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Heart Disease Prediction and Patient Segmentation

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ABSTRACT

Heart disease is one of the leading causes of death worldwide, making early prediction and patient risk assessment essential for better healthcare outcomes [1]. This project focuses on Heart Disease Prediction Using Data Mining Algorithms and Patient Segmentation [2]. Our objectives are threefold: (1) predict heart disease risk using machine learning models like Logistic Regression, Decision Trees, and k-Nearest Neighbors (k-NN) [3, 4], (2) segment patients based on shared medical characteristics to identify risk factors and trends [5, 6],Provide advice to patients based on their assigned cluster to encourage preventive measures and healthier lifestyle choices. By analyzing patient clusters, we aim to offer relevant guidance. For example, patients in high-risk clusters may focus on adopting specific dietary changes, engaging in regular physical activity, and monitoring key health indicators. Meanwhile, those in low-risk clusters might concentrate on maintaining current healthy habits and scheduling regular check-ups to ensure continued well-being. This method empowers patients with actionable insights and promotes proactive healthcare management. (3) provide a graphical interface for inputting data and visualizing predictions and segmentations [7, 8]. We implemented and tested machine learning algorithms to evaluate their accuracy in predicting heart disease, achieving promising results. Feature importance analysis highlights the significance of attributes such as cholesterol and age in risk prediction [9]. Additionally, patient segmentation revealed distinct groups based on medical profiles, which correspond to varying risk levels [5]. Our system offers an accessible interface for medical professionals and patients, combining predictive modeling with visualization tools to enhance decision-making. This project contributes to advancing heart disease research by integrating data mining techniques with user-friendly software, facilitating more effective diagnosis and patient management.

1 INTRODUCTION

Heart disease is a major global health concern, often caused by complex and interrelated risk factors such as age, cholesterol levels, and blood pressure [1, 5]. Despite the availability of advanced medical technologies, predicting heart disease remains challenging due to the diversity and complexity of patient data [2]. To address this challenge, computational techniques like data mining and machine learning are increasingly being applied in healthcare to provide more accurate and actionable insights [3, 10]. This project focuses on developing a system for predicting heart disease risk and segmenting patients using machine learning algorithms and clustering techniques [4, 8, 11]. The implementation involves analyzing patient data using algorithms such as Logistic Regression [3], Decision Trees [4], and k-Nearest Neighbors (k-NN)[8, 12] for prediction tasks. Additionally, clustering methods are applied to group patients based on shared medical characteristics, which can uncover hidden trends and inform better risk management strategies[6, 9]. The importance of this project lies in its practical application for improving heart disease diagnosis and treatment planning [7]. By using real-world patient datasets, the system identifies key features influencing heart disease risk [9, 12] and provides an interactive graphical interface for users to input data and explore predictions and segmentations [7, 10]. This interface is designed to make the system accessible to healthcare professionals and researchers who may lack technical expertise [6].

2 RELATED WORKS

Heart disease prediction has been a focal point of research in both the medical and data science communities due to its significant impact on global health [1]. The application of data mining and machine learning techniques has been extensively explored to improve the accuracy of heart disease diagnosis and risk assessment [2, 3]. This section reviews notable studies in this area, highlighting their methodologies, findings, and the gaps that our project aims to address.

Alousafat (2020) conducted a comparative analysis of various machine learning classifiers, including Decision Trees, Support Vector Machines (SVM), k-Nearest Neighbors (k-NN), and Neural Networks, for predicting heart disease [13]. The study also performed sensitivity analysis to determine the impact of different features on model performance. The findings indicated that certain classifiers, particularly Decision Trees and Neural Networks, achieved higher accuracy levels. However, the study primarily focused on model performance metrics without integrating patient segmentation to identify underlying risk patterns.

Ali et al. (2021) provided a comprehensive evaluation of supervised machine learning algorithms such as Logistic Regression, Random Forest, Gradient Boosting, and Deep Learning models using the UCI Heart Disease dataset [14]. Their research emphasized the superiority of ensemble methods like Random Forest and Gradient Boosting in terms of accuracy and robustness. Feature selection techniques were also employed to enhance model performance by eliminating redundant variables. While the study advanced the understanding of algorithm efficacy, it did not extend to patient segmentation or the development of user-friendly tools for clinical application.

Bhatla and Jyoti (2012) analyzed heart disease prediction using different data mining techniques, including Naïve Bayes, Decision Trees, and Neural Networks [15]. They concluded that Decision Trees and Neural Networks outperformed Naïve Bayes classifiers. The study underscored the importance of data preprocessing but lacked emphasis on interactive interfaces or visualization tools to aid healthcare professionals in decision-making processes. **Chandrasekhar and Peddakrishna** (2023) enhanced heart disease prediction accuracy by integrating machine learning techniques with optimization algorithms like Genetic Algorithms for feature selection [16]. Their work demonstrated that hybrid models could yield better predictive performance than standalone models. Despite these advancements, the study did not focus on patient segmentation or the practical implementation of these models in clinical settings through accessible software interfaces.

Dey and Bauratx (2014) explored data mining algorithms for healthcare decision support systems, evaluating the efficiency and accuracy of algorithms such as SVM, k-NN, and Bayesian classifiers [17]. The study highlighted the potential of data mining techniques to support medical professionals but did not provide solutions for patient segmentation or the integration of predictive models into user-friendly platforms for practitioners.

Soni et al. (2011) offered an overview of predictive data mining techniques for medical diagnosis, discussing classification, clustering, and association analysis in the context of heart disease prediction [18]. While the study acknowledged the importance of clustering methods to uncover hidden patterns in medical data, it did not implement these techniques to segment patients based on medical characteristics or develop tools for visualizing these clusters.

Despite significant advancements in applying machine learning algorithms for heart disease prediction, existing research predominantly focuses on improving model accuracy through algorithm selection and feature engineering [19]. However, notable gaps remain unaddressed. One major gap is the lack of integration of patient segmentation using clustering techniques, which can uncover hidden trends and enable personalized risk management strategies [20]. This means that while predictions are being made, the opportunity to understand underlying patient groupings based on shared medical characteristics is often missed.

Another gap is the absence of user-friendly interfaces in most studies, limiting the practical adoption of these predictive models in clinical settings [21]. Healthcare professionals without technical expertise may find it challenging to utilize these models without accessible graphical user interfaces (GUIs). Additionally, there is a scarcity of solutions that combine predictive modeling with visualization tools, which are crucial for enhancing the interpretability of models and supporting better decision-making by medical practitioners [22]. This combination could significantly aid clinicians in understanding predictions and patient segments, ultimately leading to improved patient outcomes.

3 THE PROPOSED WORK AND RESULTS

3.1 DataSet

We worked with the Heart Disease Prediction dataset available from the UCI Machine Learning Repository. The dataset can be accessed through the following link:

https://www.kaggle.com/datasets/johnsmith88/heart-disease-dataset [23]

In this project, we will explore various machine learning techniques for heart disease prediction, including Logistic Regression, Decision Trees, Naive Bayes and k-Nearest Neighbors (k-NN). We aim to gain a comprehensive understanding of these algorithms by evaluating them using important performance metrics such as accuracy, precision, and others that will be discussed in detail.

The dataset contains several features that we will consider for our machine learning models. These features are:

- **Age:** The age of the patient in years.
- **Sex:** The gender of the patient (1 = male, 0 = female).
- **Chest Pain Type:** The type of chest pain experienced, categorized into four types:
  - 0: Typical angina
  - 1: Atypical angina
  - 2: Non-anginal pain
  - 3: Asymptomatic
- **Resting Blood Pressure:** The resting blood pressure in millimeters of mercury (mm Hg).
- **Serum Cholesterol:** The serum cholesterol level in milligrams per deciliter (mg/dl).
- **Fasting Blood Sugar:** Indicates if fasting blood sugar is greater than 120 mg/dl (1 = true, 0 = false).
- **Resting Electrocardiographic Results:** Results of the resting electrocardiogram (ECG), represented by values:
  - 0: Normal
  - 1: Having ST-T wave abnormality
  - 2: Showing probable or definite left ventricular hypertrophy
- **Maximum Heart Rate Achieved:** The highest heart rate achieved during exercise.
- **Exercise-Induced Angina:** Indicates if exercise-induced angina is present (1 = yes, 0 = no).
- **Oldpeak:** ST depression induced by exercise relative to rest, which is a measure of abnormal heart activity.
- **Slope of the Peak Exercise ST Segment:** Describes the slope of the peak exercise ST segment:
  - 0: Upsloping
  - 1: Flat
  - 2: Downsloping
- **Number of Major Vessels Colored by Fluoroscopy:** The number of major blood vessels (0–3) visualized by fluoroscopy.
- **Thalassemia (*Thal*):** A blood disorder, with values indicating:
  - 1: Normal
  - 2: Fixed defect
  - 3: Reversible defect

By analyzing these features, we aim to build predictive models that can accurately assess the risk of heart disease in patients. The project not only focuses on prediction but also on understanding which features contribute most significantly to the risk, thereby providing valuable insights for medical professionals [5].

Table 1: Sample of the Heart Disease Dataset

age	sex	cp	trestbps	chol	fbs	restecg	thalach	exang	oldpeak	slope	ca	thal	target
63	1	3	145	233	1	0	150	0	2.3	0	0	1	1
37	1	2	130	250	0	1	187	0	3.5	1	0	2	1
41	0	1	130	204	0	0	172	0	1.4	2	0	2	1
56	1	1	120	236	0	1	178	0	0.8	2	0	2	1
57	0	0	120	354	0	1	163	1	0.6	2	1	3	1

3.2 System Architecture Details

The proposed system is a comprehensive framework aimed at predicting heart disease risk and grouping patients into meaningful clusters. It is designed to assist medical decision-making with a focus on being interpretable and easy to understand. The system has several layers and components, each performing a specific function:

3.2.1 Data Handling

The system offers two methods for entering data:
Batch Input: Users can upload a CSV file with patient data, allowing the system to process multiple records at once for predictions and segmentation.
Manual Input: Users can enter details for a single patient to get an immediate heart disease risk prediction and segmentation result.

This dual-mode feature provides flexibility, making it suitable for healthcare providers managing both individual patient assessments and large datasets.

3.2.2 Preprocessing Layer

The preprocessing layer prepares the input data for prediction and segmentation. It includes:

- **Categorical Variable Encoding:** One-hot encoding is applied to variables like gender, chest pain type, and exercise-induced angina to make them machine-readable [2, 14, 24].
- **Continuous Variable Normalization:** eatures such as age, cholesterol levels, resting blood pressure, and heart rate are standardized for consistent analysis [3, 5, 25].
- **Outlier Removal:** The Interquartile Range (IQR) method is used to remove outliers, improving the accuracy and robustness of the segmentation process [8, 10].
- **Missing Values:** Missing values are handled using imputation methods to maintain data integrity and minimize information loss

3.2.3 Prediction Module

The prediction module is based on a Decision Tree algorithm and Logistic Regression implemented from scratch to ensure simplicity and interpretability [3, 4, 26]. It focuses on the 7 most important features, which were identified and implemented from scratch (Figure 5) Which are cp,thal, ca,oldpeak,age,thalache,chol, reducing the amount of input data required. The module provides:

- **Real-Time Prediction:** Allows users to enter fewer features manually and receive an immediate prediction of heart disease risk for individual patients.
- **Batch Prediction:** Processes uploaded datasets to generate predictions for all records while highlighting the important features that influence the results [9, 14, 26].

This feature-based approach improves user experience by simplifying the data input process and maintaining accurate predictions.

3.2.4 Patient Segmentation Module

The system uses a patient segmentation feature based on a custom K-means clustering algorithm, created from scratch to allow deeper analysis and better use of resources. The best number of clusters (K) is chosen using the Elbow Method, and the algorithm groups patients into four clear categories.

By dividing patients into these meaningful clusters, the system makes it easier for healthcare providers to find patterns, make better decisions, and improve care quality while using resources wisely.

The cluster analysis divides patients into four distinct groups, each with unique health characteristics and specific recommendations:

- **Cluster 0:** Consists of older patients with high cholesterol levels and elevated blood pressure. For these patients, interventions such as low-cholesterol diets, blood pressure management, and regular checkups are advised [5, 25, 27].
- **Cluster 1:** Includes younger patients with normal cholesterol but moderate exercise capacity. For these patients, maintaining physical activity and adopting a healthy lifestyle are recommended [9, 20, 28].
- **Cluster 2:**Represents patients with lower heart rates and normal blood pressure, who would benefit from routine health monitoring [14, 26].
- **Cluster 3:** Represents patients with higher oldpeak values and multiple risk factors, requiring personalized care plans based on their specific health needs [11, 27, 29].

3.2.5 Visualization and Insight

The visualizations and metrics in this application provide a thorough analysis of both heart disease prediction and patient segmentation. For **heart disease prediction** performance metrics like accuracy, precision, recall, and F1 score quantitatively evaluate the model's effectiveness [2]. Confusion matrices visually represent prediction outcomes, providing insight into the balance between correctly and incorrectly classified cases [13]. Statistical significance tests, such as the Chi-squared test, assess the reliability of the results, with p-values indicating the statistical importance of the observed outcomes [3]. The ROC curve and the associated area under the curve (AUC) metric illustrate the trade-off between sensitivity and specificity, enabling a deeper understanding of the model's predictive power [10]. Additionally, the time taken for prediction offers valuable feedback on the efficiency of the implemented algorithms [12].

For **patient segmentation**, visualizations like PCA scatter plots provide a simplified, two-dimensional representation of clusters, making it easier to distinguish patterns among patient groups [8]. Silhouette plots assess the quality of clustering, with higher scores indicating more distinct and well-separated clusters [11]. Pairwise comparisons of features such as age, cholesterol, and heart rate highlight patterns and differences within and between clusters [15]. Bar plots reveal the distribution of categorical features like chest pain types and thalassemia across clusters, while summaries of continuous variables provide additional insights into group characteristics [20]. These visualizations, combined with cluster-specific guidance, enable healthcare providers to better understand the unique attributes of each group and design interventions to address specific health risks [27].

3.2.6 User Interface

The user interface is built using Streamlit to create a simple and interactive experience for users [21]. It offers both manual and batch input options, allowing users to either enter patient data one at a time or upload a CSV file for batch processing [6]. The system provides detailed clustering results, including group assignments and personalized health recommendations, making the data easy to understand and actionable [21].

The interface also features dynamic visualizations, such as pair plots for clusters and feature distributions, which give users instant feedback and a better understanding of the data [7]. Additionally, users can download the segmented data along with recommendations as a CSV file for further use [6]. With its clean layout and real-time responsiveness, the Streamlit interface is user-friendly and suitable for healthcare providers with limited technical skills [21].

3.2.7 Deployment

The system is deployed on a local Streamlit server for prototyping and testing [6]. Future enhancements could include deploying the system on cloud platforms for scalability and accessibility in real-world healthcare settings [22]. Streamlit has been shown to be an excellent tool for building interactive dashboards, specifically for medical applications, due to its simplicity and ability to handle large datasets efficiently [30]. Cloud deployment can further enhance system scalability and accessibility, ensuring the solution can reach healthcare professionals and patients in various locations [31].

3.3 Data Preprocessing

Data preprocessing is an essential step in preparing the dataset for machine learning to ensure high-quality input data and improve model performance [9, 23]. The preprocessing steps applied to the dataset focused on handling missing values, normalization, and outlier detection to create a clean and reliable dataset for training [25, 32].

Handling Missing Values: The dataset was thoroughly examined for missing values, and it was confirmed that no data was missing in any of the columns [23]. As a result, no imputation or removal of records was required, ensuring that the dataset was complete and ready for further preprocessing [23].

Normalization: Continuous variables, including age, trestbps (resting blood pressure), chol (cholesterol), thalach (maximum heart rate achieved), and oldpeak (ST depression), were standardized [19, 25]. Standardization scaled these features to have a mean of 0 and a standard deviation of 1, ensuring that variables with different scales contributed equally during model training [14, 25]. This step is especially important for machine learning algorithms like k-Nearest Neighbors, which are sensitive to the scale of features [14]. Optimizing preprocessing techniques for medical datasets ensures that the input data is transformed into a format that improves model accuracy and efficiency [32].

Outlier Detection and Removal: Outliers in continuous variables were identified based on values exceeding three standard deviations from the mean [9]. Outliers were detected in trestbps, chol, thalach, and oldpeak [27]. After removing these extreme values, the dataset size reduced from 1025 to 946 records [9, 27]. This cleaning step helped minimize noise and ensure that the dataset contained fewer extreme values that could negatively impact the accuracy of machine learning models [25]. Effective data cleaning and transformation techniques are crucial in healthcare analytics to improve model performance and ensure reliable outcomes [33].

3.4 Exploratory Data Analysis (EDA)

Continuous Data Analysis:

Figure 1 illustrates the histograms of standardized continuous variables, including age, resting blood pressure (trestbps), cholesterol (chol), maximum heart rate achieved (thalach), and ST depression induced by exercise (oldpeak). Most variables exhibit approximately normal distributions centered around zero, except for oldpeak, which shows a right-skewed distribution. These visualizations provide insights into the data's distribution and variability, highlighting potential trends and outliers for further analysis[5, 27].

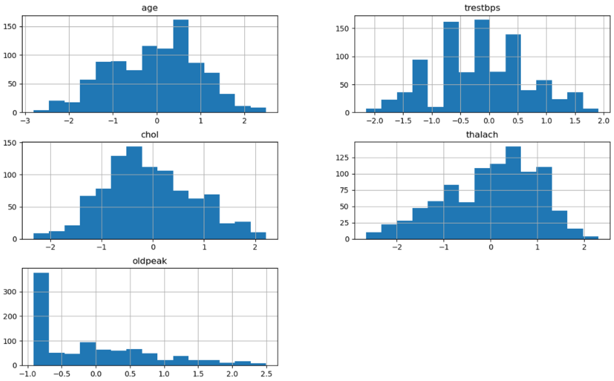


Figure 1: Histogram Of Continous Variables

Categorical Data Analysis Figure 2 shows count plots of categorical variables, including sex, chest pain type (cp), fasting blood sugar (fbs), restecg, exercise-induced angina (exang), slope, ca, thal, and the target variable. The dataset shows a higher proportion of male patients (sex=1) and varied distributions across other categories, such as chest pain types and thalassemia. These plots highlight the diversity in categorical variables, emphasizing the need for proper encoding during preprocessing to ensure accurate modeling and interpretation of heart disease risk[6, 7, 24].

Outlier Detection and Removed

Box plots in Figure 3 illustrate the continuous features like trestbps and chol after addressing the outliers identified during preprocessing. This step ensures improved model robustness by removing extreme values that could negatively impact predictions. Managing outliers is essential in medical data to maintain the reliability and accuracy of the models [9, 27].

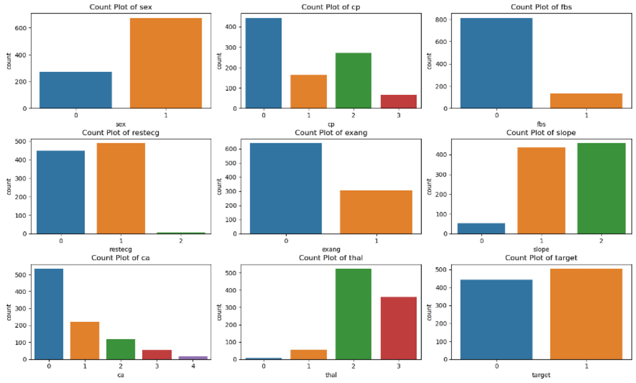


Figure 2: Count plots of categorical variables.

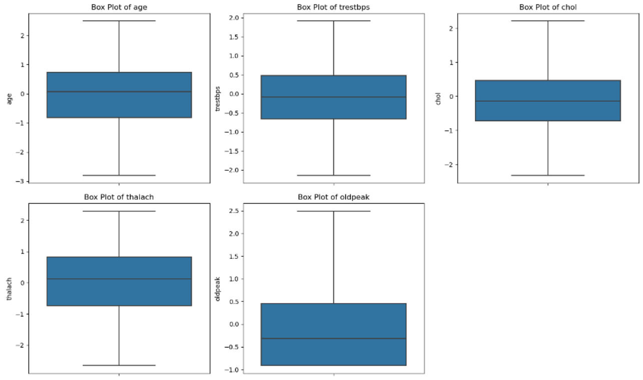


Figure 3: Box plots showing the continuous variables after removing outliers

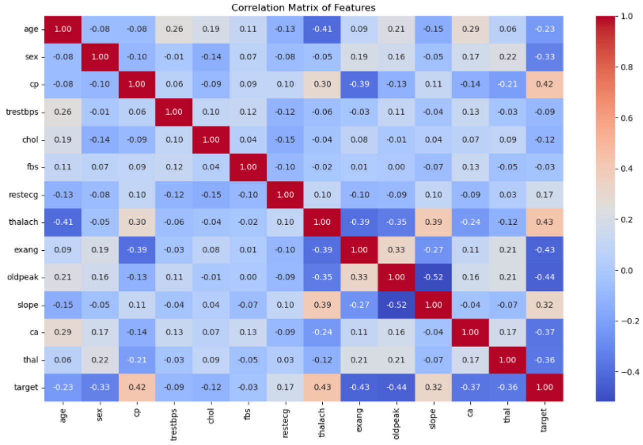


Figure 4: Correlation matrix illustrating relationships between features in the dataset

Correlation Analysis

Figure 4 illustrates the correlation matrix of features, showcasing the relationships between variables in the dataset. Notable correlations include a strong positive relationship between thalach (maximum heart rate achieved) and target (presence of heart disease), as well as a negative correlation between oldpeak (ST depression) and target. Other features, such as age and chol, exhibit weaker correlations with the target variable. These insights guide feature selection and highlight the significance of understanding variable interactions in predicting heart disease [13, 14, 19].

Feature Importance

In Figure 5, Figure 6 and Figure 7 we can see the plots that show the importance of features across three models: Decision Tree (DT), Logistic Regression (LR), and K-Nearest Neighbors (KNN). Each model ranks features based on how much they contribute to predicting the target variable. This analysis helps us understand which features are most important and supports selecting the best model. After comparing these results, we chose the Decision Tree model for our study.

In the Decision Tree plot, key features like chest pain type (cp), thalassemia status (thal), and the number of major vessels (ca) are identified as the most important. These features are medically significant for diagnosing heart conditions, making the results meaningful. Logistic Regression also shows similar important features, such as cp and oldpeak, but ranks them slightly differently. The KNN model shows more evenly distributed feature importance, which makes it less effective for identifying the most critical features.

We selected the Decision Tree model because it captures nonlinear relationships and interactions between features, which are important in datasets like this. Decision Trees are also easy to interpret, as they show clear splits based on features. This makes the model useful not only for achieving good predictions but also for explaining the results to non-technical audiences. Overall, the Decision Tree is a practical and reliable choice for our analysis [10, 12, 14].

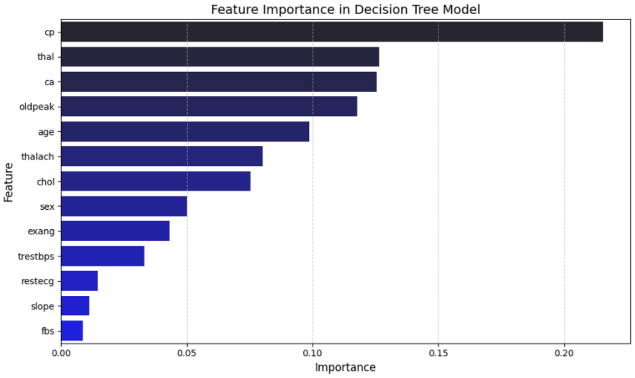


Figure 5: feature Importance In Decision Tree Model

3.5 Performance Evaluation of Scratch-Implemented Models

We implemented Decision Tree, k-Nearest Neighbors (k-NN), Logistic Regression, and Naive Bayes classifiers from scratch to explore their predictive capabilities compared to their library-based

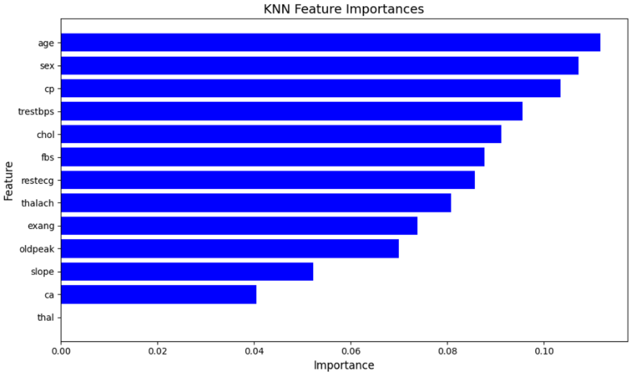


Figure 6: KNN Feature Importance

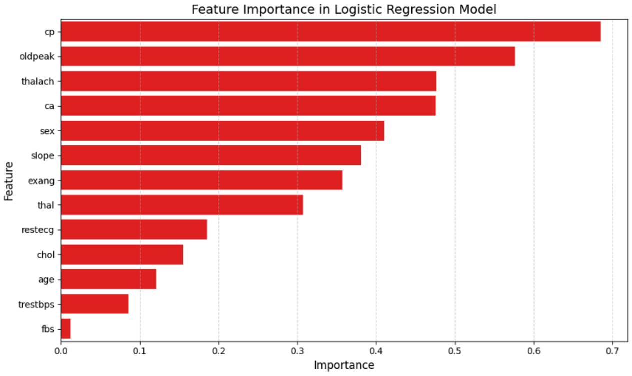


Figure 7: Logistic Regression Feature Importance

counterparts. While library implementations often utilize advanced optimization techniques and pre-built frameworks, our focus was on understanding the internal mechanics of these algorithms. By manually implementing these models, we were able to study how the components and parameters directly influence classification tasks in real-world applications [10, 15].

In Figure 8 we can see, Among the scratch-implemented algorithms, Decision Tree and Logistic Regression stood out with the highest predictive accuracy. The Decision Tree classifier achieved a mean accuracy of 90.34% (std = 1.39%), showcasing its ability to manage non-linear decision boundaries effectively. Similarly, Logistic Regression obtained a mean accuracy of 83.32% (std = 1.89%), highlighting its effectiveness in capturing linear relationships between the input features and the target variable. Although these results are slightly less accurate than their library-based counterparts, they validate the correctness of our custom implementations and demonstrate their capability in achieving accurate predictions[19, 34].

3.5.1 Description of Performance Metrics

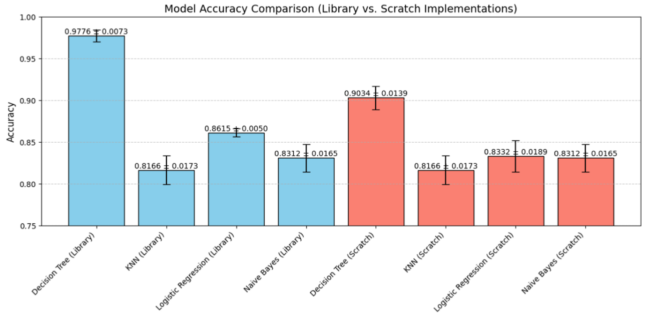


Figure 8: Model Accuracy Comparison

In Figure 9, the bar plot shows the performance metrics—Precision, Sensitivity (Recall), Specificity, F1 Score, and G-Mean—for four machine learning models implemented from scratch: Decision Tree, KNN, Logistic Regression, and Naive Bayes. Each bar represents the average value of the metric across multiple runs, and the error bars show the standard deviation, which indicates the variability in the results. The Decision Tree model performs the best in most metrics, especially in Sensitivity (Recall) and F1 Score, showing its strength in identifying positive cases while minimizing false negatives[30]. KNN and Logistic Regression have similar performance, but their precision and sensitivity are slightly lower. Naive Bayes, on the other hand, performs worse than the other models in Specificity and F1 Score[18].

The G-Mean metric, which measures the balance between Sensitivity and Specificity, shows that the Decision Tree achieves the highest balance, making it the best overall model for this dataset. KNN and Logistic Regression have competitive G-Mean values, but they are slightly lower than the Decision Tree. Naive Bayes has the lowest G-Mean, which suggests it struggles more with this dataset, especially with handling imbalanced data. This plot provides a clear comparison of the models' strengths and weaknesses, helping to understand which model is more suitable for tasks that require high recall and balanced performance. The Decision Tree is the most reliable choice for this dataset[31, 33, 34].

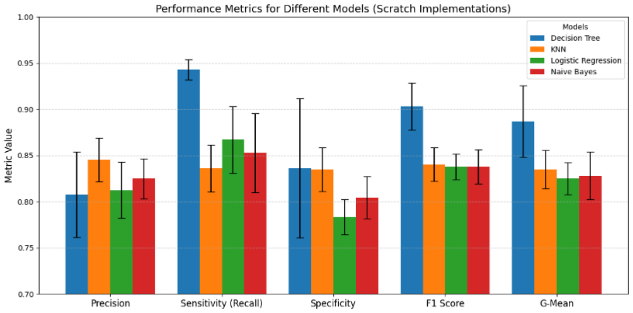


Figure 9: Bar plot showing the performance metrics for Decision Tree, KNN, Logistic Regression, and Naive Bayes.

3.5.2 Impact of Feature Selection on Classifier Accuracy

In Figure 10, the bar plots compare the accuracy of two classifiers: K-Nearest Neighbors (KNN) and Decision Tree, when trained with all features and when using only the most important features. For the KNN classifier, the accuracy using all features is slightly higher

(0.8337 ± 0.0190) compared to the accuracy with selected important features (0.8264 ± 0.0247). This suggests that KNN benefits more from considering all available features, likely due to the nature of distance-based classification where more features provide better differentiation[21, 36].

In Figure 11 we can see,In contrast, the Decision Tree classifier shows an improvement in accuracy when using important features (0.9456 ± 0.0221) compared to all features (0.9104 ± 0.0183). This result indicates that Decision Trees are more effective at focusing on the most relevant features, which reduces noise and overfitting. Overall, these plots demonstrate how feature selection impacts the performance of different classifiers, emphasizing that the effect varies depending on the classifier's working mechanism[19, 24].

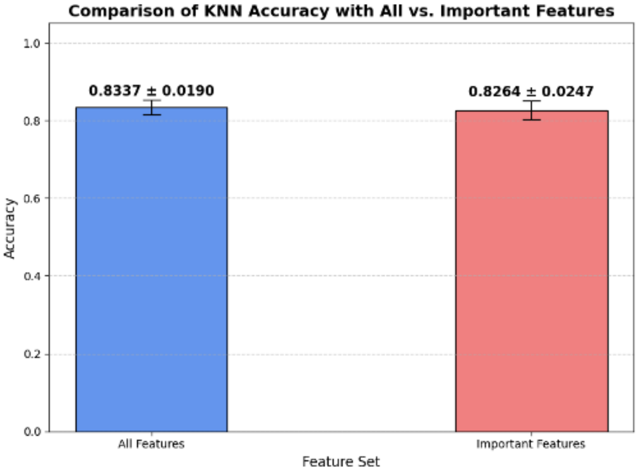


Figure 10: Comparison of KNN accuracy with all features and selected important features.

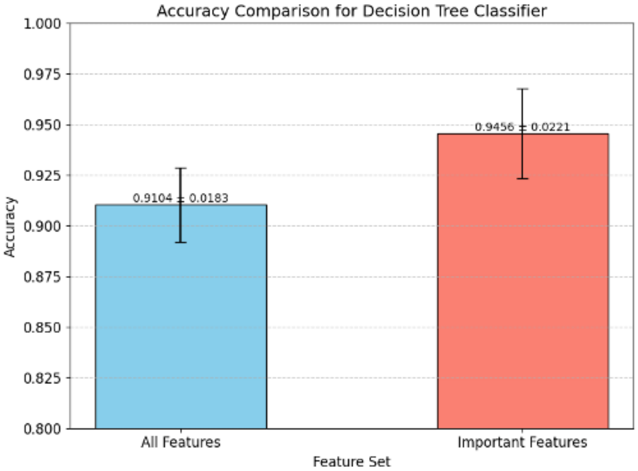


Figure 11: Comparison of Decision Tree accuracy with all features and selected important features.

3.5.3 Model Selection

As we can see in Figure 12 and Figure 13, based on the performance metrics, the Decision Tree model was selected as the preferred model for heart disease risk prediction due to its high accuracy, interpretability, and the ability to visualize feature importance. Decision Trees allow for easy identification of key predictive features, which can provide clinicians with insights into the factors contributing to heart disease risk[25, 27].

Figure 12 and Figure 13 present the confusion matrices for the Decision Tree, k-Nearest Neighbors (k-NN), Logistic Regression, and Naive Bayes classifiers, all implemented from scratch. These matrices provide an in-depth analysis of each model's predictive performance by comparing the actual and predicted labels. Among the models, the Decision Tree exhibited the highest accuracy, correctly classifying 84 instances of the negative class and 102 instances of the positive class, with only 19 misclassifications. The k-NN classifier showed competitive performance, albeit with a higher number of misclassified positive instances, indicating potential sensitivity to class distribution[10, 20].

Logistic Regression and Naive Bayes demonstrated comparable results, effectively predicting the majority of positive instances while misclassifying a notable number of negative cases. Logistic Regression showed a slightly higher rate of false positives (26 instances), which could be attributed to its linear decision boundary. Naive Bayes, on the other hand, effectively captured the patterns in the data, achieving similar results with marginally fewer false positives. These confusion matrices highlight the strengths and weaknesses of each scratch implementation, providing valuable insights into their suitability for heart disease prediction tasks[16, 33].

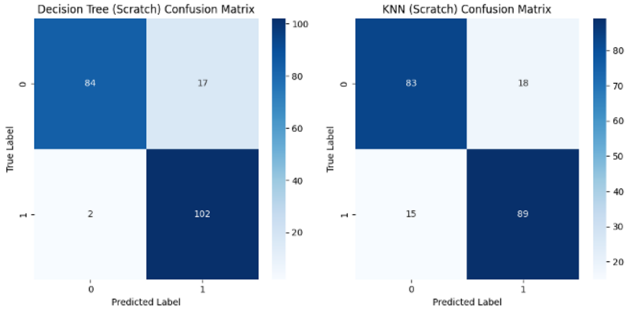


Figure 12: Confusion matrices for Decision Tree, k-Nearest Neighbors (k-NN)

3.5.4 ROC Curve Analysis

Figure 14 illustrates the Receiver Operating Characteristic (ROC) curves for the scratch implementations of Decision Tree, k-Nearest Neighbors (k-NN), Logistic Regression, and Naive Bayes classifiers. The Area Under the Curve (AUC) values provide a comparative measure of each model's performance in distinguishing between the classes. Logistic Regression achieved the highest AUC of 0.91, closely followed by the Decision Tree with an AUC of 0.90, indicating their superior ability to balance sensitivity and specificity.

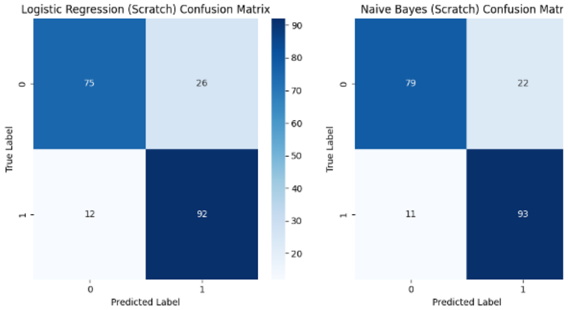


Figure 13: Confusion matrices for Logistic Regression, and Naive Bayes classifiers.

Both k-NN and Naive Bayes exhibited slightly lower AUCs of 0.85, reflecting comparable but less robust performance. These curves highlight the reliability of the scratch implementations in predicting heart disease risk, with Logistic Regression and Decision Tree demonstrating the most promising results[29, 34].

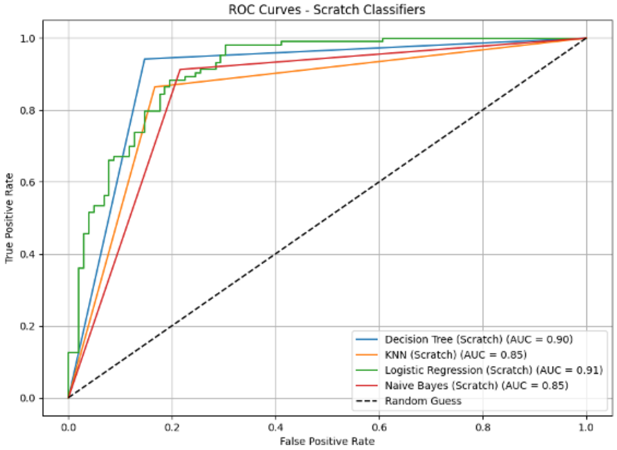


Figure 14: ROC curves for Decision Tree, k-Nearest Neighbors (k-NN), Logistic Regression, and Naive Bayes classifiers.

3.6 Segmentation

To achieve effective segmentation, we implemented K-Means, Hierarchical Clustering, and Gaussian Mixture Model (GMM) algorithms from scratch and evaluated their performance on the dataset. Among these methods, K-Means demonstrated the best results, offering well-separated, balanced clusters and computational efficiency. The Elbow Method confirmed $K = 4$ as the optimal number of clusters, achieving a good trade-off between minimizing the Total Sum of Squared Errors (SSE) and avoiding overfitting. Hierarchical Clustering, while effective in uncovering hierarchical relationships, exhibited imbalanced cluster sizes, and GMM struggled with meaningful separation due to assumptions of Gaussian distributions in the data. K-Means, with its iterative optimization and ability to handle large datasets efficiently, provided the most interpretable and reliable segmentation for identifying distinct patient groups[36].

3.6.1 Determining the Optimal Number of Clusters Using the Elbow Method

As we can see in Figure 15, thegraph illustrates the Elbow Method, which is used to determine the optimal number of clusters (K) for the dataset. The x-axis represents the number of clusters, while the y-axis shows the Total Sum of Squared Errors (SSE), a measure of how tightly data points are grouped within their clusters. As the number of clusters increases, the SSE decreases, indicating improved clustering. However, after a certain point, the rate of improvement slows significantly, forming an "elbow" shape. In this case, the elbow occurs at K=4, marked by the red dashed line. This suggests that four clusters provide a good balance between minimizing SSE and avoiding overfitting, making it the optimal choice for segmentation[30, 36].

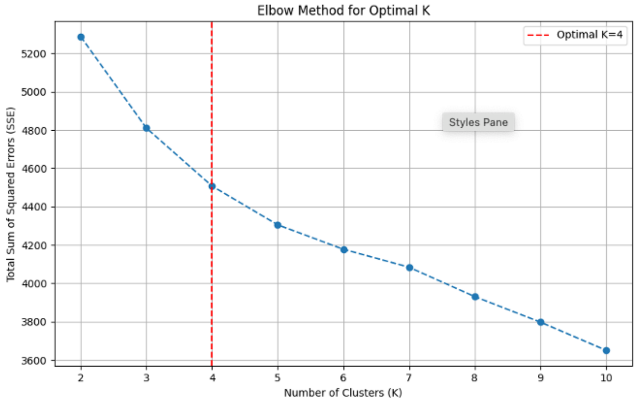


Figure 15: Elbow Method for determining the optimal number of clusters (K). The elbow occurs at K=4, marked by the red dashed line.

3.6.2 Analysis of Clustered Data Using Pairwise Scatterplots

In Figure 16 scatterplot matrix represents the relationships between five key continuous variables in the dataset: age, trestbps (resting blood pressure), chol (cholesterol level), thalach (maximum heart rate achieved), and oldpeak (ST depression induced by exercise). The dataset has been segmented into four clusters (0, 1, 2, and 3), where each cluster is represented by a unique color. The diagonal plots show the distribution of each feature within the clusters, while the off-diagonal plots highlight pairwise relationships between the variables[26].

Cluster Characteristics Based on Age and Resting Blood Pressure:

As we can see in Figure 16, the diagonal plot for age shows that Cluster 2 (pink) is primarily composed of younger individuals, as its density is highest in the lower age range. In contrast, Cluster 3 (blue) spans a much broader age range, including older individuals. Similarly, the distribution of trestbps shows that Cluster 0 (orange) and Cluster 3 (blue) are concentrated in the lower blood pressure range, suggesting these clusters may represent healthier individuals in terms of blood pressure. On the other hand, Cluster 1 (green) has a slightly higher density in the mid-range blood pressure values, which could indicate patients with moderate blood pressure levels[26].

When comparing the relationship between age and trestbps, the clusters show significant overlap. However, Cluster 2 (pink) stands out as it is concentrated around younger ages with relatively low resting blood pressure. Clusters 0 and 1 are more distributed across these two features, indicating a mix of age groups and blood pressure levels in these clusters.

Cholesterol Levels Across Clusters

The cholesterol distribution (*chol*) in Figure 16 reveals some overlap among clusters, but Cluster 2 (pink) has a sharper peak, indicating a more uniform range of cholesterol levels for its members. The scatterplots involving *chol*, such as *chol* vs. *thalach*, demonstrate moderate separation between clusters. Cluster 3 (blue) and Cluster 1 (green) are more spread out across cholesterol levels, suggesting a more diverse population in these clusters regarding cholesterol.

Exercise Capacity and ST Depression

in figure 16, the variable *thalach* represents maximum heart rate achieved, which can reflect exercise capacity. The diagonal plot for *thalach* shows that Cluster 0 (orange) and Cluster 1 (green) have higher densities in the mid-range of this feature, while Cluster 2 (pink) shows a concentration in the lower heart rate values, indicating potentially lower exercise capacity. The *oldpeak* variable, which measures ST depression induced by exercise, shows that Cluster 3 (blue) has a wider range, including individuals with both lower and higher *oldpeak* values, suggesting varied exercise tolerance levels within this cluster.

The scatterplot for *oldpeak* vs. *thalach* highlights that Cluster 0 (orange) is more tightly grouped in this space, while Cluster 3 (blue) has a broader distribution. This suggests that Cluster 0 may represent individuals with more consistent exercise tolerance levels, while Cluster 3 includes a wider variety of cases.

The scatterplot matrix shows that while there is some overlap between clusters in certain feature combinations, distinct patterns emerge in others. For example, Cluster 2 (pink) stands out for its younger members with lower blood pressure and cholesterol levels. Cluster 3 (blue) exhibits the most diversity, spanning a wide range of ages, cholesterol levels, and exercise-induced *oldpeak* values. Clusters 0 and 1 show more moderate distributions across the variables, suggesting these clusters may represent intermediate-risk groups.

This analysis provides valuable insights into the characteristics of each cluster based on key medical variables. By understanding the patterns revealed in this scatterplot matrix, healthcare professionals can better interpret the segmentation results and identify which clusters might benefit from targeted interventions. For example, younger individuals in Cluster 2 may require less intensive monitoring compared to the diverse and high-risk individuals in Cluster 3. This visualization helps bridge the gap between raw data and actionable knowledge, making it easier to develop patient-specific strategies[29].

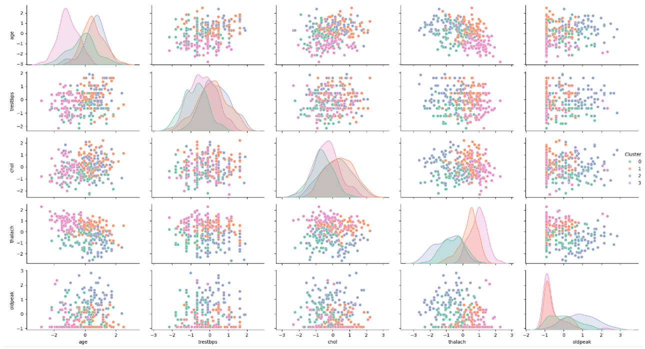


Figure 16: Pairwise Scatterplot Matrix of Key Variables Across Clusters. This matrix illustrates the relationships between age, trestbps (resting blood pressure), chol (cholesterol), thalach (maximum heart rate achieved), and oldpeak (ST depression induced by exercise). Each cluster (0, 1, 2, and 3) is represented by a unique color, with diagonal plots showing feature distributions within clusters and off-diagonal plots highlighting pairwise relationships.

3.6.3 Silhouette Plot for K-Means Clustering

Figure 17 evaluates the quality of clustering by measuring how well each data point fits within its assigned cluster. The silhouette coefficient ranges from -1 to 1, where higher values mean better clustering. Each bar represents a cluster, and its thickness shows the number of data points in that cluster. In this plot, all clusters have mostly positive silhouette scores, which means the points are well-grouped. However, some points near zero indicate overlap between clusters, where some data points might not be clearly assigned. Overall, the clustering seems reasonable but could be improved by adjusting features or the number of clusters[28].

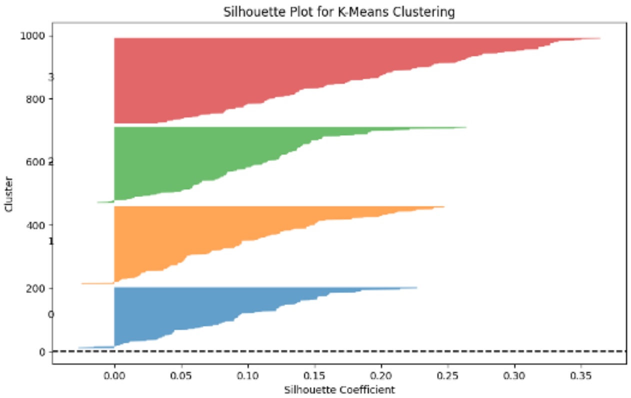
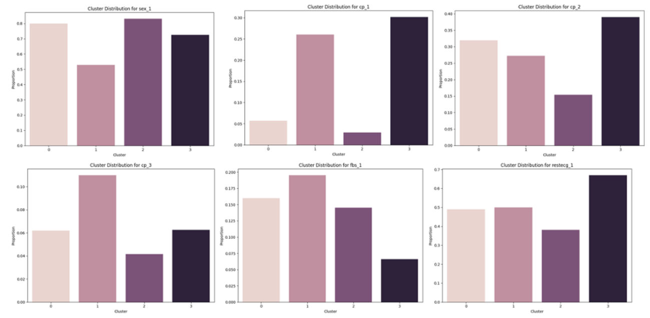


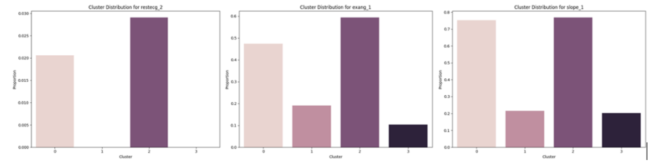
Figure 17: Silhouette Plot for K-Means Clustering. This plot shows the silhouette coefficient for each cluster, where positive values indicate well-clustered points. Overlap near zero suggests that some points may be ambiguously assigned.

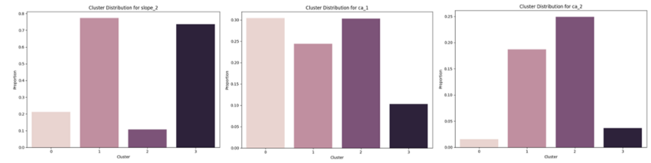
3.6.4 Cluster Distribution of Categorical Features

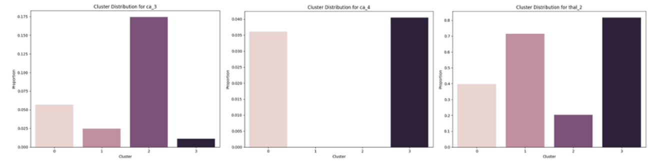
The following bar charts show how categorical features are distributed across the four clusters created by the K-means algorithm. Each chart represents a different categorical variable, such as *sex*, *cp* (chest pain type), *fbs* (fasting blood sugar), and others. The x-axis displays the cluster labels (0 to 3), and the y-axis shows the proportion of each feature within each cluster.

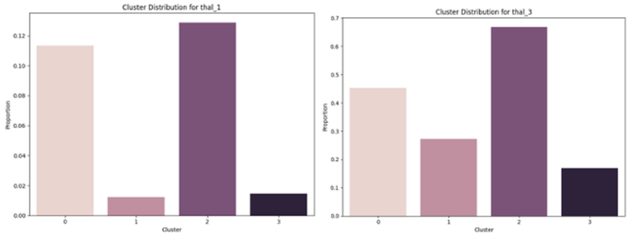
The visualizations clearly indicate that the distributions of categorical features differ among the clusters. For example, some clusters, like Cluster 2 or Cluster 3, have higher proportions of specific categories, which shows that each cluster has unique characteristics. This means the clusters are identifying meaningful patterns in the data, such as variations in chest pain types or fasting blood sugar levels. These findings can help better understand the traits of each group and support more personalized medical recommendations. Overall, the bar charts effectively demonstrate the relationship between categorical variables and the identified clusters[29].







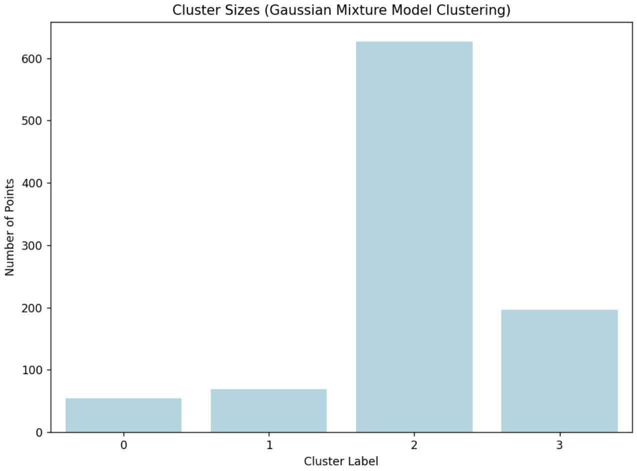




3.6.5 Cluster Distribution Analysis and Justification for Choosing K-Means

We can see in Figure 18, the plots illustrate the distribution of data points across clusters generated by K-Means, Hierarchical Clustering, and Gaussian Mixture Model. The K-Means plot shows a relatively balanced allocation of data points among the four clusters, indicating its ability to group data into similarly sized, distinct clusters. In contrast, the Hierarchical Clustering plot highlights slight imbalances in cluster sizes, reflecting its focus on hierarchical relationships rather than balanced segmentation. On the other hand, the Gaussian Mixture Model (GMM) clustering is the worst among the three, as it fails to produce meaningful or well-balanced clusters, which suggests that the underlying assumptions of GMM may not be well-suited to this dataset[37].

K-Means was chosen for this analysis due to its computational efficiency and suitability for handling large datasets with predefined cluster numbers. Additionally, its iterative optimization ensures compact and well-separated clusters, making it more appropriate for our dataset, where balanced and interpretable segmentation is critical for understanding patient group characteristics.



3.6.6 Clustering Results Comparison Using PCA

In Figure 19, the scatter plots show the clustering results created by Principal Component Analysis (PCA). Each point represents a data record, and the colors show the clusters. In the K-Means plot, the clusters are more separated and balanced, which means K-Means worked well in grouping similar data points. In the Hierarchical

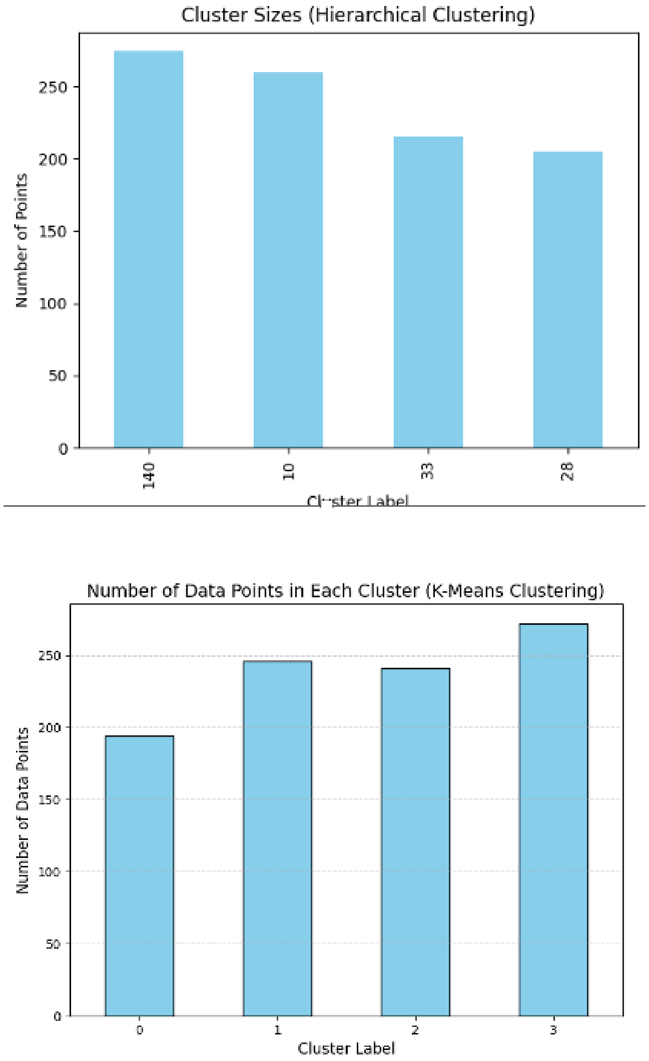


Figure 18: Comparison of cluster distributions for K-Means, Hierarchical Clustering and Guassian Mixture Model Clustering. K-Means shows balanced cluster sizes, whereas Hierarchical Clustering and Guassian Mixture Model displays slight imbalances. This comparison justifies the choice of K-Means for its efficiency and balanced segmentation.

Clustering plot, there is more overlap between clusters, making it harder to see clear groups.

K-Means was chosen because it is faster and works better with larger datasets. K-Means also improves the clusters during its process, which helps find better patterns in the data. The scatter plot for K-Means shows better separation between clusters, proving that it is a better choice for this dataset. The GMM plot reveals imbalanced cluster sizes compared to both K-Means and Hierarchical Clustering. This suggests that the GMM, which assumes that data points come from a mixture of Gaussian distributions, may not be the best fit for this dataset[26].

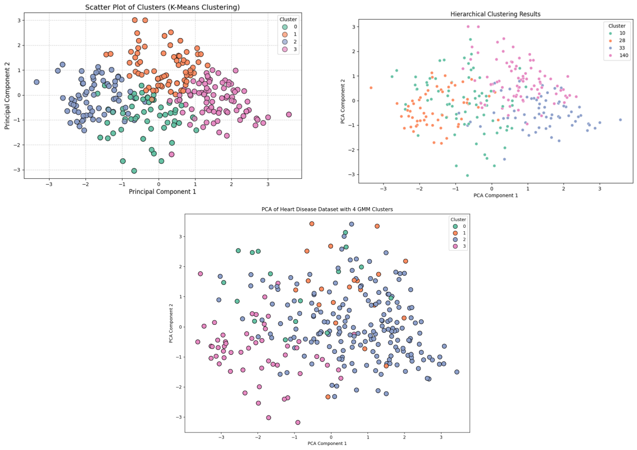
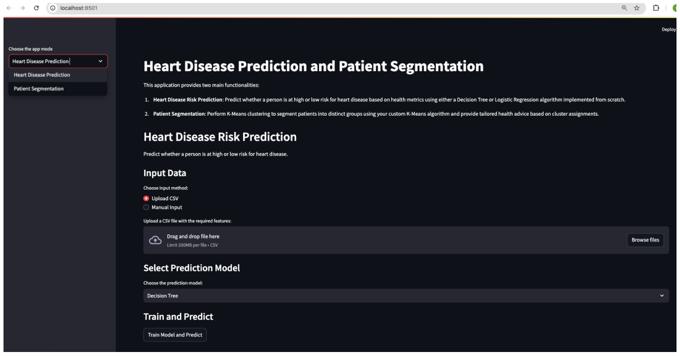


Figure 19: Scatter plots of clustering results using Principal Component Analysis (PCA) for dimensionality reduction. The left plot shows K-Means clusters with better separation and balance, while the right plot shows Hierarchical Clustering results with overlapping clusters.

3.7 Application Description and user manual

The user interface (UI) of this application is designed to support the tasks of heart disease prediction and patient segmentation in a clear and accessible way. Built using Streamlit, the interface ensures that users, including those with limited technical backgrounds, can easily interact with the system. It emphasizes usability by allowing two main functionalities: predicting heart disease risk using models like Decision Tree and Logistic Regression, and segmenting patients into clusters with a custom K-Means algorithm. The UI design reflects a focus on providing meaningful insights for healthcare applications[21].



Heart Disease Prediction and Patient Segmentation

This application provides two main functionalities:

1. **Heart Disease Risk Prediction:** Predict whether a person is at high or low risk for heart disease based on health metrics using either a Decision Tree or Logistic Regression algorithm implemented from scratch.
2. **Patient Segmentation:** Perform K-Means clustering to segment patients into distinct groups using your custom K-Means algorithm and provide tailored health advice based on cluster assignments.

Heart Disease Risk Prediction

Predict whether a person is at high or low risk for heart disease.

Input Data

Choose input method:

● Upload CSV
○ Manual Input

Upload a CSV file with the required features:

Drag and drop file here
Limit 200MB per file • CSV

Select Prediction Model

Choose the prediction model:

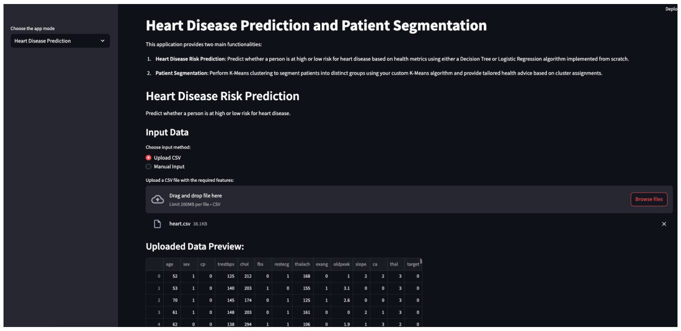
Decision Tree

Train and Predict

Figure 20: User Interface of the Heart Disease Prediction and Patient Segmentation Application.

In Figure 20, you can see the main page of the application features an intuitive layout, starting with a title and a brief introduction to the system's capabilities. The sidebar offers navigation options, enabling users to switch between **Heart Disease Prediction** and **Patient Segmentation**. The interface supports both **CSV**

file uploads for batch processing and **manual input** for individual records. This dual-mode input mechanism makes the system flexible, catering to both large-scale data analysis and single-patient assessments.



Heart Disease Prediction and Patient Segmentation

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Heart Disease Risk Prediction

Predict whether a person is at high or low risk for heart disease.

Input Data

Choose input method:

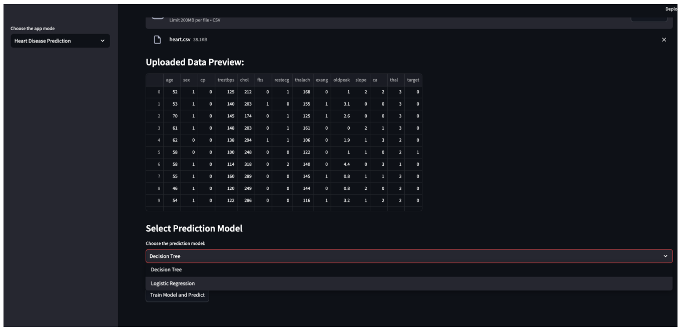
● Upload CSV
○ Manual Input

Upload a CSV file with the required features:

Uploaded Data Preview:

	age	sex	cp	trestbps	chol	fbs	restecg	thalach	exang	oldpeak	slope	ca	thal	target
0	52	1	0	125	212	0	1	168	0	1	2	2	3	0
1	53	1	0	140	203	1	0	155	1	3.1	0	0	3	0
2	70	1	0	145	174	0	1	125	1	2.6	0	0	3	0
3	61	1	0	148	203	0	1	161	0	0	2	1	3	0
4	62	0	0	138	294	1	1	106	0	1.9	1	3	2	0

Figure 21: User Interface for Heart Disease Risk Prediction.



Uploaded Data Preview:

	age	sex	cp	trestbps	chol	fbs	restecg	thalach	exang	oldpeak	slope	ca	thal	target
0	52	1	0	125	212	0	1	168	0	1	2	2	3	0
1	53	1	0	140	203	1	0	155	1	3.1	0	0	3	0
2	70	1	0	145	174	0	1	125	1	2.6	0	0	3	0
3	61	1	0	148	203	0	1	161	0	0	2	1	3	0
4	62	0	0	138	294	1	1	106	0	1.9	1	3	2	0
5	58	0	0	100	248	0	0	122	0	1	1	0	2	1
6	58	1	0	114	318	0	2	140	0	4.4	0	3	1	0
7	55	1	0	160	289	0	0	145	1	0.8	1	1	3	0
8	46	1	0	120	249	0	0	144	0	0.8	2	0	3	0
9	54	1	0	122	286	0	0	116	1	3.2	1	2	2	0

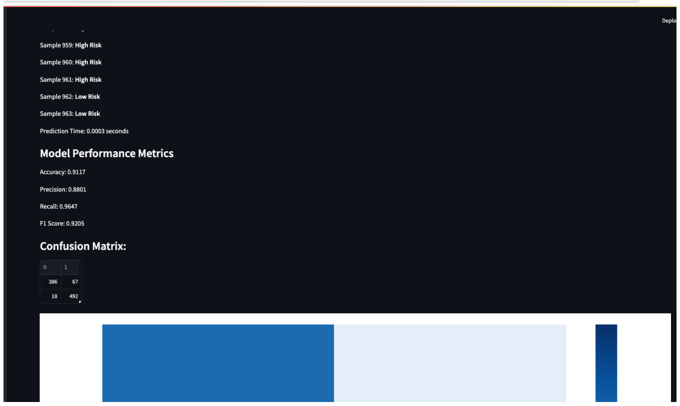
Select Prediction Model

Choose the prediction model: Decision Tree

Figure 22: User can chose between Decision Tree Or Logistic Regression For Prediction.

In figure 21, you can see for heart disease prediction, the system displays input fields for health metrics such as chest pain type, cholesterol levels, and heart rate. In figure 22, Users can train the models directly through the UI, with options to choose between Decision Tree and Logistic Regression. You can see the Logistic regression Results in Figure 26, Figure 27 and Figure 28 . In figure 23, the application provides immediate feedback on predictions, including whether a patient is at high or low risk of heart disease, along with detailed performance metrics like accuracy, precision, recall, and F1 score. Confusion matrices, ROC curves, and classification reports further enhance the interpretability of the results Figure24 Figure 25. By comparing Logistic regression and Decision Tree accuracy and Provided metrics we can see that Desicion Tree is better in heart disease prediction.

The user can also manually input data, as illustrated in Figures 29 and 30. By selecting either the Decision Tree or Logistic Regression model, the application predicts whether the individual is at high or low risk for heart disease, along with the time taken for the prediction. This functionality enables users to obtain predictions using a reduced number of features, identified through feature importance, thereby simplifying the process while maintaining predictive accuracy[38].



Sample 959: **High Risk**

Sample 960: **High Risk**

Sample 961: **High Risk**

Sample 962: **Low Risk**

Sample 963: **Low Risk**

Prediction Time: 0.0003 seconds

Model Performance Metrics

Accuracy: 0.9117

Precision: 0.8801

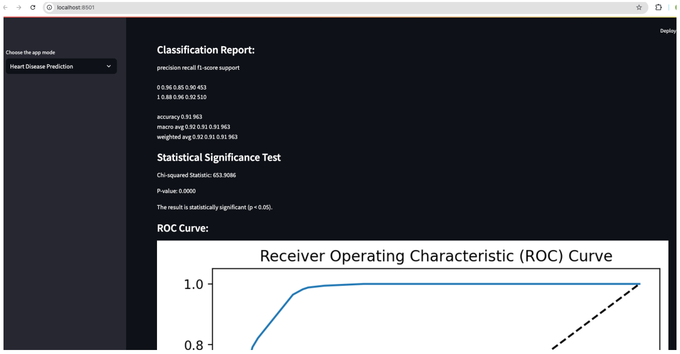
Recall: 0.9647

F1 Score: 0.9205

Confusion Matrix:

0	1
386	67
18	492

Figure 23: The application provides immediate feedback



Classification Report:

precision recall f1-score support

0 0.96 0.85 0.90 453
1 0.88 0.96 0.92 510

accuracy 0.91 963
macro avg 0.92 0.91 0.91 963
weighted avg 0.92 0.91 0.91 963

Statistical Significance Test

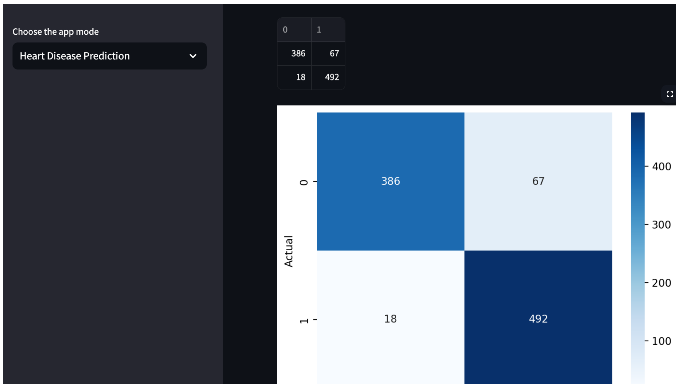
Chi-squared Statistic: 653.9086

P-value: 0.0000

The result is statistically significant ($p < 0.05$).

ROC Curve:

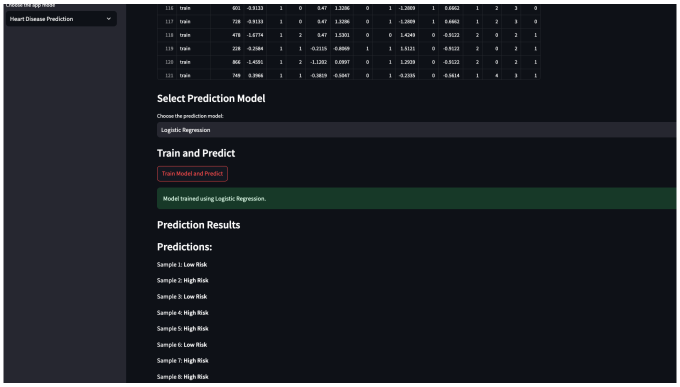
Figure 24: The application provides ROC Curve, accuracy, f1-score and other information



0	1
386	67
18	492

Figure 25: The application provides confusion matrix

In figure 31, 32, 33, 34, 35 and 36 we can see that the Patient Segmentation functionality is similarly user-friendly, guiding users through the process of uploading patient data, performing K-Means clustering, and analyzing cluster characteristics. Visual tools such as the Elbow Method for determining the optimal number of clusters and silhouette plots for evaluating clustering quality help users make informed decisions. Additionally, PCA scatter plots are used



Choose the app mode

Heart Disease Prediction

116	train	601	-0.9133	1	0	0.47	1.3286	0	1	-1.2809	1	0.6662	1	2	3	0
117	train	728	-0.9133	1	0	0.47	1.3286	0	1	-1.2809	1	0.6662	1	2	3	0
118	train	478	-1.6774	1	2	0.47	1.5301	0	0	1.4249	0	-0.9122	2	0	2	1
119	train	228	-0.2584	1	1	-0.2115	-0.8069	1	1	1.5121	0	-0.9122	2	0	2	1
120	train	866	-1.4591	1	2	-1.1202	0.0997	0	1	1.2939	0	-0.9122	2	0	2	1
121	train	749	0.3966	1	1	-0.3819	-0.5047	0	1	-0.2335	0	-0.5614	1	4	3	1

Select Prediction Model

Choose the prediction model:

Logistic Regression

Train and Predict

Model trained using Logistic Regression.

Prediction Results

Predictions:

Sample 1: **Low Risk**

Sample 2: **High Risk**

Sample 3: **Low Risk**

Sample 4: **High Risk**

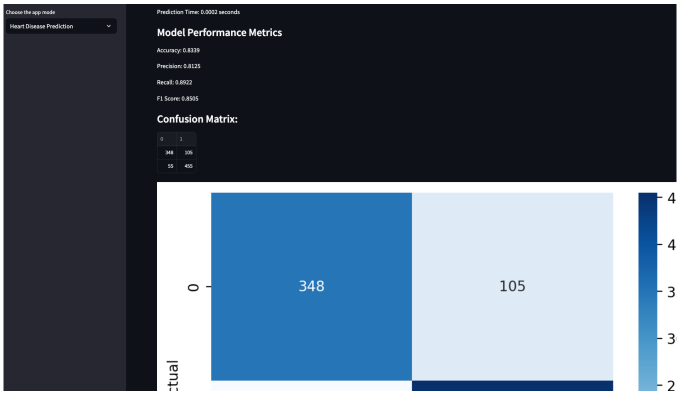
Sample 5: **High Risk**

Sample 6: **Low Risk**

Sample 7: **High Risk**

Sample 8: **High Risk**

Figure 26: Heart Disease prediction with logistic regression



Choose the app mode

Heart Disease Prediction

Prediction Time: 0.0002 seconds

Model Performance Metrics

Accuracy: 0.8339

Precision: 0.8125

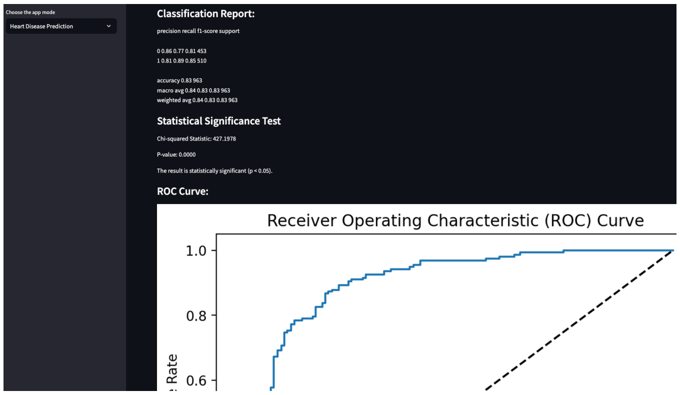
Recall: 0.8922

F1 Score: 0.8505

Confusion Matrix:

0	1
348	105
55	455

Figure 27: Heart Disease prediction with logistic regression Include Prediction Time , Accuracy, Precision, Recall, F1 Score and Confusion Matrix



Choose the app mode

Heart Disease Prediction

Classification Report:

```
precision recall f1-score support

0 0.86 0.77 0.81 453
1 0.81 0.89 0.85 510

accuracy 0.83 963
macro avg 0.84 0.83 0.83 963
weighted avg 0.84 0.83 0.83 963
```

Statistical Significance Test

Chi-squared Statistic: 427.1978

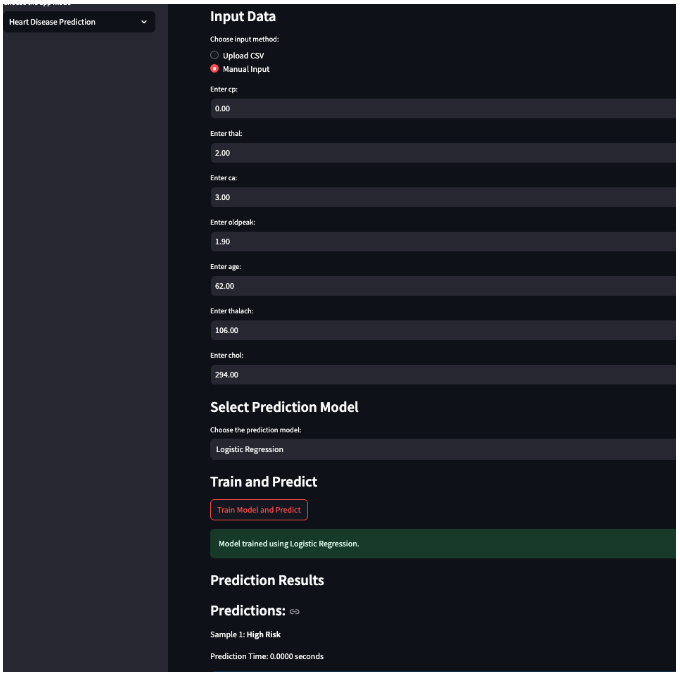
P-value: 0.0000

The result is statistically significant (p < 0.05).

ROC Curve:

Figure 28: Heart Disease prediction with logistic regression Include Prediction Time , Accuracy, Precision, Recall, F1 Score and Confusion Matrix

to visually represent the clusters, providing an easy way to understand how patients are grouped based on their health metrics.
The interface also includes dynamic visualizations like pairwise



Heart Disease Prediction

Input Data

Choose input method:

○ Upload CSV
● Manual Input

Enter cp: 0.00

Enter thal: 2.00

Enter ca: 3.00

Enter oldpeak: 1.90

Enter age: 62.00

Enter thalach: 106.00

Enter chol: 294.00

Select Prediction Model

Choose the prediction model:

Logistic Regression

Train and Predict

Model trained using Logistic Regression.

Prediction Results

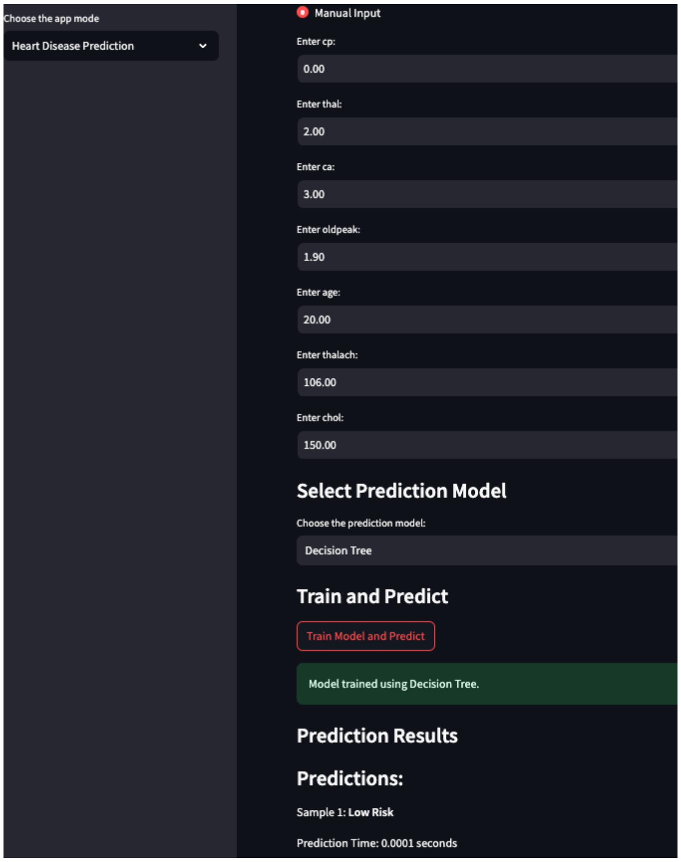
Predictions:

Sample 1: **High Risk**

Prediction Time: 0.0000 seconds

Figure 29: Heart Disease prediction with manual Input with logistic regression(Include Prediction time)

scatterplots and bar charts to analyze data distributions across clusters. For each cluster, the application provides tailored health advice based on the characteristics of the grouped patients. This feature makes the system particularly valuable for healthcare providers, who can use these recommendations to develop targeted intervention strategies.
Finally, the UI is enriched with features such as downloadable results, real-time progress indicators, and automatic outlier handling during data preprocessing. These elements make the application efficient and practical for users, ensuring it meets the needs of both technical and non-technical audiences. Overall, the interface achieves a balance between functionality and simplicity, making it a robust tool for heart disease prediction and patient segmentation[39].



Enter cp: 0.00

Enter thal: 2.00

Enter ca: 3.00

Enter oldpeak: 1.90

Enter age: 20.00

Enter thalach: 106.00

Enter chol: 150.00

Select Prediction Model

Choose the prediction model: Decision Tree

Train and Predict

Model trained using Decision Tree.

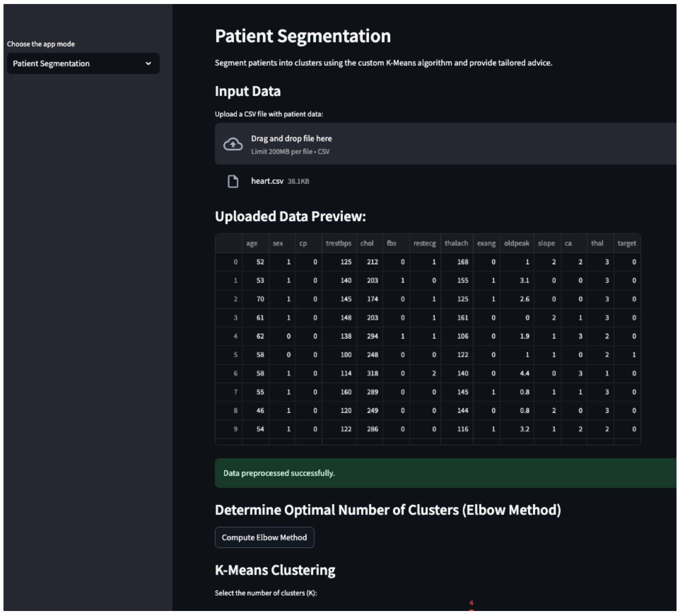
Prediction Results

Predictions:

Sample 1: **Low Risk**

Prediction Time: 0.0001 seconds

Figure 30: Heart Disease prediction with manual Input with Decision Tree(Include Prediction time)



Patient Segmentation

Segment patients into clusters using the custom K-Means algorithm and provide tailored advice.

Input Data

Upload a CSV file with patient data:

Uploaded Data Preview:

	age	sex	cp	trestbps	chol	fbs	restecg	thalach	exang	oldpeak	slope	ca	thal	target
0	52	1	0	125	212	0	1	168	0	1	2	2	3	0
1	53	1	0	140	203	1	0	155	1	3.1	0	0	3	0
2	70	1	0	145	174	0	1	125	1	2.6	0	0	3	0
3	61	1	0	148	203	0	1	161	0	0	2	1	3	0
4	62	0	0	138	294	1	1	106	0	1.9	1	3	2	0
5	58	0	0	100	248	0	0	122	0	1	1	0	2	1
6	58	1	0	114	318	0	2	140	0	4.4	0	3	1	0
7	55	1	0	160	289	0	0	145	1	0.8	1	1	3	0
8	46	1	0	120	249	0	0	144	0	0.8	2	0	3	0
9	54	1	0	122	286	0	0	116	1	3.2	1	2	2	0

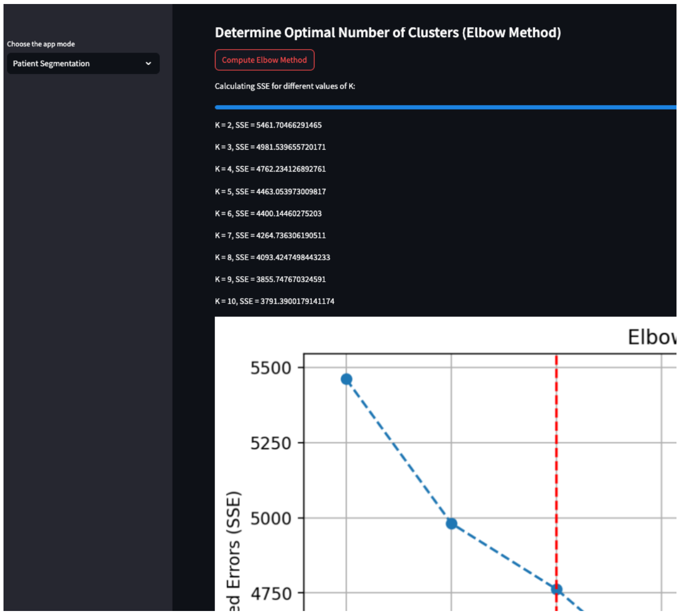
Data preprocessed successfully.

Determine Optimal Number of Clusters (Elbow Method)

K-Means Clustering

Select the number of clusters (K):

Figure 31: Patient Segmentation by K-Means

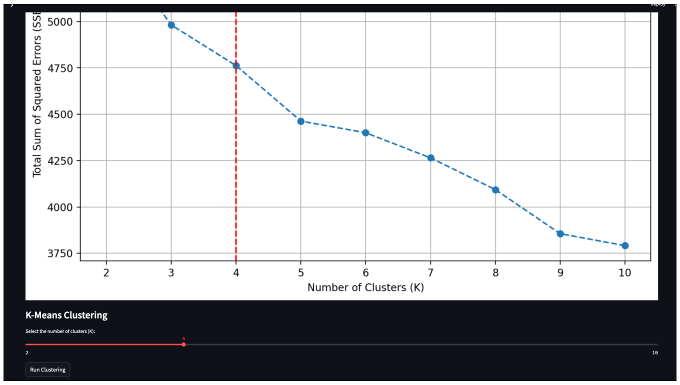


Determine Optimal Number of Clusters (Elbow Method)

Calculating SSE for different values of K:

```
K = 2, SSE = 5461.70466291465
K = 3, SSE = 4981.539655720171
K = 4, SSE = 4762.234126892761
K = 5, SSE = 4463.053973009817
K = 6, SSE = 4400.14460275203
K = 7, SSE = 4264.736306190511
K = 8, SSE = 4093.4247498443233
K = 9, SSE = 3855.747670324591
K = 10, SSE = 3791.3900179141174
```

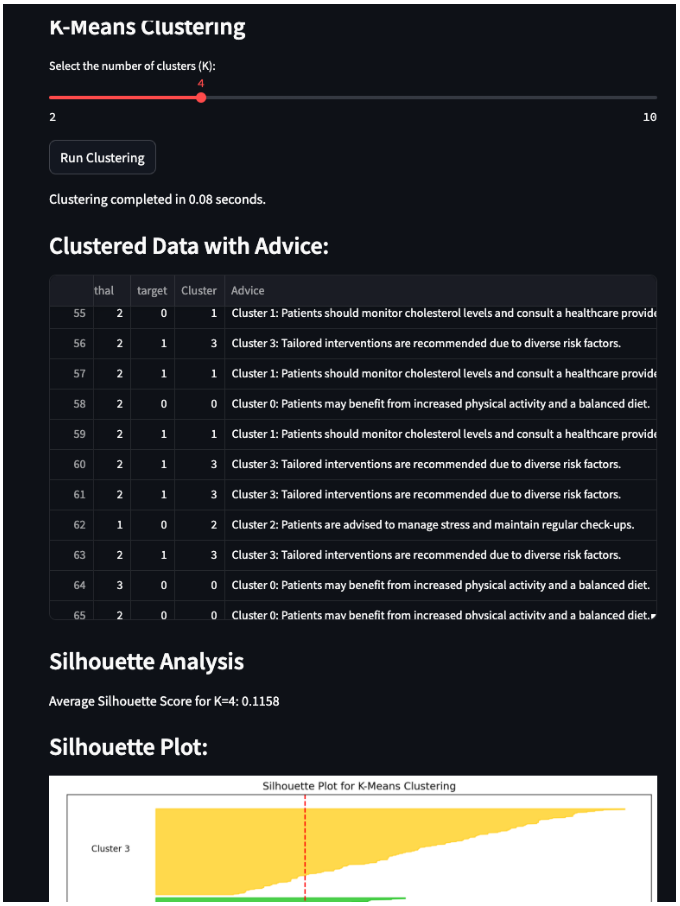
Figure 32: User by hitting "Compute Elbow Method " can see the calculating SSE for different values of K



K-Means Clustering

Select the number of clusters (K):

Figure 33: User by hitting "Compute Elbow Method " can see the calculating SSE for different values of K



K-Means Clustering

Select the number of clusters (K): 4

Run Clustering

Clustering completed in 0.08 seconds.

Clustered Data with Advice:

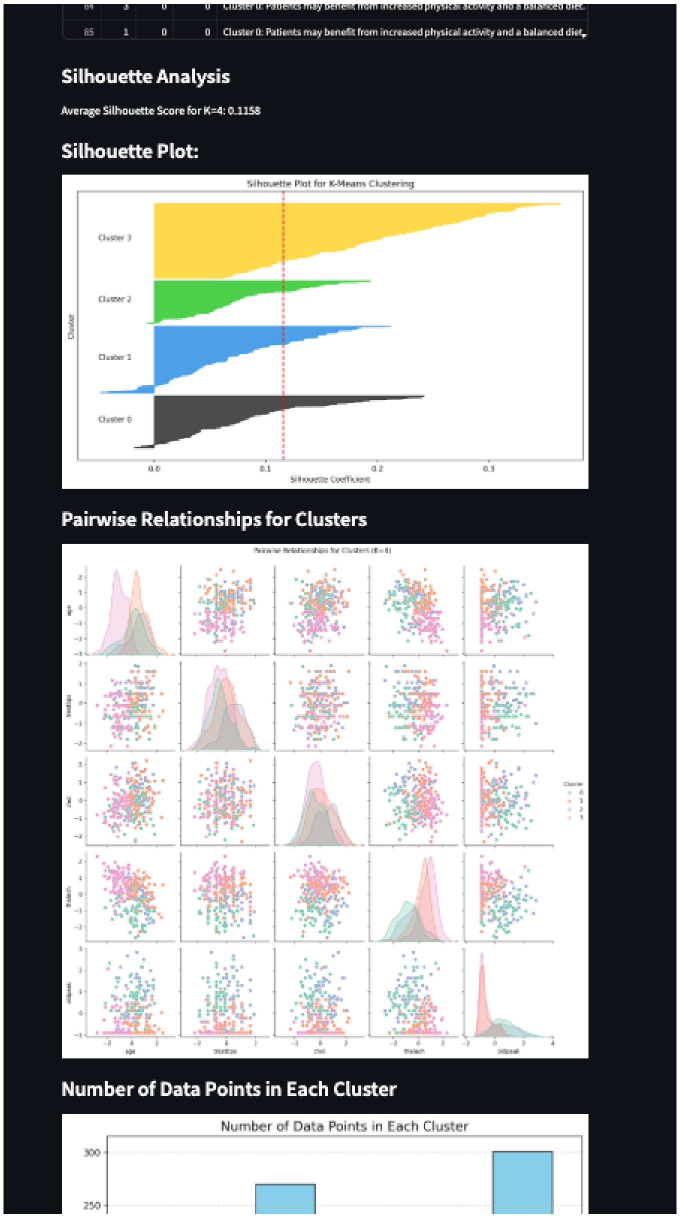
	thal	target	Cluster	Advice
55	2	0	1	Cluster 1: Patients should monitor cholesterol levels and consult a healthcare provide
56	2	1	3	Cluster 3: Tailored interventions are recommended due to diverse risk factors.
57	2	1	1	Cluster 1: Patients should monitor cholesterol levels and consult a healthcare provide
58	2	0	0	Cluster 0: Patients may benefit from increased physical activity and a balanced diet.
59	2	1	1	Cluster 1: Patients should monitor cholesterol levels and consult a healthcare provide
60	2	1	3	Cluster 3: Tailored interventions are recommended due to diverse risk factors.
61	2	1	3	Cluster 3: Tailored interventions are recommended due to diverse risk factors.
62	1	0	2	Cluster 2: Patients are advised to manage stress and maintain regular check-ups.
63	2	1	3	Cluster 3: Tailored interventions are recommended due to diverse risk factors.
64	3	0	0	Cluster 0: Patients may benefit from increased physical activity and a balanced diet.
65	2	0	0	Cluster 0: Patients mav benefit from increased ohvsical activitv and a balanced diet.

Silhouette Analysis

Average Silhouette Score for K=4: 0.1158

Silhouette Plot:

Figure 34: User can view clustered data with advice by clicking the "Run Clustering" button.



84	3	0	0	Cluster 0: Patients may benefit from increased physical activity and a balanced diet.
85	1	0	0	Cluster 0: Patients may benefit from increased physical activity and a balanced diet.

Silhouette Analysis

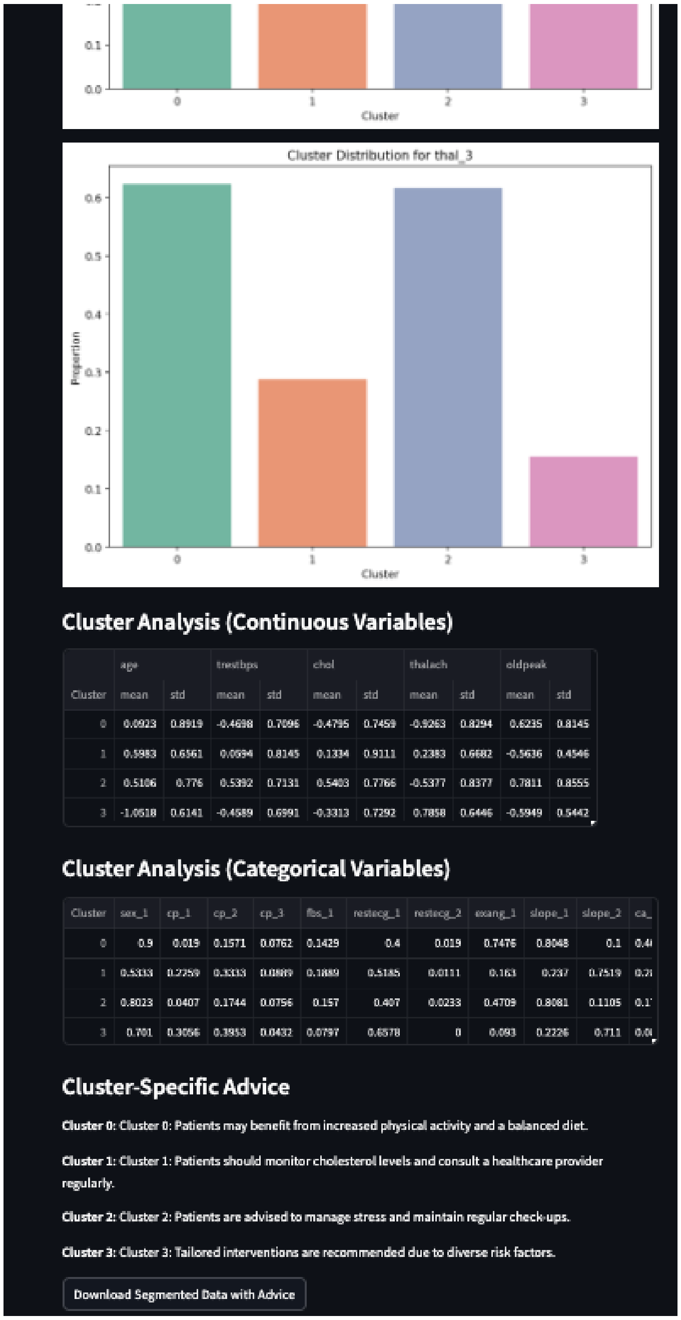
Average Silhouette Score for K=4: 0.1158

Silhouette Plot:

Pairwise Relationships for Clusters

Number of Data Points in Each Cluster

Figure 35: User can view clustered data with advice by clicking the "Run Clustering" button.



Cluster Analysis (Continuous Variables)

	age		trestbps		chol		thalach		oldpeak	
Cluster	mean	std	mean	std	mean	std	mean	std	mean	std
0	0.0923	0.8919	-0.4698	0.7096	-0.4795	0.7459	-0.9263	0.8294	0.6235	0.8145
1	0.5983	0.6561	0.0594	0.8145	0.1334	0.9111	0.2383	0.6682	-0.5636	0.4546
2	0.5106	0.776	0.5392	0.7131	0.5403	0.7766	-0.5377	0.8377	0.7811	0.8555
3	-1.0518	0.6141	-0.4589	0.6991	-0.3313	0.7292	0.7858	0.6446	-0.5949	0.5442

Cluster Analysis (Categorical Variables)

Cluster	sex_1	cp_1	cp_2	cp_3	fbs_1	restecg_1	restecg_2	exang_1	slope_1	slope_2	ca_
0	0.9	0.019	0.1571	0.0762	0.1429	0.4	0.019	0.7476	0.8048	0.1	0.4
1	0.5333	0.2259	0.3333	0.0889	0.1889	0.5185	0.0111	0.163	0.237	0.7519	0.7
2	0.8023	0.0407	0.1744	0.0756	0.157	0.407	0.0233	0.4709	0.8081	0.1105	0.1
3	0.701	0.3056	0.3953	0.0432	0.0797	0.6578	0	0.093	0.2226	0.711	0.0

Cluster-Specific Advice

Cluster 0: Cluster 0: Patients may benefit from increased physical activity and a balanced diet.

Cluster 1: Cluster 1: Patients should monitor cholesterol levels and consult a healthcare provider regularly.

Cluster 2: Cluster 2: Patients are advised to manage stress and maintain regular check-ups.

Cluster 3: Cluster 3: Tailored interventions are recommended due to diverse risk factors.

Figure 36: Provide important plots, cluster analysis for both continuous and categorical variables and at the end user can download segmented data with advise as CSV file

4 CONCLUSION AND FUTURE WORK

This project successfully highlights how data mining and machine learning can make a meaningful impact in healthcare by improving heart disease prediction and patient management. By using models like Decision Trees, Logistic Regression, and k-Nearest Neighbors, we achieved promising results in accurately predicting heart disease risk. In addition, segmenting patients into distinct groups using a custom K-Means algorithm provided deeper insights into shared characteristics and varying levels of risk among patients.

Key factors such as cholesterol levels, chest pain type, and ST depression were identified as significant predictors, offering valuable guidance for medical professionals. The user-friendly application developed as part of this project makes these advanced tools accessible to healthcare providers, allowing them to input patient data and obtain predictions and visual insights easily.

By combining predictive modeling with intuitive tools, this project has the potential to improve heart disease diagnosis and enhance patient outcomes. Looking ahead, scaling this system for real-world use and incorporating more diverse datasets could further broaden its impact, making personalized healthcare more accessible and effective.

Future work for this project includes evaluating models on larger, more diverse datasets to improve generalizability, incorporating ensemble methods like Random Forest and Gradient Boosting for better accuracy, and exploring advanced feature engineering techniques to refine predictions. Real-world deployment would require rigorous testing, EHR integration, and enhanced security, while improving the user interface with advanced visualizations and model explanations could boost usability and transparency. Additionally, extending the application to assess risks for other diseases like diabetes and stroke could make it a comprehensive healthcare tool[40].

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