International Research Journal of Medical Sciences and Health Care (IRJMSHC)
eISSN: 3087-405X
Volume03 Issue07 | Page No: - 07-16

Received: 30 May 2026, Revised: 15 June 2026, Accepted: 26 June 2026, Published: 21 July 2026

DOI: https://doi.org/10.55640/irjmshc-v03i07-02

Artificial Intelligence Enabled Healthcare Analytics for Patient Risk Assessment and Prediction

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ABSTRACT: Healthcare analytics systems based on artificial intelligence (AI) have been developed to enable early risk assessment and personalized patient treatment, thanks to the increasing rise of electronic health records (EHRs). Pressure ulcers (PUs) are a major hospital-acquired complication that require timely identification and preventive interventions. This study proposes an AI-enabled healthcare analytics framework for personalized patient risk assessment and pressure ulcer prediction using the MIMIC-IV clinical dataset. The proposed framework includes data extraction, preprocessing, missing value handling, feature engineering, normalization, and feature selection using Random Forest-based feature importance analysis. Clinically relevant features, including demographic characteristics, ICU-related parameters, vital signs, laboratory measurements, Braden scale factors, and diagnosis information, were utilized for predictive modeling. Decision Tree (DT) and Light Gradient Boosting Machine (LightGBM) are two ML models that were fine-tuned using hyperparameter tweaking to make better risk predictions. The LightGBM model was analysed using explainable AI based on SHAP (SHapley Additive exPlanations) to identify the clinical factors that contribute to pressure ulcer risk prediction. The experimental results demonstrate that the proposed LightGBM model outperformed traditional machine learning approaches, achieving 96.1% accuracy (ACC), 94.8% precision (PRE), 91.9% recall (REC), 93.1% F1-score (F1), and 99.04% ROC-AUC on average. To improve model transparency, the SHAP study identified important clinical variables linked to pressure ulcer formation. The suggested architecture offers a dependable method for pressure ulcer prediction and may find use in intelligent clinical decision-support systems and real-time healthcare monitoring.

KEYWORDS: Artificial intelligence, Healthcare systems, Patient risk prediction, Risk assessment, XAI, ML models.

1. Introduction

The exponential expansion of medical data, the ageing population, the increasing expense of healthcare, and the increasing frequency of chronic illnesses are all causing fast change in the healthcare industry. A large portion of the data generated by contemporary healthcare systems comes from electronic health records (EHRs), as well as from medical imaging, test results, and wearable devices [1][2]. The capacity to make informed clinical decisions and deliver personalised treatment to patients is dependent on the effective handling of these varied data sets. Personalised patient risk assessment aims to identify patients at high risk of contracting diseases or having unfavourable clinical outcomes through the analysis of demographic and clinical data [3][4]. Age, gender, and medical history are some of the specified risk factors used by traditional statistical approaches. However, these methods frequently miss complicated interactions between many clinical variables [5][6]. There has to be an upgrade to analytical procedures if wants better forecasts and faster therapeutic treatments [7]. AI has been a game-changer in healthcare analytics, allowing massive clinical information to be automatically learned from [8][9]. AI-based systems analyze patient records, laboratory findings, and treatment histories to support disease prediction, clinical decision-making, and personalized healthcare services. These intelligent systems facilitate early intervention, optimize resource utilization, and improve overall patient outcomes[10][11].

Healthcare prediction models have been greatly improved by recent advancements in ML and DL. These methods understand intricate associations from both structured and unstructured medical data, greatly increasing their power. ML algorithms efficiently perform classification and risk prediction using clinical attributes[12], while DL models automatically extract high-level representations from large and heterogeneous

datasets, resulting in improved prediction ACC and robustness[13]. However, many advanced ML models, particularly ensemble-based approaches, often operate as black-box models, where the decision-making process is difficult for clinicians to interpret and validate[14][15]. In healthcare settings, trust, clinical acceptability, and practical implementation can all take a hit due to this opaqueness. In order to provide predictions that can be understood, to find important clinical aspects, and to make the models more transparent, it is now vital to combine XAI methods with ML-based healthcare analytics [16]. AI-enabled healthcare analytics based on ML and explainable approaches provides a promising solution for developing accurate, reliable, and personalized patient risk assessment systems that support early intervention and improved healthcare outcomes.

Motivation and Contribution

The growing demand for patient risk prediction systems that are accurate, personalised, and explainable serves as the driving force for this work. Such systems would allow for the early detection of pressure ulcer risk and would promote successful clinical decision-making. Traditional machine learning methods have limited interpretability and struggle to handle complicated nonlinear interactions among varied clinical variables; as a result, they are not widely used in real-world healthcare environments [10]. Therefore, this study develops an AI-enabled healthcare analytics framework for personalized pressure ulcer risk assessment. The use of explainable AI analysis further enhances model transparency by revealing the role that certain clinical variables play in risk prediction. This research offers several key contributions as listed below:

- Using clinical data from the MIMIC-IV database, a thorough AI-based healthcare analytics framework is suggested for the purpose of personalised patient risk assessment and pressure ulcer prediction.
- Data cleansing, addressing missing values, feature engineering, normalisation, and Random Forest-based feature significance analysis are all steps in a comprehensive data processing pipeline that aims to discover important clinical predictors.
- The hyperparameter optimisation process allows for the accurate prediction of pressure ulcer risk using two machine learning models: DT and LightGBM.
- The proposed models are assessed using a variety of classification metrics, including REC, ACC, PRE, F1, confusion matrix, and ROC-AUC. This demonstrates their efficacy in comparison to other ML approaches.
- To decipher the LightGBM model and measure the role of certain clinical variables in pressure ulcer risk prediction, the suggested approach uses SHAP - based analysis.

The organization of the remaining parts of the paper: The Section II contains a survey of relevant literature; In Section III, examine the facts and ways in depth; The experimental results are presented in Section IV, and Section V concludes with a discussion of the study's shortcomings and recommendations for further research.

2. Literature Review

The suggested framework was developed with the help of an extensive literature analysis on personalised patient risk assessment and prediction. For example, G. Rajaram et al., (2026) provided a detailed cardiovascular risk assessment model using a patient sample of 303 patients which comprised of 13 clinical variables methodology incorporated innovative feature engineering techniques, creating 8 novel composite features including cardiovascular risk scores, exercise capacity indices, and interaction variables. The Enhanced Random Forest showed strong cross-validation performance (82.22%±6.67%) and earned the best individual performance (81.97% ACC, 84.51% F1). The ensemble model maintained comparable performance while providing enhanced reliability through model combination [17].

Another worked by A. J. D. Acosta et al., (2026) The impact of methodological improvement (using Grid Search with 5-fold cross-validation) and a feature selection technique (recursive feature removal) on the predictive capability was demonstrated by a comparative study using 32 machine learning algorithms in 4 distinct model configurations. Out of all the models tested, light gradient boosting machine performed the best (86.46). Consolidating SHapley Additive Explanations with interpret model decisions helped to decrease the gap between algorithmic correctness and clinical confidence [18]. Also, F. Salehi et al., (2025) applies a number of machine learning algorithms in an effort to foretell the onset and severity of RA. After their names were removed, 154 preclinical RA patients provided the accrual data. Cox Proportional Hazards, Linear Multi-Task Model, Neural Multi-Task Model, Support Vector Machines, Extreme Gradient Boosting Survival, Random Survival Forest, and Survival Tree were among the survival analysis models that were experimented with. With a mean C-index of 0.798, the Random Survival Forest model outperformed all of the others that were considered. This approach enabled more precise scheduling of RA clinical sessions by classifying patients as either low-, medium-, or high-risk. Key risk variables are identified using SHapley Additive Explanations (SHAP), which enhances model interpretability [19].

Then, O. Lohaj et al. (2025) use ML methods to predict the severity of COVID-19 in patients hospitalised to the hospital in Košice, Slovakia, who suffer from cardiovascular disease (CVD). This is done by analysing clinical data obtained from the Louis Pasteur University Hospital throughout the four waves of the pandemic. Once the pre-processing for missing values and categorical variables was completed, the models that were trained and evaluated using 5-fold cross-validation were XGBoost, decision trees, Gradient Boosting Machines (GBM), and logistic regression. Random Forest feature importance analysis typically found biomarkers such as IL-6, PBNP, CRP, and NLR as strong predictors. The two best methods that were tested—XGBoost and GBM—helped people make better decisions about how to care for COVID-19 patients, with mean AUC-ROC values between 0.91 and 0.94 [20]. And M. Jin et al. (2024) used the SMOTE to ensure that samples were evenly distributed across the two groups. The prediction models were built using five different machine learning methods. Among the five machine learning algorithms tested and compared for AIS risk prediction, the XGBoost method had the best results, with an AUC of 0.908 (95% CI 0.872-0.938) [21].

D. Balakrishnan et al., (2023) R-ANN, which stands for "Recursive feature elimination with ANN," is a new method that combines the two for improved Alzheimer's disease prediction and faster processing. By combining the two methods, and may reduce computational complexity and increase the ACC of illness prediction by using RFE to identify the most essential characteristics in the dataset. Comparing the suggested R-ANN to the RELM method for AD prediction, the empirical findings show that the former has 4.71% greater ACC, 4.6% better PRE, 3.41% better REC, and 3.37% better F-measure [22]. Lastly, Prakash, Mahesh and Gouthaman, (2023) The LR technique, a highly accurate and easily interpretable machine learning model, was used to construct a cardiac risk assessment system. The LR model was trained using thirteen characteristics, including gender, age, blood pressure, cholesterol levels, and blood pressure. The results showed that the LR technique was quite accurate (86.89%) in predicting the risk of CVD. Because of the algorithms' intricacy, healthcare providers have a hard time understanding the outcomes of CVD risk assessments [23].

Table I provides a synopsis of current research on individualized patient risk assessment and prediction, showcasing the studies' suggested models, datasets, important results, and obstacles to further study.

TABLE I. RECENT STUDIES ON PATIENT RISK ASSESSMENT AND PREDICTION USING MACHINE LEARNING TECHNQIUES

Author	Proposed Work	Dataset	Results	Limitations & Future Work
Rajaram et al. (2026) [17]	Developed an ensemble ML framework with feature engineering for cardiovascular risk prediction.	303 cardiovascular patient records with 13 clinical features.	Enhanced Random Forest achieved 81.97% Accuracy and 84.51% F1-score.	Limited dataset size; future work can validate on larger multi-center datasets and integrate real-time clinical data.
Acosta et al. (2026) [18]	Proposed Explainable AI (LightGBM + SHAP) for preoperative frailty risk prediction.	Clinical and laboratory data of elderly surgical patients.	LightGBM achieved AUC = 86.46%.	Requires external clinical validation and incorporation of additional patient-specific variables.
Salehi et al. (2025) [19]	Developed survival ML models for rheumatoid arthritis onset prediction using SHAP.	154 preclinical rheumatoid arthritis patients.	Random Survival Forest achieved C-index = 79.8%.	Small sample size; future work should evaluate larger cohorts and multimodal healthcare data.
Lohaj, Paralič and Klein (2025) [20]	Applied ML models for COVID-19 severity prediction in cardiovascular disease patients.	Clinical data collected across four COVID-19 waves.	XGBoost and GBM achieved AUC = 91–94%.	Generalizability across different hospitals remains to be investigated.
Jin, Nan and Fu (2024) [21]	Developed an XGBoost-based acute ischemic stroke risk prediction	Atrial fibrillation patient dataset.	XGBoost achieved AUC = 90.8%.	Future work should include prospective validation and larger patient populations.

	system with SMOTE and Flask deployment.			
Balakrishnan et al. (2023) [22]	Proposed Recursive Feature Elimination with ANN (R-ANN) for Alzheimer's disease prediction.	Alzheimer's disease clinical dataset.	R-ANN improved Accuracy by 4.71% over RELM.	Future work should validate using larger heterogeneous datasets.
Prakash, Mahesh and Gouthaman (2023) [23]	Logistic Regression-based cardiac risk assessment system.	Cardiovascular dataset with 13 clinical attributes.	Logistic Regression achieved 86.89% Accuracy.	Performance can be enhanced using advanced ensemble learning techniques.

Research gaps: Machine learning has shown promise in patient risk prediction in recent research, however most current methods are disease-specific, use small datasets, or rely on a single predictive model, all of which impair the methods' generalizability and prediction performance. Furthermore, several methods lack comprehensive data preprocessing and comparative evaluation of advanced ensemble algorithms. This paper recommends a framework for individualised patient risk assessment based on integrated healthcare data and evaluates the efficacy of two models, LightGBM and DT, to overcome these shortcomings. Higher quality patient risk prediction for better clinical decision-making and individualised treatment is the goal of the suggested method.

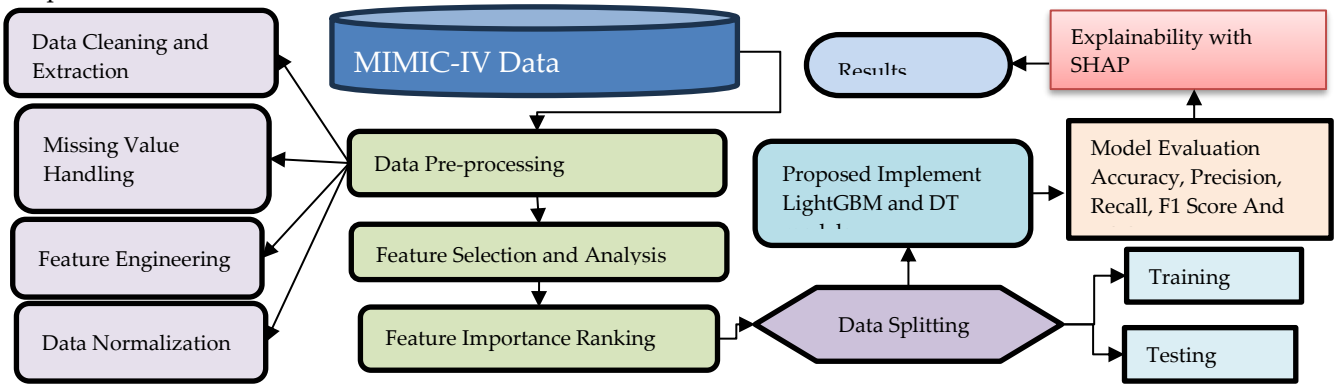

Fig. 1. Proposed flowchart for Patient Risk Assessment and Prediction using machine learning

3. Methodology

The proposed methodology presents a machine learning-based framework for personalized pressure ulcer risk prediction using the MIMIC-IV clinical dataset shows flowchart in Figure 1. Initially, patient records were extracted and integrated from the database, including demographic information, ICU-related parameters, vital signs, laboratory measurements, Braden scale assessments, and diagnosis features. The collected data underwent preprocessing steps, including data cleaning, missing value handling using debiasing/imputation techniques, feature engineering, categorical encoding, and numerical feature normalization. The foremost indications were identified via the usage of feature significance analysis based on Random Forest (Mean Decrease in Impurity). Features that are beneficial in the clinic were selected. In order to effectively create the models, the dataset was partitioned into training and testing sets after processing. Decision Tree (DT) and Light Gradient Boosting Machine (LightGBM) were both machine learning classifiers that were fine-tuned using hyperparameters to improve prediction ACC. Confusion matrix measures, including F1, REC, ACC, PRE, and ROC-AUC, were used to evaluate the proposed models at the end. A reliable decision-support system that can rapidly identify patients at high risk of developing pressure ulcers is the ultimate aim of the framework.

A comprehensive breakdown of the suggested procedure is provided in the section that follows:

A. Data collection and Analysis

The MIMIC-IV relational database, which includes all aspects of a patient's experience in a hospital, such as procedures, drugs, laboratory results, and imaging analysis, is used as the data source for the current study [24]. A bespoke HER for the entire hospital as well as a clinical information system tailored to the intensive care unit (ICU) are the two back-end databases that contributed to this database. The MIMIC-IV database did not undergo data cleaning procedures to guarantee it was representative of a real-world clinical dataset when it was being prepared. By applying a day-ago offset, de-identification causes date and time data to randomly

move into the future. While data from individual individuals is consistent with itself, there is no way to compare data from different patients across time. A PU prediction database was created using MIMIC-IV data, which included 4652 patients with PU and a control group of the same size that was randomly selected. Keep in mind that units are irrelevant to the ML classification model because they are needed to be normalized with the input variables.

Figure 2: MIMIC-IV dataset feature correlation matrix. This is the Pearson correlation between a number of variables: age, ICU stay duration, fluid intake and output, height, weight, blood pressure, glucose, O_2Sat, Braden scale scores (sensory perception, moisture, activity, mobility, nutrition, and friction/shear), total protein, albumin, and bilirubin. The heatmap also shows the relationships between these variables. Most features show weak to moderate correlations, indicating low multicollinearity and supporting their use in pressure ulcer prediction.

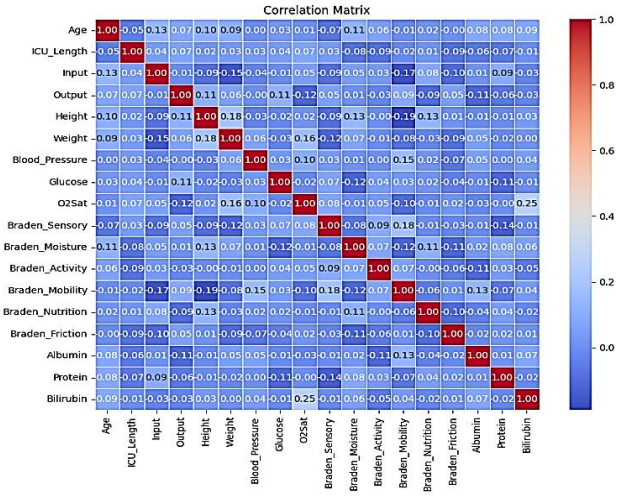

Fig. 2. Feature Correlation Matrix of the MIMIC-IV dataset

B. Data Pre-processing

The MIMIC-IV dataset was utilized for data preparation, which included data integration, cleansing, and feature engineering[25]v. The main preprocessing procedures are summarized as follows:

Data Extraction

A total of 4,652 individuals afflicted with pressure ulcers (PU) and an additional 4,652 patients without PU were culled from the MIMIC-IV relational database. The extracted data contained demographic information, ICU records, laboratory measurements, vital signs, and clinical assessments.

Data Cleaning

The dataset was prepared for cleaning by eliminating duplicate records and patients who did not survive their hospital stay, did not have their pressure ulcer diagnosis date documented, or had a high percentage of missing or null values. This ensured that only complete and reliable records were used for analysis.

Missing Value Handling

Since the clinical dataset contained missing values, a debiasing (imputation) technique was applied to estimate missing entries and reduce bias caused by incomplete data. This step improved data quality while retaining as many patient records as possible.

Feature Selection and Engineering

Twenty-three clinically relevant features were selected, including demographic information, ICU-related variables, vital signs, laboratory measurements, Braden scale scores, and diagnosis variables[26]. Feature selection was performed using the Random Forest Feature Importance (Mean Decrease in Impurity, MDI) technique, which ranks features based on their contribution to reducing impurity across DTs. Higher feature importance values indicate a greater contribution to pressure ulcer prediction. One Boolean feature was also created out of many fracture-related ICD-9 codes, and numerical representations were encoded for categorical factors like gender and ethnicity so that machine learning models could be trained.

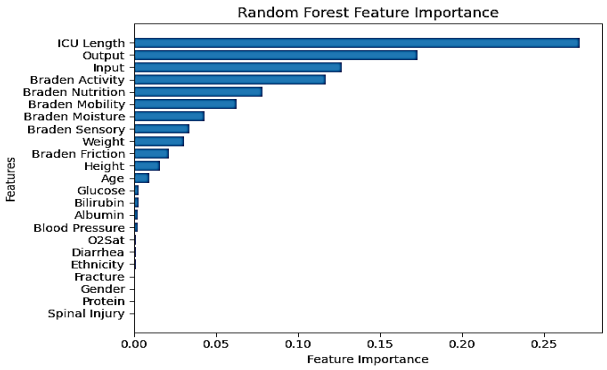

Fig. 3. Random Forest feature importance of the selected MIMIC-IV dataset features

Figure 3 bar chart presents the importance scores of the 23 input features computed using the Random Forest Mean Decrease in Impurity (MDI) technique. ICU length of stay, fluid output, fluid intake, Braden activity, and Braden nutrition were identified as the most influential predictors of pressure ulcer occurrence, while demographic and diagnosis variables showed comparatively lower importance. The chart highlights the proportional contribution of each feature to the prediction model.

Data Normalization

Normalising the numerical characteristics before training the model made sure that all the variables were on the same scale. This preprocessing procedure improved the ML models' performance by reducing the dominance of characteristics with larger numerical

ranges during learning. The Min-Max normalisation and Eq.1 were used to scale each feature to the range [0, 1]:

$$X_{\text{norm}} = \frac{X - X_{\min}}{X_{\max} - X_{\min}} \qquad (1)$$

where: X is the first value of the feature, $X_{\min}$ is is its lowest, $X_{\max}$ is its highest, and X_{norm} is its normalised value. This change guarantees that all characteristics contribute equally during model training while preserving the relative connections among the data.

C. Data Splitting

The information was cleaned up first, and then it was split into training and testing sets to see how well the ML models worked. The training set covered 80% of the data and was used to train the models. The testing set covered 20% of the data and was used to evaluate how well the models predicted unknown data. The split was performed randomly to ensure an unbiased distribution of pressure ulcer and non-pressure ulcer cases across both subsets. This method reduces the likelihood of overfitting while evaluating the model's generalisability.

D. Implementation of the Proposed Models

In this study, the proposed LightGBM and DT models were implemented for personalized patient risk assessment and prediction in healthcare analytics, enabling accurate classification of patient risk by learning complex relationships among clinical and demographic features.

Proposed Light Gradient Boosting Machine (LightGBM) Model

The suggested LightGBM is a powerful ensemble ML technique built on the GBDT architecture. To improve classification performance, reduce memory consumption, and speed up training, LightGBM uses a histogram-based optimisation technique for leaf-wise tree development. Using optimised hyperparameters, this study classified healthcare data using the suggested LightGBM model, which resulted in the prediction function shown in Equation (2) being robust and accurate.

$$F(x) = \sum_{m=1}^{M} \eta f_m(x) \qquad (2)$$

The objective function is shown in Equation (3), where $F(x)$ is the final prediction, M is the total number of trees, η is the learning rate, and $f_m(x)$ is the prediction of the m^{th} DT.

$$Obj = \sum_{i=1}^{N} L(y_i, \hat{y}_i) + \sum_{m=1}^{M} \Omega(f_m) \qquad (3)$$

The loss function between the actual and predicted outputs is denoted as $L(y_i, \hat{y}_i)$, and the regularisation term that limits the complexity of the model and reduces overfitting is denoted as $\Omega(f_m)$. Learning rate = 0.05, number of estimators = 200, maximum depth = 8, number of leaves = 31, feature fraction = 0.80, bagging fraction = 0.80, bagging frequency = 5, minimum child samples = 20, and random state = 42 were the optimised hyperparameters used to train the proposed LightGBM model. Compared to traditional boosting algorithms, LightGBM has higher generalization, faster training, and reduced memory consumption, making it ideal for large-scale clinical datasets.

Proposed Decision Tree (DT) Model

Data classification is accomplished by the suggested DT, a supervised learning method, by recursive feature space partitioning into homogenous groups. The tree begins from the root node and selects the most informative feature for splitting using an impurity measure[27]. The decision-making criteria are represented by the internal nodes, while the final class labels are represented by the leaf nodes. The proposed Decision Tree provides high interpretability, fast prediction, and efficient handling of nonlinear relationships within the healthcare dataset, Entropy is show in Equation (4).

$$Entropy(S) = \sum_{i=1}^{C} p_i log_2(p_i) \qquad (4)$$

This is where C represents the total number of classes and pi is the probability of class i. Entropy is a measure of the dataset's impurity before to splitting, and Equation (5) shows the information gain

$$Gain(S, A) = Entropy(S) - \sum_{v \in Values(A)} \frac{|S_V|}{S} Entropy(s_v) \qquad (5)$$

The given sentence describes the relationship between the total number of training samples |S|, the subset s_v that is produced after splitting on attribute A, and the selected attribute A. The DT uses the attribute that yields the newest information to make its selection. The following optimized hyperparameters were used to execute the required Decision Tree model: criterion= gini, splitter= best, maximum depth= 10, minimum samples split= 5, minimum samples leaf= 2, maximum features= sqrt, and random state= 42. DT can process numerical and categorical characteristics with ease, and it is also easy to understand and use.

E. Evaluation Metrics

Normal classification metrics were used to judge how well the proposed model worked. An initial step in summarising the classification findings was to create a confusion matrix that recorded the total number of correctly and incorrectly classified cases. From the confusion matrix, four main metrics were extracted: True Positives (TP), False Positives (FP), True Negatives (TN), and False Negatives (FN). According to the explanations in (6) to (9) below, these measurements were used to

calculate important evaluation metrics including ACC, PRE, REC, and F1:

$$\text{Accuracy} = \frac{\text{TP+TN}}{\text{TP+FP+TN+FN}} \quad (4)$$

$$\text{PR} = \frac{\text{TP}}{\text{TP+FP}} \quad (5)$$

$$\text{Recall} = \frac{\text{TP}}{\text{TP+FN}} \quad (6)$$

$$F1 - Score = 2 \times \frac{Precision \times Recall}{Precision + Recall} \quad (7)$$

The following values are used to evaluate the model's performance: ACC, PRE, REC (sensitivity), and the F1, which provide a balanced evaluation of the model, particularly for class imbalance classification tasks, by representing the harmonic mean of REC and PRE. ACC measures the overall proportion of correctly classified instances. PRE indicates the proportion of correctly predicted positive cases among all predicted positives. Furthermore, the AUC is a measure of the classifier's overall performance; a greater AUC indicates stronger prediction capacity. To evaluate the model's discriminating power, the ROC curve displays the TPR versus the FPR at different classification thresholds. All of these indicators when combined give a thorough picture of how well and how resilient the models are that have been suggested.

4. Results and Discussion

The experimental setup is described in this part, and the recommended models' effectiveness, reliability, and computation efficiency are evaluated during multiple evaluation phases using typical performance criteria. A system running Windows 11 (64-bit), with hardware specifications including an Intel Core i7-13620H CPU, 24 GB of RAM, and an NVIDIA GeForce RTX 4060 Ti (24 GB) GPU, was used for the experimental assessment. The suggested framework was built with Python 3.11 in PyCharm Community Edition 2024, and PostgreSQL 16 was utilised for database administration and data storage. Several Python libraries were used in the implementation. These included NumPy and Pandas for data manipulation and preprocessing, Scikit-learn for decision tree model implementation and performance evaluation, LightGBM for gradient boosting-based classification, Matplotlib and Seaborn for data visualisation, and SciPy for statistical computations. Training, testing, visualising, and evaluating model performance on the MIMIC-IV dataset were all made efficient using this software and hardware arrangement.

A. Experimental Results

The MIMIC-IV dataset was used to compare the proposed LightGBM and Decision Tree (DT) models for pressure ulcer prediction (Table II). With an ACC rate of 96.1%, PRE of 94.8%, REC of 91.9%, F1 of 93.1%, and ROC-AUC of 99.04%, the LightGBM model had superior classification performance compared to the competitors. A decision tree model, on the other hand, managed a 95.9% ACC rate, 90.1% PRE rate, 91.4% REC rate, 90.9% F1, and 98.02% ROC-AUC. Although both models demonstrated high predictive capability, the LightGBM model consistently outperformed the Decision Tree across most evaluation metrics, particularly in terms of PRE, F1, and ROC-AUC. These findings indicate that LightGBM provides better discrimination between pressure ulcer and non-pressure ulcer cases and is more effective for clinical risk prediction.

CLASSIFICATION RESULTS OF PROPOSED MODELS

Matrix	LightGBM	Decision Tree
Accuracy	96.1	95.9
Precision	94.8	90.1
Recall	91.9	91.4
F1-score	93.1	90.9
ROC-AUC	99.04	98.02

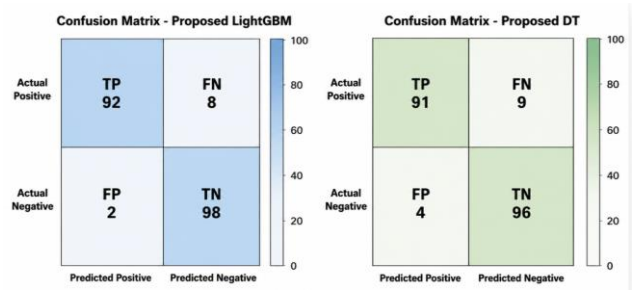

Fig. 4. Confusion Matrix for the proposed Models (LGBM and DT)

Figure 4 presents the confusion matrices of the proposed LightGBM and DT models for patient risk prediction. The proposed LightGBM model correctly classified 92 positive and 98 negative instances, with only 8 false negatives and 2 false positives, demonstrating superior classification performance. Similarly, the proposed DT model correctly identified 91 positive and 96 negative instances while producing 9 false negatives and 4 false positives. The results indicate that the proposed LightGBM model achieved fewer misclassifications than the DT model, confirming its higher prediction ACC and reliability for personalized patient risk assessment.

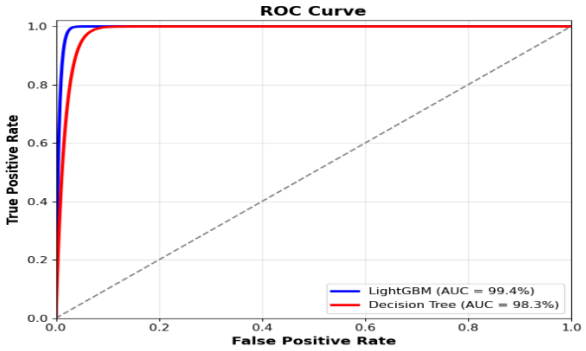

Fig. 5. ROC Curve for the proposed models

Figure 5 illustrates the classification performance of the two ML models by comparing the TPR against the FPR. Both curves remain close to the upper-left corner of the graph, indicating excellent discrimination capability

and high predictive ACC. The LightGBM model achieves a slightly higher AUC of 99.4% compared to the DT model with an AUC of 98.3%, demonstrating its superior classification performance. Overall, the figure confirms that both models effectively distinguish between the positive and negative classes, with LightGBM providing the best overall predictive results.

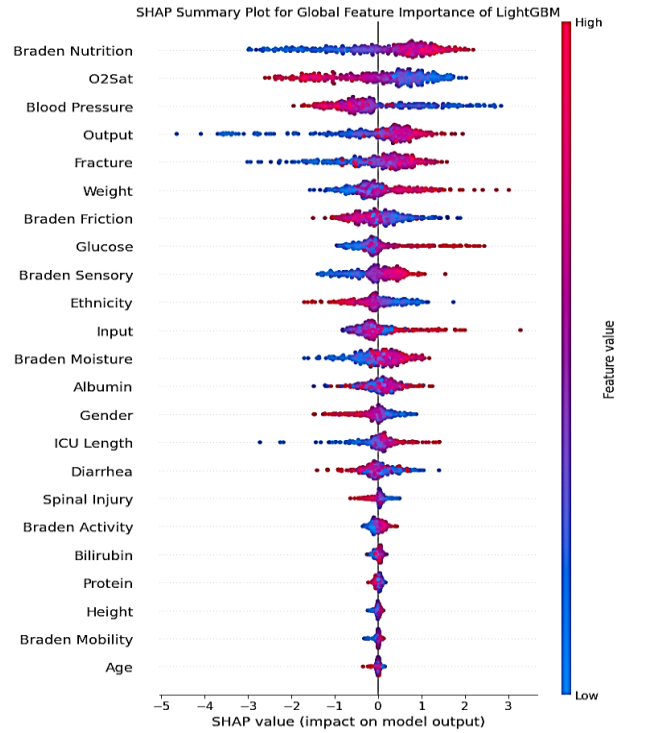

Fig. 6. Global Feature Importance Analysis of LightGBM Using SHAP

Using SHAP analysis, Figure 6 shows the global feature relevance of the proposed LightGBM model. The SHAP summary plot ranks feature by their impact on the LightGBM model's predictions. Braden Nutrition is the most influential feature, with lower values associated with increased predicted risk. O2Sat and Blood Pressure are also strong predictors, where reduced values contribute to higher risk. Other variables, including Output, Fracture, Weight, Glucose, and Braden Scale components, show moderate influence, while Bilirubin, Protein, Height, and Age have minimal impact, with SHAP values concentrated near zero.

B. Comparative Analysis

The suggested models' performance is compared to that of previously published machine learning methods in Table III. Along with the suggested DT and LightGBM models, also compare RF, KNN, SVM, XGBoost, and more. Based on the results, the suggested LightGBM outperformed all of the other approaches with respect to ACC (96.1%), PRE (94.8%), REC (91.9%), and F1 (93.1%). Additionally, the suggested Decision Tree demonstrated competitive performance, with an F1 of 90.9% and an ACC of 95.9%. This is in contrast to the inferior classification performance provided by the current RF, KNN, SVM, and XGBoost models. If these results hold, then the suggested LightGBM model outperforms the state-of-the-art machine learning approaches when it comes to personalised patient risk prediction.

TABLE II. COMPARISON OF PREDICTIVE MODELS

Model	Accuracy	Precision	Recall	F1-score
RF[28]	67.72	67.90	67.72	66.96
KNN[29]	77.82	84.45	86.31	77.57
SVM[30]	0.80	0.89	0.80	0.84
XGBoost[31]	0.8728	8690	8655	8670
Proposed DT	95.9	90.1	91.4	90.9
Proposed LightGBM	96.1	94.8	91.9	93.1

This study had a number of limitations, even if it achieved encouraging results. The suggested models may not be applicable to other hospitals or patient groups since, first, they were created and tested using data from just one database (MIMIC-IV). Secondly, imputation methods were used to fill up the dataset's missing clinical information, which might have introduced ambiguity. There is a lack of integration of unstructured data like medical photographs, real-time monitoring signals, and clinical notes into the existing models, which mostly depend on organised clinical factors. Integrate deep learning techniques with multimodal clinical information, use multi-center healthcare datasets to validate the proposed strategy, and create explainable artificial intelligence (XAI) methodologies to increase model transparency and clinical acceptability in future work. Early intervention and individualised patient care can be enhanced via the exploration of real-time deployment in healthcare environments.

5. Conclusion

Predicting a patient's likelihood of getting a disease or other health problem from their clinical and demographic data is known as patient risk prediction. Using the MIMIC-IV clinical dataset, this study suggested machine learning-based methods for personalized pressure ulcer risk prediction, such as DT and LightGBM models. Outperforming more conventional machine learning methods like XGBoost, RF, KNN, and SVM, the experimental findings showed that the suggested LightGBM model had the best prediction performance, with a ROC-AUC of 99.04% and an ACC of 96.1%. The results show that high-risk patients may be identified and early clinical decision-making can be supported to prevent pressure ulcers using machine learning approaches. However, this study has limitations, including evaluation on a single-centre dataset, dependency on structured clinical variables, and the presence of missing patient information. Future studies will focus on validating the proposed framework using multi-centre healthcare datasets, integrating multimodal data sources such as clinical notes and medical images,

applying advanced deep learning and explainable AI techniques, and developing real-time clinical decision support systems to improve personalized patient care and early intervention.

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