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Article

Integrating Risk Factors and Symptoms for Urinary Tract Infection Diagnosis Using an Explainable AI Approach in Low-Resource Regions

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Abstract

Urinary Tract Infections (UTIs) represent one of the most prevalent bacterial infections globally, posing significant health burdens, especially in low- and middle-income countries (LMICs), due to delayed diagnoses, limited access to laboratory services, and rising antimicrobial resistance. This study presents a machine learning (ML)-based diagnostic support framework for early UTI detection, leveraging structured clinical data and explainable artificial intelligence (XAI) techniques to enhance interpretability and trust among healthcare providers. A patient dataset containing 4,865 records was used in the study to train and test Extreme Gradient Boosting (XGBoost), Decision Tree (DT) and Random Forest (RF) classifiers, while class imbalance was addressed using Synthetic Minority Over-sampling Technique (SMOTE). The performance of the models was evaluated through accuracy, precision, recall, F1-score, Log Loss, and AUC-ROC, and random forest showed the best results (accuracy: 86.43%, F1-score: 86.71%, AUC-ROC: 0.8695). To ensure that such models can be adopted by stakeholders in the health sector, Local Interpret-able Model-agnostic Explanations (LIME) was integrated, which identified painful urination, urinary frequency, and suprapubic pain as primary predictors in the model. This study shows that interpretable ML models can be helpful in resource-limited regions in predicting UTIs, thereby rendering a solution to improve the management of infections in these regions.

Keywords: urinary tract infections; machine learning diagnosis; XAI; clinical decision support; low-resource healthcare

1. Introduction

Urinary Tract Infections (UTIs) are bacterial infections that affect individuals across all age groups, making them the most common infections globally. Women, older adults, and people with underlying medical conditions like diabetes and immunosuppression have a disproportionately higher burden of UTIs [1]. In paediatric populations, UTIs are a notable cause of febrile illness, particularly in infants and young children, with *Escherichia coli* responsible for more than 80% of

reported cases [2]. Clinically, UTIs are commonly classified according to the anatomical site of infection as upper or lower UTIs, and are further distinguished as uncomplicated or complicated based on patient-specific factors, such as age, sex, pregnancy status, and the presence of comorbidities. The clinical presentation of UTIs is highly variable, ranging from mild or asymptomatic bacteriuria to severe systemic manifestations. Common symptoms include increased urinary frequency, dysuria, haematuria, cloudy urine, abdominal pain, oliguria, fatigue, and fever [3,4]. Severe cases can lead to urosepsis and septic shock, which can be difficult to diagnose and treat. Real-world prescription patterns show persistent non-adherence to clear national and international clinical guidelines that discourage the indiscriminate use of broad-spectrum antibiotics, such as fluoroquinolones, for simple UTIs. The long-term efficacy of commonly used antibiotics has been compromised by this pervasive overprescription, which has been closely associated with the rising incidence of antimicrobial resistance [5,6]. Nitrofurantoin's clinical application is still restricted, despite the fact that it is acknowledged as a potential substitute for some UTI cases. Nitrofurantoin is only used in a number of nations when other safer or more potent antibiotics or chemotherapeutic agents are judged inappropriate.

UTIs pose a serious clinical and public health challenge in low- and middle-income countries (LMICs). This problem is worsened by the rampant use of antibiotics and delays in commencing proper treatment. It is also aggravated by limited access to diagnostic laboratory facilities. These challenges contribute to the growing problem of antimicrobial resistance (AMR) in these settings [7]. Neugebauer et al. [8] noted that rising bacterial resistance patterns have made it harder to select the best empirical antibiotic therapy in routine clinical practice. Research shows that many antimicrobial prescriptions are written by medical professionals who lack specific training in infection control. Prescribing decisions can be negatively affected when non-expert prescribers lack a proper understanding of antimicrobial agents and resistance mechanisms [9]. This lack of knowledge often leads to poor antibiotic choices. There is a strong need to develop diagnostic support tools that are affordable and reliable. These tools must also be easy for healthcare workers to understand and use. These systems should include the contextual factors that influence prescribing behaviour at the point of care. They should also provide prompt and easily accessible guidance.

Machine learning (ML) is transforming healthcare by analysing clinical data and generating predictive insights from patient information [10,11]. These techniques can model complex non-linear relationships that traditional statistical methods often cannot handle. ML methods are now widely used to support clinical decision-making by using patient histories, symptoms, and risk factors to make disease predictions. Traditional supervised learning algorithms such as Random Forest (RF), Decision Tree (DT), Support Vector Machine (SVM), and Extreme Gradient Boosting (XGBoost) perform well in medical prediction tasks. These models are valued for their interpretability and robustness [12]. Also, they can handle class imbalance and noisy real-world data, making them suitable for healthcare settings that rely on structured clinical data. Previous studies have reported many applications of ML techniques in diagnosing UTIs. Naik et al. [13] reported that artificial neural networks (ANN) dominate applications in this domain, followed by XGBoost, SVM, CatBoost, and ensemble learning, including RF, DT, and logistic regression [14]. de-Vries et al. [15] revealed that integrating urinalysis, Gram stain, and routine clinical parameters improves UTI prediction via semi-supervised ensembles. Furthermore, Flores et al. [1] employed RF and ANN models to predict UTIs in a large cross-sectional study and reported that their deployment influenced clinician behaviour, including antibiotic prescribing patterns and requests for urine cultures. The suggested models produced area under the curve (AUC) values ranging from 0.81 to 0.88 using data from over 8,000 cases. The model combinations produced satisfactory results.

These results imply that combining predictive models with contemporary urinalysis methods and digital health infrastructures may enhance antimicrobial stewardship initiatives, decrease laboratory workload, and improve diagnostic accuracy.

Studies have recently added Explainable Artificial Intelligence (XAI) techniques like Local Interpretable Model-Agnostic Explanations (LIME) and Large Language Models (LLMs) such as

Generative Pre-trained Transformer (GPT) to conventional ML approaches to improve the transparency of febrile disease diagnosis [16,17]. Our study evaluates the performance of three ML algorithms, RF, DT, and XGBoost, to diagnose UTIs using symptoms and risk factors from patient records. Despite the known predictive ability of conventional ML models, they are known to be black boxes, which reduces their chances of adoption in clinical settings because stakeholders in the healthcare sector often require justification for predictions [18]. Therefore, LIME is integrated in our study to generate feature-level explanations for individual model predictions, hence mitigating this limitation [19]. These XAI provide visual interpretations of how each feature influences the positive diagnosis of a medical condition, thereby assisting healthcare professionals in the interpretation and understanding of model outputs [16,20,21]. This study also addressed class imbalance within the dataset using the Synthetic Minority Over-sampling Technique (SMOTE) to enhance the performance of the classifier, reducing the risk of overfitting and ensuring balanced classification results. The main contributions of this work include:

- (i) Development of interpretable ML models for UTI diagnosis using patient symptoms and risk factors;
- (ii) Addressing class imbalance in the dataset with the SMOTE technique, to significantly improve the fairness and robustness of model training;
- (iii) Integration of XAI via LIME to aid the models in providing transparent, feature-level explanations and make clinicians understand which symptoms drive predictions. This is essential for trust and real-world use.
- (iv) Validation of predictive performance across models using appropriate metrics, to determine the most suitable model for deployment in real clinical settings.
- (v) Support the deployment of the proposed tool in low-resource settings, showing potential to improve early UTI diagnosis, reduce lab dependency, inform treatment decisions, and combat inappropriate antibiotic use.

The rest of the paper is organised as follows. Section 2 presents the methodology and experimental setup, describing and justifying the choice of predictive models used to assess UTI risk early and reduce unnecessary antibiotic use. It highlights the classical ML models with XAI for interpretability, as well as a description of the dataset and symptoms used for the study. Section 3 discusses the results, summarising the predictive performance of the models across all evaluation metrics, along with a confusion matrix and the LIME analysis to reveal the most influential features driving UTI prediction. Section 4 concludes the paper with directions for future work.

2. Materials and Methods

The workflow for UTI diagnosis is presented in Figure 1 with the important stages starting from the collection of input data, which comprises risk factors and symptoms, before the dataset undergoes preprocessing to handle missing values and encoding of categorical features. SMOTE was then employed to handle class imbalance within the dataset before training the ML models with hyperparameter optimisation using the GridSearchCV tool to enhance performance. The model was then evaluated with standard performance metrics, and LIME was integrated to clarify feature-level contributions to individual predictions. In the decision-support stage, the outputs of model predictions and explanatory insights assist healthcare professionals in making informed and transparent diagnostic decisions.

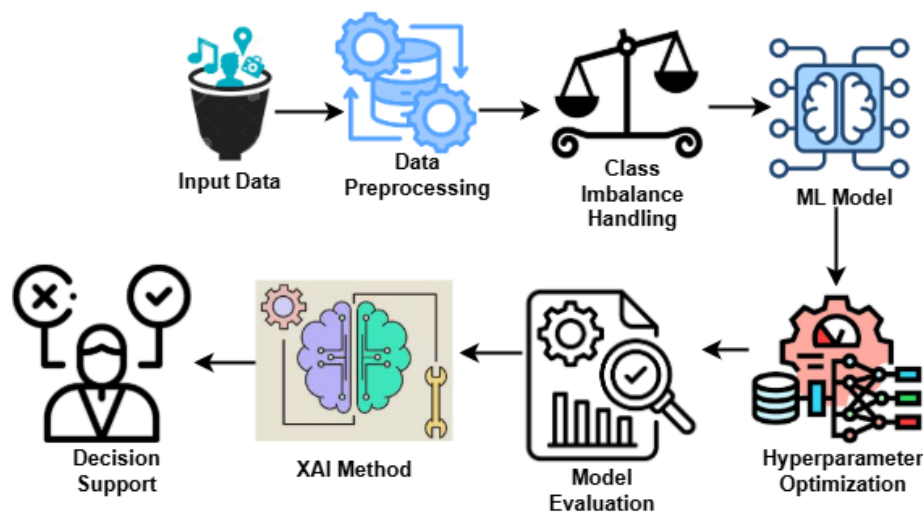


Figure 1. Study workflow.

2.1. Dataset and Preprocessing

The collected dataset from the New Frontiers in Research Fund (NFRF) project is made up of 4,870 patient records, and the patient demographic information is shown in Table 1 [22]. Patient records with missing information, such as symptoms and risk factors, were expunged, which reduced the records to 4,865, and risk factors, symptoms, as well as febrile diseases outside the scope of this study were removed as well. The final dataset only retained relevant symptoms, associated risk factors, and the target outcome variable (UTI), which is outlined in Table 2.

Table 1. Statistics of patients in the dataset.

Patient Age (Years)	Male	Female	Total
< 5	534	419	953
5 -12	346	323	669
13 – 19	150	213	363
20 – 64	1012	1605	2617
≥ 65	133	135	268
Total	2175	2695	4870

The final dataset used in the study presented a class imbalance with 961 records representing UTI-positive cases and 3,904 representing UTI-negative cases, and SMOTE was applied to address this, which transformed the dataset to 3,129 positive and 3,129 negative cases.

Table 2. Symptoms and Risk factors used in the study.

SN	Symptom/Risk Factor	SN	Symptom/Risk Factor
1	Abdominal pains (ABDPN)	11	Urinary frequency (URNFQC)
2	Bloody urine (BLDYURN)	12	Vomiting (VMT)

3	Chills and rigors (CHLNRIG)	13	High Blood Pressure (HIBP)
4	Cloudy urine (CLDYURN)	14	High Cholesterol Level (HICOLV)
5	Fatigue (FTG)	15	Poor Personal Hygiene (PPHYG)
6	Fever (FVR)	16	Intravenous Drug Use (IVNDRUS)
7	Nausea (NUS)	17	Skin Puncture (SKPUPR)
8	Upper back pain (UPBCKPN)	18	Low Fluid Intake (LWFLIN)
9	Painful urination (PNFLURNTN)	19	Underlying Chronic Illness (UNCHRIL)
10	Suprapubic pains (SPPBPN)		

2.2. Model Development, Performance Evaluation, and Explainability with LIME

RF, XGBoost, and DT algorithms were employed for this study due to their proven effectiveness in prediction tasks and suitability in dealing with structured clinical data. Hyperparameter optimisation was applied to each of the algorithms using GridSearchCV to improve the predictive performance of the models. The estimator values ranging from 100 to 200 in combination with tree depths of 3 and 5 were used for the XGBoost model; the RF model used the same range of estimators, with maximum depth values set to None and 10, while the DT model used a maximum depth of None, 10, and 20. The performance of the models was evaluated using classification metrics such as Accuracy, Precision, Recall, F1 Score, Logarithmic Loss (Log Loss), and the Area Under the Receiver Operating Characteristic Curve (AUC-ROC) due to their importance in healthcare-related datasets.

This study employed LIME to enhance the model's prediction transparency and interpretability by quantifying the contribution of individual features to the outcome of the prediction, which is essential for improving the usability of the model. The model development, training, testing and evaluation steps were carried out using a cloud-based Jupyter notebook environment (Google Colaboratory).

3. Results and Discussion

The performance evaluation results of the models are presented in this section, including the prediction performance for the SMOTE and non-SMOTE models, and the XAI method adopted in the study. The RF model was the most reliable model with a high number of true positives and true negatives, with few misclassifications as show in Figure 2 while Table 3 further presents RF's strong precision (87.12%), indicating a low rate of false positives, and high recall (86.43%), an F1 score of 86.71% and an AUC-ROC value of 0.8695, both of which highlight the model’s strong discriminative capability. Although a slight reduction in overall performance was noticed when the model was trained using SMOTE, this technique was retained to address potential class imbalance and promote

model fairness. This consideration is particularly important in clinical settings, where the underrepresentation of positive UTI cases may lead to clinically significant false negatives.

Table 3. Prediction model performance.

SMOTE Models						
	Accuracy	Precision	Recall	F1 Score	Log Loss	AUC-ROC
Random Forest	0.8643	0.8712	0.8643	0.8671	0.6057	0.8695
XGBOOST	0.8623	0.8628	0.8623	0.8625	0.4566	0.8307
Decision Tree	0.8129	0.8282	0.8129	0.8191	5.5892	0.7263
Non-SMOTE Models						
Random Forest	0.8849	0.8808	0.8849	0.8750	0.3117	0.8833
XGBOOST	0.8869	0.8816	0.8869	0.8802	0.3223	0.8835
Decision Tree	0.8674	0.8594	0.8674	0.8558	2.3150	0.7124

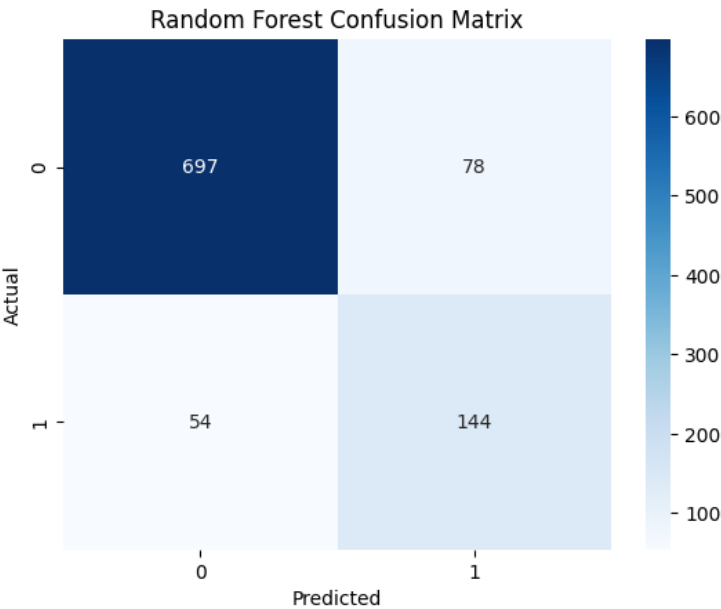


Figure 2. Random Forest Confusion Matrix.

The XGBoost model showed strong performance based on its confusion matrix (Figure 3). It achieved the lowest Log Loss (0.4566) among the three models. However, its F1 score (86.25%) and AUC-ROC (0.8307) were lower than RF, indicating slightly more misclassifications despite better probabilistic predictions. This shows that XGBoost is useful when accurate probability estimates are important. However, it does not consistently outperform RF in reliably detecting UTI cases.

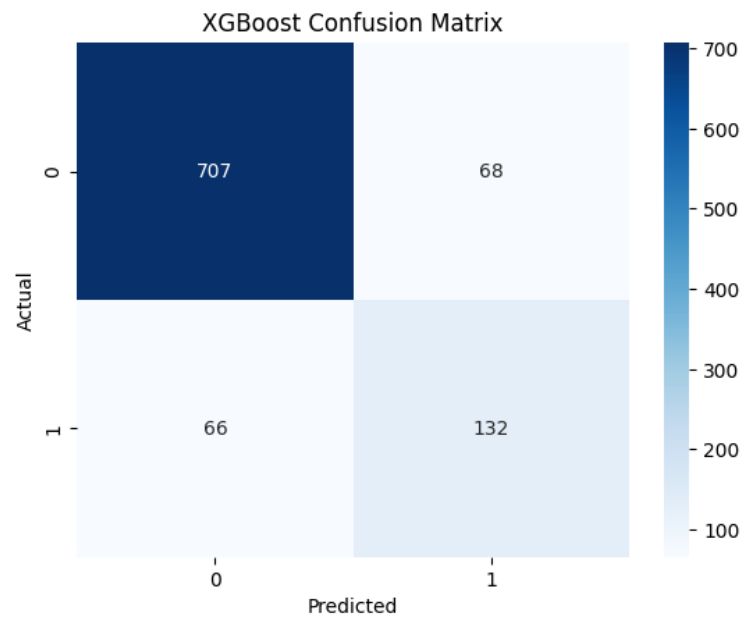


Figure 3. XGBoost Confusion Matrix.

The DT model performed worse than RF and XGBoost. It produced many misclassifications, especially false negatives and false positives (Figure 4). Its accuracy, recall, and F1 score were all around 81%. A high Log Loss (5.5892) and low AUC-ROC (0.7263) show weak confidence and poor class discrimination.

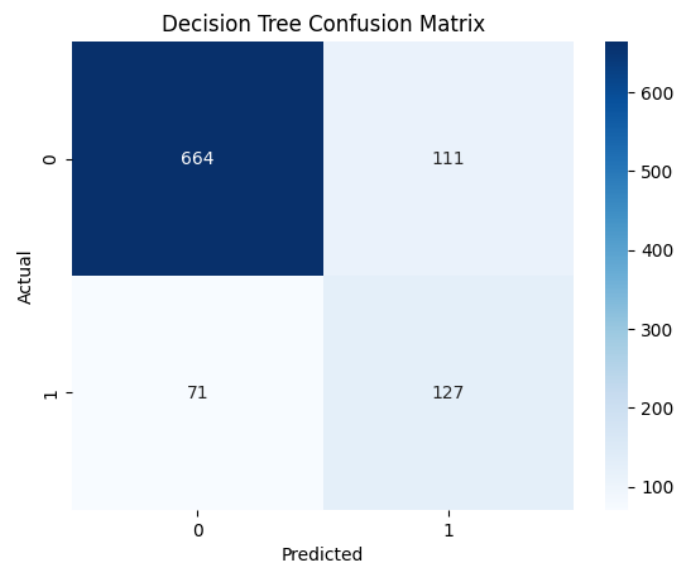


Figure 4. Decision Tree Confusion Matrix.

The LIME plots in Figures 5–7 show how different symptoms influence each model’s diagnoses across the test dataset, highlighting both positive and negative contributions. The LIME plot for the RF model in Figure 5 identifies painful urination (PNFLURNTN) as the most influential feature in predicting UTI. Other symptoms with strong positive contributions include urinary frequency (URNFQC), suprapubic pain (SPPBPN), and cloudy urine (CLDYURN). These symptoms significantly increase the likelihood of UTI predictions by the model. The results align with known clinical signs of UTI. This suggests that the RF model makes predictions based on medically meaningful patterns.

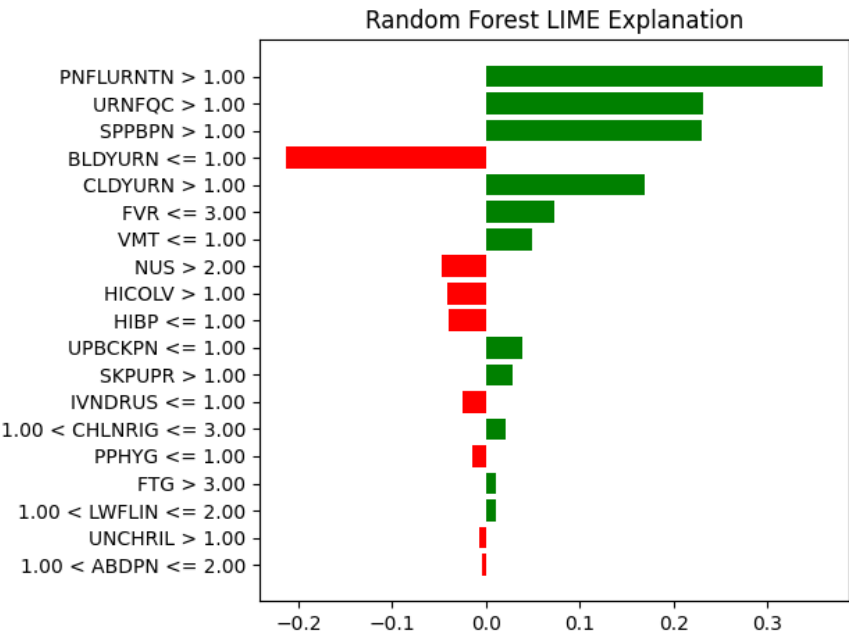


Figure 5. Random Forest LIME Diagram.

The XGBoost model in Figure 6 shows that painful urination (PNFLURNTN) is the most important predictor of UTI. Other key symptoms with positive influence are urinary frequency (URNFQC), suprapubic pain (SPPBPN), and cloudy urine (CLDYURN). The similarity in important features across models increases confidence in their predictions. Although XGBoost performs slightly lower than RF in overall metrics, it still identifies relevant clinical patterns. This indicates that the model’s predictions are medically meaningful.

The DT model in Figure 7 identifies painful urination (PNFLURNTN) and urinary frequency (URNFQC) as the most important features. However, it ranks the remaining symptoms differently from the other models. In this model, cloudy urine (CLDYURN) is considered more important than suprapubic pain (SPPBPN). Across all three models, bloody urine (BLDYURN) has a negative effect on UTI predictions. This suggests that bloody urine is more often linked to other urological conditions (e.g. kidney stones or bladder disorders) than to UTIs.

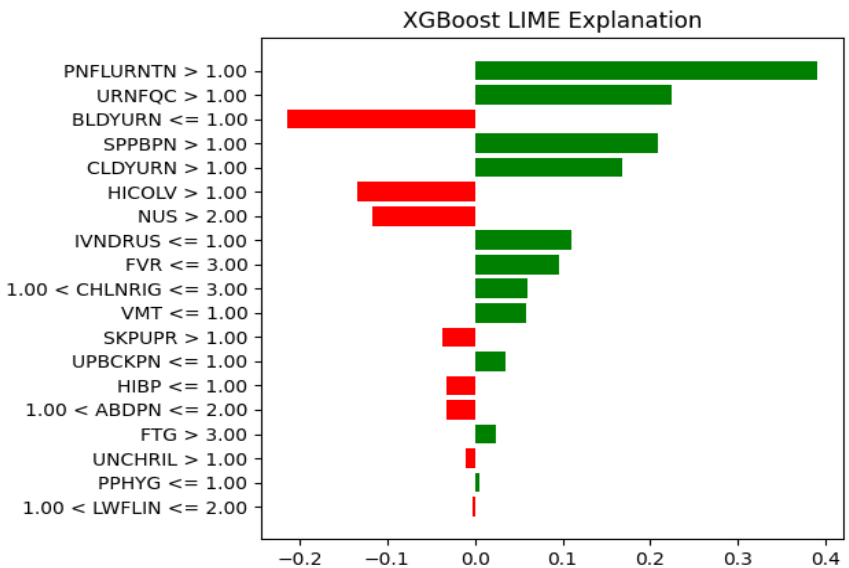


Figure 6. XGBoost LIME Diagram.

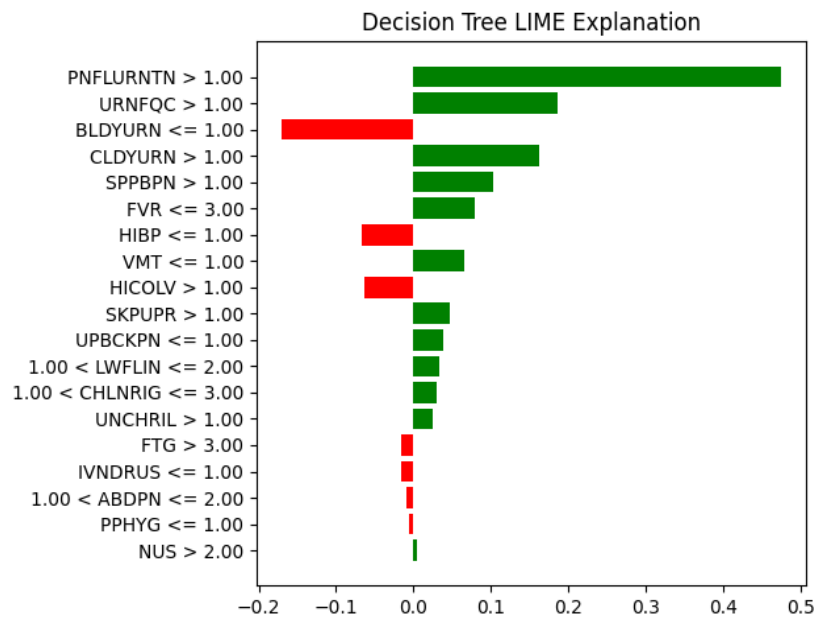


Figure 7. Decision Tree LIME Diagram.

4. Conclusions

This study shows that ML models, especially RF and XGBoost, can help diagnose UTIs where laboratory tests are not readily available. The use of explainable AI tools like LIME helps make the models’ decisions clear and understandable to clinicians. This transparency increases trust in AI-supported healthcare decisions. The results indicate that RF outperforms other models in terms of prediction accuracy, interpretability, and stability, making it suitable for use in digital health systems, particularly in LMICs. The importance of symptoms such as painful urination (PNFLURNTN) and frequent urination (URNFQC) supports the medical validity of the model’s predictions. These tools can help with early detection and better treatment decisions, especially in the face of antimicrobial resistance and diagnostic delays. Future work will involve integrating the models into mobile health platforms and testing them in real clinical settings.

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