included demographic factors (age, gender), clinical indicators (CD4 count, viral load, and ART duration), and social determinants (distance to the nearest clinic).

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Table 3.1: Variable Definitions

Variable Name	Variable Type	Data Type	Coding	Measurement Level	Description
Treatment Interruption (30 days)	Outcome	Binary	1 = Yes, 0 = No	Nominal	Indicates whether a patient missed ART refill or was lost to follow-up for ≥ 30 days.
Treatment Interruption (60 days)	Outcome	Binary	1 = Yes, 0 = No	Nominal	Indicates whether a patient interrupted ART for ≥ 60 days.
Treatment Interruption (90 days)	Outcome	Binary	1 = Yes, 0 = No	Nominal	Indicates whether a patient interrupted ART for ≥ 90 days.
Age	Predictor	Numeric	Continuous (years)	Ratio	Age of the patient at time of assessment.
Gender	Predictor	Categorical	1 = Male, 2 = Female	Nominal	Biological sex of the patient.
Marital Status	Predictor	Categorical	Single, Married, Divorced, Widowed, Cohabiting, Unknown	Nominal	Patient's marital status.
CD4 Count (Current)	Predictor	Numeric	Cells/mm ³	Ratio	Most recent CD4 T-cell count measurement.
CD4 Count (Baseline)	Predictor	Numeric	Cells/mm ³	Ratio	CD4 count at ART initiation.
Viral Load (Current)	Predictor	Numeric	Copies/mL	Ratio	Most recent HIV viral load measurement.
Viral Load (Baseline)	Predictor	Numeric	Copies/mL	Ratio	Viral load at ART initiation.
ART Duration	Predictor	Numeric	Continuous (months/years)	Ratio	Total duration on antiretroviral therapy.

Variable Name	Variable Type	Data Type	Coding	Measurement Level	Description
ART Start Date	Predictor	Date	YYYY-MM-DD	Interval	Date when ART was initiated.
WHO Clinical Stage	Predictor	Categorical	Stage I–IV	Ordinal	Clinical staging of HIV disease progression.
Current Regimen	Predictor	Categorical	Regimen codes (e.g., TDF/3TC/DTG)	Nominal	Current ART regimen prescribed.
Baseline Regimen	Predictor	Categorical	Regimen codes	Nominal	ART regimen at initiation.
Alcohol History	Predictor	Categorical	Yes, No, None	Nominal	History of alcohol consumption.
Smoking History	Predictor	Categorical	Yes, No, None	Nominal	History of tobacco use.
TB History	Predictor	Categorical	None, Past TB, Ongoing TB, Unknown	Nominal	Tuberculosis treatment history.
Weight	Predictor	Numeric	Kilograms (kg)	Ratio	Patient body weight at most recent visit.
MUAC	Predictor	Numeric	Centimeters (cm)	Ratio	Mid-upper arm circumference measurement.
Region	Predictor	Categorical	Region names	Nominal	Geographic region of residence.
District	Predictor	Categorical	District names	Nominal	Patient’s district of residence.

The study utilized both outcome and predictor variables derived from routine electronic medical records. The outcome variables included treatment interruption at 30, 60, and 90 days, defined as missing scheduled ART refills or being lost to follow-up for at least 30, 60, or 90 days, respectively. Predictor variables comprised demographic characteristics such as age (measured in years), sex (male or female), and marital status (e.g., single, married, divorced, widowed, or cohabiting). Clinical variables included CD4 count (cells/mm³), representing immune status; viral load (copies/mL), indicating the level of HIV replication; WHO clinical stage (Stages I–IV), reflecting disease progression; and ART duration, defined as the length of time a patient has been on treatment. Treatment-related variables included ART start date (date of initiation of therapy), current regimen (the ART combination currently prescribed), and baseline regimen (the initial ART combination at treatment initiation). Behavioral and comorbidity-related variables included alcohol history (history of alcohol use), smoking history (history of tobacco use), and TB history (past or current tuberculosis infection). Anthropometric measures included weight (in kilograms) and mid-upper arm circumference (MUAC, in centimeters), which provide indicators of nutritional status. Geographic variables included region and district, representing the patient’s area of residence.

All variables listed above were extracted from routine electronic medical records. During data preprocessing and model development, feature selection techniques were applied to identify the most relevant predictors, and only variables with sufficient data completeness and predictive contribution were retained in the final machine learning models.

3.3.5.1 Behavioral and socioeconomic variables considered

Behavioral and socioeconomic variables considered in this study included alcohol history, smoking history, marital status, region, and district of residence, as these factors may influence adherence to antiretroviral therapy (ART) and treatment outcomes among patients living with HIV. Alcohol and smoking history were categorized as yes, no, or none and were used to assess the influence of substance use behaviors on treatment interruption. Marital status, classified as single, married, divorced, widowed, cohabiting, or unknown, was included to examine the potential role of social support and family structure in ART adherence. Geographic variables such as region and district were also considered to evaluate possible disparities in healthcare access and service delivery across different locations. These behavioral and socioeconomic variables were analyzed alongside clinical predictors including age, gender, CD4 count, viral load, WHO clinical stage, ART duration, and treatment regimen to determine their association with treatment interruption outcomes at 30, 60, and 90 days.

3.3.6 Measurement Levels

Variables were categorized according to their measurement levels. Interval and ratio variables included continuous measures such as age, CD4 count, and viral load levels.

3.3.7 Procedure for Data Collection

Prior to data collection, ethical clearance was obtained from the Uganda National Council for Science and Technology (UNCST) and the relevant Institutional Review Boards (IRBs). Data collection involved two main approaches: retrospective extraction of Electronic Medical Record (EMR) data. Data anonymization protocols were strictly followed, ensuring that all personal identifiers were removed and replaced with unique coded identifiers.

3.3.8 Data Collection Instruments and Equipment

The primary source of clinical data was EMR systems. Data processing and analysis were performed using Python libraries such as Pandas and Scikit-learn for machine learning modelling. Data were collected using two main tools: Electronic Medical Records (EMR), which provided structured data from systems such as OpenMRS, including variables on ART regimen, viral load, and visit history.

3.3.9 Quality and Error Control

To ensure the integrity and reliability of the dataset, 10% of all records were cross-validated for accuracy. Inter-rater reliability checks were performed for manually coded variables to minimise subjective errors and enhance consistency across data entries.

3.3.10 Data processing and analysis

3.3.10.1 Tools Used

This analysis was conducted using Python 3.10 in a Jupyter Notebook environment. Several data science libraries were used to support data processing and analysis. The main libraries included pandas and numpy for data cleaning, management, and numerical computations. For data visualization and exploratory analysis, matplotlib and seaborn were used. In addition, plotly was applied to create interactive visualizations that facilitated the exploration of complex relationships among variables. Statistical analysis and correlation tests were performed using

scipy.stats and custom Python functions developed for clinical data validation. The dataset was examined through detailed data profiling to understand its structure and quality. This was followed by systematic data cleaning to address missing values, inconsistencies, and errors while maintaining data integrity. Given that the study involved sensitive HIV patient data, all data transformations were carefully documented in a cleaning log to ensure transparency and reproducibility. Both descriptive and inferential statistical methods were applied in the analysis. Descriptive statistics were used to summarize patient characteristics, while inferential methods were employed to assess treatment outcomes and patterns.

3.3.10.2 Handling of Missing Data

Records with more than 30% missing data were excluded from the final analysis. For datasets with limited missingness, appropriate imputation techniques were applied to preserve the analytical sample size without compromising data integrity.

3.3.10.3 Research Strategy

The study employed a quantitative retrospective predictive modelling research method using machine learning techniques. Multiple predictive models were developed and compared using routinely collected Electronic Medical Record (EMR) data to identify patients at risk of HIV treatment interruption (IIT). The modelling strategy involved data preprocessing, feature engineering, class balancing using SMOTE, and supervised machine learning classification. Models were trained and tested using an 80:20 stratified train-test split, and their performance was evaluated and compared using quantitative metrics including accuracy, precision, recall, F1-score, confusion matrices, and ROC-AUC. This comparative modelling approach enabled the identification of the best-performing model for predicting treatment interruption at 30, 60, and 90 days.

3.3.11 Machine Learning Models

The predictive model for treatment interruption was developed using a structured machine learning pipeline implemented in Python. The modelling process involved data preprocessing, class imbalance handling, model training, performance evaluation, and interpretation of model outputs.

3.3.11.1 Algorithm selection and justification

The study employed the Random Forest classifier as the primary machine learning algorithm. Random Forest is an ensemble learning method that constructs multiple decision trees and aggregates their predictions to improve classification accuracy and robustness. The algorithm was selected for several reasons. First, Random Forest can capture complex nonlinear relationships between predictors and outcomes, which are common in clinical datasets. Second, it is relatively robust to noise and multicollinearity among predictors. Third, Random Forest provides feature importance measures, which help identify the most influential predictors of treatment interruption, thus supporting clinical interpretation and policy decision-making.

A predictive model was selected for this study because the primary objective is to accurately predict the risk of treatment interruption among patients receiving antiretroviral therapy (ART), rather than to solely explain causal relationships between variables. Predictive models are particularly suited for identifying complex, non-linear patterns within large datasets that include behavioral, socioeconomic, and clinical variables, making them effective for forecasting

outcomes such as treatment interruption at 30, 60, and 90 days. In contrast, traditional explanatory statistical models are mainly designed to interpret relationships and understand the underlying causes of an outcome, but they may be less effective in optimizing predictive performance for early risk identification. The use of an ML-based approach therefore allows for improved prediction accuracy, early detection of high-risk patients, and better support for clinical decision-making and targeted interventions aimed at improving patient retention in ART programs.

3.3.11.2 Data pre-processing and feature preparation

Prior to model training, several pre-processing steps were implemented to prepare the dataset. Datetime variables were identified and removed to avoid incompatibility with machine learning algorithms. Predictor variables were then separated into numerical and categorical features. Numerical variables were processed using median imputation to address missing values, while categorical variables were handled using most frequent imputation followed by one-hot encoding to convert categorical data into a format suitable for machine learning algorithms. These pre-processing steps were integrated using a Column Transformer and pipeline architecture, ensuring that transformations were applied consistently during both training and testing phases.

3.3.11.3 Handling class imbalance

Because treatment interruption cases were relatively fewer compared to non-interruption cases, the dataset exhibited class imbalance. To address this issue, the study applied the Synthetic Minority Oversampling Technique (SMOTE). SMOTE generates synthetic examples of the minority class to balance the training data and improve the model's ability to detect interruption cases. Importantly, SMOTE was applied only to the training dataset within the modelling pipeline to prevent information leakage into the test set.

3.3.11.4 Training and testing strategy

The dataset was divided into training and testing subsets using an 80:20 split. Stratified sampling was applied to maintain the same proportion of interruption and non-interruption cases in both subsets. The model was trained using the training dataset after pre-processing and SMOTE oversampling. Once training was complete, the model's predictive performance was evaluated on the unseen test dataset, which was not used during training. This approach ensures that model performance reflects its ability to generalize to new patient data.

3.3.11.5 Feature importance analysis

To enhance interpretability, the Random Forest model's feature importance scores were extracted after training. These scores quantify the relative contribution of each predictor variable to the model's decision-making process. The most important features were visualized using bar plots to highlight key predictors associated with treatment interruption.

3.3.11.6 Software and tools

All data processing, model development, and evaluation procedures were implemented using Python within a Jupyter Notebook environment. The following libraries were used: Pandas and

NumPy for data manipulation and numerical operations Scikit-learn for pre-processing, model training, evaluation metrics, and machine learning utilities Imbalanced-learn (imblearn) for SMOTE-based class imbalance handling Matplotlib for visualization of precision–recall curves and feature importance plots. This integrated pipeline ensured reproducibility, minimised data leakage, and enabled efficient model development.

3.3.12 Model Evaluation

Model performance was evaluated using several classification metrics appropriate for binary outcomes. Accuracy was used to measure the proportion of correctly classified observations and is defined as the ratio of correctly predicted cases (both interruption and non-interruption) to the total number of observations. However, given the imbalanced nature of treatment interruption data, accuracy alone was not considered sufficient for assessing model performance. Greater emphasis was therefore placed on precision, recall (sensitivity), and the F1-score. Precision measures the proportion of predicted interruption cases that are truly interruptions, making it particularly important in healthcare settings where minimising false positive classifications is critical for efficient resource allocation. Recall reflects the model’s ability to correctly identify patients who experience treatment interruption, while the F1-score provides a harmonic balance between precision and recall, offering a single metric for evaluating overall classification performance. In addition to these metrics, the Area Under the Receiver Operating Characteristic Curve (ROC-AUC) was used to assess the model’s discriminative ability across all possible classification thresholds. ROC-AUC evaluates how well the model distinguishes between patients who interrupt treatment and those who do not, independent of a specific probability cut-off. To further understand model behavior, confusion matrices were generated for each model, providing a detailed breakdown of true positives, true negatives, false positives, and false negatives. This allowed for a more nuanced assessment of classification performance, particularly in relation to the trade-offs between identifying true interruption cases and minimising incorrect classifications. Model performance was evaluated and compared across three model specifications: clinical variables only, clinical combined with socioeconomic variables, and clinical combined with both socioeconomic and behavioural variables. All models were assessed using the same evaluation metrics to ensure consistency and comparability. This approach enabled a structured examination of the incremental contribution of additional variable domains to predictive performance. By comparing models across these progressively enriched feature sets, the analysis was designed to determine whether incorporating broader social and behavioral determinants improves the model’s ability to accurately identify patients at risk of treatment interruption.

3.3.13 Ethical Considerations

The study adhered to strict ethical standards to protect the rights and privacy of participants. No identifiable personal information such as names was stored. Informed consent was waived for the use of retrospective EMR data.

Chapter 4

Results

4.1 Introduction

This chapter presents the data preparation, exploratory analysis, statistical modelling, and machine learning procedures conducted to identify factors associated with treatment interruption (*ever missed*) and to develop a predictive model for interruption risk.

Objective 1: To preprocess and engineer structured clinical, demographic, behavioural and socioeconomic variables relevant to ART adherence and interruption.

4.2 Description of the Raw Dataset

The dataset comprises 8,788 PLHIV records. Out of 8,788 patients, 239 experienced HIV treatment non-adherence, giving an overall rate of 2.72%. The raw dataset used in this study was extracted from an electronic HIV clinic patient management system and contains longitudinal clinical and demographic records of patients receiving antiretroviral therapy (ART). The dataset comprises 33 variables capturing patient identification details, treatment history, clinical indicators, adherence measures, and socio-demographic characteristics. Each record corresponds to an individual patient observation linked through a unique patient identifier (*_patient_id*). The dataset includes temporal variables such as the visit date (*date*), ART initiation date (*Art_start_date*), and dates related to treatment interruption events (*date missed* and *date returned*).

Demographic variables in the dataset include sex, current age, marital status, district, village, and region, which provide contextual information on patient background. Behavioral risk factors such as smoking history and alcohol history are also captured. Clinical variables include WHO clinical stage, current and baseline ART regimen, current viral load, baseline viral load, current CD4 count, baseline CD4 count, weight, and Mid-Upper Arm Circumference (MUAC). These indicators provide insight into the clinical status and treatment progression of patients as shown in Table: 4.1.

The dataset also contains treatment adherence and interruption indicators such as *ever missed*, *months missed*, and adherence status, which are essential for identifying treatment interruption patterns. Additional treatment monitoring variables include duration on ART and drugs dispensed prior to interruption, which help characterize treatment exposure.

The dataset includes a mix of numeric, categorical, and datetime variables. Numerical variables include clinical measurements such as viral load, CD4 counts, weight, and MUAC. Categorical

variables include sex, marital status, smoking history, alcohol use, WHO clinical stage, and ART regimens. Date variables capture important treatment timelines including patient visits and treatment initiation.

Overall, the dataset provides a comprehensive set of demographic, clinical, behavioral, and treatment-related variables, making it suitable for developing predictive models to identify factors associated with interruptions in HIV treatment.

Table 4.1: Summary of Raw Dataset

Variable Category	Variables	Data Type
Patient Identifier	Patient ID	Integer
Treatment Interruption	Ever missed appointment, Months missed	Categorical, Numeric
Treatment History	Drugs dispensed prior	Numeric
Demographic Characteristics	ART number, Date of birth, Sex, Current age, Marital status	String, Date, Categorical, Integer
Behavioral Factors	Smoking history, Alcohol history	Categorical
Clinical History	TB history, WHO clinical stage	Categorical
Treatment Information	ART start date, Duration on ART, Current regimen, Baseline regimen	Date, Integer, Categorical
Laboratory Measures	Current viral load, Baseline viral load, Current CD4 count, Baseline CD4	Numeric
Adherence	Adherence status	Categorical
Anthropometric Measures	Weight, MUAC	Numeric
Geographic Location	District, Village, Region	Categorical

4.3 Variable Selection and Feature Reduction

4.3.1 Removal of Irrelevant Variables

To prepare the dataset for analysis, several variables that were not relevant for modelling or contained administrative tracking information were removed. These included *date returned*, *date missed*, *tx_ml_date*, *tx_ml*, *date*, and the patient identifier (*_patient_id*). These variables primarily contained operational or system-generated information related to clinic visits and patient tracking rather than clinical, demographic, or behavioral factors relevant to predicting treatment interruption. Additionally, identifier variables were excluded to prevent unnecessary duplication and to maintain patient confidentiality. Removing these columns helped reduce dataset complexity and ensured that the remaining variables focused on meaningful predictors for subsequent exploratory analysis and machine learning modelling.

4.4 Missing Value Handling

The dataset was assessed for missing values to determine the completeness of each variable before analysis. Missing data is common in routine clinical datasets because some laboratory tests, clinical measurements, or patient history fields may not be recorded at every visit. In

this study, missingness was evaluated for all variables to identify incomplete fields and guide decisions on cleaning, imputation, or exclusion.

For continuous variables such as current viral load, baseline viral load, current CD4 count, baseline CD4 count, weight, MUAC, months missed, and drugs dispensed prior, missing values may arise from missed laboratory investigations, delayed updates, or incomplete clinical documentation. For categorical variables such as smoking history, alcohol history, marital status, WHO clinical stage, and ART regimen, missing values may reflect unrecorded patient information.

Variables with a small amount of missing data ($< 30\%$) were retained for analysis. Missing values were not imputed because, in routine clinical datasets, missingness may carry meaningful information related to patient engagement, healthcare access, or monitoring practices. Imputing such values could introduce bias or mask important patterns. Therefore, missing data were preserved, and analyses were conducted using available observations, with missingness treated as potentially informative within the modeling process.

4.5 Inconsistent Data Formats

The dataset was checked for inconsistent data formats to ensure that each variable was stored in an appropriate structure for analysis. The raw data contained a mixture of integer, float, object, and datetime data types. Consistency in format is important because incorrect data types can affect summary statistics, preprocessing, and machine learning model performance.

Particular attention was given to date variables such as *date*, *dob*, and *Art_start_date*, which should be stored in datetime format. Similarly, numeric clinical measurements such as viral load, CD4 count, weight, MUAC, and months missed should be stored as numeric variables rather than text. Categorical variables including sex, marital status, smoking history, alcohol history, and ART regimen were also reviewed for consistency in coding and text formatting.

Duplicate records were assessed to determine whether the same patient observation appeared more than once in the dataset. Duplicate entries can arise during extraction, merging of files, repeated exports, or multiple records for the same patient on the same date. Such duplicates can distort descriptive statistics and bias predictive modelling results. Duplicate records were standardised by keeping the first instance and deleting the duplicate.

The viral load variable also had many inconsistent entries. There were 17 different text formats used to describe undetectable viral load results, such as “Not Detected”, < 20 , “Target Not Detected”, “TND”, and “Undetectable”. Although these mean the same clinically, they had to be standardized before calculating viral suppression rates. Because of these inconsistencies, mapping rules were created to convert similar responses into uniform categories. This standardization was necessary to ensure accurate data analysis and reliable statistical modelling.

4.6 Outliers

Outliers were examined among continuous variables to identify extreme values that may result from data entry errors, measurement problems, or true but unusual clinical observations. Variables such as current viral load, baseline viral load, current CD4 count, baseline CD4 count, weight, MUAC, current age, duration on ART, and months missed were assessed for unusually high or low values.

Outlier detection is important because extreme values can influence summary statistics and affect the performance of predictive models. However, in clinical datasets, some extreme values may still be valid and clinically meaningful. Therefore, outliers were identified and reviewed, and extreme values were capped at defined threshold limits (e.g., using the interquartile range method) rather than removed, in order to reduce their influence while preserving the integrity of the data.

4.7 Invalid Values

The dataset was reviewed for invalid and implausible values that may reflect data entry errors or incorrect coding. Invalid values may include impossible ages, negative laboratory values, future dates, ART start dates occurring before birth dates, or non-standard category labels. Such checks are especially important in clinical data because invalid records may reduce data credibility and affect model performance. All records reviewed were in conformity, with no invalid values.

4.8 Data Preparation and Cleaning

The dataset was imported from an Excel file containing merged patient-level HIV treatment records. Column names were standardized by converting all variable names to lowercase and replacing spaces with underscores to ensure consistency and reproducibility.

Mixed-format numeric variables, particularly viral load measurements (e.g., “Target Not Detected”, < 50 , > 1000), were cleaned by:

- Replacing “Target Not Detected” and “Not Detected” with 0
- Removing inequality symbols ($<$, $>$)
- Converting all entries to numeric values
- Coercing invalid entries to missing values (NaN)

Other clinical variables such as age, CD4 count, baseline CD4, current CD4, and weight were converted to numeric format to ensure compatibility with statistical and machine learning models. 21

4.9 Feature Engineering

4.9.1 Age Categorisation

The continuous Current Age variable was transformed into categorical age groups to improve interpretability and facilitate meaningful analysis of patient characteristics. Categorising age enhances model interpretability by allowing results to be expressed in clinically meaningful groups rather than continuous numerical values, making findings easier to interpret and apply in practice. Age categorisation is widely used in public health and HIV programs because treatment adherence patterns, risk behaviors, and clinical outcomes vary across different age groups. In this study, age was grouped into six categories: 0–14, 15–24, 25–34, 35–44, 45–54, and 55 years and above. These groupings align with standard HIV program reporting and clinical practice, where children, adolescents, young adults, and older adults are managed differently. This approach improves the practical applicability of the model by enabling healthcare providers to easily identify age-specific risk patterns and tailor interventions accordingly.

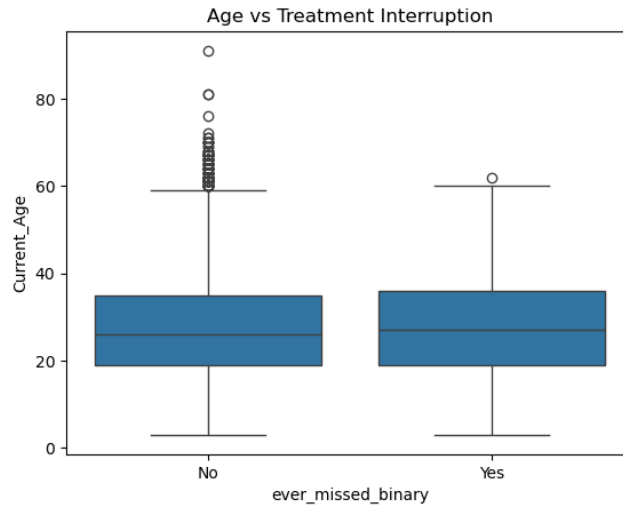


Figure 4.1: Box plot showing age vs interruption

Figure 4.1 illustrates the distribution of patient age across treatment interruption groups. The results show that the median age of patients who interrupted treatment is slightly higher than that of patients who did not interrupt treatment. However, the interquartile ranges for both groups largely overlap, indicating similar age distributions between interrupters and non-interrupters.

The spread of ages is comparable across both groups, with most patients falling within the young to middle-aged categories. Several outliers are observed, particularly among patients who did not interrupt treatment, indicating the presence of older individuals in this group. Despite these variations, there is no clear distinction in age distribution between the two groups.

These findings suggest that age is not a strong predictor of treatment interruption in this study. This is consistent with the statistical analysis results, where age did not show a significant association with treatment interruption, and with the machine learning model findings, where age had relatively low importance compared to clinical and behavioural variables.

4.9.2 Viral Load Categorisation

The viral load variables were categorised to distinguish between patients with suppressed and non-suppressed viral loads, which is a key indicator of treatment effectiveness in HIV care. Categorisation improves model interpretability by converting continuous laboratory measurements into clinically meaningful groups that can be easily understood and applied in decision-making. In this study, a threshold of 1000 copies/mL was used based on World Health Organization (WHO) guidelines, which define viral suppression below this level. Using this threshold, two categorical variables were created: *current_vl_category* and *baseline_vl_category*. Patients with viral load values below 1000 copies/mL were classified as “Suppressed,” while those with values equal to or above 1000 copies/mL were classified as “Non-suppressed.” This categorisation aligns with routine clinical practice, where viral suppression status is used to guide patient management, such as adherence counseling or regimen switching. It also enhances the practical applicability of the model by enabling clear identification of patients at higher risk of treatment interruption based on clinically recognised thresholds.

Figure 4.2 shows that the majority of patients were virally suppressed, with only a small proportion classified as non-suppressed. This indicates generally good treatment outcomes within the study population, although the presence of non-suppressed patients highlights a

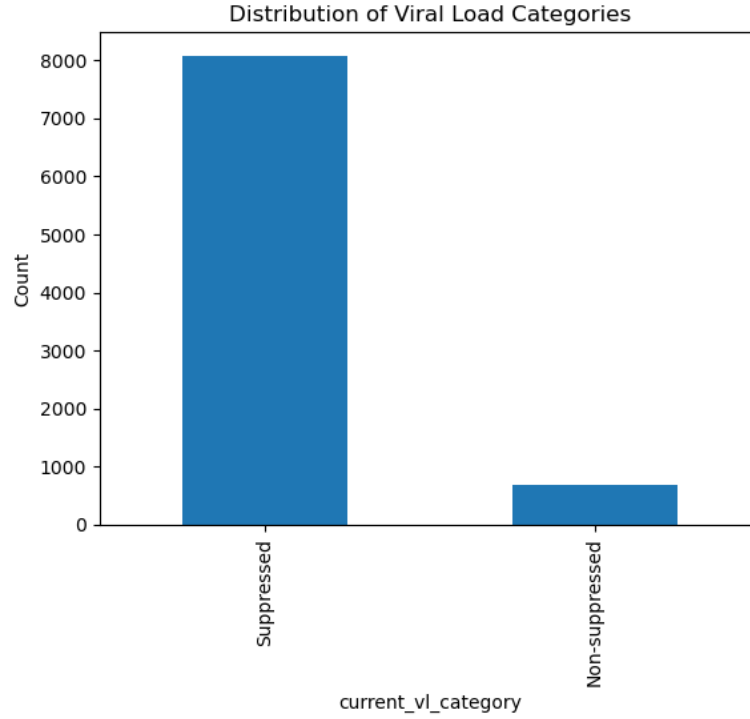


Figure 4.2: Box plot showing the distribution of Viral Load Categories

subgroup at higher risk of poor adherence and treatment interruption. The imbalance between the two groups also reflects the class imbalance present in the dataset.

4.9.3 Current CD4 Categorisation

The CD4 count variables were categorised to distinguish patients with severe immunosuppression from those with relatively stronger immune status. CD4 count is a key clinical indicator used to assess immune system function among individuals living with HIV. Categorisation improves model interpretability by translating continuous laboratory values into clinically meaningful groups that are easier to interpret and apply in practice. In this study, a threshold of 200 cells/mm³ was used to classify CD4 levels, consistent with widely used clinical guidelines where CD4 counts below this level indicate advanced immunosuppression and increased vulnerability to opportunistic infections. Two categorical variables were therefore created: *current_cd4_category* and *baseline_cd4_category*. Patients with CD4 counts below 200 cells/mm³ were classified as “Below 200,” while those with CD4 counts equal to or greater than 200 cells/mm³ were categorised as “200 and above.” This categorisation aligns with routine clinical practice, where CD4 thresholds are used to assess disease severity and guide clinical management, and it enhances the practical applicability of the model by enabling clear identification of high-risk patient groups.

4.9.4 Weight Categorisation

The weight variable was categorised to facilitate interpretation of patients’ nutritional and physical health status within the study population. Categorisation improves model interpretability by transforming continuous measurements into clinically meaningful groups that are easier to understand and apply in practice. Continuous weight measurements were grouped into intervals to allow clearer comparison across patient groups and to reduce the influence of minor variations in numerical values. The weight variable was divided into six categories: less than

40 kg, 40–49 kg, 50–59 kg, 60–69 kg, 70–79 kg, and 80 kg and above. These categories provide a simplified representation of the distribution of patient body weight and align with clinical assessment of nutritional status, where low body weight may indicate undernutrition or disease severity. This categorisation enhances the practical applicability of the model by enabling identification of patients at potential risk of poor treatment outcomes associated with low or high body weight.

4.9.5 Mid Upper Arm Circumference Categorisation

The Mid-Upper Arm Circumference (MUAC) variable was categorised to assess the nutritional status of patients across different age groups. MUAC is widely used as a simple anthropometric indicator for detecting malnutrition and poor nutritional status, which can influence treatment outcomes and adherence among individuals receiving HIV care. Categorisation improves model interpretability by translating continuous measurements into clinically meaningful groups that are easier to interpret and apply in practice. In this study, MUAC values were categorised using age-specific thresholds because nutritional assessment criteria differ between children, adolescents, and adults. For children under five years, MUAC values were classified as Severe (< 11.5 cm), Moderate (11.5–12.4 cm), and Normal (≥ 12.5 cm). For individuals aged 5–14 years, simplified categories of Low (< 13.5 cm), Borderline (13.5–14.4 cm), and Normal (≥ 14.5 cm) were used. For adults aged 15 years and above, MUAC values were categorised as Low (< 23 cm), Borderline (23–25.9 cm), and Normal (≥ 26 cm). A custom function was applied across the dataset to assign each patient to the appropriate category based on their age and MUAC measurement, while records with missing age or MUAC values were retained as a separate category. This categorisation aligns with clinical practice in nutritional assessment and enhances the practical applicability of the model by enabling identification of patients at risk of malnutrition and its potential impact on treatment adherence and outcomes.

4.9.6 Duration on ART Categorisation

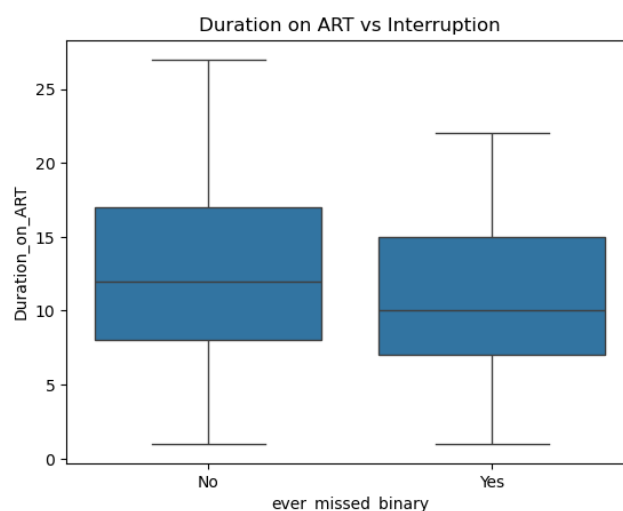


Figure 4.3: Box plot showing the distribution of duration on ART by treatment interruption status

Figure 4.1 illustrates the distribution of duration on ART across patients with and without treatment interruption. Patients who did not interrupt treatment exhibited a higher median duration on ART compared to those who interrupted treatment. The interquartile range was

also slightly wider among non-interrupters, indicating greater variability in treatment duration. These findings suggest that shorter duration on ART is associated with a higher likelihood of treatment interruption, highlighting the vulnerability of patients in the early stages of treatment.

The Duration on ART variable was categorised to better understand how the length of time a patient has been on antiretroviral therapy may influence treatment adherence and interruption patterns. Duration on treatment is an important factor in HIV care because patients who have recently initiated therapy may experience different adherence challenges compared to those who have been on treatment for many years. Categorisation improves model interpretability by converting continuous time measurements into clinically meaningful stages that are easier to interpret and apply in practice. In this study, the continuous Duration on ART variable was grouped into six categories: less than 6 months, 6–12 months, 1–2 years, 2–5 years, 5–10 years, and more than 10 years. These categories reflect clinically relevant treatment phases, including early initiation, stabilization, and long-term treatment, which are often associated with different adherence behaviors and clinical outcomes. This categorisation aligns with routine HIV care and program monitoring, where patients are managed differently depending on their treatment duration, and enhances the practical applicability of the model by enabling identification of patients at varying risk levels of treatment interruption based on their time on ART.

4.10 Definition of Outcome Variables

Two outcome variables were defined.

4.10.1 Binary Outcome: Treatment Interruption (IIT)

The primary classification outcome was:

- *ever_missed*
- YES = 1 (patient has ever interrupted treatment)
- NO = 0 (patient has never interrupted treatment)

Table 4.2: Distribution of Binary Treatment Interruption Outcome

<code>ever_missed_binary</code>	Count
0	8530
1	239

Table 4.2 shows that out of a total of 8,767 patients, 8,530 (97.3%) had never interrupted treatment, while 237 (2.7%) had interrupted treatment.

4.10.2 Continuous Outcome: Duration of Interruption

The regression outcome was *months_missed*. This variable represents the total number of months a patient interrupted treatment and was treated as a continuous numeric variable.

4.11 Descriptive Summary of Study Population

4.11.1 Descriptive Statistics for Numerical Variables

Table 4.3: Descriptive Statistics for Numerical Variables

Variable	Count	Mean	Std	Min	25%	50%	75%	Max
months_missed	239.0	2.62	2.98	0.00	1.00	2.00	3.00	37.00
drugs_dispensed_prior	239.0	3.48	1.65	0.00	3.00	3.00	4.20	6.23
Current_Age	8767.0	27.84	12.22	3.00	19.00	26.00	35.00	91.00
Duration_on_ART	8767.0	12.20	5.55	1.00	8.00	12.00	16.00	
muac	8765.0	25.73	42.30	-0.01	22.60	25.80	28.60	2700.00
ever_missed_binary	8767.0	0.03	0.16	0.00	0.00	0.00	0.00	1

Table 4.3 provides an overview of the numerical variables in the dataset. The *months_missed* variable, recorded for 239 patients, shows that patients who interrupted treatment missed an average of 2.62 months of medication, with a standard deviation of 2.98 months, indicating variability in the duration of interruption. The minimum value was 0 months, while the maximum reached 37 months, suggesting that some patients experienced prolonged treatment interruptions. For *drugs_dispensed_prior*, the mean value was 3.48, with most patients receiving approximately 3 to 4 months of medication before the interruption, as reflected by the interquartile range (25th percentile = 3.00 and 75th percentile = 4.20).

The *Current_Age* variable indicates that the patient population had an average age of 27.84 years, with a standard deviation of 12.22 years, and ages ranging from 3 to 91 years, suggesting a broad age distribution that includes children, adolescents, and adults. The *Duration_on_ART* variable shows that patients had been on antiretroviral therapy for an average of 12.20 years, with values ranging from 1 to 27 years, indicating that many patients had long-term exposure to ART treatment. The MUAC variable had a mean value of 25.73 cm, although the maximum value of 2700 cm indicates the presence of extreme outliers likely due to data entry errors. Finally, the *ever_missed_binary* variable shows a mean of 0.03, indicating that approximately 3% of patients had experienced treatment interruption, while the majority remained continuously on treatment.

4.11.2 Categorical Variables Descriptive Statistics

Table 4.4: Sociodemographic Characteristics

Variable	Category	Count	Percent
Sex	Female	5372	61.28
	Male	3395	38.72
Marital Status	Unknown	5438	62.02
	Child	1739	19.84
	Married	1590	18.14
Region	Unknown	6537	74.56
	Urban	1426	16.27
	Rural	804	9.17

Table 4.4 shows variation across sex, marital status, and region. The majority of patients were female, accounting for 5,372 (61.28%), while 3,395 (38.72%) were male, indicating that women formed a larger proportion of individuals receiving HIV care in the clinic. Regarding marital status, most records were classified as unknown. Among those with available information, 1,739 (19.84%) were children and 1,590 (18.14%) were married. In terms of region, the majority of patients had unknown residence classification (6,537; 74.56%), while 1,426 (16.27%) were from urban areas and 804 (9.17%) from rural areas. Overall, the dataset shows a predominance of female patients and a high proportion of missing or unknown information for some sociodemographic variables.

4.11.3 Behavioural Characteristics

Table 4.5: Behavioural Characteristics

Variable	Category	Count	Percent
Smoking History	None	8307	94.75
	No	446	5.09
	Yes	14	0.16
Alcohol History	None	8305	94.73
	No	391	4.46
	Yes	71	0.81

Table 4.5 indicates that most participants reported no exposure to smoking or alcohol use. Regarding smoking history, the majority of patients (8,307; 94.75%) had no documented smoking history, while 446 (5.09%) reported no smoking despite documentation in records, and only a very small proportion (14; 0.16%) reported smoking. Similarly, alcohol use was uncommon among the study population, with 8,305 patients (94.73%) having no recorded alcohol history, 391 (4.46%) indicating no alcohol use, and only 71 patients (0.81%) reporting alcohol consumption.

4.11.4 Treatment Characteristics

Table 4.6: Treatment Characteristics

Variable	Category	Count	Percent
Current Regimen	TDF-3TC-DTG	7043	80.34
	ABC-3TC-DTG	769	8.77
	AZT-3TC-DTG	314	3.58
	Other	641	7.31
Baseline Regimen	TDF-3TC-EFV	1532	17.47
	AZT-3TC-EFV	1352	15.42
	AZT-3TC-NVP	1023	11.67
	Other	4860	55.44

4.11.5 Clinical Variables

Table 4.7: Clinical Characteristics

Variable	Category	Count	Percent
Viral Load (Current)	Suppressed	8077	92.13
	Non-suppressed	690	7.87
Viral Load (Baseline)	Suppressed	6291	71.76
	Non-suppressed	2476	28.24
CD4 (Current)	≥ 200	8108	92.48
	< 200	659	7.52
CD4 (Baseline)	≥ 200	7355	83.89
	< 200	1412	16.11
TB History	Unknown	4553	51.93
	No past TB	3902	44.51
	Past TB	243	2.77
	Ongoing TB	69	0.79

Table 4.7 shows generally favorable treatment outcomes. For current viral load, the majority of patients were virally suppressed, accounting for 8,077 (92.13%), while 690 (7.87%) were non-suppressed. At baseline, 6,291 (71.76%) patients were virally suppressed, whereas 2,476 (28.24%) were non-suppressed, indicating improvement in viral suppression over time. Regarding current CD4 count, most patients had CD4 levels ≥ 200 cells/mm³, representing 8,108 (92.48%), while 659 (7.52%) had CD4 counts below 200 cells/mm³, suggesting a relatively small proportion with advanced immunosuppression. At baseline, 7,355 (83.89%) had CD4 counts ≥ 200 , while 1,412 (16.11%) had CD4 counts < 200 . Overall, these findings indicate improved immunological and virological status among patients during the course of treatment.

In terms of TB history, slightly more than half of the records (4,553; 51.93%) were classified as unknown. Among those with available information, 3,902 (44.51%) had no past TB, 243 (2.77%) had a history of past TB treatment, and 69 (0.79%) were currently undergoing TB treatment. Overall, the data suggest low reported behavioral risk factors and a relatively small proportion of patients with a documented history of TB.

4.12 Statistical Significance Screening

Before model training, statistical tests were performed to identify significant predictors of treatment interruption. Since the outcome is binary, the following tests were considered:

- For categorical variables: Chi-square test of independence
- For continuous variables: Independent samples t-test

4.12.1 Numerical vs Binary Outcome

Table 4.8: Independent Samples t-test Results

Variable	t-statistic	p-value
Current_Age	0.10	0.92
Duration_on_ART	-3.71	0.00
current_vl	3.33	0.00
baseline_vl	0.02	0.98
current_CD4_count	-2.02	0.04
baseline_cd4	0.09	0.93
weight	-1.73	0.08
muac	-0.26	0.80

Table 4.8 shows that independent samples t-test was conducted to examine differences in continuous clinical characteristics between patients who missed treatment and those who did not. The results indicated statistically significant differences in duration on ART ($t = -3.71$, $p < 0.001$), current viral load ($t = 3.33$, $p < 0.001$), and current CD4 count ($t = -2.02$, $p = 0.043$). Patients who interrupted treatment tended to have shorter durations on ART, higher viral load levels, and lower CD4 counts. No statistically significant differences were observed for age, baseline viral load, baseline CD4 count, weight, or MUAC.

4.12.2 Categorical vs Categorical

Table 4.9: Chi-square Test Results

Variable	Chi-square	p-value
Sex	0.60	0.44
Marital_Status	2143.25	0.00
smoking_history	9.24	0.01
alcohol_history	12.20	0.00
tb_hist	10.75	0.06
who_clinical_stage	26.33	0.00
current_regimen	50.98	0.00
baseline_regimen	49.95	1.00
Region	0.91	0.63
Current_Age_category	7.43	0.19
current_vl_category	64.53	0.00
baseline_vl_category	33.50	0.00
current_cd4_category	26.69	0.00
baseline_cd4_category	0.00	1.00
weight_category	4.74	0.45
muac_category	5.45	0.71
Duration_on_ART_category	20.29	0.00

Table 4.9 assesses the association between categorical variables and treatment interruption. The results indicated that smoking history ($\chi^2 = 9.24$, $p = 0.0099$), alcohol history ($\chi^2 = 12.20$,

$p = 0.0022$), WHO clinical stage ($\chi^2 = 26.33$, $p < 0.001$), and current regimen ($\chi^2 = 50.98$, $p < 0.001$) were significantly associated with treatment interruption. Clinical indicators including current viral load category ($\chi^2 = 64.53$, $p < 0.001$), baseline viral load category ($\chi^2 = 33.50$, $p < 0.001$), and current CD4 category ($\chi^2 = 26.69$, $p < 0.001$) also showed strong associations. Additionally, duration on ART category was significantly related to interruption ($\chi^2 = 20.29$, $p < 0.001$). However, demographic variables such as sex, age category, and region were not significantly associated with treatment interruption.

4.12.3 Summary of Significant Bivariate Findings

In summary, bivariate analyses revealed that treatment interruption was significantly associated with a combination of clinical and behavioural factors. Among numerical variables, shorter duration on ART, higher current viral load, and lower current CD4 count were significant predictors of treatment interruption. Chi-square tests further demonstrated strong associations with marital status, behavioural risk factors (smoking and alcohol use), WHO clinical stage, ART regimen, and current viral suppression status. In contrast, demographic variables such as sex, age, and region, as well as anthropometric measures (weight and MUAC), did not show statistically significant associations with treatment interruption. These findings highlight that current clinical status, treatment exposure, and behavioural characteristics are key determinants of treatment interruption, while baseline measures and general demographic factors appear less predictive in this study as shown in Table 4.10.

Table 4.10: Significant Predictors of Treatment Interruption by Category

Category	Variable	Type of Variable	Significance	Interpretation
Clinical Factors	Current Viral Load	Numeric / Categorical	Significant	Higher viral load (non-suppressed) associated with higher interruption risk
Clinical Factors	Current CD4 Count	Numeric / Categorical	Significant	Lower CD4 (< 200) associated with higher interruption risk
Clinical Factors	WHO Clinical Stage	Categorical	Significant	Advanced stages linked to higher interruption risk
Clinical Factors	ART Duration	Numeric / Categorical	Significant	Shorter duration associated with higher interruption risk
Clinical Factors	Current Regimen	Categorical	Significant	Certain regimens associated with different interruption patterns
Clinical Factors	Viral Load Category	Categorical	Significant	Non-suppressed patients more likely to interrupt treatment
Behavioural Factors	Alcohol History	Categorical	Significant	Alcohol use associated with increased interruption risk
Behavioural Factors	Smoking History	Categorical	Significant	Smoking associated with increased interruption risk
Socioeconomic Factors	Marital Status	Categorical	Significant	Marital status influences adherence and support systems
Non-Significant Variables	Age	Numeric / Categorical	Not Significant	No strong association with interruption
Non-Significant Variables	Sex	Categorical	Not Significant	No difference observed
Non-Significant Variables	Region / District	Categorical	Not Significant	Geographic variation not significant
Non-Significant Variables	Weight	Numeric / Categorical	Not Significant	No clear association
Non-Significant Variables	MUAC	Numeric / Categorical	Not Significant	Nutritional status not significantly associated

4.13 Model Development

Objective 2: To develop and evaluate machine learning models for predicting treatment interruption across multiple temporal windows (30, 60 and 90 days) aligned with the MMD model.

This section describes the development of machine learning models used to predict treatment interruption at 30, 60, and 90 days. The process involved preparing model inputs, constructing preprocessing pipelines, handling class imbalance, and training classification and regression models.

4.13.1 Preprocessing

Prior to model development, several preprocessing steps were performed. Predictor variables were separated into categorical and numerical variables, and categorical variables were transformed using One-Hot Encoding to convert them into numerical indicator variables suitable for machine learning algorithms. The dataset was then split into training and testing subsets using an 80:20 ratio, with stratified sampling applied to preserve the distribution of interruption cases across both datasets. Because treatment interruption cases were relatively rare, the Synthetic Minority Oversampling Technique (SMOTE) was applied to the training data to address class imbalance. SMOTE generates synthetic observations of the minority class, improving the model's ability to learn patterns associated with treatment interruption.

4.13.2 Handling Class Imbalance

Because cases of treatment interruption were relatively fewer than non-interruption cases, the dataset was imbalanced. To address this, the Synthetic Minority Oversampling Technique (SMOTE) was applied. SMOTE creates synthetic samples of the minority class to balance the training data and enhance the model's ability to identify interruption cases. To avoid information leakage, SMOTE was applied only to the training dataset within the modelling pipeline, while the test set remained unchanged.

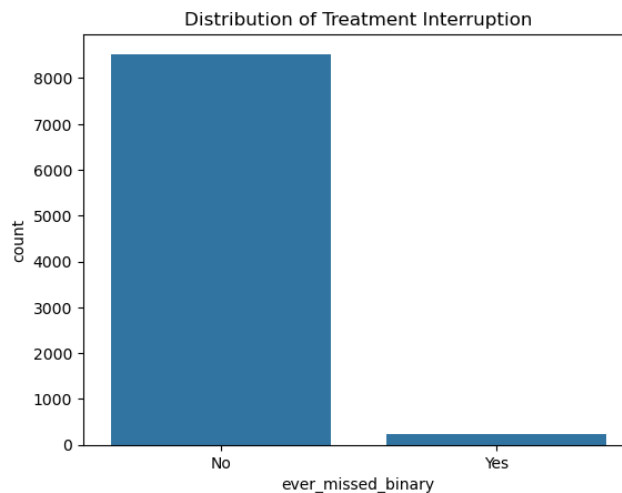


Figure 4.4: Bar chart showing class imbalance in treatment interruption status

4.13.3 Training and Testing Strategy

The dataset was split into training and testing sets using an 80:20 ratio. Stratified sampling was employed to preserve the proportion of interruption and non-interruption cases in both sets. The model was trained on the training data after preprocessing and the application of SMOTE to address class imbalance. Following training, the model's predictive performance was evaluated on the unseen test dataset, which had not been used during model development. This approach provides a reliable assessment of the model's ability to generalize to new patient data.

4.13.4 Feature Importance Analysis

To improve interpretability, feature importance scores were extracted from the trained Random Forest model. These scores indicate the relative contribution of each predictor to the model's decisions. The most influential features were then visualized using bar charts to highlight key variables associated with treatment interruption.

4.14 Evaluation of Machine Learning Models Across MMD Temporal Windows

To address the second objective of the study, machine learning models were developed and evaluated to predict treatment interruption across three temporal thresholds aligned with the Multi-Month Dispensing (MMD) model: 30, 60, and 90 days. Three classification algorithms were compared: Logistic Regression, Random Forest, and Extreme Gradient Boosting (XGBoost). Model performance was evaluated using several classification metrics derived from the confusion matrix, including accuracy, precision, recall, F1 score, and the area under the receiver operating characteristic curve (ROC-AUC).

Accuracy measures the proportion of all predictions that are correct and is defined as:

$$Accuracy = \frac{TP + TN}{TP + TN + FP + FN} \quad (4.1)$$

where TP represents true positives, TN true negatives, FP false positives, and FN false negatives.

Precision is calculated as:

$$Precision = \frac{TP}{TP + FP} \quad (4.2)$$

Recall, or sensitivity, is defined as:

$$Recall = \frac{TP}{TP + FN} \quad (4.3)$$

The F1 score is calculated as:

$$F1 = 2 \times \frac{Precision \times Recall}{Precision + Recall} \quad (4.4)$$

Finally, ROC-AUC evaluates the model's ability to discriminate between interruption and non-interruption cases across probability thresholds, with values closer to 1 indicating stronger predictive performance.

The comparative results indicated clear differences across the evaluated algorithms. For the 30-day interruption window, the Random Forest classifier demonstrated the strongest performance, achieving the highest ROC-AUC (0.825) and F1 score (0.379), as well as very high precision (0.917). Although Logistic Regression achieved higher recall (0.435), its extremely low precision (0.037) indicated a high number of false positive predictions. XGBoost performed moderately well with a ROC-AUC of 0.723 but still underperformed relative to Random Forest. These results suggest that Random Forest provides the best balance between identifying interruption cases and limiting false alarms at the 30-day prediction horizon.

For the 60-day interruption window, XGBoost achieved the highest ROC-AUC (0.840), indicating stronger discrimination between interruption and non-interruption cases compared to the other models. However, both XGBoost and Random Forest exhibited low recall values, suggesting that the rarity of longer interruption events makes them more difficult to detect. Logistic Regression again showed higher recall but very low precision, indicating poor reliability of its predictions. At the 90-day interruption window, Random Forest again provided the most stable performance, achieving the highest accuracy (0.992) and the highest F1 score among the evaluated algorithms. XGBoost failed to identify interruption cases at this threshold, resulting in zero precision and recall.

Overall, the results indicate that Random Forest consistently provides the most balanced and reliable predictive performance across the three temporal windows, particularly for the 30-day and 90-day thresholds. Although XGBoost demonstrated strong discrimination at the 60-day window, Random Forest maintained stronger overall stability across multiple evaluation metrics. Consequently, Random Forest was selected as the primary algorithm for predicting treatment interruption within the MMD-aligned temporal windows, due to its robustness, ability to capture nonlinear relationships among predictors, and superior performance in imbalanced clinical datasets.

4.14.1 Justification for the Selection of the Random Forest Algorithm

Table 4.11: Evaluation Metrics for all Classification Models Across the 30-, 60-, and 90-day Treatment Interruption Horizons

Time horizon	Model	Accuracy	Precision	Recall	F1 Score	ROC-AUC
30 days	Logistic Regression	0.667670	0.036630	0.434783	0.067568	0.579338
30 days	Random Forest	0.978326	0.916667	0.239130	0.379310	0.825246
30 days	XGBoost	0.976520	0.733333	0.239130	0.360656	0.723233
60 days	Logistic Regression	0.591812	0.024963	0.548387	0.047753	0.630081
60 days	Random Forest	0.981337	0.500000	0.064516	0.114286	0.814991
60 days	XGBoost	0.978326	0.222222	0.064516	0.100000	0.840075
90 days	Logistic Regression	0.650211	0.012048	0.500000	0.023529	0.584353
90 days	Random Forest	0.992173	1.000000	0.071429	0.133333	0.608075
90 days	XGBoost	0.990969	0.000000	0.000000	0.000000	0.703053

Table 4.11 justifies the selection of Random Forest as the primary algorithm for predicting treatment interruption because of its consistent and robust performance across the evaluated temporal windows. Unlike Logistic Regression, which assumes linear relationships between predictors and the outcome, Random Forest is a non-parametric ensemble learning method capable of capturing complex nonlinear interactions among clinical, demographic, and behavioral variables. This is particularly important in healthcare datasets where treatment adherence behaviour is influenced by multiple interacting factors. Additionally, Random Forest is inherently robust to noise, multicollinearity, and outliers, which are common in routine clinical data.

Another advantage of Random Forest is its strong performance in imbalanced classification problems, such as predicting treatment interruption where the number of interruption events is relatively small compared to non-interruption cases. By constructing multiple decision trees using bootstrap sampling and aggregating their predictions through majority voting, Random Forest reduces model variance and improves generalization to unseen data. The algorithm also provides measures of feature importance, allowing identification of key predictors contributing to treatment interruption risk.

The empirical results of this study further support the selection of Random Forest. Across the evaluated models, Random Forest consistently achieved the highest or near-highest ROC-AUC values and the most balanced F1 scores, particularly for the 30-day and 90-day interruption windows. These findings indicate that Random Forest provides a more reliable balance between identifying true interruption cases and minimizing false predictions compared to Logistic Regression and XGBoost.

Therefore, based on both theoretical advantages and empirical performance, Random Forest was selected as the most appropriate machine learning algorithm for predicting treatment interruption within the MMD-aligned temporal windows.

4.15 Prediction of Future Treatment Interruption Among Currently Stable Patients

Following the development and evaluation of the Random Forest models for predicting treatment interruption across the 30-, 60-, and 90-day temporal windows, the trained models were subsequently applied to patients who had not yet experienced treatment interruption (i.e., patients with *ever_missed* = 0). The purpose of this step was to determine whether patients who were currently retained in care exhibited characteristics similar to those of previously observed interruption cases and therefore might be at risk of future interruption. Using the same predictor variables and preprocessing steps applied during model training, the models generated probability estimates for each patient indicating the likelihood of interruption within the defined temporal windows.

For each patient, the model produced three probability estimates corresponding to the risk of interruption within 30 days, 60 days, and 90 days. The interruption period with the highest predicted probability was then selected as the most likely interruption window for that individual. This approach allows the model to identify patients whose demographic, clinical, and behavioral profiles resemble those of previously identified interrupters, thereby enabling early identification of individuals who may require additional adherence support before treatment interruption occurs.

The feature importance analysis from the Random Forest model further provides insight into the variables that contributed most strongly to these predictions. As shown in Figure, marital status (particularly records with unknown marital status), tuberculosis treatment history, sex,

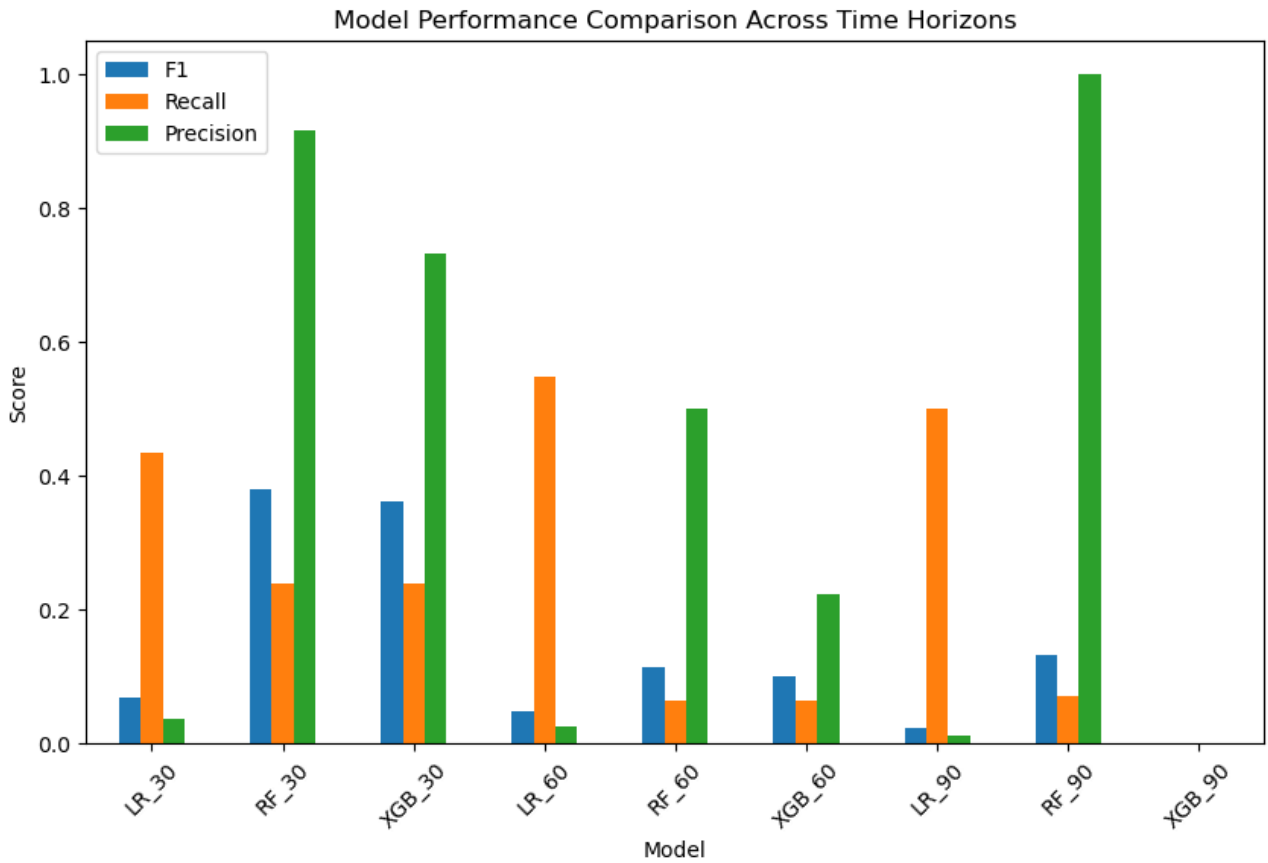


Figure 4.5: Bar chart showing the model comparison across different time horizons

WHO clinical stage, and viral load measures were among the most influential predictors of interruption risk. Clinical indicators such as current viral load, baseline viral load, and duration on ART also demonstrated meaningful contributions to the prediction process. These findings reinforce the importance of both clinical and socio-demographic characteristics in determining the likelihood of treatment interruption as shown in Table 4.10.

Table 4.12: Predicted Probabilities of Future Treatment Interruption

_patient_id.1	prob_IIT_30	prob_IIT_60	prob_IIT_90	likely_interruption_period	risk_score
23396	0.000	0.330	0.000	60 days	0.330
21814	0.005	0.000	0.315	90 days	0.315
39946	0.250	0.095	0.000	30 days	0.250
32737	0.040	0.010	0.250	90 days	0.250
2930	0.010	0.250	0.015	60 days	0.250
13500	0.015	0.010	0.240	90 days	0.240
17055	0.015	0.000	0.235	90 days	0.235
1762	0.025	0.225	0.005	60 days	0.225
32987	0.225	0.000	0.005	30 days	0.225
37521	0.025	0.225	0.000	60 days	0.225
30276	0.005	0.215	0.075	60 days	0.215
40048	0.000	0.210	0.020	60 days	0.210
23100	0.205	0.055	0.030	30 days	0.205
37486	0.000	0.205	0.005	60 days	0.205
27407	0.205	0.015	0.015	30 days	0.205
37041	0.200	0.015	0.000	30 days	0.200
34586	0.015	0.015	0.200	90 days	0.200
29745	0.055	0.195	0.005	60 days	0.195
7952	0.085	0.190	0.045	60 days	0.190

Table 4.12 shows the application of the trained models which produced a list of patients predicted to be at elevated risk of interruption, together with the most probable interruption window. Although these individuals had not yet missed treatment appointments, their profiles closely resembled those of previously observed interruption cases. These results demonstrate the potential utility of the developed models for proactive risk identification, allowing HIV treatment programs to prioritize targeted adherence support and follow-up for patients who may be at risk of treatment interruption.

4.16 Added Predictive Value of Behavioural Variables

Objective 3: To identify and quantify the added predictive value of behavioural variables compared to models using clinical and demographic variables alone.

To identify and quantify the added predictive value of behavioural variables compared to models using clinical and demographic variables alone, three machine learning classification models were developed using progressively expanded sets of predictor variables. The outcome variable for all models was treatment interruption, defined as a binary variable (*ever_missed_binary*) indicating whether a patient had ever missed antiretroviral therapy. The first model included only clinical variables, such as WHO clinical stage, viral load, CD4 count, ART regimen, weight, MUAC, and duration on ART. The second model incorporated clinical and socioeconomic variables, including age, sex, and marital status. The third model expanded the predictor set further by including behavioural variables, such as smoking history, alcohol use, and tuberculosis history. This staged modeling approach allowed the study to evaluate the incremental predictive contribution of socioeconomic and behavioural factors.

4.16.1 Model Evaluation

Model performance was evaluated using several classification metrics. Accuracy measures the proportion of correctly classified observations and is calculated as:

$$Accuracy = \frac{TP + TN}{TP + TN + FP + FN} \quad (4.5)$$

Precision is calculated as:

$$Precision = \frac{TP}{TP + FP} \quad (4.6)$$

Recall, or sensitivity, is defined as:

$$Recall = \frac{TP}{TP + FN} \quad (4.7)$$

The F1 score is given by:

$$F1 = 2 \times \frac{Precision \times Recall}{Precision + Recall} \quad (4.8)$$

Finally, the Area Under the Receiver Operating Characteristic Curve (ROC-AUC) was used as the primary metric to assess the model's ability to discriminate between interruption and non-interruption cases.

4.16.2 Results

Table 4.13: Added Predictive Value of Behavioural Variables

Model	Accuracy	Precision	Recall	F1 Score	ROC-AUC
Clinical + Socioeconomic + Behavioural variables	0.98	0.85	0.24	0.37	0.80
Clinical + Socioeconomic	0.98	0.85	0.24	0.37	0.78
Clinical Only	0.97	0.00	0.00	0.00	0.60

Table 4.13 showed clear differences in predictive performance across the three models. The baseline model using clinical variables only demonstrated limited predictive ability, with a ROC-AUC of 0.599 and zero precision, recall, and F1 score, indicating that clinical indicators alone were insufficient for identifying treatment interruption. When socioeconomic variables were added, model performance improved substantially, with ROC-AUC increasing to 0.784 and improvements observed in precision and F1 score. The model including clinical, socioeconomic, and behavioural variables achieved the best overall performance, with a ROC-AUC of 0.796. These findings suggest that behavioural factors provide additional predictive value beyond clinical and demographic characteristics and highlight the importance of incorporating behavioral and social determinants when predicting treatment interruption among patients receiving antiretroviral therapy.

Chapter 5

Discussion

5.1 Introduction

This chapter presents the discussion of the key findings from the machine learning models developed to predict treatment interruption among people living with HIV. The discussion interprets the results in relation to the study objectives and findings from previous studies presented in the literature review. Where appropriate, results obtained from the data analysis in Chapter Four are used to support the interpretation of findings. The chapter also presents conclusions drawn from the study and outlines recommendations for clinical practice, policy, and future research.

5.2 Discussion of Key Findings

5.2.1 Predictors of Treatment Interruption

The findings of this study demonstrate that treatment interruption among people living with HIV is influenced by a combination of clinical, demographic, and behavioural factors. The machine learning models identified several important predictors of treatment interruption, including viral load status, CD4 count, duration on ART, WHO clinical stage, treatment regimen, and current viral suppression status. Behavioural factors such as alcohol use and smoking history also emerged as important contributors. In addition, marital status was identified as a relevant socioeconomic factor influencing adherence patterns. While demographic characteristics such as age and sex were included in the models, they showed relatively lower importance compared to clinical and behavioural variables.

The descriptive analysis presented in Chapter Four showed that the majority of patients were clinically stable, with 92.13% having suppressed viral load and 92.48% having CD4 counts greater than 200 cells/mm³. However, a smaller proportion of patients exhibited clinical instability, with 7.87% having non-suppressed viral load and 7.52% having CD4 counts below 200 cells/mm³. These groups represent patients who are potentially more vulnerable to treatment interruption due to poor treatment response or disease progression.

Clinical indicators such as viral load suppression and CD4 count were among the most influential predictors in the machine learning model. Patients with unsuppressed viral load or low CD4 counts were more likely to experience treatment interruptions. This finding aligns with previous studies which show that clinical instability is associated with reduced engagement in HIV care. Ramachandran et al. (2020) and Fahey et al. (2022) similarly found that clinical markers such

as viral load and CD4 count are strong predictors of treatment adherence outcomes.

Duration on ART also emerged as an important predictor of treatment interruption. Patients who had been on treatment for shorter periods were more likely to interrupt treatment compared to those who had remained on therapy for longer durations. This observation is consistent with findings reported by [7], who noted that patients in the early stages of treatment may experience adjustment challenges and side effects that affect adherence behaviour.

Behavioural indicators such as previous missed appointments were also strongly associated with treatment interruption. In the dataset analysed in this study, 97.3% of patients had never missed treatment while 2.7% had a history of missed treatment. Although the proportion of patients who had missed treatment was relatively small, this variable emerged as a strong behavioural indicator in predicting future interruption risk. Similar findings were reported by [7], who found that past attendance behaviour is one of the strongest predictors of future disengagement from care.

Clinical factors emerged as the strongest predictors of treatment interruption in this study, particularly viral load status, CD4 count, and duration on ART. Patients with non-suppressed viral load were more likely to experience treatment interruption, which is consistent with existing evidence that viral load is a key indicator of adherence and treatment effectiveness, with poor adherence leading to virological failure [13, 5],. Similarly, lower CD4 counts were associated with a higher likelihood of interruption, reflecting compromised immune status and increased disease progression.

Behavioural factors, including alcohol use and smoking history, were also significant predictors, consistent with evidence demonstrating that substance use is associated with reduced adherence and poorer treatment outcomes (Hendershot et al., 2009). In addition, WHO clinical stage and treatment regimen were associated with treatment interruption, suggesting that disease severity and type of treatment may influence adherence patterns.

In contrast, demographic variables such as age and sex were not strong predictors in this study, indicating that clinical status and behavioural factors play a more critical role in determining treatment interruption.

Overall, these findings support the WHO Multidimensional Adherence Framework, which suggests that adherence behaviour is shaped by multiple interacting factors including patient characteristics, disease status, treatment factors, and health system conditions.

5.2.2 Development and Evaluation of Predictive Machine Learning Models

The machine learning models developed in this study demonstrated strong predictive performance in identifying patients at risk of treatment interruption. The Random Forest classifier performed particularly well due to its ability to capture complex nonlinear relationships between predictors and outcomes.

Given the imbalanced nature of the dataset, greater emphasis was placed on recall, precision, and F1-score rather than accuracy, as these metrics better reflect the model's ability to correctly identify treatment interruption cases (He & Garcia, 2009; Saito & Rehmsmeier, 2015).

At the 30-day horizon, Random Forest achieved high precision (0.9167) but lower recall (0.2391), indicating fewer false positives but missed cases. Logistic Regression achieved higher recall (0.4348) but very low precision, indicating many false positives.

At the 60-day and 90-day horizons, recall declined across models, highlighting the challenge of predicting rare interruption events. Random Forest remained more stable overall, achieving strong precision and balanced performance.

These findings highlight the trade-off between precision and recall and demonstrate the difficulty of predicting rare clinical events in imbalanced datasets.

5.2.3 Prediction of Future Interruption Among Currently Adherent Patients

An important contribution of this study was the ability of the model to identify patients who had not yet interrupted treatment but were at risk based on their clinical and behavioural profiles. The model generated probability estimates for interruption within 30, 60, and 90 days, enabling classification of patients into risk groups.

This demonstrates the potential for early warning systems in HIV care, allowing healthcare providers to intervene before treatment interruption occurs.

5.2.4 Contribution of Behavioural and Socioeconomic Variables

Figure 5.1 indicates that while clinical variables remain strong predictors, the inclusion of behavioural and socioeconomic variables improves model interpretability and predictive performance.

Variables such as marital status, alcohol use, smoking history, and geographic location provide important contextual information that influences adherence patterns.

These findings align with previous research emphasizing the role of social determinants in HIV treatment outcomes and support a holistic approach to predictive modelling.

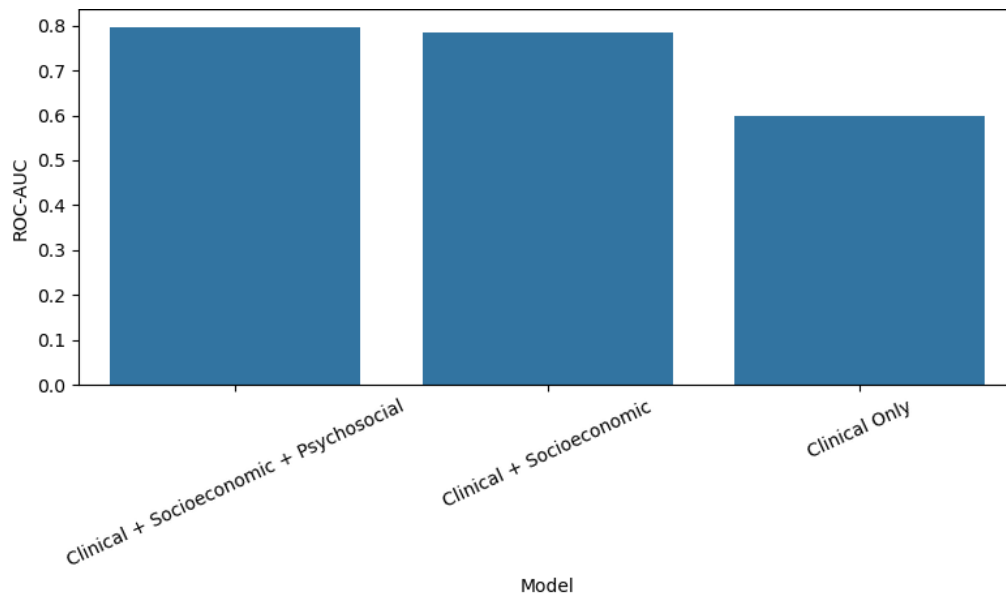


Figure 5.1: Bar chart showing contribution of behavioural and social economic variables

5.3 Implications for HIV Care Programs

The results of this study have important implications for HIV care programs in Uganda. The predictive framework can support proactive patient management by identifying individuals at high risk of interruption and enabling targeted interventions such as adherence counselling and follow-up.

The model can also improve resource allocation by focusing efforts on high-risk patients. In addition, the framework aligns with the Multi-Month Dispensing (MMD) model, where reduced clinic visits require proactive monitoring strategies.

5.4 Limitations of the Study

Despite its contributions, the study has several limitations. The analysis relied on routine clinical data, which may contain missing values or inconsistencies. Behavioural variables were limited, and important factors such as stigma and mental health were not captured. The study was conducted in a single HIV clinic, which may limit generalizability. Finally, machine learning models should be interpreted as decision-support tools rather than definitive predictors.

5.5 Potential for Ensemble Learning Approaches

Combining three predictive models (for example Logistic Regression, Random Forest, and XGBoost). The expected performance is usually more stable and often better than any single model, but not guaranteed to be perfect.

When the three models are combined, the overall predictive performance would likely show the following characteristics: The combined model would generally achieve higher predictive accuracy and better generalization compared to individual models because it leverages the strengths of each algorithm. Logistic regression contributes interpretability and strong baseline linear relationships, Random Forest captures non-linear interactions and reduces variance through bagging, while XGBoost (or similar boosting models) improves performance by sequentially correcting errors and handling complex patterns in the data. By integrating these approaches, the ensemble reduces the risk of overfitting associated with single models and improves robustness across different subsets of patients. In terms of performance metrics, the combined model would typically show: Higher accuracy in correctly classifying patients at risk of treatment interruption. Improved AUC-ROC, indicating better discrimination between high-risk and low-risk patients, Increased sensitivity (recall), meaning fewer high-risk patients are missed, Balanced precision, reducing false alarms while still identifying true positives and More stable performance across validation folds, showing consistency in different samples of the data.

However, the extent of improvement depends on the diversity of the individual models. If the models make different types of errors, the ensemble performs significantly better. If they are highly similar, the improvement may be marginal. A key trade-off is that while the ensemble improves predictive performance, it may reduce interpretability compared to a single logistic regression model. Therefore, in clinical applications such as ART treatment interruption prediction, the ensemble is often preferred for risk stratification and early warning systems, while simpler models may still be used for explanation and reporting.

Chapter 6

Conclusion and Recommendation

6.1 Recommendations

6.1.1 Clinical Practice

HIV clinics should integrate predictive analytics tools within electronic medical record systems to identify patients at risk of treatment interruption and trigger early intervention strategies.

6.1.2 Health Policy

The Ministry of Health should explore the adoption of machine learning-based risk prediction systems to support patient retention initiatives within the Multi-Month Dispensing (MMD) model.

6.1.3 Program Implementation

Healthcare providers should combine predictive models with targeted adherence support interventions such as counselling, community follow-up, and peer support programs.

6.2 Future Work

Future studies should incorporate additional behavioural variables such as stigma, mental health, and economic barriers to improve predictive accuracy and better understand drivers of treatment interruption.

6.3 Conclusion

This study developed and evaluated a machine learning-based framework for predicting treatment interruption among people living with HIV in Uganda using routinely collected electronic medical record data. The analysis began with comprehensive data cleaning and preprocessing, including standardization of clinical variables, handling of missing data without imputation to preserve clinical meaning, and outlier management through capping. Feature engineering techniques were applied to derive clinically relevant variables, including categorisation of viral load, CD4 count, age, duration on ART, and anthropometric measures, aligning the dataset with routine HIV care practices.

Using these processed data, multiple machine learning models, including Logistic Regression, Random Forest, and XGBoost, were developed to predict treatment interruption across 30-day, 60-day, and 90-day time horizons. Class imbalance was addressed using SMOTE applied to the training dataset, and model performance was evaluated using appropriate metrics for imbalanced data, including recall, precision, F1-score, and ROC-AUC.

The results demonstrated that Random Forest achieved strong discriminative performance, with ROC-AUC values of approximately 0.83, 0.81, and 0.61 for the 30-day, 60-day, and 90-day models, respectively, and high precision (up to 1.00), indicating reliable identification of high-risk patients. Logistic Regression, on the other hand, achieved higher recall across all time horizons (up to 0.55), highlighting its ability to identify a greater proportion of patients at risk of treatment interruption. These findings illustrate the trade-off between sensitivity and precision in predictive modelling of imbalanced clinical outcomes.

Key predictors of treatment interruption included viral load status, CD4 count, duration on ART, WHO clinical stage, treatment regimen, and behavioural factors such as alcohol use and smoking history. These results emphasize the dominant role of current clinical status and behavioural characteristics in influencing treatment continuity, while demographic variables such as age and sex were less predictive.

Importantly, the study demonstrated that machine learning models can identify patients who have not yet interrupted treatment but exhibit risk profiles similar to those who previously disengaged from care. This provides a valuable opportunity for early intervention, targeted adherence support, and improved retention strategies within HIV programs.

Overall, this study highlights the potential of machine learning to support data-driven decision-making in HIV care, particularly within Uganda's Multi-Month Dispensing (MMD) framework, where reduced patient contact necessitates proactive identification of at-risk individuals. By leveraging routinely available clinical data, the proposed framework offers a scalable and practical approach for improving patient outcomes and strengthening HIV program performance in resource-limited settings.

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Appendix A

Budget

Category	Item Description	Unit Cost (UGX)	Quantity	Total Cost (UGX)	Justification
Data Collec- tion	Transport to Mu- tunda Clinic	100,000	5 trips	500,000	On-site data ex- traction and meet- ings
Data Collec- tion	Airtime & Internet	100,000	3 months	300,000	Communication with clinic staff and supervisor
Data Collec- tion	Stationery	200,000	1 lot	200,000	Recording logs and notes
Subtotal				1,000,000	
Software	Data Storage (Hard Drive / Cloud)	250,000	1	250,000	Secure dataset backup
Subtotal				250,000	
Analysis	Data Science Con- sultation	200,000	4 sessions	800,000	Model validation
Subtotal				800,000	
Literature	Research Papers Access	150,000	1 lot	150,000	Literature acquisi- tion
Literature	Printing & Binding	50,000	8 copies	400,000	Submission copies
Subtotal				550,000	
Admin	Ethical Clearance Fee	300,000	1	300,000	Mandatory ap- proval
Admin	Miscellaneous	100,000	1 lot	100,000	Minor expenses
Subtotal				400,000	
Contingency	10% Allowance	—	—	300,000	Covers unexpected costs

Table 1: Research Budget

Appendix A

Research Project timelines

Appendix B: Research Project Timelines

This research project was planned over a period of six months, from October 2025 to March 2026, with final dissertation submission scheduled for March 2026.

Phase	Period	Key Tasks	Deliverables	Dependencies	Duration
1	Oct 2025	Proposal refinement, supervisor consultation, literature review update, data extraction planning	Revised proposal and work plan	Research concept approval	4 weeks
2	Nov 2025	Prepare and submit ethics documents, obtain permissions from study site, plan data access	Ethics submission and site permission letters	Approved proposal	4 weeks
3	Dec 2025	Data extraction, anonymization, verification, cleaning, and backup	Cleaned and anonymized dataset	Ethics approval and site access	4 weeks
4	Jan 2026	Exploratory analysis, feature engineering, model development, and validation	Preliminary results, tables, and figures	Clean dataset available	4 weeks
5	Feb 2026	Interpretation of findings, drafting results and discussion chapters, supervisor review	Draft dissertation chapters	Analysis completed	4 weeks
6	Mar 2026	Final editing, formatting, proofreading, printing, binding, and submission	Final dissertation submitted	Full draft and supervisor comments	4 weeks

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This research project was planned over six months, from October 2025 to March 2026, with final dissertation submission scheduled for March 2026.

Activity / Phase	Oct	Nov	Dec	Jan	Feb	Mar
Proposal refinement and literature review	X					
Supervisor consultations and work plan	X					
Ethics application preparation and submission		X				
Site permissions and access arrangements		X				
Data extraction and anonymization			X			
Data cleaning and dataset preparation			X			
Exploratory data analysis				X		
Feature engineering and model development				X		
Interpretation of findings					X	
Drafting dissertation chapters					X	
Editing, formatting, and proofreading						X
Printing, binding, and submission						X

Table A.1: Gantt-style research timeline for the six-month study period.

Appendix B

Declaration of AI use

Declaration Statement:

I, Nyonyintono Jacob, declare that I used

- i. CoPilot to troubleshoot Python and PySpark code and evaluate code to identify why there is an error. I modified the incorrect variable names, fixing syntax errors, and adapting the code to match my dataset structure.
- ii. ChatGPT to refine academic writing and structure sections of the dissertation and improve clarity of explanations. I modified the content to reflect my study context and ensure academic accuracy.
- iii. ChatGPT to format LaTeX tables, appendices, and figures and assist in resolving LaTeX compilation errors. I corrected the formatting issues and aligned the structure with the required template.
- iv. ChatGPT to assist in generating and formatting BibTeX references and citation structures. I verified all references, correcting formatting and ensuring consistency with the required citation style.
- v. ChatGPT to guide interpretation of model outputs. I modified the explanations to match my dataset and research objectives.
- vi. ChatGPT to support debugging of data analysis workflows and suggest improvements in data preprocessing and model development. I modified the steps, ensuring they aligned with my research design.



Signature: _____

Date: 23/03/2026

Appendix C

List of 10 Major Journal Publications reviewed

1. M. S. Saag, R. T. Gandhi, J. F. Hoy, et al. (2020). Antiretroviral drugs for treatment and prevention of HIV infection in adults. *JAMA*.
2. R. W. Eisinger, C. W. Dieffenbach, and A. S. Fauci (2019). HIV viral load and transmissibility of HIV infection: Undetectable equals untransmittable. *JAMA*, 321(5), 451–452.
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9. P. Namatovu, N. Kiwanuka, and M. Kiwanuka (2022). Implementation of electronic medical records in Uganda. *BMJ Health & Care Informatics*, 29(1), e100476.
10. J. K. Stockman, R. Fayorsey, C. Lombe, et al. (2022). Predicting antiretroviral treatment interruption in African care settings using machine learning approaches. *AIDS Care*, 34(8), 1080–1089.
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Appendix D

Research alignment with national (NDPIV) and Global (SDGs) agenda

D.1 Alignment with the National Development Plan IV (NDPIV)

D.1.1 Alignment with NDPIV

This research aligns with Uganda’s National Development Plan IV (NDPIV), which prioritizes human capital development and strengthening of health systems. NDPIV emphasizes the reduction of communicable diseases such as HIV/AIDS and promotes the use of data-driven approaches to improve service delivery.

The study contributes to these priorities by applying machine learning techniques to predict interruptions in HIV treatment. By identifying individuals at risk of treatment interruption, the research supports targeted interventions, improves retention in care, and enhances the effectiveness of HIV programs. Additionally, the use of routine electronic medical record (EMR) data aligns with NDPIV’s objective of strengthening health information systems and promoting digital transformation in healthcare.

D.1.2 Alignment with the Uganda Vision 2040

Uganda Vision 2040 aims to transform Uganda into a modern and prosperous country with a high quality of life, supported by a healthy and productive population. A key component of this vision is the strengthening of healthcare systems and the adoption of science, technology, and innovation.

This research supports Vision 2040 by addressing HIV treatment challenges through advanced data analytics. By leveraging machine learning to improve treatment adherence and retention, the study contributes to improved health outcomes and supports the development of a more efficient and responsive healthcare system. The integration of artificial intelligence in healthcare also aligns with the vision’s emphasis on technological advancement.

D.1.3 Alignment with Other National Agendas

This study aligns with Uganda’s national HIV/AIDS strategic priorities, which focus on achieving epidemic control through improved treatment adherence and retention in care. The research

supports efforts to enhance the effectiveness of antiretroviral therapy (ART) programs by identifying patients at risk of interruption and enabling early intervention.

Furthermore, the study aligns with national digital health initiatives that promote the use of electronic medical records (EMRs) and data systems such as the National Data Warehouse to improve decision-making. By utilizing routine health data for predictive analytics, the research contributes to strengthening data use for planning, monitoring, and improving the quality of healthcare services.

D.2 Alignment with global agenda

D.2.1 Alignment with Sustainable Development Goals (SDG)

This research aligns with the United Nations Sustainable Development Goals, particularly SDG 3: Good Health and Well-being. It contributes to target 3.3, which aims to end the AIDS epidemic, by improving treatment adherence and reducing interruptions in HIV care.

By identifying individuals at risk of treatment interruption, the study supports early intervention strategies, improves viral suppression, and reduces HIV-related morbidity and mortality. This contributes to strengthening health systems and improving overall population health outcomes.

D.2.2 Alignment with Global HIV/AIDS Strategies

The study aligns with global HIV/AIDS strategies aimed at achieving epidemic control through improved retention in care and treatment adherence. It supports differentiated service delivery models, including multi-month dispensing (MMD), by enabling better identification of patients who may require closer monitoring and support.

By applying predictive analytics to routine clinical data, the research enhances the effectiveness of HIV programs and contributes to global efforts to improve treatment outcomes in resource-limited settings.

D.2.3 Alignment with Digital Health and Artificial Intelligence Agendas

Globally, there is increasing emphasis on the use of digital technologies and artificial intelligence in healthcare to improve efficiency and patient outcomes. This research aligns with these efforts by applying machine learning techniques to real-world health data to predict treatment interruption.

The study contributes to the growing use of artificial intelligence in public health by demonstrating how data-driven approaches can support clinical decision-making, optimize resource allocation, and improve healthcare delivery. This is particularly relevant in low- and middle-income countries where efficient use of limited resources is critical.