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Machine Learning Models for Metabolic Syndrome Identification with Explainable AI

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Abstract

Metabolic syndrome (MetS) is a cluster of interrelated risk factors, including hypertension, dyslipidemia, central obesity, and insulin resistance, significantly increasing the likelihood of cardiovascular diseases and type 2 diabetes. Early identification of hypertension, a key component of MetS, is essential for timely intervention and effective disease management. This research aims to develop a hybrid machine learning model that integrates XGBoost classification with K-Means clustering to enhance or strengthening of hypertension prediction and identify distinct patient subgroups based on metabolic risk factors. The dataset consists of 1,878 patient records with metabolic parameters such as systolic and diastolic blood pressure, fasting glucose, cholesterol levels, and anthropometric measurements. Model performance was assessed using accuracy, precision, recall, F1-score, and ROC-AUC. The proposed XGBoost model achieved an outstanding classification performance with 98% accuracy, 98% precision, 98% recall, 98% F1-score, and an ROC-AUC of 1.00. K-Means clustering further identified five distinct patient subgroups with varying metabolic risk profiles. The findings underscore the potential of machine learning-driven decision support systems in improving hypertension diagnosis and MetS management.

Keywords : *Explainable AI, Hypertension, K-Means, Machine Learning, Metabolic Syndrome, XGBoost.*

1. INTRODUCTION

Metabolic syndrome, characterised by hypertension, hyperglycemia, dyslipidaemia, and central obesity, elevates the risk of cardiovascular disease, type 2 diabetes, and further metabolic disorders[1]. Due to the often non-specific and gradual onset of metabolic syndrome symptoms, early identification is essential. Hypertension, a principal risk factor for this condition, is characterised by persistently elevated blood pressure, potentially damaging essential organs[2]. This study employs machine learning and explainable AI to identify metabolic syndrome, emphasising hypertension. This study examines a hybrid model that integrates K-Means clustering with XGBoost to tackle the challenge of identifying complex situations involving several risk indicators. K-Means, an unsupervised learning technique, may uncover latent patterns in intricate clinical data, while XGBoost, a robust boosting algorithm, is proficient in classification and prediction tasks[3]. This work aims to develop a model that precisely identifies metabolic syndrome, including hypertension, by integrating the advantages of both algorithms and offering enhanced understanding of the relationships among its constituent risk factors[4]. Metabolic syndrome (MetS) denotes a collection of risk factors that elevate the likelihood of cardiovascular disease and diabetes. Obesity, especially central obesity, hypertension, dyslipidaemia (elevated triglycerides and diminished HDL cholesterol), insulin resistance, and an unhealthy lifestyle

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are the predominant risk factors[5]. Central obesity is critical due to the production of adipokines by abdominal adipose tissue, which fosters inflammation and metabolic dysfunction [6][7]. Hypertension and Metabolic Syndrome (MetS) exhibit a reciprocal association, wherein hypertension induces MetS and vice versa. Dyslipidaemia is often associated with insulin resistance and obesity. Insulin resistance is a hallmark of Metabolic Syndrome, leading to increased blood glucose levels. Unhealthy lifestyle choices, including insufficient physical exercise and inadequate nutrition, contribute to the onset of MetS [8],[9]. The correlation between hypertension and other metabolic illnesses suggests a same pathophysiological process, including insulin resistance and activation of the sympathetic nervous system[10],[11]. Hypertension serves as both a diagnostic indicator for MetS and a predictor of more severe manifestations, including non-alcoholic fatty liver disease and cardiovascular complications[5]. Hypertension is currently regarded as a critical element of metabolic syndrome due to its role in elevating the risk of target organ damage[12].

K-Means is an effective clustering algorithm for identifying concealed patterns in large, complex medical datasets. The fundamental principle of K-Means is to decrease intra-cluster variance while maximising inter-cluster variation via an iterative methodology[13]. The method commences with the random selection of K initial centroids, followed by the allocation of each data point to the nearest centroid based on a distance metric[14],[15]. Subsequent to the allocation of data points to clusters, the algorithm recalibrates the centroids by computing the mean of all data points inside each cluster. This procedure will persist until the termination criteria are satisfied. K-Means offers benefits regarding processing speed and the ability to identify concealed patterns without labelled data. K-Means has limitations, including sensitivity to the initial location of centroids and assumptions regarding cluster forms[16]. XGBoost is a proficient boosting technique capable of addressing several challenges in medical data classification, including overfitting and large datasets [17]. XGBoost excels in predictive tasks due to its ability to manage complex data and nonlinear interdependencies among variables. The integration of K-Means and XGBoost can enhance the accuracy of hypertension prediction[18]. This hybrid model leverages the attributes of both methodologies, utilising K-Means for data segmentation and XGBoost for enhanced classification and prediction accuracy[19]. This hybrid methodology can diminish data noise, enhance computational efficiency, and yield more dependable forecasts. Utilising Explainable AI (XAI) in conjunction with the SHAP approach enhances model interpretability, facilitating a more lucid comprehension of each feature's impact on predictions[20].

Previous research has shown that K-Means and XGBoost are good at classifying things and finding patterns in medical data, which is why they were chosen for this study. K-Means is a clustering algorithm that puts patient data into groups based on metabolic traits that are similar[21]. This makes it easier to find hidden patterns in the dataset. This fits with earlier research that showed K-Means could effectively divide patients at risk of high blood pressure into groups based on physiological factors. XGBoost is a decision tree-based algorithm that is known for being able to handle large datasets and accurately show how variables are related in ways that aren't linear[22]. Previous research has shown that XGBoost is better than other machine learning methods at diagnosing chronic diseases like high blood pressure[23]. It does this by being more accurate and easier to understand. The integration of these two methods facilitates a more precise identification of hypertension through a data-driven approach, while simultaneously creating opportunities for personalized health recommendations derived from patterns observed within patient groups.

The implementation of Explainable Artificial Intelligence (XAI) enhances the interpretability of predictive results, providing medical professionals with a clearer understanding of the model's decision-making process[24]. Transparency is essential for cultivating trust and facilitating the therapeutic application of these approaches. This project seeks to enhance the development of robust and

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interpretable decision support systems in healthcare for the early detection and management of metabolic disorders.

Previous studies on hypertension and MetS diagnosis using machine learning have primarily focused on single-method classification approaches, such as Support Vector Machines and Random Forest, without considering the heterogeneity of patient metabolic profiles. In previous research in [25], the random tree forest model provided the best performance in predicting hypertension, which had previously been compared with six other machine learning algorithm models. Then in the study [26], it was proven that in classifying arterial hypertension, linear quadratic DA would be more relevant, These approaches have high classification scores and low deviations over different realizations.

The next research on hypertension detection uses SSVM or swarm-based support vector machine, which can be considered acceptable because, based on comparisons with seven other models, SSVM provides the best performance[27]. These methods often overlook hidden subgroups within the data, limiting their ability to provide personalized risk assessments. Additionally, existing models struggle to handle complex nonlinear interactions between metabolic risk factors, reducing predictive accuracy and interpretability. To address these gaps, this study introduces a hybrid approach that integrates K-Means clustering and XGBoost classification, allowing for both patient segmentation and enhanced predictive modeling. This novel combination not only improves hypertension detection accuracy but also identifies distinct metabolic subgroups, enabling more personalized interventions. Furthermore, the incorporation of Explainable AI (XAI) using SHAP analysis enhances model transparency, ensuring that clinical decision-making is both data-driven and interpretable, which is often lacking in previous studies.

Additionally, the incorporation of Explainable AI (XAI) using SHAP analysis ensures that the decision-making process remains transparent and interpretable, addressing a critical challenge in AI-driven medical diagnostics[28]. By clearly identifying key predictors such as systolic and diastolic blood pressure, waist circumference, and fasting glucose, the model enhances clinical decision support systems (CDSS), fostering trust among medical practitioners. This research paves the way for AI-powered precision medicine, improving early intervention strategies and reducing the long-term burden of cardiovascular diseases and diabetes in global healthcare systems.

2. METHOD

This section explains in detail the methodological steps applied in this study, from data collection to the evaluation model. This study concentrates on hypertension and utilises advanced machine learning (ML) methods alongside Explainable Artificial Intelligence (XAI) to identify metabolic syndrome (MetS) through a quantitative, cross-sectional research approach. The methodological framework comprises data preparation, feature selection, model creation, validation, and interpretability analysis, which will be displayed in Figure 1.

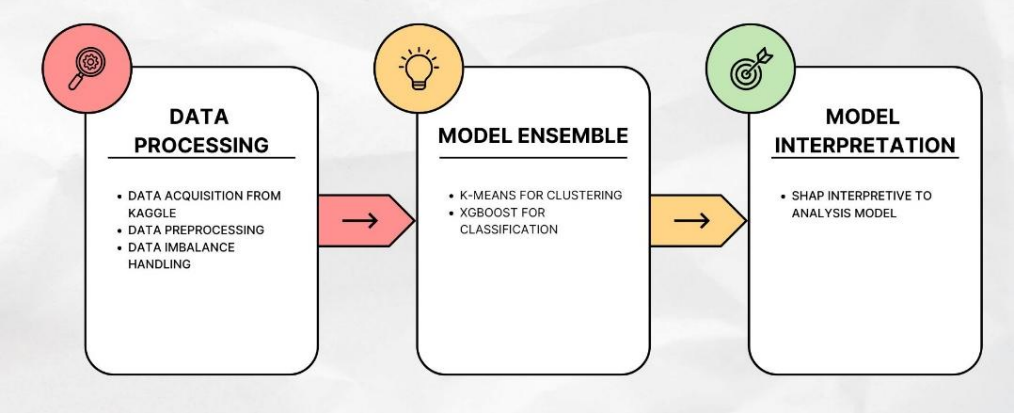

Figure 1. Technical Approach

2.1. Data Processing

2.1.1. Data Acquisition

Individuals engaged in research utilize the dataset available from the Kaggle repository. The dataset encompasses essential clinical characteristics such as systolic and diastolic blood pressure, fasting plasma glucose levels, lipid profiles (including HDL, LDL, and triglycerides), body mass index (BMI), waist circumference, as well as behavioral factors like physical activity and dietary patterns. From the total of 1.878 data samples in the dataset, we noted.

2.1.2. Data Preprocessing

This investigation undertakes comprehensive preprocessing to improve data quality and bolster model robustness. The process of data cleaning involves the elimination of duplicates, thereby improving data quality and aiding in the preparation phase that follows.

2.1.3. Data Imbalance Handling

This research applies 5-Fold Cross-Validation to evaluate the model's performance more accurately and ensure stable results across various data subsets. This technique divides the dataset into five folds, where each fold is alternately used as test data while the other folds are used for training. This approach helps reduce bias due to data imbalance and improves the model's generalization in classifying hypertension.

2.2. Model Ensemble

2.2.1. Machine Learning Models

Two fundamental algorithms were implemented: K-Means Clustering and XGBoost Classifier. K-Means is employed for unsupervised learning to identify hidden patterns in the dataset[29]. The algorithm systematically refines centroids to reduce intra-cluster variance. The centroid is modified based on the number of clusters required to ascertain the severity of the patient's hypertension. The XGBoost Classifier was utilized for supervised learning tasks, taking advantage of its gradient boosting framework to improve classification performance. In contrast to adaptive and gradient boosting, XGBoost employs advanced regression trees within its algorithm, leading to the development of what is now referred to as a reborn tree. In contrast to gradient boosting, the XGBoost tree initiates with a single leaf rather than multiple leaves. The regularization and gradient boosting steps of XGBoost are essential components that cannot be overlooked. XGBoost has established itself as one of the leading boosting algorithms available for a significant period.

2.2.2. Model Training and Evaluation

The dataset was partitioned into training (80%) and testing (20%) subsets using stratified sampling to preserve class distribution. Model performance was rigorously evaluated using Classification Metrics, such as accuracy, precision, recall, F1-score, and Matthews correlation coefficient (MCC). Next, Clustering Validation include silhouette score, Davies-Bouldin index, and Calinski-Harabasz index. And ROC-AUC Curve for assessing the discriminative power of classification models.

2.3. Model Interpretation

2.3.1. Explainable AI (XAI) Integration

To improve transparency, SHapley Additive exPlanations (SHAP) were incorporated to clarify feature contributions to model predictions. SHAP summary plots, dependence plots, and force plots

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offered detailed insights into model decision-making, enhancing clinical interpretability and trust. SHAP functions elucidate the impact of key determinants in identification, highlighting which variable predominantly influences the prediction output. Prior to achieving a strong approach to interpretability, XAI will naturally have some risks and failures in AI predictions, just like any new medical technology, treatment, or drug. XAI should be regarded as a supplementary tool rather than a substitute for conventional medical practice, with expert supervision remaining essential for final decision-making[28].

3. RESULT

3.1. Data Processing

This table outlines the demographic and clinical characteristics of the study population. Important factors encompass age, BMI, blood pressure, both systolic and diastolic measurements, HbA1c, fasting glucose levels, and lipid profiles.

Table 1. Dataset Description and Analysis

Feature	Mean	Std Dev	Min	Max
Age	55.04	20.52	20.00	90.00
BMI	27.69	7.19	15.03	39.99
SystolicBP	134.05	25.61	90.00	179.00
DiastolicBP	89.86	17.33	60.00	119.00
FastingBloodSugar	135.20	37.52	70.07	199.94
HbA1c	6.98	1.74	4.00	9.99
CholesterolTotal	225.01	43.37	150.06	299.99
CholesterolLDL	124.66	42.91	50.06	199.90
CholesterolHDL	60.06	23.32	20.01	99.96
CholesterolTriglycerides	227.39	101.07	50.15	399.89

Table 1 presents the statistical summary of key health-related features in the dataset, including central tendency and variability measures such as mean, standard deviation, minimum, and maximum values.The dataset includes Age, with an average of 55.04 years (ranging from 20 to 90 years), and BMI, which has a mean of 27.69 and a standard deviation of 7.19, indicating variability in body mass index values. Blood pressure measurements are provided, including Systolic Blood Pressure (SystolicBP) and Diastolic Blood Pressure (DiastolicBP), which have mean values of 134.05 mmHg and 89.86 mmHg, respectively. These values suggest a population with elevated blood pressure levels, as systolic and diastolic readings exceed normal thresholds. Fasting Blood Sugar levels vary widely, with a mean of 135.20 mg/dL and a standard deviation of 37.52, suggesting the presence of individuals with high glucose levels. Similarly, HbA1c levels, an indicator of long-term glucose control, have a mean of 6.98%, with a maximum of 9.99%, suggesting a high prevalence of diabetes or prediabetes in the dataset. Cholesterol-related features are also included, showing varying levels of lipid profiles. Total Cholesterol has a mean of 225.01 mg/dL, while LDL Cholesterol averages 124.66 mg/dL. HDL Cholesterol, which is considered beneficial, has a mean of 60.06 mg/dL. Lastly, Triglycerides show a high mean of 227.39 mg/dL, with a standard deviation of 101.07, indicating significant variations in fat levels among individuals.

The next step is to perform data imbalance handling, where the author used 5-fold cross-validation, the results are shown in Table 2.

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Table 2. Cross-Validation

Fold	Accuracy Score
1	0.9873
2	0.9841
3	0.9873
4	0.9905
5	0.9905
Mean Accuracy	0.9879
Standard Devation	0.0024

The choice of 5-Fold Cross-Validation in this study was based on how well it balances model accuracy, computational efficiency, and reducing bias caused by uneven data. This method provides a compromise between bias and variance, where a smaller number of folds can lead to biased accuracy estimates, while a larger number can increase variance due to smaller data subsets. When it comes to efficiency, this method works really well for K-Means and XGBoost-based models, which are very complicated to compute, compared to slower methods like 10-Fold or Leave-One-Out Cross-Validation. Additionally, the use of stratified 5-fold cross-validation helps maintain a proportional class distribution in each fold, thereby reducing the risk of bias toward the majority class and enhancing the model's ability to recognize the minority class. According to the validation results in Table 2, the method works 98.79% of the time with a standard deviation of 0.0024. This means that it is stable and consistent when evaluating models without losing efficiency or overfitting. Therefore, 5-Fold Cross-Validation was chosen as the optimal validation method in this study.

3.2. Model Ensemble

3.2.1. K-Means (Clustering Analysis)

Prior to clustering, the machine learning process involved data cleaning, which included the removal of duplicate entries. A total of 303 data points were identified as suitable for removal to enhance overall quality. The K-Means algorithm was employed to ascertain optimal clustering through the application of the Elbow method and the evaluation of Silhouette scores. The clustering outcomes identified unique patient subgroups defined by differing degrees of metabolic risk factors. Figure 2 below illustrates the separation of clusters in the feature space.

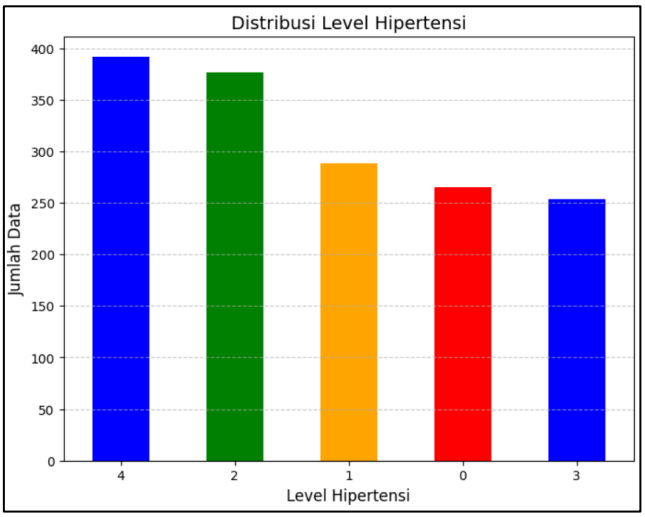

Figure 2. Cluster Visualization

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This study categorizes hypertension clustering into five levels: a score of 0 indicates low blood pressure, 1 signifies normal blood pressure, 2 represents pre-hypertension, 3 denotes first-stage hypertension, and 4 corresponds to second-stage hypertension, which poses the highest danger.

The results of the PCA analysis in Figure 3, show that the hypertension data can be broken down into two main parts that each have their own unique structure. This makes four separate clusters. The color variation in the scatter plot signifies a robust association between the hypertension labels and the data distribution patterns, indicating that the employed features provide substantial discriminative ability. The distinct separation of clusters suggests a significant potential for employing machine learning techniques to enhance the accuracy of hypertension prediction and classification.

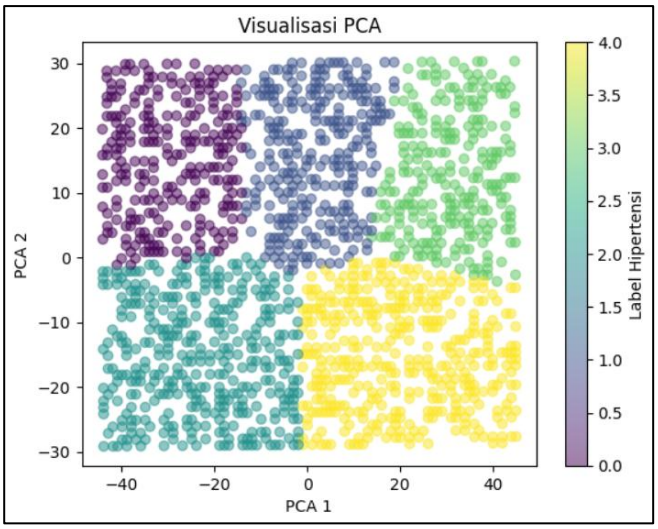

Figure 3. PCA Visualization

3.2.2. Xgboost (Classification Performance)

The XGBoost classifier demonstrated robust performance in identifying hypertension. The optimised XGBoost model attained an accuracy of 98.10% and an MCC score of 0.9759, indicating excellent performance in classification. From Table 3, the classification report indicates that each class exhibits great precision, recall, and F1-score, particularly classes 0, 2, and 4, which attain about 100% prediction accuracy. Classes 1 and 3 exhibit marginally lower results, although remain above 95%, showing the model's proficiency in pattern recognition. The macro and weighted averages (macro avg. and weighted avg.) attained 98%, signifying a balanced prediction across categories. This model is highly dependable for classification jobs with an adequate data dispersion.

Table 3. Performance Metrics of the XGBoost Model

Accuracy After Tuning: 0.9810				
Classification Report:				
	Precision	**Recall**	**F1-Score**	**Support**
0	1.00	1.00	1.00	47
1	0.96	0.95	0.95	56
2	0.99	0.99	0.99	81
3	0.96	0.98	0.97	48
4	0.99	0.99	0.99	84
Accuracy			0.98	316
Macro avg	0.98	0.98	0.98	316
Weighted avg	0.98	0.98	0.98	316

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Grid search with many parameter combinations was used for XGBoost model hyperparameter tuning process. The learning rate is set low at 0.05 to guarantee steady learning; max depth is changed between 3 and 4. We use between 250 and 300 n_estimators; a subsample of 0.7 aids in preventing overfitting. Setting Colsample_bytree to 0.5 helps to regulate the feature count in every tree. To establish the minimum number of samples per leaf, Min_child_weight was evaluated with values 3 and 5. Along with gamma (0, 0.1) as a control for tree branch pruning to enhance model generalization, regularization is also evaluated with reg_alpha (0, 0.1) and reg_ lambda (1, 2) to avoid too great model complexity.

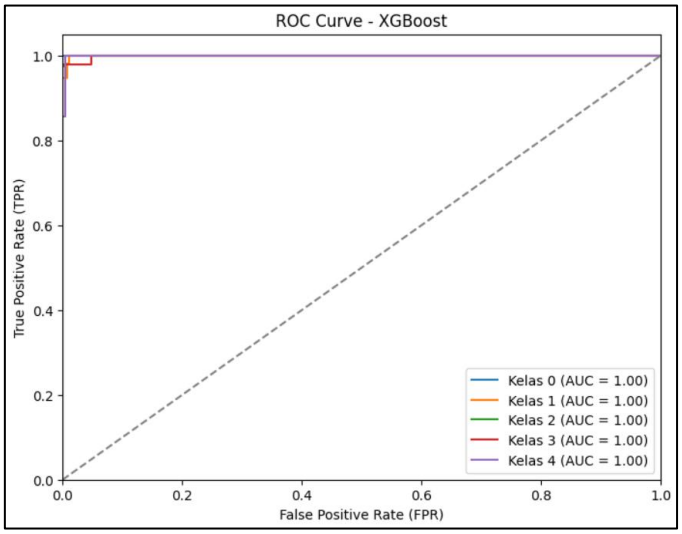

Figure 4. ROC-AUC Curve

Figure 4 shows the model's performance in distinguishing classes using the Receiver Operating Characteristic (ROC) Curve. The X-axis represents the False Positive Rate (FPR), while the Y-axis shows the True Positive Rate (TPR). Based on the results, all classes (0, 1, 2, 3, and 4) have an AUC (Area Under Curve) of 1.00, which means the model has perfect performance in separating positive and negative classes without error. It can be concluded that the XGBoost model used in this classification has very high accuracy, with AUC-ROC reaching 1.00 for all classes. This shows that the model is able to distinguish each class perfectly, without a trade-off between sensitivity and specificity.

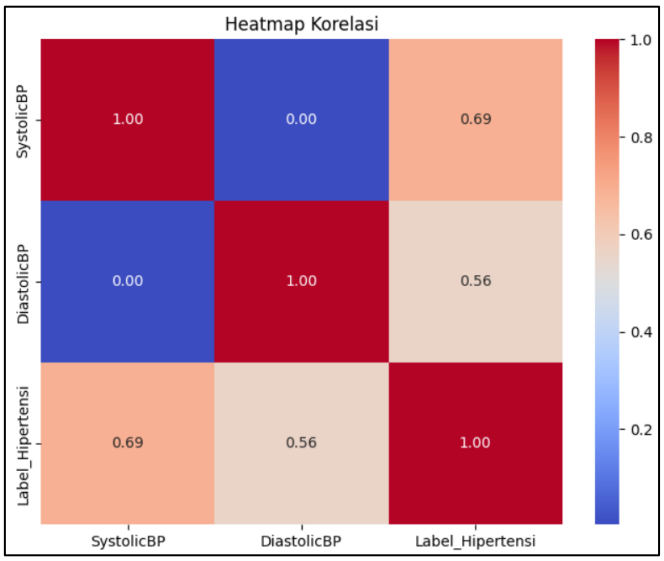

Figure 5. Heatmap Correlation

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Correlation heatmaps in statistical analysis and machine learning reveal the relationships between traits in a dataset. In Figure 5 shows there is a link between the factors SystolicBP, DiastolicBP, and Label_Hypertension in this correlation heatmap. Range of correlation values: -1 to 1. Values close to 1 show a strong positive correlation, while numbers close to 0 show there is no significant link. This heatmap shows that systolic blood pressure is strongly linked to high blood pressure (r = 0.69). With a value of 0.56, diastolic blood pressure is also linked to high blood pressure, but not as strongly as systolic blood pressure. Also, there is no relationship between SystolicBP and DiastolicBP (0.00), which means that they are two separate traits.

3.3. Model Interpretation

SHAP analysis identified the most influential features contributing to hypertension classification. Key predictors included systolic and diastolic blood pressure.

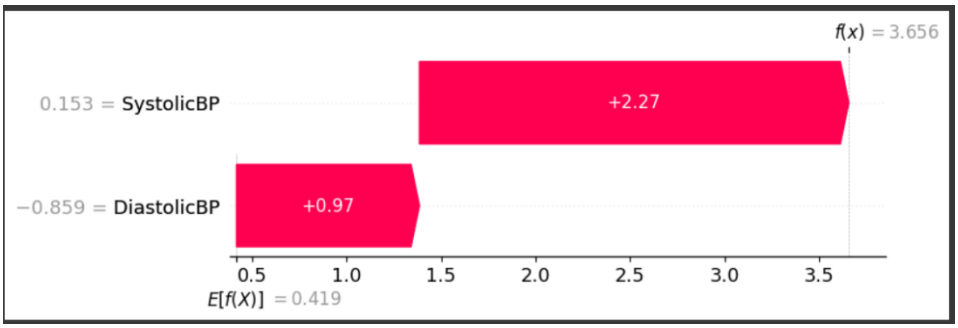

Figure 6. SHAP Waterfall Plot

The graphic on Figure 6 shows how features contribute to the prediction of the model using a SHAP waterfall plot. Whereas after considering the contribution of the features, the final prediction becomes 3.656 (f(x)); the baseline value of the model before considering individual features is 0.419 (E[f(X)). Systolic BP and diastolic BP are the two main variables affecting this prediction; systolic BP contributes more with a rise of +2.27, while diastolic BP also positively impacts the outcome with a rise of +0.97. In particular, the rise in the prediction value is primarily determined by Systolic BP, indicating that the combination of these two elements significantly influences the model's outcomes.

3.4. Model Validation

Validation metrics confirmed the reliability of the model across different subsets. Sensitivity analysis demonstrated the model's stability under varying parameter settings.

Table 4. Validation Metrics

Class	Sensitivity	Specificity
0	1.0000	1.0000
1	0.9464	0.9923
2	0.9877	0.9957
3	0.9792	0.9925
4	0.9881	0.9957

Table 4 above displays the evaluation results of the XGBoost model in the form of performance metrics, including accuracy, MCC score, and classification report, as well as sensitivity and specificity per class. The model shows very good performance with an accuracy of 98.10% and an MCC score of 0.9759, indicating a good balance between positive and negative predictions. The classification report shows the precision, recall (sensitivity), and F1-score values for each class. In the report, it is evident

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that the model has high precision and recall, especially for class 0, which reached 100% in all metrics, indicating that the model is able to recognize this class perfectly without any errors. The macro average and weighted average scores also show high values at 0.98, confirming that the model has consistent performance across all classes.

In addition, the evaluation results also include Sensitivity (Recall) and Specificity for each class. Sensitivity measures the extent to which the model can recognize the correct class, while specificity measures its ability to avoid misclassifying other classes. Class 0 has perfect sensitivity and specificity (1.0000), which means there are no classification errors for this class. The other classes also show high performance with sensitivity between 0.9464 and 0.9881 and specificity between 0.9923 and 0.9957, indicating that the model has a very low classification error rate. These evaluation results conclude that the XGBoost model is highly reliable in performing classification with a very low error rate.

4. DISCUSSIONS

4.1. Key Findings

The study demonstrates the effectiveness of integrating K-Means clustering and XGBoost for the identification of hypertension. The hybrid model achieved high accuracy, precision, recall, and F1-score, highlighting its robust predictive performance. The clustering analysis showed different groups of patients with different hypertension risk profiles. The SHAP analysis, on the other hand, showed which features were most important, focusing on systolic blood pressure, waist circumference, and fasting glucose as the most important predictors. In previous hypertension prediction research[30] proposed a model that combines KNN and LightGBM, showing that the model is reliable and achieves accuracy and recall rates of more than 86% and 92%, respectively. but below the score of the combined K-Means and XGboost model. Then there is also research related to [18] using information gain and random forest techniques that show an accuracy of 92.555%. It can be concluded that the combination of K-means and XGBoost achieved the best performance in predicting hypertension.

4.2. Interpretation Of Results

It is in line with previous research that the XGBoost classifier works very well at processing complex and high-dimensional medical data to find people with high blood pressure. The recognition of systolic blood pressure as a key predictor reinforces its critical role in diagnosing hypertension, a major risk factor for cardiovascular diseases. This finding supports previous studies emphasizing the importance of accurate blood pressure assessment in the early detection and management of hypertension.

Furthermore, the clustering analysis reveals variations among individuals with hypertension, suggesting that different subgroups may exist based on distinct risk profiles. This underscores the need for personalized interventions tailored to specific patient characteristics. Identifying these subgroups could enhance hypertension management strategies by enabling targeted treatment approaches, ultimately improving patient outcomes and reducing the overall burden of hypertension-related complications.

4.3. Clinical Implications

The findings have significant clinical implications, particularly in the early identification of hypertension. The hybrid model can assist healthcare professionals in detecting hypertension at an early stage, allowing for timely interventions to prevent severe complications such as heart disease and stroke. The model improves clinical decision-making by correctly identifying systolic and diastolic blood pressure as key predictors. This leads to more accurate and proactive management of hypertension.

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Furthermore, the integration of explainable AI (XAI) increases model transparency, fostering greater trust and adoption in medical practice. Understanding key risk factors associated with hypertension can help guide targeted lifestyle interventions, such as dietary modifications and physical activity, as well as personalized treatment plans. This approach enables more effective hypertension management, reducing the long-term risks associated with uncontrolled high blood pressure.

4.4. Limitations

The findings have significant clinical implications, particularly in the early identification of hypertension. Using a hybrid model trained on publicly available datasets from Kaggle, this study demonstrates the potential of machine learning in detecting hypertension at an early stage. Although the model is not developed with real-world hospital data, its ability to identify systolic and diastolic blood pressure as key predictors supports its validity. By leveraging advanced algorithms, the model enhances clinical decision-making, allowing for timely interventions to prevent severe complications such as heart disease and stroke. This contributes to a more accurate and proactive approach to hypertension management. Adding explainable AI (XAI) to models also makes them more clear, which builds trust and makes it easier to use in medical research and possible clinical applications. There are some problems with the dataset that need to be thought about, but finding the main risk factors for high blood pressure can still help with targeted lifestyle changes like eating less and exercising more, as well as making personalized treatment plans. Future studies incorporating hospital-based datasets could further validate and refine the model, ensuring its reliability in real-world healthcare settings.

4.5. Future Research Directions

Future research should focus on enhancing the model's robustness and clinical applicability by utilizing large-scale, real-world hospital data. Along with blood pressure readings, including a wide range of metabolic parameters, like fasting blood glucose, lipid profiles, and inflammatory markers, will help us learn more about the factors that raise the risk of developing high blood pressure. A dataset made up of different types of patients from different healthcare institutions would make models more general by reducing the biases that come with publicly available datasets like Kaggle. Adding machine learning to hospital-based electronic health records (EHRs) could also improve the accuracy of predictions and allow for real-time risk assessment of high blood pressure.

Future studies should also explore longitudinal data to assess how metabolic changes over time influence hypertension progression. Moreover, the next phase of research should focus on developing deep learning systems that not only diagnose hypertension but also provide personalized health recommendations and self-care treatment plans for patients. By offering tailored lifestyle modifications, dietary guidelines, and acupressure-based interventions, the model can empower individuals to manage their condition independently. This approach ensures that AI-driven hypertension diagnostics not only support clinical decision-making but also enhance patient autonomy and proactive disease management.

5. CONCLUSION

This research shows that the hybrid model based on K-Means and XGBoost has excellent performance in identifying hypertension. With a high accuracy of 98.10% and an MCC score of 0.9759, this model is able to classify blood pressure accurately based on clinical parameters. The analysis results show that systolic and diastolic blood pressure are the main predictors in the diagnosis of hypertension. In addition, this model also has high sensitivity and specificity in each class, ensuring that hypertension detection can be performed with a very low error rate. Although this model has shown promising performance, this research still has limitations because it only uses a dataset from Kaggle, which may not fully reflect clinical conditions in the real world. Therefore, future research needs to use original

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data from hospitals with a larger sample size and include a broader range of metabolic parameters, such as blood glucose levels and lipid profiles. In addition to improving prediction accuracy, future research should also produce a health recommendation system that allows patients to receive self-care advice, including lifestyle changes and acupressure-based therapy. Thus, this model not only supports clinical decision-making for healthcare professionals but also empowers patients to manage hypertension independently.

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