African Journal of Biology and Medical Research
ISSN: 2689-534X
Volume 9, Issue 2, 2026 (pp. 1-16)
www.abjournals.org

STABILITY AND TRANSFORMATION PREDICTION OF HIV VIRAL LOAD USING THE APPLICATION OF MACHINE LEARNING AND PRINCIPAL COMPONENT ALGORITHMS

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Article DOI: 10.52589/AJBMR-YWFMQGV9
DOI URL: https://doi.org/10.52589/AJBMR-YWFMQGV9

Cite this article:

Kabiru Bala, Ilker Etikan, Ismail Mahmoud, Isa Abba Sani, Abdullahi Garba Usman (2026), Stability and Transformation Prediction of HIV Viral Load Using the Application of Machine Learning and Principal Component Algorithms. African Journal of Biology and Medical Research 9(2), 1-16. DOI: 10.52589/AJBMR-YWFMQGV9

Manuscript History

Received: 3 Apr 2026

Accepted: 6 May 2026

Published: 13 May 2026

ABSTRACT: *The current antiretroviral therapy (ART) medication gives hope to people living with human immunodeficiency virus (HIV) and those with acquired immunodeficiency syndrome (AIDS). This great development contributes to and improves the lives of HIV-treated patients. Lacking education and awareness among pupils in Nigeria and Africa about HIV is the reason we are suffering from an increasing number of new cases of HIV/AIDS. This study judges the ability of Machine Learning (ML) algorithms of Multilayer perceptron (MLP), Neuro fuzzy (NF), and Principal Component Analysis (PCA) to predict a retrospective cohort study of ART-treated patients at the Federal Teaching Hospital, Gombe (FTHG), State, Nigeria. The modelling used data from 1500 patients, including variables such as ART drug, hospital status, BP, viral load, age on ART, and birth and age groups. The ML models employed the ("coefficient of determination_DC and mean square error_MSE") to measure the model accuracy, however, factor loading, the rotated component matrix, and the scree plot (variance and cumulative) employed PCA to evaluate the dimensionality of the components. Before the real prediction, the data underwent thorough proofed of (training 75%) and testing 25%). The NF demonstrated superior performance, achieving (91% and 90%) accuracy in both training and testing over MLP (90% and 89%). By applying PCA to simplify the high-dimensional data, three significant components were identified that met the Kaiser Criterion with eigenvalues of 1.946, 1.070, and 1.047. Together, these components effectively reduce the complexity of the original dataset while retaining more than 58% of the total information. The rotated component matrix showed that Component 1 was defined by a strong positive cluster of age group and patient age (both 0.985). Component 2 included positive loadings for hospital status (0.576) and SBP (0.726). Finally, Component 3 showed a mixed pattern, with a negative loading on viral load (-0.641) and a positive loading on ART start year (0.699). With an accuracy of 91%, the AI model confirms that years of ART treatment align with the 90-90-90 HIV/AIDS targets. Additionally, since the PCA components preserve over 58% of the original variance, this approach proves to be a robust method for clinical predictions.*

KEYWORDS: AI Algorithm, Factor loading, PCA transformation, Scree plot, Viral Load Stability.

INTRODUCTION

Human Immunodeficiency Virus (HIV), a complex “retrovirus” within the Lentivirus genus, poses a severe threat to human life by systematically dismantling the immune system. If left untreated, the infection progresses to Acquired Immune Deficiency Syndrome (AIDS), which is fatal without early clinical intervention and strict adherence to antiretroviral therapy. HIV is categorized into two distinct types (HIV-1 and HIV-2), which vary significantly in their biological behavior and epidemiological reach. While (‘‘HIV-2 remains largely restricted to specific populations in West Africa”)**,** HIV-1 has emerged as the primary driver of the global pandemic (Ismail et al., 2026; Peng et al., 2023). The current ART medications are better drugs for fighting HIV-1 and HIV-2 than ever before, which have been the only medications found to be effective in the fight against HIV/AIDS. (Charpentier et al., 2025; Magomere et al., 2025). The HIV-1 and HIV-2 protease enzymes are nearly identical in action. When these protease enzymes are not properly regulated, they can cause AIDS and lead to death. Regarding this accomplishment, the endorsed ongoing ART is the only acceptable treatment for HIV both locally and globally. The progress in ART from test, treatment, and decline in mortality was on the right track (Okesanya et al., 2025). Within “ML” discipline, the application of artificial intelligence (AI) to biological research has created a particular niche.

Evidence across different professions around the world indicates that computational intelligence models are becoming more dependable and effective in improving HIV treatment and medicine. A wide range of uses for these technologies has been highlighted by recent research: AI models have been crucial in improving diagnostic testing, managing immunological results, and monitoring therapy (Ngcobo et al., 2025), MLP studied the risk factors causing HIV and the relevance of treatment (Nazeera Sedeeq Kareem Barznji, 2025), ML predicted life quality in HIV treated people (Xie et al., 2025), ANN and MLP investigated the sequence of HIV drug supply, focusing on dual minimization of costs and delivery times (Ali et al., 2025), ML models studied the duration of viral suppression so that predictive factors among ART can be resolved (Orowe, 2025), In Milan, Italy, neural networks (NN) were effectively used to predict the risk of cardiovascular disease (CVD) in patients receiving antiretroviral medication (ART) (Cernuschi et al., 2025). Additionally, AI is being used to address difficult ethical and accessibility issues while also enhancing early diagnosis and personalizing treatment approaches (Senel & Beka, 2025). Optimization of a multipurpose preventative hydrogel formulation containing (Tenofovir-TNF and Cyanovirin-N -CV-N) was predicted using ANN (Oyediran et al., 2025), CD4+T cells were examined using a neural network (Riaz et al., 2024). A mixed model of Neural NN and a NN Graph evaluated the progress of ART treatment in HIV-1 (Di Teodoro et al., 2025). Fuzzy logic and voice-enabled technology studied health application software for diagnosing HIV related problems (Oluwagbemi et al., 2025). However, in numerous studies, scholars mixed ML models and statistical models to predict HIV/AIDS. Neural network and multivariate analysis predicted the association between HIV infection and osteoporosis risk (Li et al., 2025), Cox proportional hazard models, eXtreme Gradient Boosting, Random Forest, SVM, and MLP predicted HIV-treated people (Cai et al., 2025).

Based on the foregoing, several multivariate statistical models used a different route, including adopting a mixed-effects statistical model to predict the duration of ART in HIV-1 (Bayón-Gil et al., 2020), “Multidrug-resistant” (MDR) “Staphylococcus aureus” in patients with “HIV” predicted using logistic regression (He et al., 2021), Percentage of HIV-1 subtypes and transmitted medication resistance among ART patients was determined using logistic regression (Kim et al., 2025). Logistic regression examines the features of recently diagnosed HIV cases in South Korea's (Yoo et al., 2022), In older HIV-positive individuals, the prevalence of cognitive fragility and the factors that contribute to it were examined (Xu et al., 2025). Health metrics and bibliometric analysis views regarding the social stigma of individuals living with HIV/AIDS were evaluated using correlation (Picón-Jaimes et al., 2025), Longitudinal viral Load clustering in HIV was examine using PCA (Ma et al., 2025), Logistic regression models and General estimating equations were utilized to investigate ("babies delivery with and without HIV") due to ("Systemic Inflammation and Growth") (Evans et al., 2026), Conversely, researchers utilized survival analysis to examine ART-treated follow-up cases in Henan Province (Deng et al., 2025), Hemoglobin level and treatment defaulters in female HIV-positive patients were investigated (Muhie & Tegegne, 2025).

In the field of dimensionality techniques, scholars employed PCA to investigate how socioeconomic factors cause morbidity and mortality in ART-treated patients (Nikolaev, 2025), In addition, the molecular interactions between HIV subtype C and the CD4 receptor were examined (Mishra et al., 2025). MCA and random forest were used to assess factors associated with high HIV-RNA viral load (Soogun et al., 2022), MCA and cluster analysis investigated the relationship between ART interruption, sociodemographic, and clinical variables in people living with HIV (da Silva Ziani et al., 2025). MCA, multiple logistic regression, and latent class analysis (LCA) evaluated public awareness, attitudes, and perceptions regarding HIV, focusing on community pharmacy-based provision (El-Osta & Bagkeris, 2026). MDS, CFA, and Chi-square examining social support perception among HIV/AIDS treated People in Vietnam (Kieu et al., 2023). This study establishes a novel predictive framework by integrating supervised machine learning with Principal Component Analysis (PCA) to map the stability and transformation levels of ART medication. Unlike traditional models, our approach quantifies stability through a dual lens of predictive performance and 'performance distance' metrics, offering a more granular understanding of patient-specific drug behavior.

MATERIALS AND METHODS

This retrospective cohort study was conducted at "FTHG" in Gombe State, Nigeria. The settings of the Nigerian population comprise (36 states, including the Federal Capital Territory (FCT), Abuja), which are divided into six geopolitical zones. FTHG is a tertiary health facility located in the North-Eastern geopolitical zone. The hospital serves as a key regional referral center, attracting HIV patients from all six states (Gombe, Bauchi, Yobe, Borno, Adamawa, and Taraba) within the zone. The study sample consisted of clinical records from a cohort of 1,500 HIV patients receiving AART follow-up care at FTHG. To predict patient outcomes, the following clinical and demographic variables were extracted (including age, age group, drug, hospital status, blood pressure, viral load, and ART year).

Data Processing and Predictive Modelling

Data management and initial pre-processing were conducted using Microsoft Excel, and predictive modelling was implemented within the MATLAB environment. Three distinct computational and machine learning approaches were utilized to predict the clinical stability and status transformation of the patients: MLP, NF, and PCA. Before model training and evaluation, the dataset was partitioned using a standard holdout validation split (training 75% and testing 25%).

AI Machine Learning models

Developing computational methods for creating and improving perfect predictions of model performance using data is the focus of ML. The ML tool uses its algorithms to control the data and build models that can solve certain scientific problems based on the useful information received about the data. In addition, it deals with real-world issues by utilizing them to create statistical models. Also, various ML tools can be used to understand and handle the exploration and analysis of data with different problems.

Multilayer_perceptron_neural_network (MLP)

The multi-layer perceptron (MLP) networks use more than one layer of adaptive weights. These layers constitute three units of values, and each layer is fostered by the previous layer's term as Jump Connection Network (JCN). The MLP is unique among FFNNs; it organizes its neurons in a one-directional manner, with data passing between three parallel sets of layers known as the input, hidden, and output layers, respectively. As a result, the connections between the layers are used to classify the weights that are fixed therein; therefore, the MLP uses each to present a summation and activation function, in which the product of inputs, weights, and bias is summed by the summation function defined as,

$$s_j = \sum_{i=1}^{n} w_{ij} I_i + \beta_j \qquad (1)$$

Where $n \, and \, I_i$ stand for inputs and input variable, i, β_j represents the bias term, and w_{ij} symbolizes the connection weight. Consequently, the activation function is going to be applied using the output of equation 1. Figure 1 demonstrates the MLP sketching. The MLP used a variety of activation functions, one of which is the S-shaped curved or sigmoid function (Ramchoun et al., 2016). It is described as,

$$f_j(x) = \frac{1}{1+e^{-s_j}} \qquad (2)$$

Thus, the output of the neuron j can be achieved using the equation below:

$$y_i = f_j\left(\sum_{i=1}^{n} w_{ij} I_i + \beta_j\right) \qquad (3)$$

The MLP is a network type that works with only two numbers of weighted connections, concurrently it possesses the ability to map any function (ESANN 2001 : European Symposium on Artificial Neural Networks, 2001) symbolically defined as

$$"y_k = f_{outer}\left[\sum_{j=1}^{M} w_{kj}^{(2)} f_{inner}\left[\sum_{i=1}^{d} w_{ji}^{(1)} x_i + w_{j0}^{(1)}\right] + w_{k0}^{(2)}\right]" \qquad (4)$$

Where y_k is “the k^{th} output”, f_{outer} refers to “the output layer transfer function”, f_{inner} refers to “the input layer transfer function”, "w” denotes “the weights and biases”, and ("i") symbolizes the "i^{th} layer”.

Article DOI: 10.52589/AJBMR-YWFMQGV9
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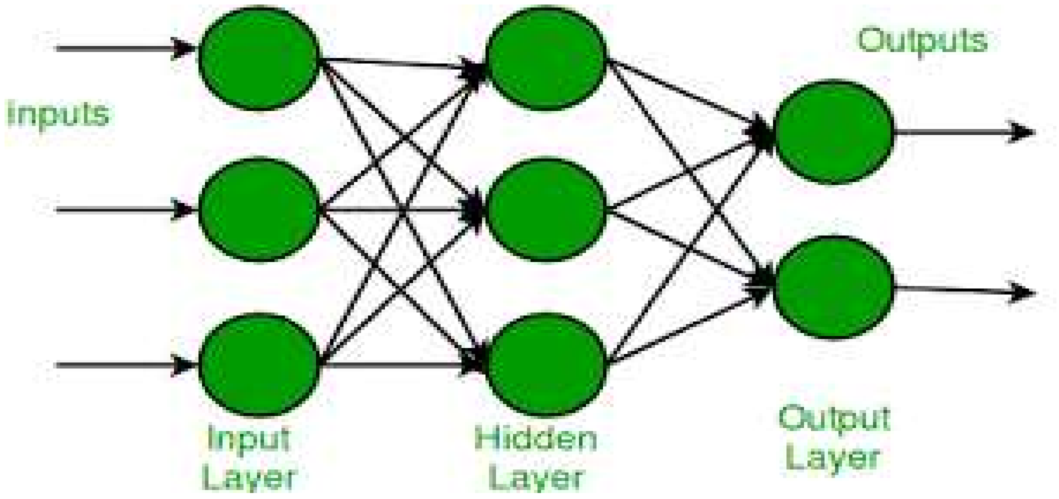
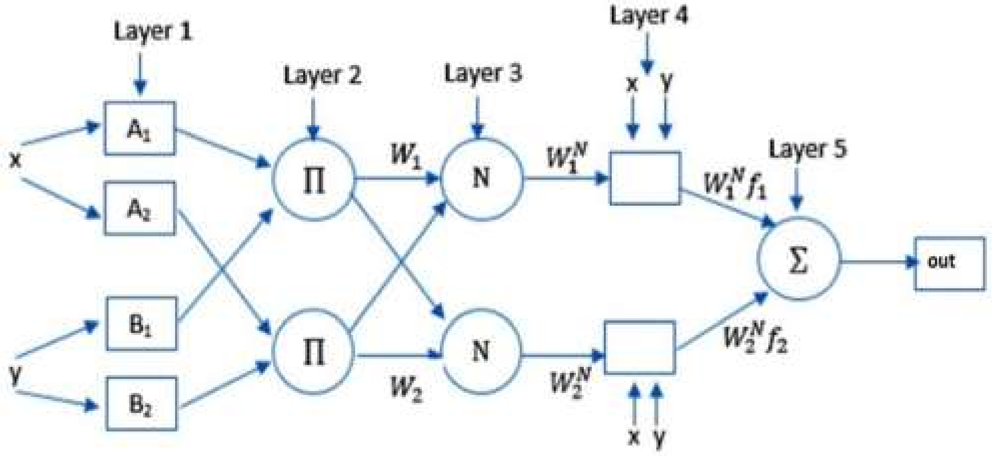
Figure 1. Multilayer perceptron (MLP) network flow chart



Neuro-fuzzy system

The NF system is a machine learning technique that enables a learning algorithm to be constructed from the theory of neural networks and to identify fuzzy sets and fuzzy rules (parameters) to process the sample. Figure 2 gives the organized shape of the fuzzy neural network. NF, in the context of ML, is a learning mechanism that uses sample data to design a neural network and enable it to handle specified parameters. Via the algorithm, which involves learning that takes place during the modeling process, the neural networks answer unclear events, such as “uncertainty about human thinking” by translating “knowledge” into “numeric computation” and then focusing towards the imprecise judgment given by the neural networks (Abba et al., 2017; Mei & Zhao, 2018).

Figure 2. Fuzzy neural system structure

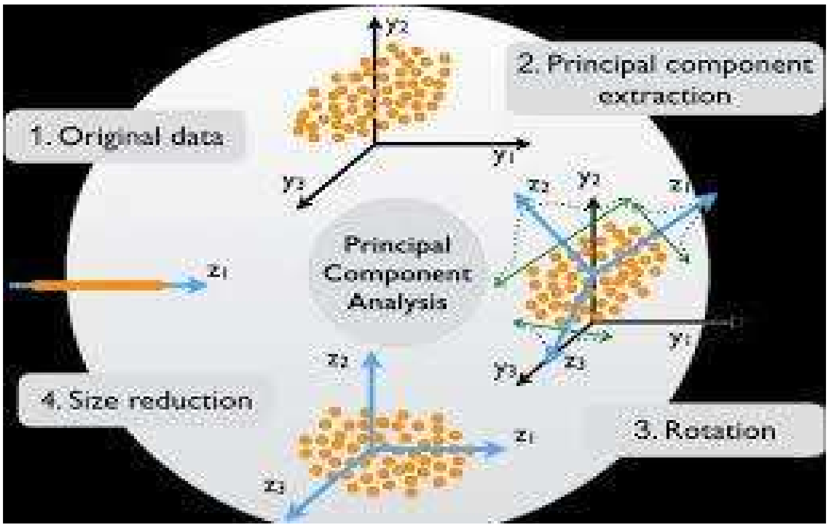


The PCA Algorithms

Algorithms are compatible with regression and are built to be trained on labeled datasets. During the process of training, each sample of data requires a target and a feature to allow the understanding of mapping between the inputs and outputs for the model to produce precise predictions on fresh data that has not been tested (Greenacre et al., 2022; James et al., 2023) .

The PCA is a technique that can preserve most of its variance and present the set of data on an orthogonal basis of transformation. However, the computation of the covariance matrix for a given data set helps in realizing the “eigenvalues and eigenvectors of the matrix”. To summarize the dimensions of the data set, a few eigenvectors can be selected from many eigenvalues larger to form the transformation matrix (Rodarmel & Shan, 2002). The PCA (“identified and accounts for most of the variance in the data.)” Secondly, it (“accounts for the second largest amount of variance in the data”) and is (“uncorrelated with the first principal component”) and so on (Suhr, n.d.). Figure 3 illustrates the dimensionality reduction architectural workflow of the PCA algorithm.

Figure 3. Schematic view of the PCA algorithm



3 ML MODELS RESULTS AND DISCUSSION

The supervised ML singles models evaluation centered on the Coefficient of determination (DC), Multiple correlations (R), Mean square error (MSE), and Root mean square error (RMSE). The findings in Table 1 show that the models performed better, explaining more than 88% of the coefficient of determination for the variables, despite the poor performance exhibited by MLP. The evaluation of the supervised single machine learning models centered on the (“ Determination Coefficient-DC/R^2”), (“Correlation-Coefficient-ρ”), (“Mean Squared Error- MSE”), and (“Root Mean Squared Error-RMSE”). As shown in Table 1, the models performed well, with the coefficient of determination explaining over 88% of the variance for the variables, despite the poor performance exhibited by the multilayer perceptron (MLP). The Neuro-Fuzzy (NF) model achieved the highest R-square values in both training (0.902418) and testing (0.895384), outperforming the multilayer perceptron (MLP), which scored 0.899187 and 0.889916, respectively. Similarly, the Adaptive Neuro-Fuzzy Inference System (ANFIS) demonstrated superior performance by yielding lower mean squared errors (MSE) in training (8.066743) and testing (9.508287) compared to the higher MSE values of the MLP (8.333905 and 10.00526). The high accuracy and minimal fluctuations that allow the NF model to outperform the MLP mirror the precision required to meet the (“UNAIDS 2020 90-90-90") direction for HIV “testing, treatment, and viral load suppression” (Global HIV Statistics, n.d.; Ssekalembe et al., 2020). The predictive performances of the developed models are illustrated

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using a bar chart and a pie chart in Figures 4 and 5, respectively, while Figure 6 displays the scatter plot of predicted versus observed values.

Table 1. Computations of supervised ML of single models and results

	Training				Testing			
Models	DC	R	MSE	RMSE	DC	R	MSE	RMSE
MLP	0.899187	0.948254	8.333905	2.88685	0.889916	0.943354	10.00526	3.163109
NF	0.902418	0.949957	8.066743	2.840201	0.895384	0.946247	9.508287	3.083551

Figure 4. Training and Testing DC performance

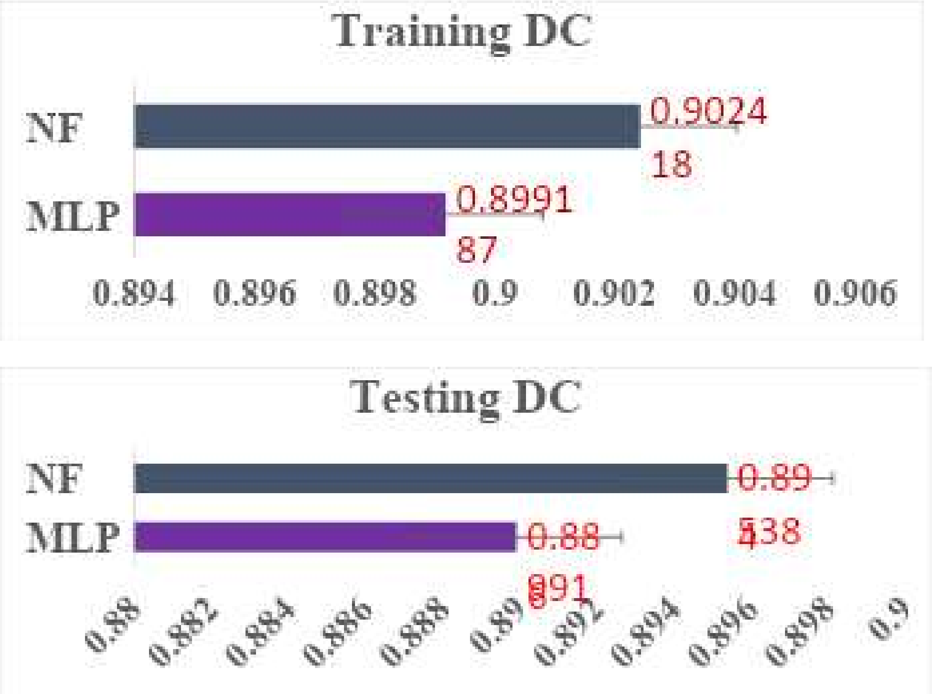
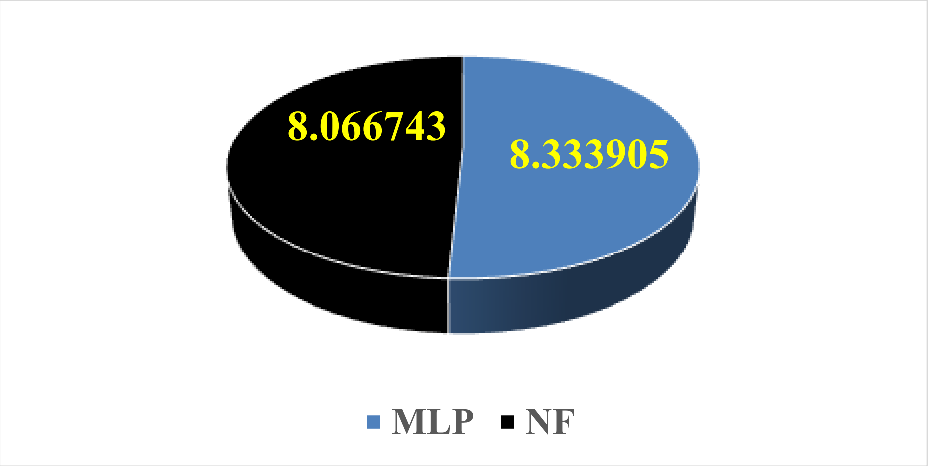


Figure 5. Training and Testing MSE performance



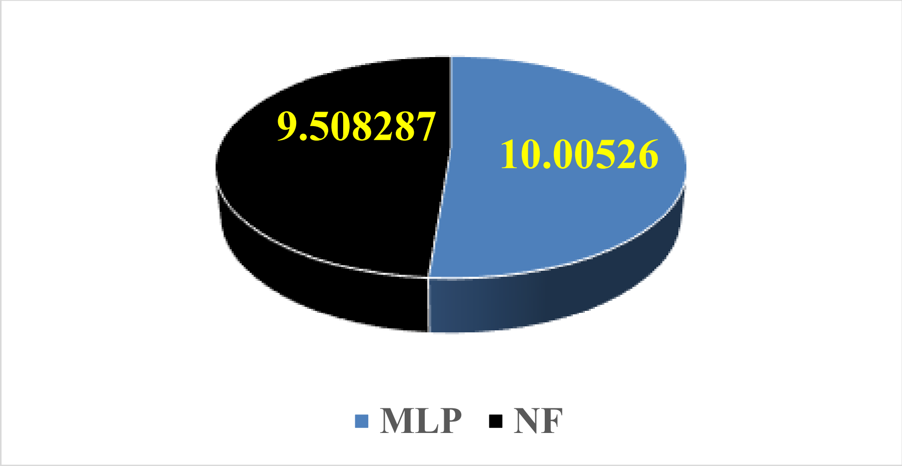
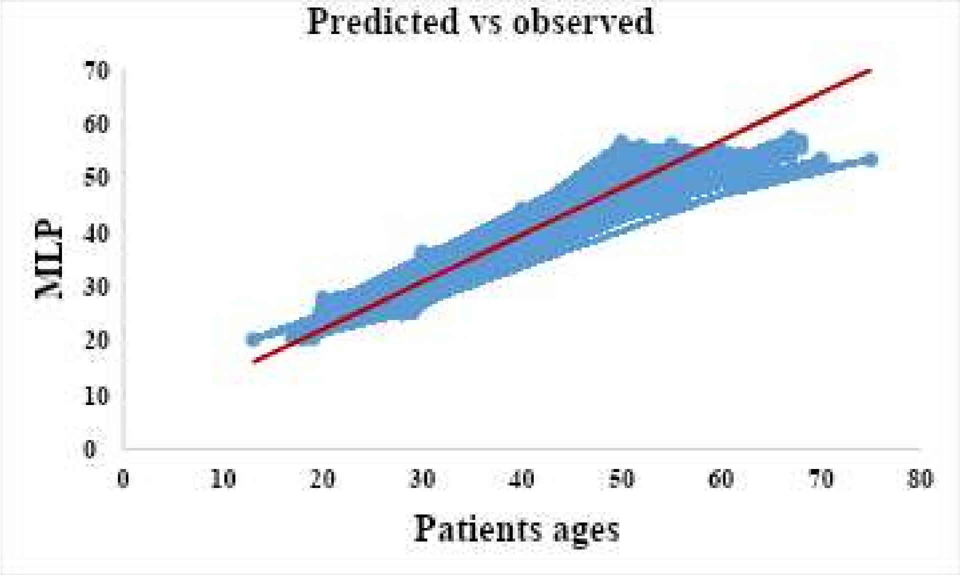
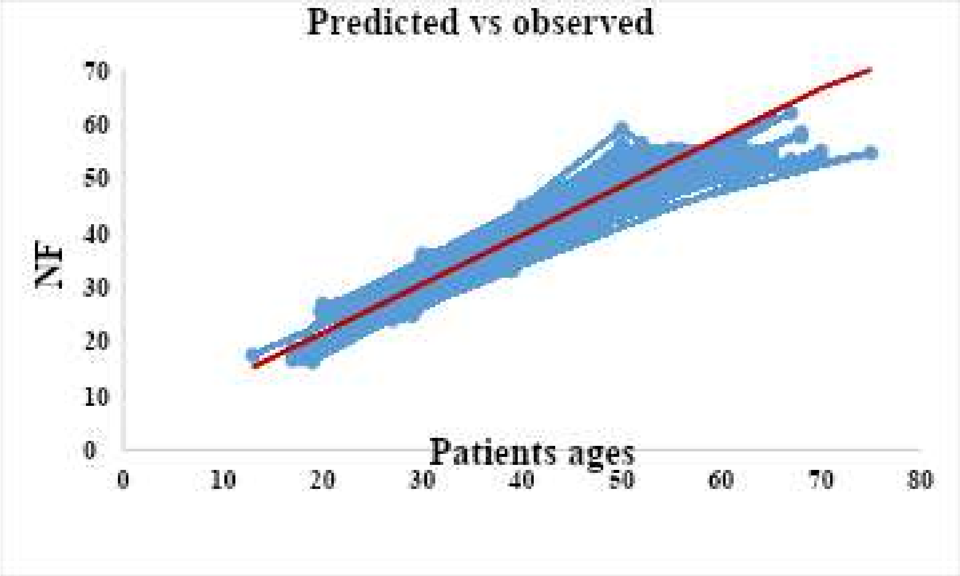


Figure 6. Predicted values for MLP, NF, against the duration in ART years





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The PCA R-square and factor loading of communalities results.

The PCA was evaluated using indices such as (“communality (R^2), total variance explained, initial eigenvalues, percentage of variance, cumulative percentage, and rotated component”), respectively. The factor loading results in Table 2, loaded higher communalities of 97.1% in the age group and patients' ages, compared to the remaining factors. This variance distribution and factor loading hierarchy are visually illustrated in Figure 7.

Table 2. Factor loading of communality results.

Variables	Extraction
ART drug	0.195
Hospital status	0.423
SBp	0.531
Viral load	0.436
Beginning of the ART year	0.537
Age group	0.971
Patients ages	0.971

Figure 7. Is the extracted performance of the factor loading

The PCA total explained variance results

The Initial eigenvalues constitute the total variance cumulative percentage. The results in Table 3 capture the total represented by the scree plot. The total initial eigenvalues for the first three target values above 1 are found in component 1 (1.946), 2 (1.070), and 3 (1.047), respectively. In addition, the retained and non-retained component were utilized for displaying the scree plot captured in Figure 8**.** The variance percentage constituted the cumulative percentage of 27.803, 15,2682 and 14.958 to account for about 58.045 factor rotation converged from seven iterations to retain only 3 components with a total initial eigenvalue greater than 1. The eigenvalue distribution and component retention criteria are visually illustrated in Figure 9.

Table 3. Total explained variance (% variance and cumulative)

Total Variance Explained			
Component	Initial Eigenvalues		
	Total	% of Variance	Cumulative %
1	1.946	27.803	27.803
2	1.070	15.282	43.085
3	1.047	14.958	58.045
4	0.989	14.131	72.176
5	0.971	13.869	86.045
6	0.921	13.160	99.204
7	0.056	0.796	100.00

Figure 8. Scree plot for the retained and unretained components

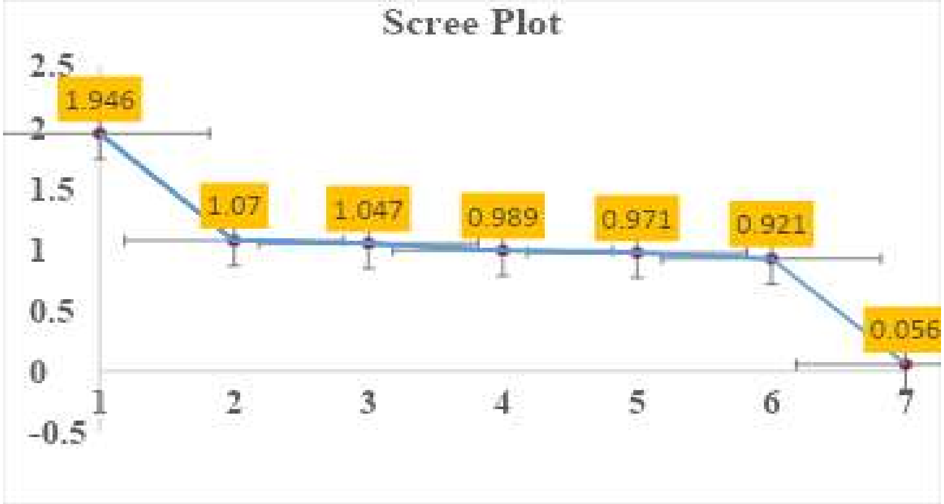
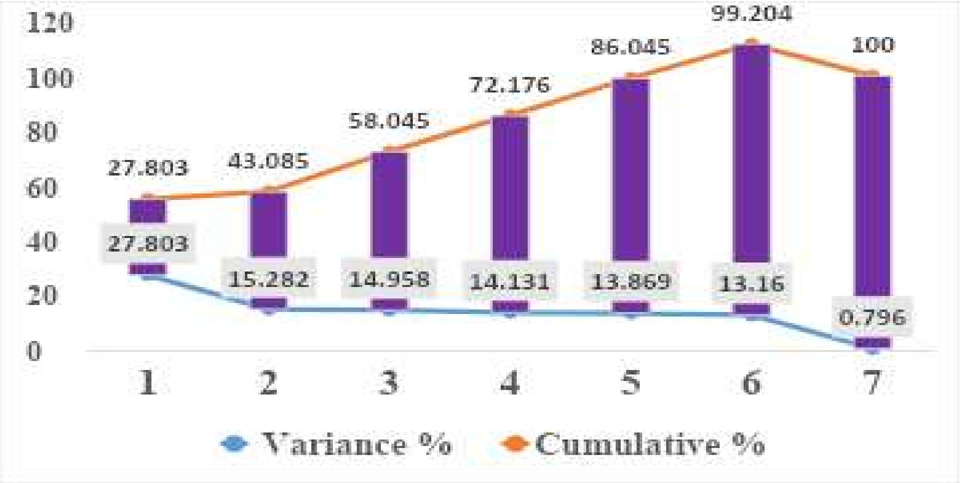


Figure 9. % of variance and cumulative



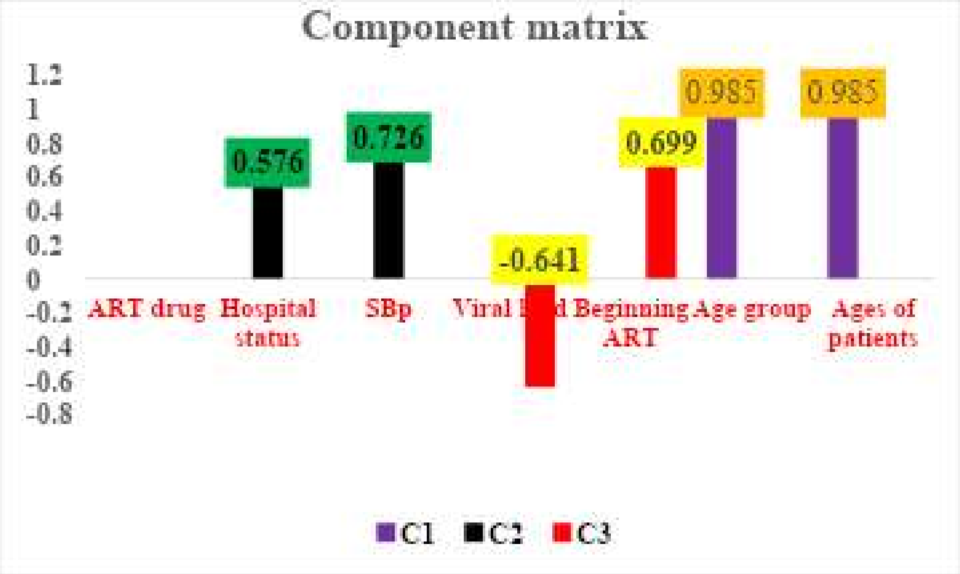
Rotated_component_matrix

The ("rotated component matrix") results in Table 4 show that age group and patients' age exhibited nearly identical, strong positive loading of 0.985. This demonstrated that the two variables represent the same underlying demographic dimension within the dataset. However, Hospital status (0.576**)** and systolic blood pressure (SBp) (0.726**)** both loaded positively on this component. This suggests a notable relationship between the type of facility providing care and the physiological management of the patients' blood pressure. ART starting year loaded positively (0.699) and viral load loaded negatively (-0.641). The inverse relationship between timing of treatment and clinical outcomes indicates that patients who started ART in more recent years tend to have lower viral loads, potentially reflecting improvements in modern treatment efficacy or earlier intervention strategies. The spatial distribution and alignment of these variable loadings are visually mapped in Figure 10.

Table 4: Rotated component matrix variables

Component	Variables	Rotated component values
C1	Age group	0.985
	Patients ages	0.985
C2	Hospital status	0.576
	SBp	0.726
C3	Viral load	-0.641
	Beginning of the ART year	0.699

Figure 10. Bar chart representing a rotated space component matrix



CONCLUSION

The embedding of NF, MLP, and PCA in this study to predict the stability and transformation in ART (treated patients) yielded a superior accuracy of performance in the NF model over the MLP model. The 91% NF coefficient of determination (DC) for this study concurs with the goal target (90%, 90%, 90%) of UNAIDS and WHO success progression in HIV/AIDS achievement. The dimensionality techniques of the PCA retained more than 58.1% variation for the new components, reflecting a transformation in the ART life cycle. These results proved that commitment and consistency in year of ART drugs can prolong HIV/AIDS patients. In the future, we suggest that more advanced methods, like ensemble or hybrid techniques, MDS, and MCA, need to be attempted.

Author contribution: Study design: All-authors; data collection: K Bala; data analysis and interpretation: All-authors; manuscript preparation and review: All-authors. Proofreading: I Etikan, S.I. Abba, A.G Usman

Conflict of interest: No conflict of interest between the authors

Acknowledgments

The authors express their gratitude to the management of the Federal Teaching Hospital, Gombe State, Nigeria, for granting the ethical approval necessary to conduct this research. We are also grateful to the anonymous reviewers for their insightful observations and comments, which significantly improved the quality of this paper. Finally, we thank the Tertiary Education Trust Fund (TETFund) and Taraba State Polytechnic, Suntai, for their invaluable support and contributions throughout the research process.

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