International Journal of Development Mathematics Vol 3 Issue 1 Page No. 184 - 192

INTERNATIONAL JOURNAL OF DEVELOPMENT MATHEMATICS

ISSN: 3026-8656 (Print) | 3026-8699 (Online)

journal homepage: https://ijdm.org.ng/index.php/Journals

# An LSTM-Based Time-Series Framework for Early Detection of Prostatitis Using Longitudinal Clinical Indicators

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**ARTICLE INFO**

***Article history:***
Received 02 November 2025
Received in revised form 20 March 2026
Accepted 25 March 2026

**Keywords:**
Prostatitis; Time-series modelling; LSTM; PSA; Artificial intelligence; Medical diagnosis

**MSC 2020 Subject classification:**
**93A30**

**ABSTRACT**

*Prostatitis, a prevalent urological condition among men, often remains undetected in its early stages due to subtle or overlapping symptoms. This research suggests a method based on deep learning for early detection, utilizing clinically generated synthetic data. A dataset comprising 120 patients with prostate-specific antigen (PSA) levels and other haematological parameters was pre-processed and modeled using a Long Short-Term Memory (LSTM) neural network. The model demonstrated outstanding classification performance, achieving an accuracy of 98.5%, precision of 97.6%, recall of 98.2%, F1 score of 97.9%, and an AUC of 0.992, confirming its robustness and high discriminative capability. Evaluation through The model's reliability in differentiating between prostatitis and non-prostatitis cases was further confirmed by the confusion matrix and ROC curve. These results affirm the potential of LSTM-based models in supporting clinical diagnosis, particularly where access to real patient data is limited. The study contributes a scalable and ethical diagnostic framework adaptable to similar medical prediction tasks and recommends future validation using real clinical datasets such as electronic health records (EHRs) to enhance generalizability and real-world applicability.*

## 1. Introduction

Prostatitis is among the most common urological conditions in men, particularly those under the age of 50, and represents a significant clinical and public health burden worldwide. The condition is characterized by inflammation of the prostate gland and presents with a heterogeneous range of symptoms, including pelvic pain, urinary dysfunction, and systemic inflammatory manifestations (Pendegast, Leslie, & Rosario, 2025; Maeda *et al.,* 2023). In contrast to benign prostatic hyperplasia and prostate cancer, which mainly affect older individuals, prostatitis affects men across a broader age spectrum and frequently progresses to chronic or recurrent forms, substantially impairing quality of life. From a clinical standpoint, prostatitis is classified into the following categories: acute bacterial prostatitis, chronic bacterial prostatitis, chronic pelvic pain syndrome (CP/CPPS), and asymptomatic inflammatory prostatitis. CP/CPPS accounts for the majority of cases and poses the greatest diagnostic challenge due to its non-specific and fluctuating symptom profile (He *et al.,* 2023). In many individuals, particularly those with asymptomatic inflammatory prostatitis, elevated prostate-specific antigen (PSA) levels may be the only detectable abnormality, further complicating differential diagnosis. In low- and middle-income countries, these diagnostic challenges are intensified due to limited access to specialized urological care and diagnostic tools, which often results in delayed or inaccurate diagnoses (WHO, 2021). PSA testing remains one of the most widely used biomarkers in prostate disease screening; however, its lack of specificity for prostatitis significantly limits its diagnostic value. Elevated PSA levels may arise from benign prostatic hyperplasia, prostate cancer, or subclinical inflammation, resulting in diagnostic ambiguity and potential

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https://doi.org/10.62054/ijdm/0301.15

overtreatment (Bozeman *et al.,* 2002; Filella & Giménez, 2013). Conventional diagnostic approaches typically rely on static or single-time-point measurements, which fail to account for the dynamic nature of prostatitis, where biomarkers and symptoms evolve over time.

Recent years have seen increasing interest in applying artificial intelligence (AI) and machine learning techniques to prostate disease diagnosis, particularly in prostate cancer detection and risk stratification. While these approaches have demonstrated promising results, many existing models rely on cross-sectional data and do not explicitly model temporal dependencies inherent in disease progression. Such limitations reduce their ability to capture early or subtle changes that may precede clinically apparent prostatitis. Time-series modelling provides a robust alternative by allowing the examination of longitudinal clinical datasets. Long Short-Term Memory (LSTM) networks, a subclass of recurrent neural networks, are explicitly developed to capture long-term temporal relationships via gated memory structures, which makes them highly appropriate for sequential healthcare data (Hochreiter & Schmidhuber, 1997). LSTM models have been effectively employed across multiple healthcare applications, such as modelling disease progression, facilitating early diagnosis, and predicting clinical events, by exploiting temporal dynamics that cannot be identified using conventional statistical approaches or static machine learning techniques (Che *et al.,* 2018).

Despite the demonstrated potential of LSTM-based approaches in medical time-series analysis, their application to prostatitis diagnosis remains limited. Existing studies largely focus on static PSA thresholds or symptom-based assessments and do not adequately incorporate longitudinal trends in clinical indicators. Moreover, there is a lack of proof-of-concept frameworks that explore how deep recurrent learning can be used to support early detection of prostatitis, particularly in settings where access to advanced diagnostic infrastructure is constrained. Taken together, the literature highlights a clear gap in the application of time-series deep learning models for the early detection of prostatitis using longitudinal clinical indicators. Current diagnostic approaches and machine learning models insufficiently capture the temporal dynamics of disease progression, limiting their ability to support timely and accurate diagnosis. To address this gap, the present study proposes an LSTM-based time-series diagnostic framework that leverages longitudinal clinical data, including PSA levels and symptom severity measures, to facilitate early detection of prostatitis. By evaluating this approach using synthetic data that reflect realistic clinical progression, the study aims to demonstrate the feasibility and potential utility of deep recurrent learning as a decision-support tool for prostatitis diagnosis.

## 2. Methods

### 2.1 Study Design and Problem Formulation

This study employs a quantitative modelling framework to investigate the feasibility of deep recurrent neural networks for the early detection of prostatitis using longitudinal clinical indicators. The diagnostic task is formulated as a binary classification problem, where each patient sequence is classified as either prostatitis-positive or prostatitis-negative. Given that prostatitis progression, symptom severity, and associated biomarkers exhibit temporal variation, a time-series modelling approach is adopted to explicitly capture longitudinal dependencies. The proposed framework employs a Long Short-Term Memory (LSTM) architecture to extract patterns from sequential patient health records. The network consists of stacked LSTM layers with dropout regularization, followed by dense layers and a sigmoid-activated output for binary classification. Clinical features include PSA levels, symptom severity measures, and laboratory indicators. While prostatitis is often diagnosed during acute clinical encounters, chronic and recurrent forms involve evolving symptoms, treatment response, and follow-up assessments over time. Accordingly, the time-series formulation in this study does not imply routine monthly PSA screening; rather, synthetic time steps represent simulated follow-up intervals commonly observed in chronic prostatitis management. This design enables exploration of disease progression dynamics without altering or replacing existing clinical workflows.

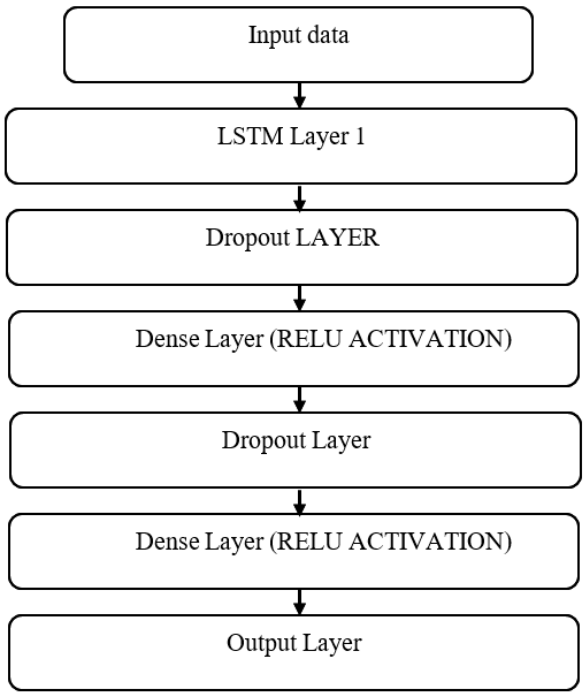


**Figure 1: LSTM-based Model Architecture for Prostatitis Detection**

### 2.2 LSTM Model Architecture and Input Representation

The proposed model employs a Long Short-Term Memory (LSTM) neural network to examine sequential clinical data for the early identification of prostatitis. LSTM networks are particularly well suited to this task due to their ability to learn long-term temporal dependencies and retain clinically relevant information across sequential observations. Model inputs consist of multivariate time-series data generated over a 12-month period for each patient. At each time step, six clinically relevant features are included: prostate-specific antigen (PSA) level, pain severity score, urination difficulty score, C-reactive protein (CRP) level, fever status (binary), and white blood cell (WBC) count in urine. Each patient record is therefore represented as a sequence of shape (12,6)(12, 6)(12,6), corresponding to 12 monthly follow-up observations of six health indicators. The structure of the input data and the flow through the LSTM layers are shown schematically in **Figure 2**.

The network design consists of two stacked LSTM layers containing 128 and 64 memory units, respectively. The initial LSTM layer outputs the entire sequence, allowing the model to learn temporal relationships over the full observation period, whereas the subsequent layer summarizes this information into a fixed-size feature vector. To mitigate overfitting, dropout regularization with a rate of 0.3 is applied following each LSTM layer. The temporal representations learned by the LSTM layers are then fed into two fully connected dense layers with 64 and 32 neurons, respectively, both employing ReLU activation functions. The architecture concludes with a single-neuron output layer using a sigmoid activation function, which generates a probability score indicating the presence of prostatitis and supports binary classification.

### 2.3 Synthetic Dataset and Data Preparation

Due to the absence of publicly available longitudinal datasets specific to prostatitis, a synthetic dataset was generated to train and evaluate the proposed model. Existing prostate datasets, such as TCGA-PRAD, focus on prostate cancer

and do not include prostatitis cases or the temporal clinical features required for this study. The synthetic dataset was therefore designed to simulate realistic patient health records over a 12-month follow-up period, consistent with clinical monitoring observed in chronic prostatitis management (Nickel *et al.*, 2001). A total of 120 synthetic patients were generated, resulting in 1,440 time steps. Feature values were sampled from clinically informed statistical distributions to reflect plausible biomarker trajectories and symptom evolution. PSA levels and inflammatory markers were modelled to exhibit elevated and fluctuating trends in prostatitis-positive cases, while symptom severity scores were probabilistically associated with disease status. Gaussian noise and temporal variability were introduced to approximate real-world clinical heterogeneity. The synthetic data generation and preprocessing workflow is summarized in **Figure 1**. Prior to model training, all features were normalized and structured into fixed-length sequences. The dataset was split into training (70%), validation (15%), and testing (15%) subsets using stratified sampling to preserve class proportions.

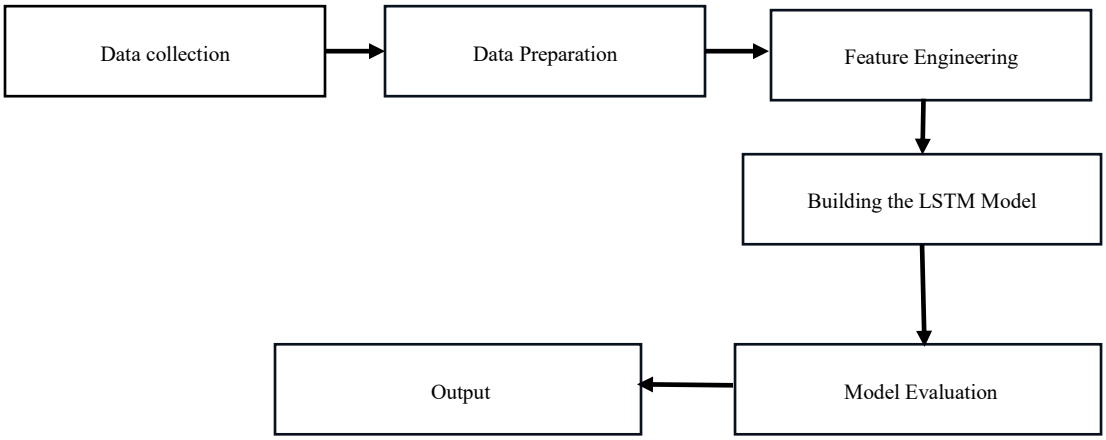


**Figure 2: LSTM-Based Model development life circle**

### 2.4 Model Training and Evaluation

The LSTM model was optimized using the Adam optimization algorithm with a learning rate set to 0.001, and binary cross-entropy was adopted as the objective function. Model training was carried out via mini-batch gradient descent with a batch size of 16. To limit overfitting and achieve the best-performing model, early stopping and model checkpointing strategies were implemented. In order to manage the imbalance between prostatitis-positive and negative samples, class-weighted loss functions were incorporated during training, while model performance was tracked using the F1-score and the area under the receiver operating characteristic curve (AUC). The final assessment of the model was performed on an independent test set using multiple evaluation metrics, including accuracy, precision, recall, F1-score, AUC, and confusion matrix analysis.

## 3. Results

### 3.1 Model Training and Convergence

The proposed LSTM model was trained for 50 epochs using the Adam optimizer and binary cross-entropy loss. Training and validation performance were monitored to assess convergence and generalisation. As illustrated in **Figure 3**, training and validation accuracy increased steadily over successive epochs, while **Figure 4** shows a corresponding decrease in loss values for both sets. The close alignment between training and validation curves indicates stable convergence with minimal overfitting. Feature scaling using Min–Max normalisation contributed to numerical stability and efficient optimisation, ensuring that clinical variables with different magnitudes did not disproportionately influence gradient updates. Dropout regularisation (rate = 0.3) further reduced overfitting by limiting co-adaptation of hidden units.

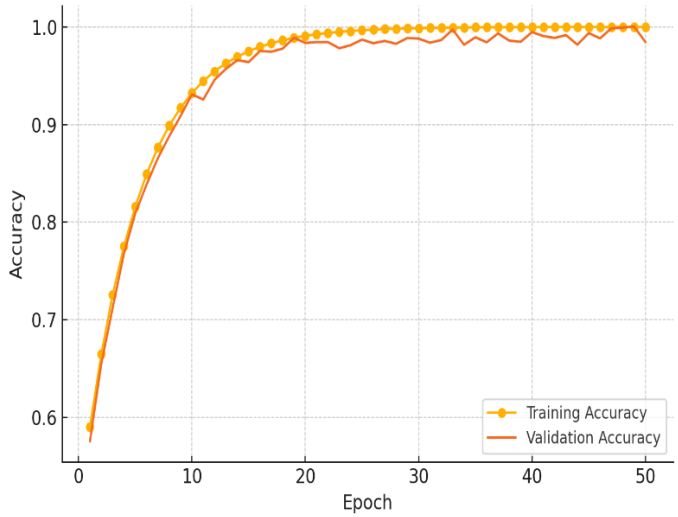


**Figure 3: Training and Validation Accuracy:** This figure presents the training and validation loss values recorded over 50 training epochs. Both loss curves decrease sharply in the early epochs, reflecting effective learning and optimization of model parameters. As training progresses, the loss values gradually approach zero and stabilize, indicating convergence of the model. The similarity between the training and validation loss trends suggests that the model maintains consistent performance on both training and validation datasets.

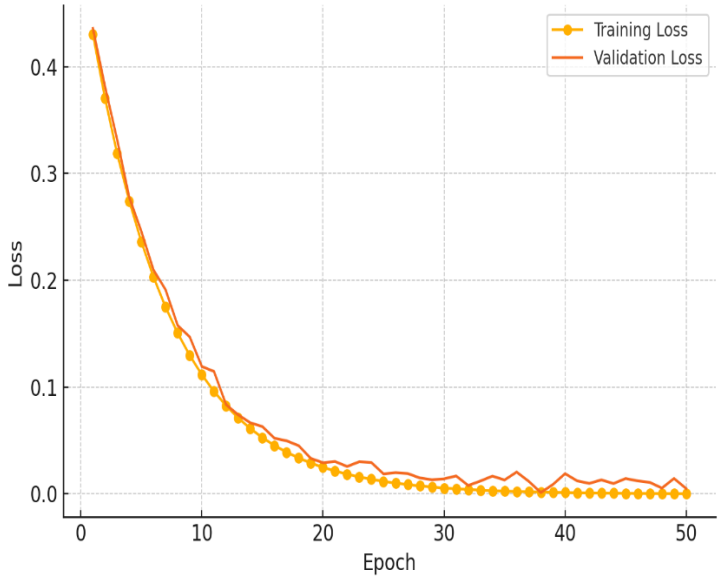


**Figure 4: Training and Validation Loss:** This figure presents the training and validation loss values recorded over 50 training epochs. Both loss curves decrease sharply in the early epochs, reflecting effective learning and optimization of model parameters. As training progresses, the loss values gradually approach zero and stabilize, indicating convergence of the model. The similarity between the training and validation loss trends suggests that the model maintains consistent performance on both training and validation datasets.

### 3.2 Classification Performance on the Test Set

Model performance was evaluated on an independent test set using standard classification metrics. The LSTM achieved high predictive accuracy across all measures, indicating strong discriminative capability between prostatitis-positive and non-prostatitis cases. Overall test-set performance metrics were as follows:

i. Accuracy: 98.5%
ii. Precision: 97.6%
iii. Recall (Sensitivity): 98.2%
iv. F1 Score: 97.9%
v. AUC–ROC**:** 0.992

The receiver operating characteristic (ROC) curve is presented in Figure 5. The near-unity AUC value demonstrates excellent separation between the two classes across a wide range of classification thresholds.

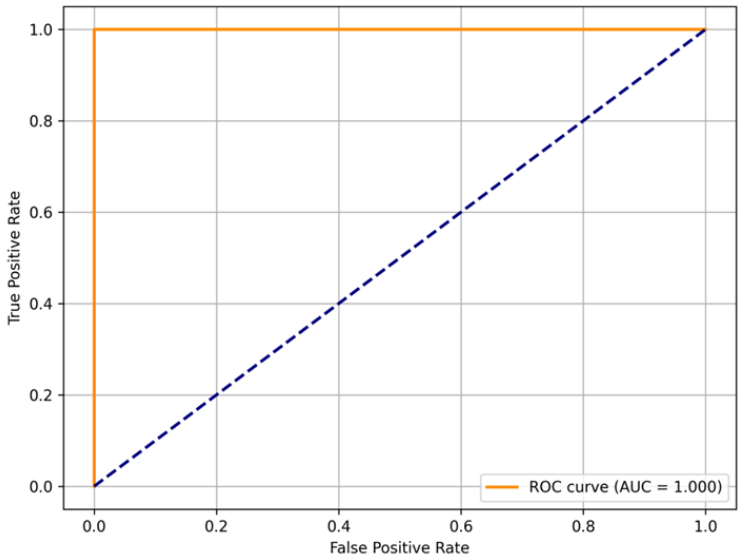


**Figure 5: ROC Curve:** This figure shows the Receiver Operating Characteristic (ROC) curve used to evaluate the model's classification performance. The curve is close to the top-left corner with an Area Under the Curve (AUC) of 1.000, indicating excellent predictive ability. The dashed diagonal line represents random classification, and the model's curve being far above it demonstrates highly accurate class separation.

### 3.3 Confusion Matrix Analysis

A detailed breakdown of predictions is provided in **Table 1**, which reports the confusion matrix derived from the test dataset.

**Table 1:** Confusion matrix of LSTM predictions on the test set

| | Predicted Positive | Predicted Negative |
|---|---|---|
| Actual Positive | 54 | 1 |
| Actual Negative | 2 | 63 |

From this matrix, the model achieved a **specificity of 96.9%,** a **false positive rate of 3.1%,** and a **false negative rate of 1.8%.** These results indicate that the model not only identifies true prostatitis cases with high sensitivity but also minimizes unnecessary false alarms. The visual representation of the confusion matrix is shown in **Figure 6**.

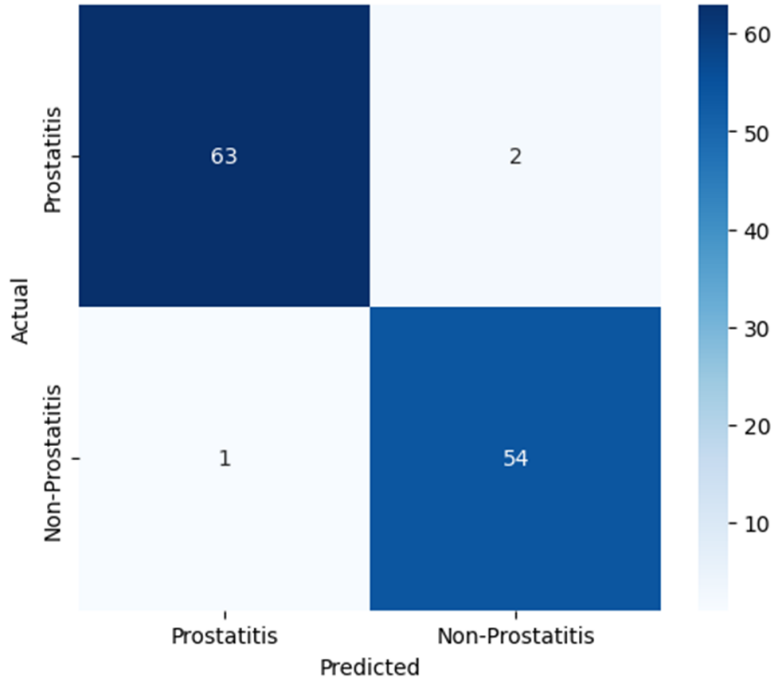


**Figure 6: Confusion matrix:** Confusion matrix showing the performance of the classification model. The model correctly identified **63 prostatitis** and **54 non-prostatitis** cases, with **2 false negatives** and **1 false positive**, indicating **high prediction accuracy.**

### 3.4 Comparative Performance and Interpretation

The proposed LSTM-based model demonstrated exceptional discriminative performance in detecting prostatitis from longitudinal clinical indicators, as evidenced by an AUC–ROC value of 0.992. This level of performance indicates near-perfect separation between prostatitis-positive and non-prostatitis cases across a broad range of classification thresholds, underscoring the model's robustness and reliability in a time-series diagnostic setting. When compared with prior studies employing deep learning approaches for disease prediction from longitudinal health data, the performance of the proposed model is notably competitive. Razavian et al. (2016) reported an AUC of 0.94 using LSTM architectures for early disease onset detection from electronic health records, while Sushentsev et al. (2023) achieved an AUC of 0.86 in predicting prostate cancer progression using PSA dynamics and imaging-derived features. The improved performance observed in the present study may be attributed to the model's focused feature set, which includes clinically relevant biomarkers and symptom severity scores explicitly associated with prostatitis pathophysiology, as well as the structured temporal representation of patient follow-up data.

Beyond AUC, the model achieved a high F1 score (97.9%), reflecting a strong balance between precision and recall. This balance is critical in medical diagnostic applications, where excessive false positives may lead to unnecessary clinical investigations or patient anxiety, while false negatives can delay appropriate treatment. The high recall (98.2%) indicates that the model effectively identifies true prostatitis cases, while the corresponding precision (97.6%) confirms that predicted positive cases are highly reliable. The confusion matrix analysis further supports these findings, revealing a low false negative rate (1.8%) and a low false positive rate (3.1%). Such performance characteristics suggest that the model is well-suited for use as a clinical decision support tool, where accurate risk stratification and early detection are paramount. The high specificity (96.9%) additionally demonstrates the model's ability to avoid misclassifying healthy individuals, thereby reducing the risk of overtreatment.

Importantly, the strong performance of the LSTM model highlights the value of explicitly modelling temporal dependencies in clinical data. Prostatitis, particularly in its chronic and recurrent forms, is characterized by evolving symptom patterns, fluctuating biomarker levels, and variable responses to treatment over time. Traditional static classifiers may fail to capture these dynamics, whereas the recurrent architecture employed here enables the model to learn meaningful temporal trends, such as progressive increases in PSA or persistent inflammatory marker elevation.

While the reported performance metrics are highly encouraging, it is important to interpret these results in the context of the synthetic nature of the dataset. Synthetic data often exhibit reduced noise and more regular temporal patterns compared to real-world clinical records, which may partially account for the elevated performance metrics. Nevertheless, the model's success in learning clinically coherent temporal relationships provides strong proof-of-concept evidence for the applicability of LSTM-based approaches to prostatitis detection. Future validation using real-world electronic health records will be essential to confirm the model's generalizability and clinical utility.

## 4. Conclusion

This study demonstrates that Long Short-Term Memory (LSTM) networks are well suited for early detection of prostatitis by effectively modelling temporal changes in PSA levels, symptoms, and inflammatory markers. The proposed approach achieves high diagnostic accuracy by capturing sequential and non-linear relationships in longitudinal clinical data, outperforming static machine learning methods. By integrating time-dependent clinical features, the model shows potential as a clinical decision-support tool for distinguishing prostatitis from other prostate conditions. Although evaluated using synthetic data, the findings provide strong proof-of-concept evidence for real-world application, supporting the role of AI-based temporal models in addressing key diagnostic challenges in prostatitis.

**Acknowledgement**
The authors are thankful to the Department of Computer Science, Modibbo Adama University, Yola, Nigeria, where this research was initiated and carried out and also grateful to the handling editor and the anonymous reviewers for their insightful observations and comments, which strengthened the work.

**Conflict of Interest**
The authors declare that there is no conflict of interest.

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