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Application of Machine Learning in the Classification of HIV Medical Care Status for People Living with HIV in Oshana Region of Namibia

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ABSTRACT

Background: Monitoring of viral load among pregnant and breastfeeding women augments remote patient management, reduces the risk of mother-to-child transmission of Human Immunodeficiency Virus (HIV), helps prevent treatment failure and virological rebound.
Objective: This study aimed to develop a machine learning (ML) model that effectively classifies the medical care status of HIV patients, particularly among pregnant and breastfeeding women, using integrated historic data of people living with HIV (PLHIV) in Oshana region, Namibia.
Method: A quantitative approach was employed to a cross-sectional dataset of 27,768 patients, from which 22,347 active patients were selected. Feature selection using a Random Forest classifier was used to reduce the risk of model overfitting. Three supervised learning models Convolutional Neural Network (CNN), Long Short-Term Memory (LSTM), and a hybrid CNN-LSTM were trained using an 80/20 train-test split. Models were trained under two scenarios: (1) using all 71 demographic and clinical features and (2) using a reduced set of 5 top feature.
Results: The hybrid CNN-LSTM achieved the highest performance (99.98% accuracy, 98.46% recall, 99.22% F1-score) and maintained strong results even with fewer features. In contrast, CNN and LSTM models showed reduced recall, highlighting the hybrid model's superior ability to minimize false negatives, critical for identifying high-risk PBFW.
Conclusion: ML models can enhance healthcare decision making by providing accurate predictions to strengthen continuity of HIV care.
Unique Contribution: This study provides localized evidence on HIV care in Oshana region, Namibia by applying deep learning to classify the medical care status of pregnant and breastfeeding women. It demonstrates how routine clinical data can support scalable, data-driven interventions to improve continuity of care and reduce treatment failure in resource-limited settings.
Key recommendation: Future research should explore alternative hybrid deep learning architectures, optimize complex hyperparameters, and evaluate diverse feature selection techniques. Testing on larger datasets is also recommended to assess scalability and generalizability.

Keywords: Pregnant and breastfeeding women; medical care status; HIV care; viral load monitoring.

INTRODUCTION

Sub-Saharan Africa continues to bear the highest global burden of Human Immunodeficiency Virus (HIV), accounting for over two-thirds of all HIV positive individuals approximately 25.7 million people many of whom face persistent challenges in accessing prevention, diagnosis, treatment, and care services (Belay et al., 2022; Aligwe et al., 2019). in response, the Joint United Nations Programme on HIV/AIDS (UNAIDS) launched the 95-95-95 targets, aiming for 95% of people living with HIV (PLHIV) to know their status, 95% of those diagnosed to be on treatment, and 95% of those on treatment to achieve viral suppression (Kweku et al., 2021). Despite these efforts, pregnant and breastfeeding women (PBFW) continue to face barriers such as delayed diagnosis, irregular viral load monitoring, social stigma, and disengagement from care that compromise both maternal and child health outcomes (UNAIDS, 2024; Mwamba et al., 2018; Nweze et al., 2020).

These challenges underscore the need for data-driven approaches that support early identification of patients at risk of poor outcomes and promote targeted interventions. Machine learning (ML) has emerged as a valuable tool in this regard, offering opportunities to predict retention in care, identify individuals at risk of virological failure, and improve data use for more responsive HIV programming (Godfrey et al. 2022; Mahalie et al. 2024; Olatosi et al. 2021a). Tailoring these technologies to support PBFW is particularly important given their elevated vulnerability during the perinatal period.

Namibia has achieved substantial progress in meeting the UNAIDS targets. By 2023, the country reported that 95% of PLHIV knew their HIV status, 97% were on ART, and 94% had achieved viral suppression (UNAIDS, 2022). However, despite these national-level successes, gaps remain among specific subpopulations. For instance, in 2021, viral load (VL) monitoring among PBFW was below 83%, and only 90% of those monitored achieved suppression (Ministry of Health and Social Services (MoHSS), 2017). These figures suggest ongoing challenges in patient retention, monitoring, and treatment adherence in this key group.

To address these challenges, Namibia has implemented Differentiated Service Delivery (DSD) models, including Multi-Month Dispensing (MMD), Multi-Month Prescriptions (MMP), community ART groups, and fast-track ART services. These models aim to personalize HIV care, improve retention, and reduce health system burden (WHO.,2021; Long et al., 2020). However, the implementation has been inconsistent. For example, although MMD coverage rose to 53% during the COVID-19 pandemic, it dropped to 31% by mid-2022 (MOHSS, 2023). revealing gaps in continuity and sustainability especially for high-risk groups like PBFW.

Namibia's national electronic HIV surveillance system, the Quantum electronic Patient Monitoring System (QePMS), contains rich clinical and demographic data collected routinely from patients. While this resource holds great potential for advancing data science applications in healthcare, its use for predictive analytics and ML based risk classification remains underdeveloped. Internationally, ML approaches have been used in countries like Ethiopia and the United States to predict care outcomes and identify patients at risk of virological failure using

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routine health data (Olatosi et al. 2021a; Seboka et al. 2023). However, most of these studies focus on general HIV-positive populations and are conducted in better-resourced settings. There remains limited evidence on the effectiveness and relevance of ML models tailored for pregnant and breastfeeding women in low-resource environments like northern Namibia.

Moreover, while traditional ML algorithms have been widely studied, there is a lack of exploration into the application of advanced deep learning methods on real-world programmatic data from such contexts. Little has been done to test how these models perform when applied to routine HIV datasets, nor how they can be integrated with DSD factors to improve risk stratification and personalized care for PBFW.

This study addresses these gaps by developing a machine learning model to classify the medical care status of HIV-positive pregnant and breastfeeding women using historical clinical data from the Oshana region in Namibia. Specifically, it aims to: (1) identify factors influencing the prediction of medical care status among people living with HIV (PLHIV) using differentiated service delivery (DSD) indicators; (2) integrate these factors into a machine learning model to enhance predictive accuracy; and (3) evaluate the model's performance in classifying the medical care status of this vulnerable population. By focusing on a high-risk group often overlooked in existing studies, and by utilizing routinely collected national programmatic data, this research contributes to the growing but limited body of evidence on applying artificial intelligence to strengthen HIV care outcomes in sub-Saharan Africa.

METHOD

The study employed an experimental strategy associated with quantitative research design. This study was conducted in the Oshana region, Namibia, which has a population of approximately 205,000 people, representing about 8% of the national population. Among adults aged 15 years and older, an estimated 24,000 individuals are living with HIV (UNAIDS, 2023). The study population consisted of patients who were active in HIV care within the region. From the initial dataset of 27,768 records, 22,347 active patients who met the inclusion criteria being currently on ART or, if lost to care, having been lost within the past 28 days were selected for analysis. Data were extracted from the QePMS. Patients who were deceased, transferred out, or had stopped ART were excluded. The entire eligible dataset was used to ensure representativeness and an adequate sample size. Data preprocessing was conducted prior to splitting the dataset into training (80%) and testing (20%) sets for experimental model development.

A modelling intervention was implemented during the experimental design phase. To evaluate the effectiveness of the feature selection technique, all models were trained under two scenarios: (1) using the full set of 71 features, and (2) using a reduced subset of the top 5 most important features identified by the Random Forest classifier. This comparison aimed to assess the impact of feature reduction on model performance by comparing accuracy before and after feature selection.

The study utilised data from the QePMS database, which is an electronic health record system that contains comprehensive historical health records of PLHIV in Namibia. This dataset offers a

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rich foundation for the training and development of ML models tailored to this context. Furthermore**,** the experiments on Google Colab, an open-source cloud-based platform that offers computational resources for efficient model training were conducted. Data were initially checked for completeness, cleaned by handling missing values, and standardised where necessary. TensorFlow and Keras were used for training, testing, and evaluating the deep learning models (Pillai et al., 2020). Additionally, libraries such as NumPy, Pandas, Matplotlib, and Scikit-learn were employed for data pre-processing, visualization, and statistical analysis.

RESULT

The study evaluated three deep learning models single CNN, single LSTM, and a hybrid CNN-LSTM for classifying HIV patients as low-risk or high-risk. Two experimental scenarios were tested: (1) using all 71 features from the dataset and (2) using the top 5 features selected by a Random Forest classifier. Model performance was assessed through accuracy, precision, recall, F1-score, loss, and training time. Confusion matrices were analysed to further understand classification outcomes.

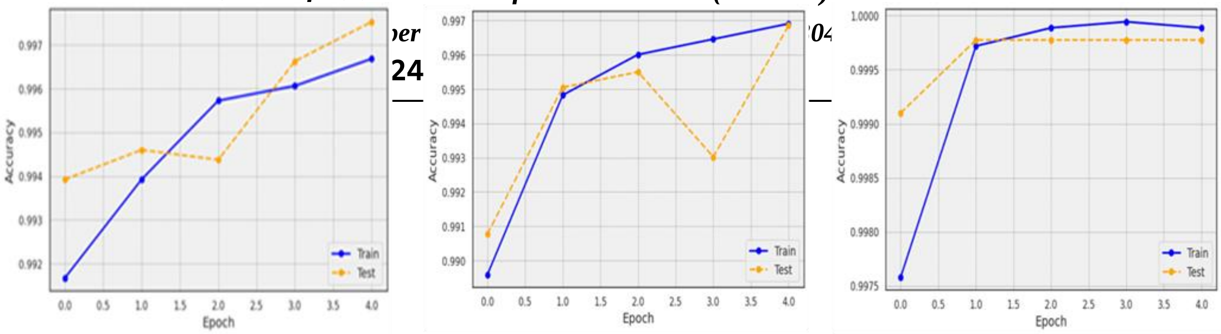
Scenario One: Model Performance with All Features

In the first scenario (Table 1 and Figure 1), both the single CNN and single LSTM models were evaluated using all Seventy-one (71) features to identify HIV patients as Low-risk or high- risk. The CNN model achieved a high accuracy of 99.73% and an F1-score of 89.43%. This indicates a good generalization across all features. However, CNN's recall was low at 84.61%, meaning it missed several true positive. On the other hand, the single LSTM model had a slightly lower accuracy of 99.67% and F1-score of 85.71% than CNN and took much longer to train - 59.561 seconds. The LSTM model also obtained a lower recall of 83.08%. This shows that the LSTM struggled more than CNN to recognize true positives cases.

Table 1: Performance with all features

Model	Accuracy (%)	Loss (%)	Precision (%)	Recall (%)	F1-score (%)	Training Time (s)
Single CNN	99.73	0.008	94.82	84.61	89.43	18.306
Single LSTM	99.67	0.010	88.52	83.08	85.71	59.561
Hybrid CNN-LSTM	99.98	0.001	100	98.46	99.22	51.081

The hybrid CNN-LSTM model outperformed the single CNN and LSTM models in all metrics. It scored a nearly perfect accuracy of 99.98%, a precision of 100%, a recall of 98.46%, and an F1-score of 99.22%. The high recall shows that the hybrid model accurately identified almost all high-risk patients, thus reducing false negatives. Although the hybrid model took longer to train than the CNN model (-51.081 seconds), it outperformed LSTM. The high performance of the hybrid model demonstrates that combining different architectures allows us to handle complex patterns in data, subsequently achieving better performance, especially in applications requiring high accuracy and reliability in identifying high-risk patients.



a) CNN b) LSTM c) Hybrid CNN_LSTM

Figure 1: Accuracy comparison on the train and test sets with all features

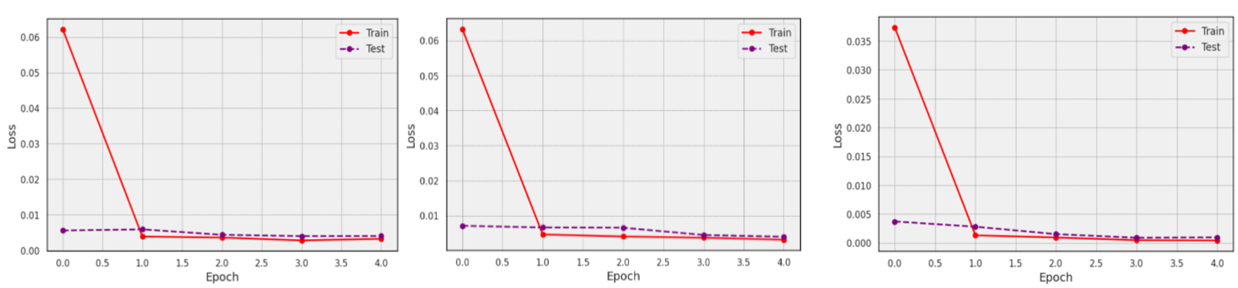
Scenario Two: Model Performance with Reduced Features

Using only the 5 most important features, the hybrid model maintained superior performance (99.98% accuracy, 98.46% recall), demonstrating robustness to feature reduction. The CNN and LSTM models improved precision to 100%, but recall remained at approximately 87.7% (Table 2), reflecting some failure to detect all high-risk patients. Training time for the CNN model increased slightly, while LSTM time decreased but remained longer than CNN.

Table 2: Performance with all reduced features

Model	Accuracy (%)	Loss (%)	Precision (%)	Recall (%)	F1-score (%)	Training Time (s)
Single CNN	99.82	0.0073	100	87.69	93.44	24.447
Single LSTM	99.82	0.0064	100	87.7	93.44	53.949
Hybrid CNN-LSTM	99.98	0.0015	100	98.46	99.22	51.081

The hybrid CNN-LSTM model continued to outperform the single models with a reduced number of features. As seen in Table 2, it achieved high precision and an impressive recall of 98.46%. This performance highlights the hybrid model's robustness and ability to adapt to different scenarios while retaining high classification accuracy. This adaptability makes it a suitable choice for applications where the availability of comprehensive feature sets is limited.



a) CNN b) LSTM c) Hybrid CNN_LSTM

Figure 2: Loss comparison on the train and test sets with the best five features

As shown in Table 2 and Figure 2, all models displayed low loss values, indicating that they made minimal errors in predicting patient risk levels. The single CNN and LSTM models had slightly higher loss values of 0.0073 and 0.0064, respectively. However, the hybrid model achieved the lowest loss value of 0.0015. This suggests that the hybrid model is highly accurate in distinguishing between low- and high-risk patients, making it a suitable and reliable option for our application.

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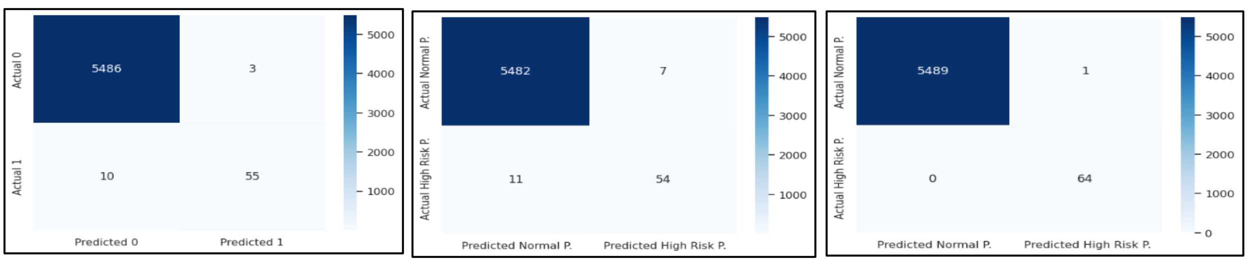
Confusion Matrix Insights

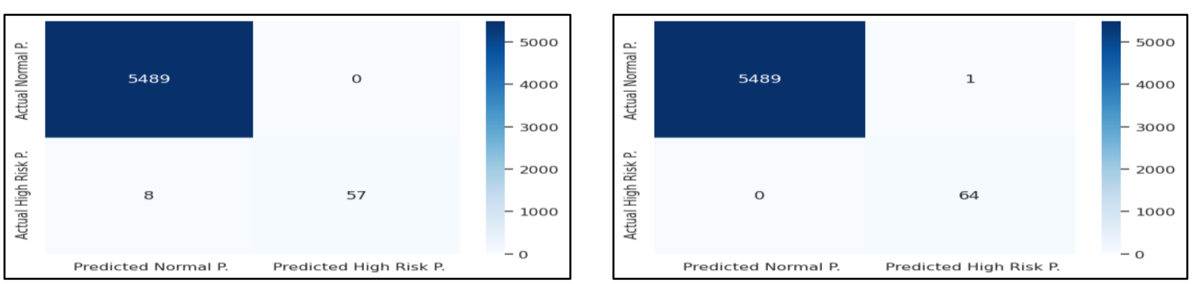
When trained with all features, the single CNN model achieved a high true negative rate, correctly identifying 5,486 low-risk patients with only 3 false positives, but it missed 10 high-risk cases Figure 3 (a). The LSTM model performed slightly worse, with 5,482 true negatives, 7 false positives, and 11 missed high-risk cases Figure 3(b). This shows that both models struggled to capture all positive cases despite using the full feature set. In contrast, the hybrid model produced only 1 false positive and zero false negatives, successfully identifying all high-risk patients without compromising accuracy for low-risk cases. This strong performance confirms the hybrid model's robustness in fully leveraging the feature set to classify patient risk level accurately, aligning with the test set distribution.



a) CNN b) LSTM c) Hybrid CNN_LSTM

Figure 3: Confusion matrix with all selected features

After reducing the features, we can see that in Figure 4(a) both the single CNN and LSTM models obtained the same and 100% accurate true negative rate. This indicates that as we used only the most important features, both models were able to accurately identify every low-risk patient and had no false positives. However, eight false negatives were still present in each model. This indicates that several high-risk cases were overlooked by the single models. When using fewer features, these models struggle to detect all positive cases, which is a major shortcoming as such missed cases might have serious consequences and possibly result in poor medical treatment in sensitive applications like ours.



a) CNN and LSTM b) Hybrid CNN-LSTM

Figure 4 Confusion matrix with reduced features

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However, Figure 4(b) shows that the hybrid CNN-LSTM model did exceptionally well, just like it did when trained with all features. It maintained zero false negatives and just one false positive. This shows that even with a smaller feature set, the hybrid model can reliably identify between patients who are at low and high-risk. This performance makes our hybrid model a great potential for real-world applications where fewer features may be available as it minimises both false positives and false negatives

Comparative Insights

The hybrid CNN-LSTM model consistently outperformed the single CNN and LSTM models across all metrics in both feature scenarios. While the single models showed strong accuracy, they struggled with recall and produced more false negatives especially with fewer features. The hybrid model maintained high recall and F1-score throughout, making it more reliable for identifying high-risk patients. Despite a slight increase in training time, its superior performance makes it ideal for clinical applications where minimizing false negatives is critical.

DISCUSSION

Accurately predicting the medical care status of people living with HIV (PLHIV) remains a vital tool in advancing targeted interventions and improving clinical outcomes, particularly among pregnant and breastfeeding women (PBFW) receiving antiretroviral therapy (ART). This population faces elevated risks of virological failure and vertical transmission, which underscore the need for practical, data-driven approaches to risk stratification. Accordingly, this study evaluated the predictive utility of three machine learning (ML) models using routinely collected clinical data to classify the medical care status of HIV positive PBFW in Namibia. The findings demonstrate that ML can serve as a reliable and scalable tool for informing clinical decision-making and enhancing care continuity.

Among the models tested, the hybrid Convolutional Neural Network–Long Short-Term Memory (CNN-LSTM) model demonstrated superior performance, achieving an accuracy (99.98%), a recall (98.46%), and an F1-score (99.22%) when trained on all 71 available features. Remarkably, the model retained high predictive accuracy even when limited to just 5 clinically significant features: ART duration, ART adherence, viral load testing intervals, recent viral load availability, and treatment outcomes. These findings align with those of Olatosi et al. (2021a) and Seboka et al. (2023), who reported that routinely collected clinical data particularly ART adherence and viral load information are strong predictors of HIV treatment outcomes. However, unlike these broader population-based studies, the current research focuses specifically on PBFW in a southern African context. This population is often underrepresented in ML based HIV studies, despite having distinct clinical vulnerabilities. Therefore, this study extends existing knowledge by tailoring predictive modelling to the maternal HIV care context and demonstrating its feasibility in a low-resource setting.

The model's high performance using a reduced set of features also mirrors findings by Seboka et al. (2023), who found that models based on fewer, yet contextually meaningful inputs can yield accurate results. This is particularly important in settings where comprehensive datasets are not

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always available. In the present study, the presence of a recent viral load result especially within a three-month period, emerged as a key indicator of effective clinical monitoring. Conversely, individuals on ART for extended periods without an updated viral load result were at an increased risk of disengagement and virological failure. These results suggest structural limitations in routine monitoring and highlight gaps in care continuity, similar to observations in studies by Hans et al. (2023), who noted that such monitoring gaps are common drivers of treatment failure among PBFW.

The hybrid model's superior performance may be attributed to the synergy between the CNN's ability to detect complex feature patterns and the LSTM's capacity to model non-linear relationships within the structured data. This combination likely explains the enhanced risk stratification observed compared to simpler models. Importantly, the model's low false negative rate is particularly beneficial in public health settings, where failing to identify high-risk individuals can have serious consequences, especially in preventing mother-to-child HIV transmission.

Furthermore, the study supports the integration of predictive tools into national health information systems, such as the QePMS. Unlike conventional black-box models, the reduced feature approach ensures model interpretability and practical relevance for health workers. While Olatosi et al. (2021b) did not focus specifically on explainability, they acknowledged the importance of usable and scalable ML tools in HIV care. This study contributes to this dialogue by demonstrating how interpretable, simplified models can be effectively embedded into clinical workflows.

Findings from the thematic literature review also align with the model's outputs. Variables such as ART adherence, viral load, CD4 counts, comorbidities, and socio-economic conditions have long been recognized as key determinants of treatment outcomes and patient retention, particularly within the framework of differentiated service delivery (DSD). These results are consistent with those reported by Seboka et al. (2023) and Hans et al. (2023), who emphasized that targeted programmatic strategies including Multi-Month Dispensing (MMD) and community-based ART delivery require accurate patient segmentation to be effective. The predictive framework developed in this study offers a practical approach to operationalizing such strategies by enabling the early identification of pregnant and breastfeeding women (PBFW) at heightened risk of vertical HIV transmission.

This study adds to the growing body of literature on ML in HIV care by providing a context-specific application focused on a high-priority yet underrepresented population. It demonstrates not only that ML can achieve high accuracy in classifying care status using routine clinical data, but also that simplified and interpretable models can be practically deployed in real-world, resource-constrained health systems. These findings offer a scalable approach for improving patient retention, optimizing resource allocation, and advancing progress toward Namibia's HIV response objectives and the global 95-95-95 targets.

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CONCLUSION

The study successfully developed and evaluated a robust model to classify the medical care status of HIV positive patients, with a special focus on pregnant and breastfeeding women. The use of routine health data and selection of critical features such as ART duration and viral load testing intervals enabled accurate classification, even in simplified scenarios. The hybrid CNN-LSTM model performed with exceptional reliability and offers a promising tool to support targeted interventions. These findings underscore the importance of timely and efficient data use in strengthening HIV care, especially in high-burden settings.

A major strength of this study is its use of programmatically relevant data extracted from QePMS and its application in developing a robust model tailored to the HIV context. The model's ability to perform well with a small number of features makes it adaptable and scalable. However, the limited dataset size may affect generalizability. While cross validation was applied, larger and more diverse datasets are needed to validate the findings further**.**

For future work, the study recommends exploring other alternative hybrid architectures and optimizing other complex hyperparameters. To also experiment with different feature selection methods to refine the model performance. Additionally, to assess the model's performance on other large datasets and test its scalability in larger applications to provide more comprehensive insights.

Ethical Clearance: Ethical approval and permission to carry out the study was obtained from the NUST Research and Ethics Committee (FREC-24/24), the Ministry of Health and Social Services (Ref: 22/4/2/3) and the Regional Health Director of Oshana in Namibia. The privacy of individuals personal information was protected from unauthorized access or disclosure through encryption and adherence to confidentiality agreements. Anonymity was maintained by removing personal identifiers from the dataset, ensuring security and data ownership throughout the study.

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Data Availability Statement: Data generated during this study is available on password protected databases. This will be availed upon successful approval of this manuscript.

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