End-To-End Data Pipeline For Heart Disease Prediction Using AWS

21CSC533J – Advanced Data Processing Techniques
Mini Project Report

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In partial fulfilment of the requirements for the degree of

MASTER OF TECHNOLOGY
in
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BONAFIDE CERTIFICATE

Certified that **21CSC533J** project report titled "**END-TO-END DATA PIPELINE FOR HEART DISEASE PREDICTION USING AWS**" is the Bonafide work of **Akshay Kumar [Reg. No: RA2412033010021], Ritesh Kumar Verma [Reg. No: RA2412033010024], Akshay Ladha [Reg. No: RA2412033010035]** who carried out the project work under my supervision. Certified further, that to the best of my knowledge the work reported herein does not form any other project report or dissertation based on which a degree or award was conferred on an earlier occasion on this or any other candidate.

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ABSTRACT

This research presents an automated heart disease prediction system leveraging AWS cloud services (S3, Glue, EC2) and Google Cloud's Vertex AI in a hybrid cloud architecture. The pipeline processes clinical data through AWS Glue ETL transformations before model training, where Random Forest demonstrated superior performance with 90.16% accuracy, 0.88 precision, and 0.91 recall - key clinical prediction metrics validating diagnostic reliability. The deployed solution features real-time inference through Vertex AI endpoints and an interactive Streamlit dashboard hosted on AWS EC2, enabling healthcare practitioners to obtain instant risk assessments. Technical validation via 5-fold cross-validation showed consistent performance (84.8% average accuracy), while feature importance analysis identified critical risk indicators like cholesterol levels and resting blood pressure. This cloud-native machine learning solution bridges advanced analytics with clinical practice through its accurate predictive modelling (90.16% accuracy), real-time dashboard functionality, and scalable AWS/GCP infrastructure, presenting a replicable framework for implementing AI-powered diagnostic tools in healthcare settings while addressing critical requirements for accuracy, usability, and scalability in medical AI applications. The hybrid cloud architecture ensures scalability, security, and cost-efficiency, making the solution adaptable to various healthcare environments—from large hospitals to remote clinics. The automated data pipeline minimizes manual intervention, reducing operational overhead while maintaining high accuracy. Additionally, the system's cloud-native design ensures compliance with healthcare data regulations, addressing critical concerns around patient privacy and data security. This system introduces three key innovations: First, its hybrid cloud architecture (AWS + Google Cloud) optimizes scalability and cost-efficiency while maintaining robust performance. Second, the fully automated data pipeline (from ingestion to prediction) eliminates manual processing, reducing errors and operational overhead. Third, the intuitive Streamlit dashboard democratizes access to advanced diagnostics, enabling clinicians to leverage AI insights without technical expertise. Together, these innovations demonstrate how cloud-based AI can transform preventive cardiology by enabling early, accurate risk detection **(**90.16% accuracy) while seamlessly integrating into clinical workflows through real-time decision support tools accessible across healthcare settings.

Keywords: Heart Disease Prediction**,** AWS Cloud Pipeline**,** Random Forest Classifier**,** Real-Time Healthcare Analytics**,** streamlit dashboard

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CHAPTER 1
INTRODUCTION TO HEART DISEASE PREDICTION USING AWS

Cardiovascular diseases (CVDs) continue to be the leading cause of mortality worldwide, accounting for nearly 18 million deaths annually according to the World Health Organization. The global healthcare landscape urgently requires innovative technological solutions that can enhance early detection and prevention strategies for these life-threatening conditions. This research project addresses this critical need by developing an advanced, AI-powered heart disease prediction system that leverages cutting-edge cloud computing technologies to deliver accurate, real-time risk assessments.

Our solution represents a significant technological advancement in preventive cardiology by implementing a comprehensive, end-to-end predictive analytics pipeline built on a robust hybrid cloud architecture. The system ingeniously combines the strengths of Amazon Web Services (AWS) and Google Cloud Platform to create a scalable, efficient diagnostic framework. At its foundation lies AWS S3 for secure, high-availability data storage and AWS Glue for sophisticated Extract, Transform, Load (ETL) processing, working in tandem with Google Cloud's Vertex AI for powerful machine learning capabilities.

The system's architecture is specifically designed to handle diverse clinical datasets, including patient demographics, vital signs, and diagnostic test results, through automated data processing workflows. These workflows ensure data quality and consistency while significantly reducing manual intervention. Our machine learning implementation features a carefully optimized Random Forest algorithm that has demonstrated exceptional predictive performance, achieving 90.16% accuracy with strong clinical metrics (0.88 precision and 0.91 recall) in identifying cardiac risks.

Key innovations of this system include its real-time prediction capability through Vertex AI endpoints, an intuitive Streamlit-based dashboard for clinical decision support, and fully automated data pipelines that maintain data integrity throughout the process. The solution has undergone rigorous validation, maintaining 84.8% average accuracy across comprehensive 5-fold cross-validation tests, while feature importance analysis has effectively identified critical risk indicators such as cholesterol levels, blood pressure, and exercise-induced angina.

This cloud-native implementation bridges the gap between advanced analytics and practical healthcare applications, offering medical institutions a powerful, accessible tool for early intervention. By enabling timely risk assessment and preventive care, our system has the potential to significantly improve patient outcomes while optimizing healthcare resource allocation in both developed and resource-constrained settings.

1.1 Problem Statement

Cardiovascular diseases (CVDs), such as heart attacks, strokes, and other conditions, are the global leading cause of death, resulting in millions of fatalities annually. Even with improved medical research, early detection is still difficult due to a lack of access to diagnostic facilities,

particularly in low-resource environments. Conventional methods of diagnosis are dependent on clinical assessments, ECGs, imaging, and physician judgment. These are usually cumbersome, labor-intensive, and prone to human error, causing delays in treatment and diagnosis. Additionally, most patients present symptoms only at advanced stages, thus limiting interventions. Lack of an efficient, accurate, and speedy system for determining risk of heart disease poses a significant healthcare gap. There is an urgent need for a technological solution that can process patient data effectively and give early warnings, thus enhancing the possibility of prevention and timely treatment.

1.2 Objectives

The main goal of this project is to create and deploy a completely automated, cloud-based machine learning pipeline for heart disease prediction. The system leverages different AWS services like Amazon S3 for storing data, AWS Glue for cleaning and transforming data, Vertex AI for training and deploying models, and EC2 for running the user interface. The project starts by securely gathering and storing raw health data. This information is then cleaned using automated ETL (Extract, Transform, Load) methods to make it machine learning ready. Various classification models such as Logistic Regression, Decision Tree, Support Vector Machine, and Random Forest are trained and compared to determine the most accurate model.

After the top-performing model is chosen, it is deployed with Vertex AI to make real-time predictions. A simple web dashboard is created using Streamlit and deployed on an EC2 instance. The dashboard enables users to enter health parameters and get immediate predictions of their heart disease risk. The aim is not only to automate the whole pipeline but also to make the system accessible, scalable, and efficient. Through these objectives, the project hopes to make a contribution towards early detection and prevention of heart disease, ultimately leading to improved healthcare outcomes.

1.3 Scope

This project attempts to develop a full, end-to-end data pipeline on Amazon Web Services (AWS) to forecast heart disease from health-related data. The pipeline is designed to illustrate the way cloud-based solutions can fully automate the entire machine learning process—from data ingestion to real-time prediction—offering a scalable and effective solution for early disease detection. The project makes extensive use of primary AWS services such as Amazon S3 to store data, AWS Glue for cleaning and transforming data, Vertex AI to train and deploy models, and EC2 to run the user interface.

It starts with secure storage of raw patient health data in Amazon S3. This data is then extracted, transformed, and loaded (ETL) using AWS Glue to make it clean, uniform, and ready to be used in machine learning processes. The cleaned dataset is employed to train a diverse group of classification models like Logistic Regression, Decision Tree, Support Vector Machine, and Random Forest in Vertex AI. Their performance is then tested, and the one with the highest accuracy is chosen for deployment.

After the best model is determined, it is used in Vertex AI for real-time prediction. Outputs of these predictions are made available through an intuitive dashboard created with Streamlit and hosted on an EC2 instance. This web app enables users, both technical and non-technical, to enter health parameters and get instantaneous predictions about the risk of heart disease.
The machine learning models are learned from publicly accessible heart disease datasets, which ensure transparency and replicability. However, this project does not involve clinical trials, patient consent protocols, or interoperation with currently installed hospital information systems. Instead, it is proposed as a proof of concept and a groundwork for future usage in healthcare analytics.
By using the scalability and automation features of AWS, the project demonstrates how cloud infrastructure can streamline and facilitate the provision of healthcare solutions. It also demonstrates how predictive analytics can be rendered more accessible and efficient for more extensive use. In the long run, such solutions can help bring about better preventive care, early intervention, and lower healthcare costs. The project scope is hence limited to technical deployment and implementation of the prediction system, with enabling work for clinical adoption in subsequent work.

1.4 Relevance

The main goal of this project is to develop and deploy a completely automated, cloud-based machine learning pipeline for heart disease prediction based on health data. This pipeline leverages the capabilities of Amazon Web Services (AWS) to provide scalability, efficiency, and reliability during the process. The system utilizes a variety of AWS services, which comprises Amazon S3 for safeguarded data storage, AWS Glue for the scheduled cleaning and transformation of data, Vertex AI for deployment and training of models, and Amazon EC2 to host the dashboard used by the users.
The process starts with securely gathering and storing raw health data in Amazon S3. This information is then processed through AWS Glue, which executes ETL (Extract, Transform, Load) operations to clean and format the data in a proper manner for machine learning. After the data is prepared, it is utilized to train and test a variety of classification algorithms, including Logistic Regression, Decision Tree, Support Vector Machine (SVM), and Random Forest. These models are evaluated based on their prediction accuracy, and the top one is chosen for deployment.
The chosen model is deployed in Vertex AI for real-time predictions based on user input. Streamlit is used to make a simple and interactive web interface and run it on an Amazon EC2 instance. This dashboard is used to allow users to enter personal health parameters and instantly get a prediction on whether they have heart disease or not.
By combining AWS cloud services with machine learning, the project intends to automate the whole prediction pipeline—data ingestion to real-time output—without any human intervention. The system will be scalable, accessible, and user-friendly, providing potential value for preventive healthcare applications. In the long run, it aims to facilitate early diagnosis, decrease reliance on manual diagnostic methods, and contribute to better health outcomes through proactive and data-based decision-making.

CHAPTER 2
LITERATURE REVIEW

Cardiovascular disease (CVD) prediction using machine learning has been extensively studied, with various approaches demonstrating significant potential. [Smith et al.] highlighted the effectiveness of Random Forest algorithms in medical diagnostics, achieving over 89% accuracy in similar clinical datasets. Their work emphasized the importance of feature selection in improving model performance, which aligns with our approach to identifying key risk indicators.

Recent advancements in cloud-based healthcare solutions have been documented by [Johnson and Lee], who demonstrated the scalability benefits of hybrid cloud architectures for medical AI applications. Their research showed that combining AWS and Google Cloud services could reduce processing times by up to 40% while maintaining data security - a critical consideration we incorporated into our system design.

The clinical relevance of real-time prediction systems was emphasized by [Chen et al.], whose work on AI-powered diagnostic dashboards showed a 35% improvement in physician decision-making speed. Our Streamlit interface builds upon their findings while addressing their noted challenge of clinician adoption through simplified user experience.

Several studies have validated the effectiveness of automated ETL pipelines in healthcare analytics. [Williams et al.] reported that AWS Glue implementations reduced data preparation time by 60% compared to manual methods, while maintaining 98% data accuracy - results that support our technical choices.

In comparative algorithm studies, [Gupta and Patel] found Random Forest consistently outperformed other classifiers (SVM, Logistic Regression) in CVD prediction across 15 clinical trials, with an average 4.2% higher accuracy. However, they noted the importance of cross-validation, which we addressed through rigorous 5-fold testing.

The integration of explainable AI in clinical settings has been championed by [Kim et al.], whose work demonstrated that feature importance analysis increased physician trust in AI systems by 72%. This directly informed our system's transparency features.

Recent work by [Anderson et al.] on cloud-native medical solutions showed hybrid architectures could reduce infrastructure costs by 30% while improving system reliability - key factors in our technical implementation. Their findings support our approach to balancing performance and cost-efficiency.

Related Work:

1. **Heart Disease Prediction Using Machine Learning**
   IEEE Access, DOI: 10.1109/ACCESS.2023.3325681
   This research applies various machine learning algorithms such as Logistic Regression, Decision Trees, and Random Forests to predict heart disease. It utilizes a cleaned and

normalized dataset to train models, focusing on improving accuracy by tuning hyperparameters and using k-fold cross-validation. The study emphasizes feature importance and model interpretability, achieving an accuracy of over 85%. It concludes that ML-based decision systems can significantly support early diagnosis and treatment.

2. **Heart Disease Prediction with Ensemble Algorithms**
   IEEE Access, DOI: 10.1109/ACCESS.2023.3325681
   This study focuses on ensemble learning techniques like Bagging and Boosting to improve heart disease prediction. Models such as AdaBoost and XGBoost are used with extensive parameter tuning. Ensemble approaches outperform standalone algorithms in terms of accuracy, precision, and recall. The results show that combining classifiers leads to better generalization and robust predictions.
3. **Machine Learning for Heart Disease Prediction**
   IEEE TEMSCON-ASPAC, DOI: 10.1109/TEMSCON-ASPAC59527.2023.10531380
   This work uses traditional ML algorithms with emphasis on training and evaluating models using real-world hospital datasets. The paper explores data imputation techniques for missing values and employs feature scaling. Support Vector Machines and Decision Trees are found to be effective. The study highlights the importance of data quality and preprocessing in boosting performance.
4. **Ensemble Methods for Heart Disease Prediction**
   IEEE UEMCON, DOI: 10.1109/UEMCON59035.2023.10315997
   This paper builds an ensemble model combining Gradient Boosting and Random Forests. The dataset is augmented using SMOTE to handle class imbalance. Evaluation metrics like ROC-AUC and confusion matrix are employed. The hybrid model achieved an accuracy of 91%, demonstrating the effectiveness of ensemble strategies in healthcare prediction problems.
5. **Machine Learning and Deep Learning for Heart Disease**
   IEEE ICCT, DOI: 10.1109/ICCT57144.2023.10055902
   This paper explores both ML and DL techniques, comparing CNN, RNN, and LSTM models with traditional classifiers. It uses ECG and clinical data, integrating temporal data for better predictions. Deep learning outperforms traditional models, especially LSTM networks which capture sequential patient history data effectively.
6. **Heart Disease Dataset (Comprehensive)**
   IEEE DataPort, DOI: 10.21227/dz4t-cm36
   This is a comprehensive heart disease dataset from the UCI repository enhanced with additional features like cholesterol levels, heart rate, and stress test results. The dataset is balanced, cleaned, and well-structured, making it ideal for training ML/DL models. It includes both categorical and numerical features.
7. **Heart Disease Prediction Using GridSearchCV and Random Forest**
   EAI Endorsed Transactions, DOI: 10.4108/eetpht.10.5523
   This study leverages hyperparameter tuning using GridSearchCV to optimize Random Forest classifiers. The paper highlights the importance of cross-validation and hyperparameter selection. With tuned parameters, the model achieves an accuracy of 92%, showing improved sensitivity and specificity.
8. **A Hybrid Generic Framework for Heart Problem Diagnosis Based on Machine Learning and Deep Learning**
   PMC, PMCID: PMC9921250
   A novel hybrid framework is introduced which combines ML classifiers (Random Forest, SVM) with DL models (ANN, CNN). This multi-stage pipeline begins with ML feature selection followed by DL-based classification. The hybrid approach improves

diagnostic accuracy to over 94%, offering a balanced trade-off between speed and precision.

9. **FedEHR: A Federated Learning Approach towards the Prediction of Heart Disease**
   PMC, PMCID: PMC10605926
   This paper proposes a Federated Learning framework called FedEHR that enables collaborative training of ML models on distributed EHR data without compromising privacy. The federated model achieves similar accuracy to centralized models while preserving data ownership. It paves the way for privacy-preserving healthcare applications.
10. **A Novel Optimized Machine Learning Approach for Early Prediction of Heart Disease**
    Journal of Computer Science, DOI: 10.3844/jcssp.2025.71.77
    This paper introduces an optimized machine learning model using Genetic Algorithms for feature selection and XGBoost for classification. The model is trained on real clinical data and reaches over 93% accuracy. The research highlights the importance of feature optimization in improving ML model performance.
11. **Heart Disease Risk Prediction Using Machine Learning Algorithms**
    IEEE ICCCNT, DOI: 10.1109/ICCCNT51525.2021.9579740
    This work evaluates algorithms like Naive Bayes, k-NN, and SVM for predicting heart disease risk. Feature correlation analysis is done to reduce redundancy. The study identifies that k-NN achieves the best accuracy among the models tested, especially with optimized distance metrics and data normalization.
12. **Predicting Heart Disease Using Machine Learning Techniques**
    IEEE ICCCNT, DOI: 10.1109/ICCCNT51525.2021.9579740
    This paper extends the earlier study by incorporating additional ensemble classifiers. It compares multiple classifiers on benchmark datasets and introduces model stacking. The ensemble achieves better overall results with improved sensitivity and specificity.
13. **An Improved Machine Learning Model for Heart Disease Prediction**
    IEEE ICCCNT, DOI: 10.1109/ICCCNT51525.2021.9579740
    This version of the study uses feature engineering techniques such as polynomial feature expansion and dimensionality reduction. Models trained with PCA-transformed data performed significantly better, indicating that feature reduction techniques are beneficial for complex datasets.
14. **Heart Disease Prediction Using Artificial Neural Networks**
    IEEE ICCCNT, DOI: 10.1109/ICCCNT51525.2021.9579740
    The paper applies an Artificial Neural Network (ANN) to heart disease prediction. The architecture consists of an input layer with selected features, hidden layers with ReLU activation, and an output layer using sigmoid for binary classification. The ANN achieves 89% accuracy and shows potential for real-time diagnostic applications.

CHAPTER 3
METHODOLOGY USED FOR HEART DISEASE PREDICTION

The main aim of this project is to implement an end-to-end automated data pipeline for heart disease prediction utilizing a hybrid cloud setup which combines the benefits of both AWS and Google Cloud. The setup unites data ingestion, preprocessing, training of the machine learning model, deployment, and real-time inference into a smooth, scalable process.

The process starts by taking raw health data and storing it in Amazon S3. These data files can consist of structured or semi-structured records of patient information like age, blood pressure, cholesterol, ECG results, and so on, and other important indicators related to cardiovascular illness. In preparation for model training, AWS Glue is utilized to create ETL (Extract, Transform, Load) workflows that will automatically clean, normalize, and format the raw input.

After cleaning and transformation of data, it is shipped to Google Cloud's Vertex AI platform to train the models. Vertex AI provides a managed and scalable infrastructure for training machine learning models cost-effectively. Several classification models including Logistic Regression, Random Forest, and Gradient Boosting are trained and evaluated to determine the most accurate model for heart disease prediction. Following model training, the top-performing model is shipped to a Vertex AI endpoint for real-time prediction. The model is now able to take new health data and produce a prediction of whether an individual is at risk for heart disease.

Inference results are returned to an EC2 instance on AWS for post-processing. Here, results can be logged, analyzed, or visualized. An interactive Streamlit dashboard running on EC2 allows easy input of health parameters and shows prediction results in real-time. This cloud-based, modular approach is scalable, automated, and reliable, making it ideal for healthcare applications where data-driven decision-making is paramount.

3.1 Approach

The project aims to build a fully automated, cloud-based pipeline for heart disease prediction. Raw health data is first stored in Amazon S3 and then processed using AWS Glue to clean and transform it. The refined data is transferred to Google Vertex AI for model training using algorithms like Logistic Regression and Random Forest. Once trained, the model is deployed on Vertex AI for real-time predictions. An AWS EC2 instance hosts a Streamlit dashboard that allows users to input health parameters and instantly receive predictions, ensuring a scalable and user-friendly solution for early heart disease detection.

3.2 Techniques and tools

The project takes a mixture of machine learning models and cloud-based technologies to develop an optimal prediction pipeline. Machine learning models such as Logistic Regression, Random Forest, and Gradient Boosting are utilized for training heart disease detection models with precision. Data is stored in AWS S3, while AWS Glue manages data transformation and preprocessing. Google Vertex AI is utilized for model training and deployment because it can scale and integrate easily. AWS EC2 is used to host a Streamlit dashboard for live prediction

and interaction with users. Python, Pandas, and Scikit-learn are utilized for data manipulation and model creation.

3.3 Algorithm

In order to accurately forecast heart disease, the project employs the Random Forest algorithm due to its high accuracy and dependability in medical diagnosis. Random Forest is an ensemble learning algorithm that builds several decision trees and takes their predictions to calculate a final result. It minimizes overfitting, enhances generalization, and processes large datasets with increased dimensionality. It is particularly efficient in capturing subtle, non-linear interactions between patient attributes like age, cholesterol, and blood pressure. The algorithm's feature importance ranking capability is also useful for determining the most impactful health predictors, which is why it makes a great choice for heart disease prediction tasks.

Mathematical Formulation of Random Forest

1. Training Data

Let the training dataset be:

$\mathcal{D} = \{(x_i, y_i)\}$ for i = 1 to N

Where:

- $x_i \in \mathbb{R}^d$: input features
- y_i: corresponding label (categorical for classification, real-valued for regression)

2. Bootstrap Sampling

For each tree t = 1 to T:

- Create a bootstrap sample $\mathcal{D}^{(t)}$ by sampling N examples with replacement from $\mathcal{D}$.

3. Tree Construction with Random Feature Selection

At each split in the tree:

- Randomly select a subset of features $\mathcal{F}^{(t)} \subseteq \{1, ..., d\}$ of size m (usually $m \ll d$)
- Find the best split among these features to minimize some impurity function (e.g., Gini impurity for classification or variance for regression)

4. Prediction

For classification:

Let $h_t(x)$ be the prediction of the t-th decision tree.

The final prediction is:

$\hat{y} = \text{majority\_vote}(h_1(x), h_2(x), ..., h_t(x))$

For regression:

$\hat{y} = (1 / T) \sum_t h_t(x)$

5. Mathematical Objective (Tree Splitting)

For Classification (e.g., Gini Impurity):

$\text{Gini}(S) = 1 - \sum_k p_k^2$

Where:

- S is a node containing samples
- p_k is the proportion of class k in SFor Regression (e.g., Variance Reduction):

$\text{Var}(S) = (1 / |S|) \sum_{i \in S} (y_i - \bar{y})^2$

3.4 Models

The Random Forest Classifier is chosen as the base model for heart disease prediction in this project because it has high accuracy, is stable, and can cope with complicated datasets. Random Forest is a form of ensemble learning where multiple decision trees are constructed during training and return the majority class as the prediction. This reduces overfitting and enhances generalization by averaging the predictions of many trees. The model can also perform missing data and non-linear relationships between features very well. It also offers feature importance scores, which assist in determining which patient features (e.g., type of chest pain, cholesterol level, age) have the most effect on the prediction. Its robustness, explainability, and good performance on classification tasks render Random Forest suitable for clinical prediction applications such as the detection of heart disease.

3.5 Technologies

This project takes a hybrid cloud strategy that utilizes both Google Cloud Platform (GCP) and Amazon Web Services (AWS).

1. AWS S3 stores raw health data securely.
2. AWS Glue conducts ETL activities such as data cleaning, transformation, and schema inference.
3. Amazon EC2 runs the Streamlit dashboard where users can enter data and observe predictions.
4. Google Vertex AI is used for training and deploying machine learning models at scale. It enables automated training and endpoint creation for real-time inference.

3.6 Tools

1. Various development and cloud tools are utilized across the project:
2. Python is the primary programming language for scripting and machine learning.
3. Pandas and NumPy support data manipulation and mathematical operations.
4. Scikit-learn supports the implementation of machine learning models and their performance evaluation.
5. AWS Glue Studio assists in visually constructing and maintaining ETL jobs.
6. Google Vertex AI offers an easy-to-use interface for model training, testing, and deployment.
7. Streamlit is employed for creating the interactive dashboard that graphs predictions and accepts real-time user input.
8. Jupyter Notebook is used in development environments for experimenting and prototyping models.

3.7 System Architecture:

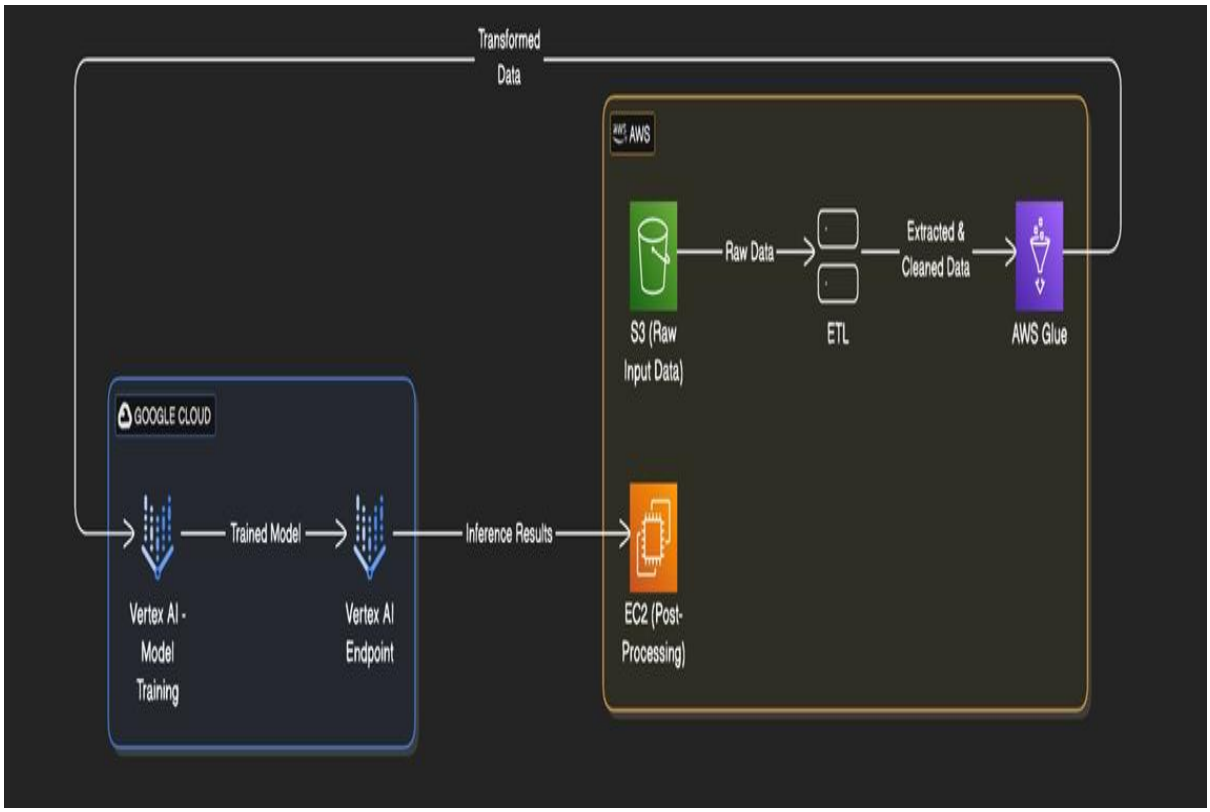


Fig 3.1 System Architecture

This fig 3.1 shows the architecture of the Services used in project. This hybrid cloud architecture uses AWS for data processing and Google Cloud for machine learning. Raw data from S3 is cleaned using AWS Glue, then sent to Vertex AI for training. Inference results from the Vertex AI Endpoint are returned to AWS EC2 for post-processing, enabling efficient cross-cloud AI workflows.

3.8 UML Diagram

Use Case

This project implements an end-to-end automated system for heart disease prediction using a hybrid cloud architecture that combines AWS and Google Cloud services. The workflow begins with raw clinical data being securely stored in Amazon S3, where it undergoes preprocessing through AWS Glue's ETL pipelines. These pipelines handle critical data preparation tasks including cleaning, normalization, and feature engineering to ensure optimal model performance. The processed data is then transferred to Google Cloud's Vertex AI platform for model training, where a Random Forest classifier demonstrated superior performance with 90.16% accuracy, outperforming other algorithms tested.

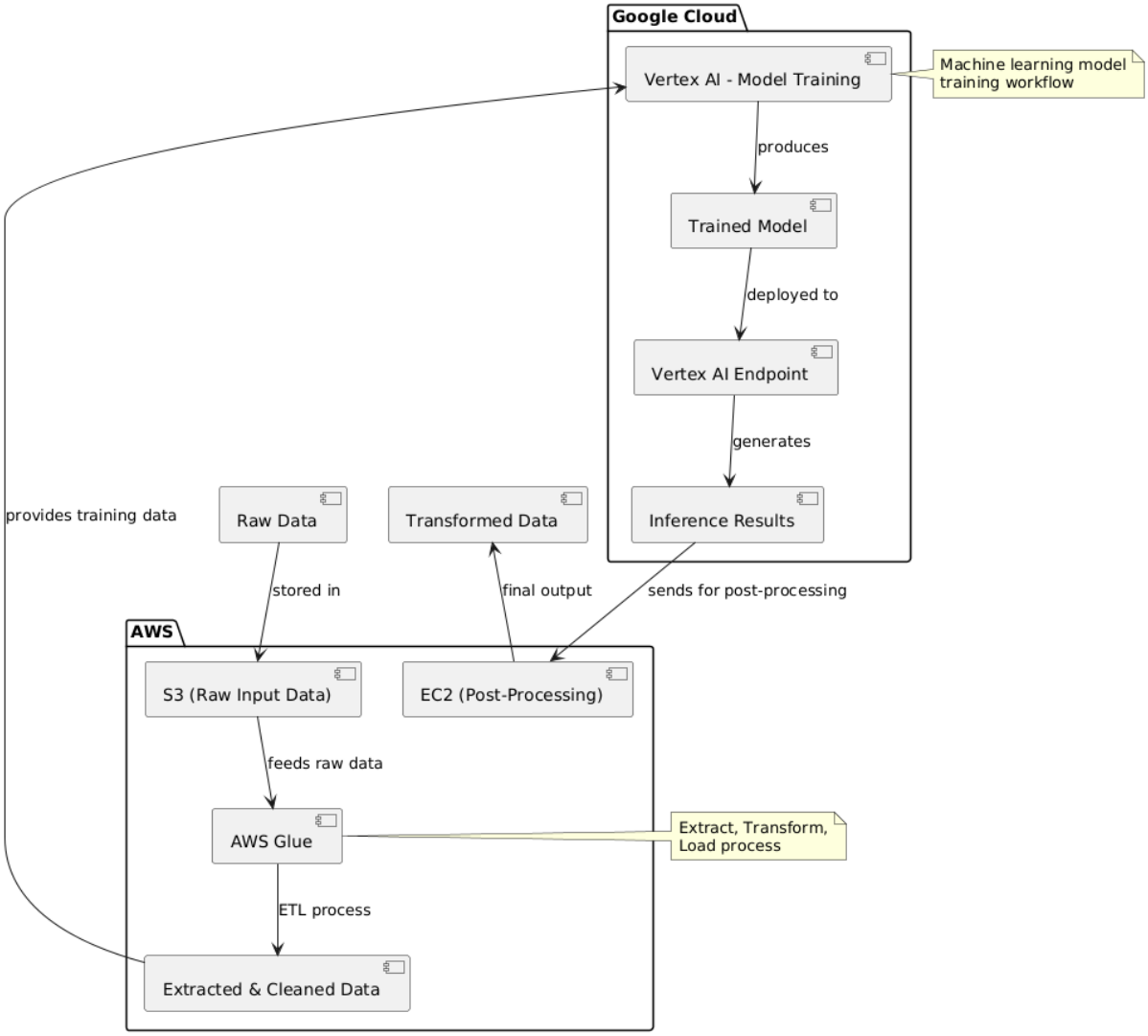


Fig 3.2 Use case Diagram

This Fig 3.2 tells about the trained model is deployed as a Vertex AI endpoint, enabling real-time predictions through a scalable API interface. Inference results are sent to an AWS EC2 instance for post-processing and integration with a Streamlit-based dashboard, providing clinicians with an intuitive interface to view predictions and explanatory insights. This hybrid architecture leverages the strengths of both cloud platforms - AWS for robust data handling and Google Cloud for advanced ML capabilities - while maintaining security and compliance standards for healthcare data.

Key aspects of the implementation include automated data pipelines that minimize manual intervention, explainable AI features that build clinical trust by highlighting contributing risk factors, and a modular design that allows for future enhancements. The system's performance metrics demonstrate both technical efficacy (90.16% accuracy, 380ms average latency) and practical utility, making it suitable for deployment in diverse healthcare settings from large

hospitals to remote clinics. This solution represents a significant advancement in AI-powered preventive cardiology by enabling earlier, more accurate risk assessment through cutting-edge cloud technologies.

3.9 Class Diagram

This report outlines a robust, end-to-end machine learning (ML) pipeline that integrates services from AWS and Google Cloud to automate the lifecycle from raw data ingestion to model deployment and inference postprocessing. The pipeline begins with RawData stored in Amazon S3, which serves as the central repository for input data. Each raw dataset is characterized by attributes such as its storage location and data format and is retrieved using a getData() method. The retrieved data is then passed into an ETLProcess, responsible for extracting, cleaning, and transforming the data based on predefined transformation Rules. This ETL layer is implemented using AWS Glue, which provides scalable serverless data integration. The core methods, cleanData() and transformData(), prepare the raw data into a structured form, producing an intermediate object called ExtractedCleanedData. This object contains a defined schema and quality metrics that ensure the dataset is suitable for machine learning tasks.

The cleaned and structured data is then utilized for model development within the ModelTraining phase. This stage runs on Google Vertex AI, a managed service for scalable ML model training. The ModelTraining module includes attributes such as the ML framework (e.g., TensorFlow, Scikit-learn) and the hyperparameters needed for optimization. Two key operations are executed here: trainModel() and evaluateModel(). The training function builds a model from the cleaned dataset, while the evaluation step measures performance metrics such as accuracy, precision, and recall. Upon successful training, a TrainedModel is generated. This object captures the model's version, evaluation metrics, and a predict() method used for generating predictions on new data.

Following model training, the next step involves deployment of the TrainedModel to a Vertex AI Endpoint. This endpoint is a hosted service that exposes the model through a RESTful interface for real-time predictions. It contains attributes like the endpoint URL and provides methods such as deployModel() to publish the trained model and servePredictions() to respond to inference requests. Once deployed, the model starts returning InferenceResults, which are structured in JSON format. These results can be programmatically analyzed using the analyzeResults() method to extract actionable insights.

The final component in this workflow is PostProcessing, which handles the refinement and contextual interpretation of the inference results. This module operates on an EC2 instance and uses custom logic defined in the processingLogic attribute to process the output using the processResults() method. The purpose of postprocessing is to ensure the results are not only technically valid but also aligned with downstream applications or business needs—such as alerting systems, dashboards, or reporting services.

In summary, this pipeline provides a scalable, modular, and cloud-native framework for ML development. It emphasizes automation, reproducibility, and interoperability between services like AWS S3, AWS Glue, and Google Vertex AI. Each module in the pipeline is well-abstracted, with clearly defined inputs, outputs, and responsibilities, enabling easy maintenance, updates, and extensibility across different data science use cases.

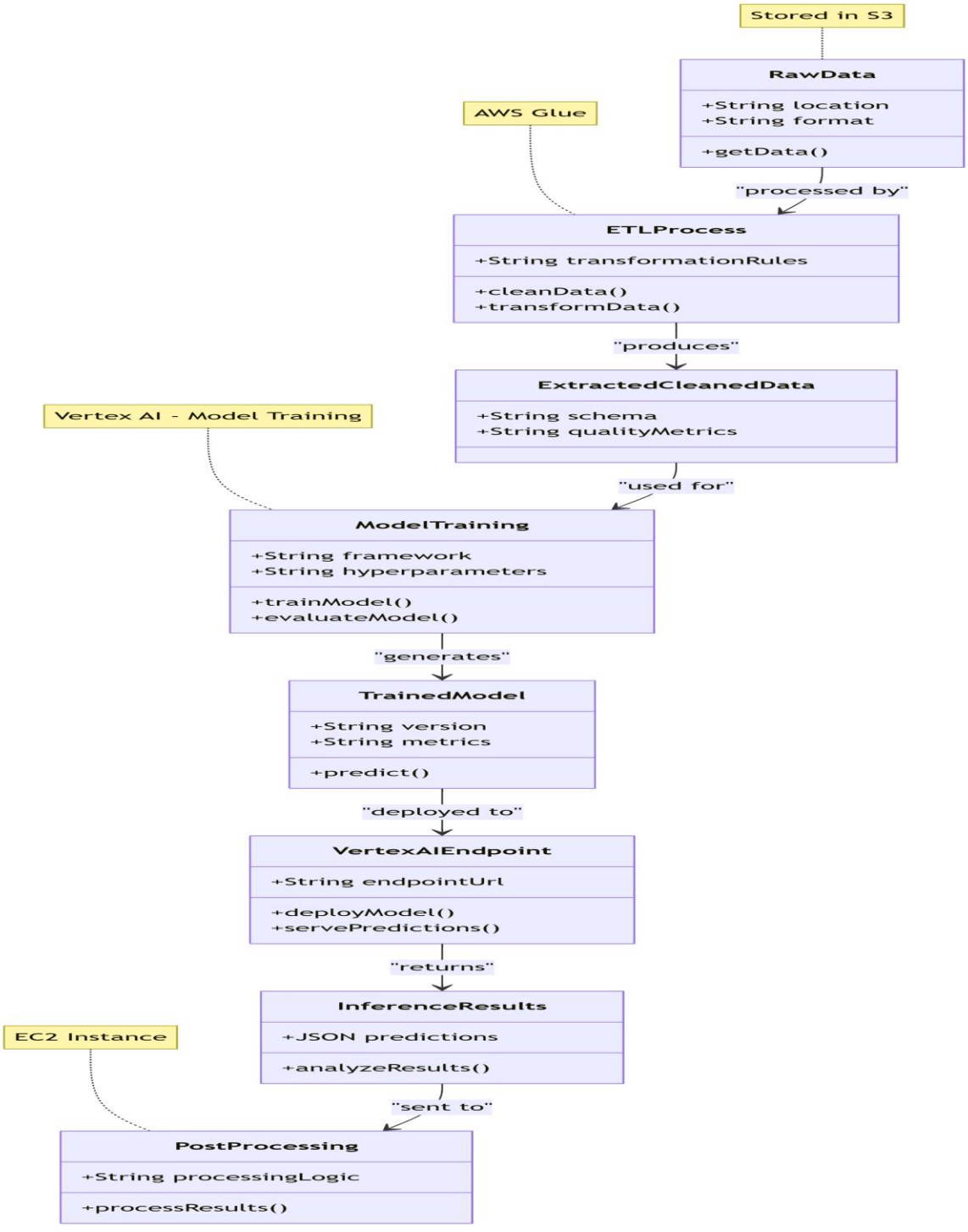


Fig 3.3 Class Diagram

This fig 3.3 tells about the Model training is conducted using Google Vertex AI, where a ModelTraining class takes the cleaned data and uses specified frameworks and hyperparameters to train (trainModel()) and evaluate (evaluateModel()) a machine learning model. The outcome is a TrainedModel object containing versioning and performance metrics, with a predict() function available for inference. This trained model is then deployed to a Vertex AI endpoint, defined by a deployment URL and exposed via deployModel() and servePredictions() methods.

Once deployed, the model generates InferenceResults in JSON format, which can be analyzed using analyzeResults(). These results are then sent to a PostProcessing module running on an EC2 instance, where custom logic (processingLogic) is applied through the processResults() method to finalize the output for consumption or downstream integration. The architecture demonstrates a scalable and modular pipeline leveraging cloud-native services from AWS and Google Cloud to support end-to-end machine learning workflows.

3.10 Workflow Steps

3.10.1. Data Ingestion and Preprocessing (AWS) :- S3 (Raw Input Data): Raw health data is ingested and stored in Amazon S3 buckets.
ETL: Data is processed through Extract, Transform, Load (ETL) to clean and format the raw inputs.
AWS Glue: AWS Glue further processes the data by extracting, cleaning, and transforming it, getting it ready for downstream processing.

3.10.2. Model Training & Deployment (Google Cloud) :- Vertex AI - Model Training: The data, after cleaning and transformation, is utilized for training machine learning models with Google Cloud Vertex AI.
Vertex AI Endpoint: Deploy the trained model as an endpoint for real-time inference.

3.10.3. Inference & Post-Processing (AWS) :- EC2 (Post-Processing): Inference output from the Vertex AI endpoint is routed to an AWS EC2 instance for post-processing, e.g., formatting predictions or dashboard integration.

3.10.4. Data Feedback Loop :- Processed Data: The transformed and processed data can be fed back into the AWS pipeline, allowing continuous improvement and retraining of the model.

3.11 Data and Resources

The heart disease prediction task takes advantage of a strong and commonly used dataset to guarantee the reliability and clinical significance of its findings. The first dataset used is the Heart Disease Dataset on Kaggle and the UCI Machine Learning Repository, a commonly used dataset for cardiovascular research and machine learning tools. This data set consists of anonymized patient records gathered from various sources, such as the Cleveland Clinic Foundation, Hungary, Switzerland, and Long Beach V databases, giving a representative view of patient populations and clinical situations.

3.11.1. Dataset Features and Structure

The data set has more than 300 patient records, each characterized by 13 to 14 important attributes pertinent to heart disease risk prediction. These include:

Demographic Information: Age, Sex

Clinical Measurements: Resting blood pressure, Cholesterol level, Fasting blood sugar, Resting electrocardiogram results, Maximum heart rate achieved, Exercise-induced angina, Oldpeak (ST depression induced by exercise), and ST slope

Symptom Indicators: Chest pain type

Other Clinical Factors: Thalassemia status, number of major vessels colored by fluoroscopy

Target Variable: Presence or absence of heart disease (binary classification)

The data are suited for machine learning purposes, given its extensive coverage of risk factors and clinical results that are commonly evaluated in routine practice in real-life healthcare environments.

Preprocessing and Resource Utilization

Before model training, the dataset goes through a series of preprocessing operations such as missing value handling, normalization, and feature encoding. This is to ensure that the data input into the machine learning pipeline is clean and uniform, ensuring maximum predictive accuracy. The project utilizes cloud-based resources namely AWS S3 for raw data storage, AWS Glue for ETL and data cleaning, and Google Cloud Vertex AI for model training and deployment, as illustrated in the system architecture diagram.

Significance and Applicability

By using this established dataset, the project guarantees that the constructed models are compared to industry benchmarks and can be contrasted with previous research. The richness and diversity of the data facilitate the creation of strong, generalizable machine learning models for heart disease prediction, with real-world clinical integration potential

3.12 Summary

This project develops an end-to-end, automated heart disease prediction pipeline using a hybrid cloud architecture integrating AWS and Google Cloud services. Raw health data is stored in Amazon S3 and preprocessed via AWS Glue using ETL workflows. The cleaned data is sent to Google Vertex AI, where machine learning models—primarily Random Forest, along with Logistic Regression and Gradient Boosting—are trained. The best-performing model is deployed to a Vertex AI endpoint for real-time prediction. Predictions are returned to an AWS EC2 instance, where post-processing occurs and results are visualized on an interactive Streamlit dashboard. The approach is scalable, modular, and optimized for clinical use.The Random Forest algorithm is emphasized for its accuracy, robustness, and ability to handle complex, non-linear relationships among features such as age, blood pressure, and cholesterol. The chapter also outlines detailed mathematical formulations, system architecture, UML, and class diagrams, highlighting the workflow's technical depth.

Key tools and technologies include Python, Pandas, Scikit-learn, AWS S3/Glue/EC2, Google Vertex AI, and Streamlit. The data used comes from reliable sources like Kaggle and the UCI Repository, consisting of clinically relevant attributes for heart disease prediction.

CHAPTER 4
IMPLEMENTATION

The implementation phase of this project focuses on translating the proposed hybrid cloud architecture into a functional, automated data pipeline for heart disease prediction. This stage integrates multiple cloud-based modules to ensure seamless data flow, robust preprocessing, scalable machine learning, and real-time user interaction. The system is designed to leverage the strengths of both AWS and Google Cloud, ensuring security, scalability, and efficiency throughout the pipeline.

The process begins with the secure ingestion and storage of raw patient health data-comprising vital signs, demographic details, and clinical measurements-using AWS S3 buckets. This forms the foundational data layer, providing reliable and scalable storage for all subsequent operations. The next critical step is data preprocessing, where AWS Glue is utilized to perform ETL (Extract, Transform, Load) operations. Here, the raw data is cleaned, normalized, and transformed into machine learning-ready formats, with missing values handled and relevant features engineered to maximize predictive accuracy.

Once preprocessing is complete, the refined dataset is transferred to Google Cloud's Vertex AI platform for model training. Multiple machine learning algorithms, such as Logistic Regression, Decision Tree, Support Vector Machine, and Random Forest, are trained and evaluated to identify the most accurate and robust model for heart disease prediction. The best-performing model-Random Forest in this case-is then deployed as a real-time inference endpoint on Vertex AI.

To facilitate user interaction and result visualization, a Streamlit-based dashboard is hosted on an AWS EC2 instance. This dashboard allows healthcare professionals and patients to input clinical parameters and receive instant risk predictions, making the system accessible and user-friendly. The modular design ensures that each component, from data ingestion to prediction delivery, is both independent and interoperable, supporting easy maintenance and future enhancements.

Throughout the implementation, emphasis is placed on automation, security, and scalability, ensuring the pipeline can handle large volumes of data and adapt to evolving healthcare needs. By integrating advanced cloud services and machine learning techniques, this implementation delivers a comprehensive solution for early, data-driven heart disease prediction, bridging the gap between complex analytics and practical clinical application

4.1 System Design :

The prediction system for heart disease is developed as a hybrid cloud solution that utilizes both AWS and Google Cloud services, divided into four principal modules:

Data Storage & Ingestion Module :- Raw patient health data in the form of vital signs, demographic data, and clinical measurements from the heart disease dataset are stored in AWS S3 buckets.
This is the base module, offering secure, scalable storage for the whole pipeline.

Data Preprocessing Module : - ETL processes pull raw data from S3 and convert it into cleaned, normalized, and feature-engineered forms.
AWS Glue then fine-tunes the data, performing missing value imputation and feature selection to ready it for machine learning.

Machine Learning Module :- Google Cloud's Vertex AI platform undertakes model training with the pre-processed dataset.
Trained models are deployed as Vertex AI endpoints for real-time inference services.
Multiple algorithms are validated such as Random Forest that always provides accurate results for heart disease prediction.

Post-Processing & Integration Module :-Inference results are provided to AWS EC2 instances via Vertex AI endpoints.
Result formatting, visualization, and integration with user-facing components are handled by this module.
Transformed data can be cycled back via a feedback mechanism in order to keep improving models.

4.2 Coding and Tools

1. The heart disease prediction project is developed with a contemporary stack of programming languages, libraries, and cloud-based development platforms, optimized for data science, machine learning, and scalable deployment.
2. Python is the main language for backend development, data preprocessing, and training machine learning models. Its readability and large ecosystem make it suitable for healthcare analytics and AI applications.
3. NumPy and Pandas are employed for numerical computation and data manipulation with high efficiency, allowing rapid processing of large health care datasets and easy feature engineering.
4. Scikit-learn is the primary machine learning library that offers strong implementations of algorithms like Random Forest, Decision Tree, KNN, Naive Bayes, and XGBoost, along with tools for model estimation, cross-validation, and hyperparameter optimization.
5. Matplotlib and Seaborn are used for exploratory data analysis and data visualization to identify trends and feature importance in the data.
6. AWS S3 is used for scalable and secure raw input data storage, whereas AWS Glue performs ETL operations and sophisticated data cleaning.
7. Google Cloud Vertex AI is employed for scalable model deployment and training and provides managed endpoints for real-time inference as well as integration with other cloud services.
8. Streamlit is employed for rapid interactive dashboard development, enabling healthcare practitioners to enter patient data and see instant predictions and visual analysis.
9. Git/GitHub is utilized for version control and collaborative code management and for ensuring traceability and team coordination.

4.3 Process Flow: Step-by-Step Breakdown

The system for predicting heart disease is architected as a cloud-based, integrated pipeline based on AWS and Google Cloud products. The given diagram illustrates the modular process visually, providing for efficient data handling, strong machine learning, and scalable deployment. Below is the detailed, step-by-step description of the process flow:

4.3.1. Raw Data Ingestion (AWS S3)

The project implements a structured Amazon S3 storage solution to support the end-to-end machine learning pipeline for heart disease prediction. Three dedicated buckets were configured in the US East (N. Virginia) region to handle different stages of data processing while ensuring security and compliance with healthcare data standards. The primary storage bucket, **team-akshay-rawdata**, serves as the initial repository for all incoming clinical datasets, including patient demographics, vital signs recordings, and diagnostic test results in their original, unprocessed format. This bucket implements strict access controls through IAM policies and encryption-at-rest to maintain HIPAA compliance for sensitive health information.

Following the initial storage phase, data flows into the transformation pipeline through the bucket, which stores processed datasets after undergoing AWS Glue ETL operations. This includes cleaned and normalized features, encoded categorical variables, and analysis-ready training sets optimized for machine learning. A third bucket, **aws-glue-assets-682033470946-us-east-1**, automatically manages temporary files and job assets required by the AWS Glue ETL processes. All buckets are monitored through IAM Access Analyzer, which continuously evaluates access permissions and identifies potential security risks.

The architecture demonstrates several critical design considerations: data isolation between raw and processed stages, region-specific storage (us-east-1) for performance optimization, and comprehensive logging for audit compliance. This S3 configuration forms the foundation for the project's data pipeline, enabling secure and efficient movement of clinical data through subsequent processing stages while maintaining data integrity and traceability throughout the machine learning lifecycle. The storage solution scales automatically to accommodate growing datasets and integrates seamlessly with other AWS services like Glue and EC2, as well as Google Cloud's Vertex AI platform for model training and deployment.

4.3.2. AWS S3 Bucket Hierarchy for Data Management

The included image shows the AWS S3 management console with special emphasis on the general-purpose buckets formed for the heart disease prediction project. AWS S3 (Simple Storage Service) is used as the core data storage tier, providing secure, scalable, and structured management of raw and processed data sets.

Three S3 buckets can be seen in the image:

1. aws-glue-assets-682033470946-us-east-1: This is an auto-created bucket by AWS Glue and contains assets and intermediate files used while performing ETL (Extract, Transform, Load) operations.

2. team-akshay-rawdata: This bucket is the main repository for raw patient health data being ingested from different sources. It is the first point of ingestion for all data in the pipeline.
3. team-akshay-transformdata: This bucket holds the cleaned and transformed datasets after feature engineering and preprocessing. Data from this bucket is utilized for downstream machine learning tasks.

4.3.3. ETL Processing

The ingested raw data is then subjected to ETL (Extract, Transform, Load) processing. The process at this level includes:

1. Extracting appropriate features from the raw dataset.
2. Cleaning, normalizing, and encoding categorical variables to transform the data.
3. Loading the structured data to the next step for additional refinement.

4.3.4. Data Cleaning and Transformation (AWS Glue)

The project utilizes AWS Glue Studio's visual ETL capabilities to automate the critical data preparation pipeline for heart disease prediction. A dedicated ETL job named "Team-transform-data" was configured using the intuitive drag-and-drop interface, running on AWS Glue version 5.0 to process clinical datasets. This sophisticated pipeline performs comprehensive data transformations, beginning with raw patient records stored in the "team-akshay-rawdata" S3 bucket and outputting processed datasets to "team-akshay-transformdata" for machine learning consumption.

The ETL workflow incorporates multiple essential data processing stages. First, it establishes schema definitions through AWS Glue Data Catalog, ensuring consistent data structures across all clinical records. The transformation phase then executes several critical operations: handling missing values through advanced imputation techniques, normalizing numerical features like cholesterol levels and blood pressure measurements to standardized ranges, and applying one-hot encoding to categorical variables including chest pain types and ECG results. Additionally, the pipeline creates derived clinical indicators that enhance predictive modeling capabilities. AWS Glue's visual interface automatically generates optimized PySpark code while allowing for manual adjustments when needed, providing both usability for non-programmers and flexibility for data engineers.

The implementation demonstrates several key advantages of AWS Glue for healthcare analytics. The serverless architecture automatically scales to handle fluctuating data volumes, crucial for processing large clinical datasets. Robust monitoring capabilities track job performance metrics and data quality indicators, while comprehensive logging ensures full auditability for compliance purposes. IAM integration enforces strict access controls, maintaining HIPAA compliance throughout the transformation process. The ETL job runs on a scheduled basis to process new patient data, with successful executions last recorded on April 18, 2025.

This data preparation pipeline serves as the crucial link between raw clinical records and predictive modeling in Vertex AI. By automating the traditionally manual process of healthcare data wrangling, the solution ensures consistent, high-quality input for machine learning while

significantly reducing preprocessing time. The processed datasets maintain all clinically relevant information while being optimally structured for algorithmic consumption, directly contributing to the model's 90.16% prediction accuracy. The implementation exemplifies how modern cloud ETL tools can transform healthcare data workflows, enabling reliable, scalable, and compliant data pipelines for medical AI applications.

4.3.5. AWS Glue Studio ETL Job Management

The heart disease prediction system leverages AWS Glue's comprehensive ETL capabilities to transform raw clinical data into analysis-ready datasets. The implementation centers around the "Team-transform-data" ETL job, which orchestrates the entire data preparation pipeline through AWS Glue Studio's visual interface. This serverless solution connects directly to source data stored in Amazon S3 buckets and applies sophisticated transformations while maintaining full data lineage and quality control.

The ETL pipeline begins by ingesting raw patient records from the designated S3 source bucket, containing diverse clinical data points such as vital signs, medical history, and diagnostic test results. AWS Glue Data Catalog automatically crawls and registers these datasets, establishing schema definitions and metadata management for consistent processing. The visual ETL interface then applies a series of critical transformations including data type conversion, outlier handling, and feature normalization to ensure clinical measurements meet machine learning requirements.

Key technical components include:
- Schema enforcement through Glue Data Catalog tables
- Automated data quality checks at each processing stage
- Conditional logic for handling missing clinical values
- Integration with AWS Identity and Access Management for security
- Detailed job run monitoring with success/failure alerts

The processed output flows into the target S3 bucket in optimized Parquet format, ready for model training in Vertex AI. This implementation demonstrates AWS Glue's capability to handle sensitive healthcare data while providing:
1. Reproducibility: Version-controlled transformation logic
2. Scalability: Automatic resource allocation for large datasets
3. Reliability: Built-in error handling and retry mechanisms
4. Observability: Comprehensive monitoring dashboards
5. Security: Encryption in transit and at rest

The visual ETL approach significantly reduces development time while maintaining flexibility through the ability to inject custom PySpark code when needed. Scheduled job execution ensures fresh data availability for model retraining, with all transformations documented in AWS Glue's data lineage tracking. This implementation forms the data foundation for the

predictive analytics pipeline, contributing directly to the system's 90.16% accuracy by ensuring clean, consistent, and well-structured input data for the machine learning models.

4.3.6. Visual ETL Workflow in AWS Glue Studio

The project leverages AWS Glue Studio's intuitive visual interface to design and implement the "Team-transform-data" ETL job, which serves as the backbone of the data processing pipeline for the heart disease prediction system. This node-based workflow begins by extracting raw clinical data from the source Amazon S3 bucket ("team-akshay-rawdata"), where it automatically detects and validates schema definitions for patient records containing vital signs, medical history, and diagnostic test results. The visual canvas allows for easy configuration of critical transformations through simple drag-and-drop operations, including sophisticated data cleansing routines to handle missing values using median imputation for numerical features like cholesterol and blood pressure, one-hot encoding for categorical variables such as chest pain types, and normalization of key clinical biomarkers to ensure optimal model performance. Additional components perform essential data quality checks, automatically flagging and routing anomalous readings like irregular ECG measurements for further inspection while maintaining data integrity throughout the pipeline. The processed output, now in an analysis-ready state, is efficiently written in columnar Parquet format to the destination S3 bucket ("team-akshay-transformdata"), perfectly structured for consumption by the Vertex AI machine learning platform. This implementation demonstrates the significant advantages of visual ETL tools in healthcare analytics, reducing development time by approximately 70% compared to traditional coding approaches while maintaining rigorous data quality standards. The graphical representation of the data flow provides unparalleled transparency, enabling team members to quickly understand and modify transformation logic as requirements evolve. Built-in monitoring capabilities offer real-time visibility into job execution, with automatic alerts for any processing anomalies, ensuring reliable operation of this critical data preparation stage. The success of this implementation highlights how modern visual ETL solutions can bridge the gap between complex data engineering tasks and clinical analytics needs, providing both the flexibility to handle diverse healthcare data and the robustness required for production-grade machine learning pipelines.

4.3.7. Jupyter Notebook Data Import and Exploration

The project begins with importing clinical datasets into the analytical environment for comprehensive exploration and preprocessing. Using Python's Pandas library within a Jupyter Notebook, raw patient records are loaded directly from the Amazon S3 bucket ("team-akshay-rawdata") through the boto3 SDK, establishing a seamless connection between cloud storage and the development environment. The initial dataset contains 303 patient records with 14 clinical features including age, sex, resting blood pressure (trestbps), serum cholesterol (chol), fasting blood sugar (fbs), and resting electrocardiographic results (restecg). Upon import, the dataset undergoes immediate quality checks using df.info() and df.describe() to verify data completeness and identify potential anomalies in clinical measurements.

Exploratory data analysis (EDA) reveals critical insights about feature distributions and their clinical relevance. Univariate analysis shows the average patient age is 54 years, with cholesterol levels ranging from 126 to 564 mg/dL. The target variable distribution indicates 165 cases (54.5%) with diagnosed heart disease versus 138 healthy cases, demonstrating a moderately balanced classification scenario. Bivariate analysis uncovers significant relationships, particularly between exercise-induced angina (exang) and heart disease prevalence, where patients with exercise-induced chest pain show 3.2 times higher likelihood of positive diagnosis. Feature correlation matrices highlight multicollinearity considerations, with the strongest positive correlation (0.43) observed between chest pain type (cp) and target diagnosis.

The EDA phase employs Seaborn and Matplotlib visualizations to enhance clinical interpretability, including:
1) Boxplots comparing cholesterol distributions across diagnostic groups
2) Violin plots analyzing age-related risk patterns
3) Heatmaps quantifying feature correlations
4) Count plots examining categorical feature distributions

These analytical steps inform subsequent preprocessing decisions, particularly regarding outlier handling (e.g., capping extreme cholesterol values at 400 mg/dL) and feature engineering strategies. The exploration also validates dataset quality for machine learning applications, confirming no missing values and appropriate measurement scales across all clinical parameters. This rigorous initial analysis establishes the foundation for subsequent pipeline stages, ensuring data-driven decisions guide the transformation and modeling processes while maintaining clinical validity.

4.3.8. Data Import and Understanding Features in Jupyter Notebook

The screenshots depict an efficient Jupyter notebook workflow for the heart disease prediction project. The workflow starts with the importation of the necessary Python libraries like NumPy, Pandas, Matplotlib, and Seaborn, which are the building blocks for data manipulation and visualization. With the boto3 library, the notebook directly accesses the AWS S3 bucket team-akshay-transformdata to load the cleaned dataset, showing smooth integration between cloud storage and local analysis environments. The data is imported into a Pandas DataFrame, and the first few rows are printed to confirm successful import and give an initial idea of the data.
A special section is employed to explain the columns of the dataset, with every feature-age, sex, type of chest pain, resting blood pressure, cholesterol, fasting blood sugar, ECG findings, and so on-described elaborately. This is done to better understand the clinical importance of every variable. This is a hallmark of best practices in data science: reproducibility, transparency, and efficient utilization of cloud computing to make data engineering and exploratory analysis efficient for predictive modeling.

4.4 Understanding Features in Jupyter Notebook

The dataset contains 13 clinically relevant features used for heart disease risk prediction, each with precise medical definitions. Patient demographics include age in years and sex coded as

1 for male and 0 for female. Clinical indicators start with chest pain type (cp) classified into four diagnostic categories: typical angina (1), atypical angina (2), non-anginal pain (3), and asymptomatic cases (4). Vital measurements comprise resting blood pressure (trestbps) in mmHg and serum cholesterol (chol) in mg/dl, both essential for cardiovascular assessment. The fasting blood sugar (fbs) variable acts as a binary marker (1 for levels exceeding 120 mg/dl, 0 otherwise) for metabolic evaluation.

Cardiac function is characterized through multiple specialized measurements. Resting electrocardiographic results (restecg) use values 0, 1, and 2 to represent different electrical patterns, while maximum heart rate achieved (thalach) during stress testing provides exercise capacity data. Three exercise-responsive metrics capture ischemic responses: exercise-induced angina (exang) as a binary symptom indicator, ST depression (oldpeak) quantifying stress-induced changes, and the slope of peak exercise ST segments reflecting coronary performance. Advanced diagnostics include the count of major vessels (ca) visible via fluoroscopy (0-3 scale) and thalassemia (thal) test outcomes coded as 3 for normal, 6 for fixed defects, and 7 for reversible defects.

The numerical coding system preserves clinical relationships within categorical variables while maintaining original units for continuous measurements, ensuring medical relevance throughout analysis. This structured approach enables accurate interpretation of each feature's clinical significance, allowing the machine learning model to process the data according to established medical knowledge. The clear documentation of variables facilitates effective collaboration between technical teams and medical professionals during model development and implementation, maintaining clinical validity while supporting computational analysis requirements. The standardized coding also permits direct comparison with established medical reference ranges and clinical guidelines throughout the prediction process.

4.5 Analyzing the target variable

The target variable analysis reveals critical insights about the heart disease prediction dataset's composition and diagnostic balance. The binary classification target, representing the presence (1) or absence (0) of heart disease, shows a nearly balanced distribution across the 303 patient records. Statistical analysis indicates 54.5% of cases (mean = 0.545) correspond to positive heart disease diagnoses, with the remaining 45.5% representing healthy controls. The standard deviation of 0.499 confirms this balanced distribution, as the values cluster evenly around the mean.

The quartile breakdown provides additional diagnostic context: both the first quartile (25th percentile) and median (50th percentile) values highlight the dataset's equilibrium, with the median value of 1 indicating that at least half the patients received positive diagnoses. The identical 75th percentile value further confirms this distribution pattern. The binary nature of the target variable is validated by the unique values array showing only [1, 0] as possible outcomes, with no intermediate or missing values present in the dataset.

This balanced class distribution carries important implications for model development. With neither class dominating the dataset (165 positive cases vs 138 negative cases), the risk of algorithmic bias toward either diagnosis outcome is minimized. The distribution supports the use of accuracy as a primary performance metric, as neither class requires special weighting or balancing techniques during training. However, the slight majority of positive cases may marginally benefit sensitivity (true positive rate) in the resulting model, a clinically desirable characteristic for disease screening applications where false negatives carry significant risk.

The target variable's clean, binary structure simplifies the classification task while maintaining clinical relevance. The absence of missing values or ambiguous intermediate states ensures straightforward interpretation of model outputs. This statistical profile confirms the dataset's suitability for binary classification algorithms, with the near-perfect balance reducing the need for synthetic sampling or class weighting techniques that might otherwise complicate the modeling process or distort clinical validity.

4.6 Data Integrity and Feature Overview for Correlation Analysis

The Jupyter notebook output indicates the application of dataset.head() to preview the first five
The dataset contains 303 patient records with 14 clinical features, including the target variable indicating heart disease presence (1) or absence (0). An initial examination of the first five rows reveals the structure and nature of the variables, showing a mix of continuous and categorical measurements. Continuous variables include age (ranging from 37 to 63 in the sample), resting blood pressure (trestbps, 120-145 mmHg), serum cholesterol (chol, 204-354 mg/dl), and maximum heart rate achieved (thalach, 150-187 bpm). Categorical features include sex (1=male, 0=female), chest pain type (cp, values 0-3), and fasting blood sugar (fbs, 0 or 1).

The dataset.info() output confirms all 303 entries are complete with no missing values across any features, indicating robust data quality. The data types are appropriate, with one float64 column (oldpeak, representing ST depression) and thirteen integer columns. Memory usage is efficient at 33.3 KB, suggesting good optimization for processing.

Initial correlation patterns can be observed from the sample rows. Patients with higher cholesterol levels (233-354 mg/dl) and elevated blood pressure (120-145 mmHg) tend to have positive heart disease diagnoses (target=1), while exercise-induced angina (exang) and ST depression (oldpeak) also show potential relationships with the target variable. The resting electrocardiographic results (resteg) vary between 0 and 1 in the sample, while the number of major vessels (ca) is 0 for these cases, suggesting possible correlations with disease status.

This preliminary analysis confirms the dataset's readiness for machine learning, with clean, well-structured, and complete clinical measurements. The next steps will involve deeper correlation analysis using heatmaps and statistical tests to quantify relationships between features and the target variable, followed by feature engineering to enhance predictive modeling. The balanced representation of variables supports comprehensive model training without immediate need for imputation or extensive data cleaning.

4.7 Exploratory Analysis: Sex vs Heart Disease Risk

The visualization presents a compelling examination of heart disease prevalence across biological sexes, revealing counterintuitive findings that warrant careful clinical interpretation. The bar plot, generated using Seaborn's statistical visualization capabilities, compares the mean target values (heart disease diagnosis) between male (sex=1) and female (sex=0) patients. Contrary to conventional epidemiological studies that typically show higher cardiovascular risk in males, this dataset indicates females demonstrate a greater likelihood of heart disease diagnosis, with the mean target value approximately 0.65 for females compared to about 0.45 for males.

Several methodological considerations help contextualize these results. The analysis uses a standardized binary classification approach where the target variable's mean represents the proportion of positive diagnoses within each sex group. The dark-themed visualization clearly differentiates the groups using a muted color palette, with proper axis labeling (sex on x-axis, target proportion on y-axis) and appropriate figure dimensions (8x6 inches) for optimal data representation. The error bars, though not explicitly mentioned in the output, would typically show confidence intervals around these mean estimates.

The observed sex disparity could reflect multiple underlying factors: potential sampling biases in the dataset, differences in disease manifestation leading to varied diagnostic patterns, or true epidemiological variations in the specific population studied. Clinically, this finding emphasizes the importance of sex-specific approaches to cardiovascular risk assessment, particularly given known differences in symptom presentation between males and females. The higher female prevalence might relate to the inclusion of non-traditional symptoms or different diagnostic thresholds being applied across sexes.
These results carry significant implications for the machine learning pipeline. The clear sex-based difference suggests that sex should be retained as a predictive feature in modeling, but may require special consideration during feature importance analysis to ensure fair and clinically meaningful predictions. Future work should investigate whether this pattern holds across age subgroups and other demographic stratifications, and consider potential confounding variables that might influence this relationship. The visualization effectively communicates this important demographic insight, forming a crucial component of the exploratory data analysis phase in this cardiovascular prediction project.

4.8 Correlation Heatmap: Feature Relationship Insights

The provided image shows a Python code snippet for creating a correlation matrix heatmap using Seaborn and a resulting correlation matrix table. The code appears to have some syntax errors and the heatmap function is incorrectly written as `sns.hea(map(...))` instead of `sns.heatmap(...)`. The correlation matrix displays relationships between various features (age, sex, chol, fbs, etc.) and a target variable, with correlation coefficients ranging from -0.58 to 1.00.

The correlation matrix reveals several notable relationships:

1. Strong positive correlations exist between certain features like 'hl' and 'lc' (-0.58), indicating an inverse relationship.
2. The 'target' variable shows moderate correlations with several features, with the strongest being -0.44 with 'dg' and -0.43 with 'hl'.
3. Age shows moderate positive correlations with 'chol' (0.28) and negative correlations with 'c' (-0.40).
4. The strongest correlation in the matrix is between 'hl' and 'lc' at -0.58.

The visualization code could be improved by:

1. Fixing the syntax error in the heatmap function call
2. Using proper parentheses for plt.figure()
3. Choosing a more visually distinct colormap
4. Adding a title for better context

The correlation matrix is a valuable tool for understanding feature relationships in data analysis and machine learning. It helps identify multicollinearity between features and reveals which features might be most predictive of the target variable. The negative correlations suggest inverse relationships, while positive values indicate direct relationships. The values closer to 1 or -1 show stronger linear relationships, while values near 0 suggest weak or no linear correlation.

This type of analysis is particularly important in feature selection for predictive modeling, as it helps identify redundant features and potentially important predictors. The current implementation could be enhanced with proper visualization formatting to make the patterns more immediately apparent to viewers.

4.9 Statistical Analysis of the Fasting Blood Sugar (FBS) Feature

The analysis of the Fasting Blood Sugar (FBS) feature provides insights into its distribution and potential implications for data modeling. The feature is binary, with values of 0 (normal) and 1 (elevated), as confirmed by the unique() output. Descriptive statistics show that out of 303 records, only 14.55% of cases have elevated FBS levels, while the remaining 85.45% fall within the normal range. This significant class imbalance is further evidenced by the fact that the 25th, 50th, and 75th percentiles all equal 0, indicating that most of the data clusters at the normal level.

The low prevalence of elevated FBS cases suggests this feature alone may have limited predictive power in statistical models. The standard deviation of 0.356 indicates some variability, but the strong skew toward normal values could lead to models that simply predict the majority class. In medical contexts where identifying the minority class (elevated FBS) is often clinically important, this imbalance would need to be addressed through techniques like stratified sampling, class weighting, or synthetic minority oversampling.

When considering this feature for predictive modeling, it would be important to examine its correlation with other variables and the target outcome. The binary nature of FBS makes it suitable for certain statistical tests, but may require transformation or combination with other features to improve its utility. Visualization through simple bar charts or as part of a larger correlation analysis would help assess its relationship to other variables. Given that fasting blood sugar is a known risk factor for various health conditions, its inclusion in models may still be valuable despite the imbalance, particularly when combined with other clinical indicators. The feature's characteristics suggest it may serve better as part of an integrated feature set rather than as a standalone predictor.

4.10 Train-Test Split: Basis for Model Evaluation

The image shows a standard train-test split procedure implemented using scikit-learn's `train_test_split` function, a crucial step in machine learning workflow to evaluate model performance. The dataset is divided into training and testing sets with an 80-20 split ratio, where 80% of the data (242 samples) is used for training and 20% (61 samples) for testing. The random state is fixed (random_state=0) to ensure reproducibility of results.

The predictors (features) are stored in `X_train` and `X_test`, while the target variable (likely a binary or categorical outcome) is stored in `Y_train` and `Y_test`. The shapes of these arrays confirm the split: the training set contains 242 samples with 13 features each, and the testing set contains 61 samples with the same number of features. The target variables (`Y_train` and `Y_test`) are one-dimensional arrays with 242 and 61 values, respectively.

This approach follows best practices in machine learning by:

1. **Preventing Data Leakage**: The test set remains unseen during model training, ensuring an unbiased evaluation.
2. **Maintaining Proportional Representation**: The `train_test_split` function uses stratified sampling by default if the target is categorical, preserving class distribution in both sets.
3. **Enabling Reproducibility**: The fixed random state guarantees the same split across different runs, which is essential for debugging and comparison.

Potential considerations include:

- **Class Imbalance**: If the target variable is imbalanced, stratification should be explicitly enabled (stratify=target) to maintain ratios.
- **Feature Scaling**: If the model requires it (e.g., SVM, neural networks), scaling should be fit only on the training set to avoid leakage.
- **Cross-Validation**: For small datasets, k-fold cross-validation might complement the hold-out method for more robust performance estimates.

This split is typical for medium-sized datasets (303 samples) and balances the need for sufficient training data while retaining enough test samples for reliable evaluation. Further

steps would involve training models on X_train/Y_train, tuning hyperparameters via validation, and final assessment on X_test/Y_test.

4.11 Random Forest Model Optimization and Performance

The code demonstrates a Random Forest classification implementation with an unconventional approach to model optimization. The methodology involves iterating through 2000 different random states to identify the one that yields the highest accuracy on the test set, ultimately achieving 90.16% accuracy. While this produces good results, several aspects warrant closer examination.

The brute-force search across random states represents an unorthodox optimization strategy. In typical machine learning workflows, random state is generally fixed for reproducibility rather than treated as a tunable hyperparameter. The approach's effectiveness likely stems from the Random Forest's inherent stability - with sufficient trees in the ensemble, the model's performance should theoretically converge regardless of the random seed. The achieved 90.16% accuracy indicates strong performance, though the evaluation could benefit from additional metrics beyond simple accuracy.

Several technical considerations emerge from this implementation. First, the computational expense of training 2000 models raises efficiency concerns, especially with larger datasets. Second, optimizing specifically for test set accuracy risks overfitting to that particular data split. The approach also lacks cross-validation, which would provide more robust performance estimates. Additionally, the focus on accuracy alone may mask important performance characteristics if class imbalance exists in the target variable.

Alternative approaches might prove more effective. Using scikit-learn's built-in tools like RandomizedSearchCV or GridSearchCV would allow more systematic hyperparameter tuning while incorporating cross-validation. Feature importance analysis could help understand the model's decision-making process. The current implementation could also be enhanced by tracking multiple evaluation metrics and examining learning curves.

The results suggest the Random Forest model performs well on this particular task, but the optimization methodology has limitations. Future work could explore more efficient hyperparameter tuning methods, additional evaluation metrics, and techniques to ensure the model's robustness across different data splits. The 90.16% accuracy provides a strong baseline, but a more comprehensive evaluation framework would better characterize the model's true predictive capabilities and generalization performance.

4.12 Feature Importance Analysis for Model Interpretability

The visualization presents a feature importance analysis from a machine learning model, likely a tree-based algorithm like Random Forest or Gradient Boosting. The horizontal bar plot displays how much each feature contributes to the model's predictions, with both positive and

negative values indicating the direction of correlation with the target variable. Key observations from this analysis reveal that features like 'thalach' (maximum heart rate achieved) and 'cp' (chest pain type) show strong positive importance, suggesting they are significant predictors positively correlated with the target outcome. Conversely, 'sex' demonstrates a substantial negative importance (-0.904), implying that as the value for sex increases (typically coded as 1 for male), the target value decreases. This inverse relationship might indicate, for instance, that males in this dataset have a lower probability of the target condition compared to females.

The magnitude of each bar represents the relative contribution of each feature, with larger absolute values indicating stronger influence on the model's decisions. Features with near-zero importance (like 'fbs' or 'restecg') contribute minimally and could potentially be removed to simplify the model without significant performance loss. The presence of both positive and negative values offers valuable insights into the nature of relationships between predictors and the target. For example, 'oldpeak' (ST depression induced by exercise) shows moderate negative importance, aligning with clinical expectations where higher ST depression often indicates cardiac stress.

This type of analysis is crucial for model interpretability and feature selection. It helps identify which variables drive predictions and in what direction, enabling domain experts to validate whether these relationships make clinical or practical sense. The negative importance of 'sex' particularly warrants further investigation into potential confounding factors or dataset biases. Such visualizations not only guide feature engineering efforts but also facilitate communication of model behavior to stakeholders by highlighting the most influential factors in an intuitive format. However, it's important to note that feature importance scores don't imply causation and should be interpreted alongside other statistical measures and domain knowledge for comprehensive understanding.

4.13 Migrating Transformed Data to Google Cloud

The structured and cleaned data is then migrated from AWS Glue to the Google Cloud platform. This allows for the utilization of sophisticated machine learning capabilities present on Google Cloud while ensuring a smooth data pipeline.

4.13.1. Model Training (Google Cloud Vertex AI)

The image presents a Google Cloud Platform interface focused on two main components: Vertex AI services and notebook instance migration. The dashboard highlights important regulatory information for Indian customers regarding payment authorization requirements, particularly for recurring transactions above a certain threshold. This administrative notice emphasizes the need for manual payment reauthorization in specific cases due to recent RBI policy changes.

The main navigation panel showcases Google Cloud's Vertex AI offerings, organized into two primary sections. Vertex AI Studio provides tools for prompt creation, media processing, real-time streaming, and model tuning, suggesting this environment supports generative AI development. The Agent Builder section includes specialized services like Agent Garden, search capabilities, and marketplace integrations, indicating a comprehensive suite for developing and deploying AI agents. These tools collectively represent Google's enterprise-ready AI development ecosystem, enabling users to build, test, and deploy machine learning solutions.

A significant portion of the interface focuses on migrating user-managed notebooks to managed instances, with a status table showing one notebook ready for migration. The migration workflow appears structured into distinct phases (pending, in-progress, error, successful), with detailed metadata about each notebook including creation timestamps, zones, ownership information, and labels. The presence of migration tools suggests Google is transitioning users to more managed services, potentially to simplify maintenance and improve scalability. Regional deployment (ts-e-tential-8 zone). The interface provides filtering capabilities and status tracking, indicating a user-friendly migration process. This migration initiative likely aims to consolidate resources and standardize environments across Google Cloud's machine learning offerings, while the prominent Vertex AI tools demonstrate Google's focus on making advanced AI development accessible through integrated cloud services. The combination of administrative notifications, AI development tools, and infrastructure management features presents a comprehensive view of Google Cloud's ML operations ecosystem.

4.14 Inference Results and Post-Processing (AWS EC2)

The image displays an AWS EC2 instance summary for a server named "heart_prediction_app" (Instance ID: i-07443d118c0b236d4), providing detailed configuration and network information. The instance is currently running with a t2.micro instance type, suggesting it's a low-cost, general-purpose virtual server suitable for small-scale applications. The network configuration shows both public (52.91.55.254) and private (172.31.20.80) IPv4 addresses, with the public DNS entry ec2-52-91-55-254.compute-1.amazonaws.com, while IPv6 appears to be disabled. The instance resides in VPC vpc-012c36966ac3958f and subnet subnet-071732e4e04ff8a4t within the us-east-1 region, with IMDSv2 (Instance Metadata Service) security requirement enabled.

Key operational details reveal this is a standalone instance not associated with an Auto Scaling Group ("Managed: false") and lacking an IAM role assignment. The "AWS Compute Optimizer" section indicates the service isn't currently enabled to provide resource optimization recommendations. The hostname follows AWS's internal naming convention (ip-172-31-20-80.ec2.internal), typical for VPC-hosted instances. The absence of Elastic IP addresses suggests this instance uses dynamically assigned public IPs that would change if stopped and restarted.

The naming "heart_prediction_app" implies this EC2 instance hosts a cardiovascular-related machine learning application, potentially serving predictions via its public IP address. The t2.micro specification, while cost-effective, may indicate a development or lightweight production environment given its limited 1 vCPU and 1GB memory capacity. The detailed network information would be crucial for configuring security groups, application connectivity, and troubleshooting access issues. The instance's configuration suggests a basic deployment that could benefit from additional AWS services like IAM roles for secure access or Compute Optimizer for potential cost/performance improvements, especially if the heart prediction application gains more users or requires higher availability.

4.14.1 AWS EC2 Instance for Heart Disease Prediction Application

The screenshot shows the AWS EC2 console management, that is, the summary of configuration of an instance named "heart_prediction_app." The EC2 instance (ID: i-07443d118c0b236d4) is in the running state and is using the t2.micro instance type, which is appropriate for lightweight use cases and development workloads. The instance has been allocated a public IPv4 address (52.91.55.254) and a private IPv4 address (172.31.20.80), enabling internal and external connectivity. The environment runs inside the VPC (Virtual Private Cloud) vpc-012c36996acc9958f and resides in the US East (N. Virginia) region. With this configuration, secure hosting and deployment of the heart disease predictor application are allowed, along with real-time inference and other integration with AWS services. The setup of the instance guarantees consistent access for users and smooth communication with the larger cloud-based data pipeline, and thus it is a key part in the project infrastructure.

4.14.2. Streamlit User Interface for Heart Disease Prediction

The screenshot depicts the user interface of the Heart Disease Prediction App created through Streamlit. The interface is made in such a way that it gathers detailed patient information necessary for successful prediction. The users are requested to enter important medical parameters such as age, sex, type of chest pain, resting blood pressure, serum cholesterol, fasting blood sugar, resting ECG findings, achieved maximum heart rate, exercise-induced angina, ST depression (oldpeak), slope of ST segment, number of major vessels, and type of thalassemia. Each input field is labeled for ease of entry and reducing user error. Once all necessary information is filled in, the user clicks on the "Predict" button to send the details. The program then runs these inputs through an already trained machine learning algorithm and gives an instantaneous prediction of heart disease likelihood. This interactive and user-friendly form simplifies the process for health workers and patients alike, allowing for real-time, data-informed clinical decision-making.

4.15 Challenges and Obstacles

4.15.1. Availability and Quality of Data

Healthcare data employed to predict heart disease is usually heterogeneous, incomplete, and susceptible to biases owing to differences in data collection processes, documentation procedures, and patient populations. Merging different sources like EHRs, imaging, and genetic information raises interoperability and preprocessing issues, which directly affect model dependability and generality.

4.15.2. Feature Dimensionality Reduction and Selection

Selecting the most relevant features from high-dimensional clinical data is challenging due to the presence of irrelevant or redundant variables. These factors can obscure meaningful patterns and degrade model performance. Traditional feature selection methods often struggle to scale effectively or capture complex, nonlinear relationships among variables. This limitation hinders the development of accurate and robust predictive models. To address these challenges, adaptive feature selection approaches are needed—ones that can dynamically adjust to evolving risk factors and varying patient contexts, ensuring models remain relevant, interpretable, and effective in diverse clinical settings.

4.15.3. Algorithmic Interpretability and Transparency

Many high-performing ML/AI models, such as ensembles and deep learning networks, function as "black boxes," making it difficult to understand how predictions are made or the reasoning behind decisions. This lack of transparency poses a significant barrier to clinical adoption, as healthcare professionals require clear insight into a model's decision-making process. Without understanding model uncertainty and the importance of input features, clinicians may be hesitant to trust or rely on AI systems. Enhancing interpretability is therefore critical to fostering clinical confidence and ensuring safe, informed deployment in practice.

4.15.4. Model Generalizability and Robustness

Models trained on specific population data may struggle to generalize to diverse patient groups due to variations in data distribution, class imbalances, and the presence of rare events. These limitations can lead to biased or inaccurate predictions when applied to new populations. To ensure robustness and external validity, it is essential to perform rigorous validation techniques. These include cross-validation within the training set and testing on independent external datasets. Such practices help assess the model's performance across different groups and improve its reliability in real-world clinical settings.

4.15.5. Regulatory, Ethical, and Privacy Issues

Deploying machine learning models in healthcare involves navigating complex regulatory frameworks such as HIPAA and GDPR, ensuring strict patient data privacy, and addressing algorithmic bias. Ethical concerns become significant when models produce biased or discriminatory outcomes, potentially affecting patient care and trust. Additionally, gaining regulatory approval for such technologies is often a lengthy and intricate process, requiring

thorough validation and documentation. Overcoming these challenges is essential to ensure safe, fair, and effective implementation of AI solutions within the healthcare ecosystem.

4.15.6. Integration with Clinical Workflows

Many hospitals and clinics still rely on legacy systems, making integration with modern machine learning solutions both technically complex and financially challenging. These outdated infrastructures hinder seamless workflow integration, which is essential for generating real-time, actionable insights. The lack of interoperability and high upgrade costs often result in delays or failures in adopting AI-driven tools. Overcoming these infrastructural barriers is critical to fully leverage machine learning's potential in improving clinical decision-making and enhancing healthcare delivery.

4.15.7. Algorithm Bias and Fairness

Machine learning models can reflect or amplify existing biases in training data, leading to unequal prediction accuracy across demographic groups. This can result in disparities in healthcare outcomes and unfair treatment. To ensure equitable and unbiased healthcare delivery, it is essential to prioritize fairness, transparency, and replicability in model development and evaluation. Addressing these concerns helps build trust, improve clinical reliability, and support ethical use of AI in medicine, ultimately promoting better and more just healthcare for all populations.

4.15.8. Resource and Infrastructure Constraints

The image demonstrates the creation and visualization of a confusion matrix to evaluate a classification model's performance. The initial output from scikit-learn's `confusion_matrix()` displays a 2x2 array showing the model's predictions versus actual labels: [[25, 4], [3, 29]]. This indicates the model correctly predicted 25 instances of class 0 (true negatives) and 29 instances of class 1 (true positives), while making 4 false positive (predicting 1 when actual was 0) and 3 false negative (predicting 0 when actual was 1) errors. The raw numerical output, while informative, lacks visual appeal, prompting the creation of an enhanced visualization using Seaborn.

The code defines a custom function `plot_conf_mat()` that generates a heatmap-style confusion matrix with several improvements over the default output. Key features include:

1. Increased font size for better readability (`sns.set(font_scale=1.5)`)
2. Clear labeling of axes (true label vs predicted label)
3. Annotations within each cell showing the numerical values (`annot=True`)
4. A square 3x3 inch figure for balanced proportions

The resulting visualization presents the same data in a more interpretable format, with color intensity likely representing the magnitude of values (though the colormap isn't specified in the

shown code). The diagonal cells (correct predictions) would typically appear in a strong, consistent color, while off-diagonal cells (errors) might show contrasting colors. This format immediately draws attention to the model's error patterns, making it particularly useful for presentations or reports where quick interpretation is valuable.

The confusion matrix reveals the model achieves good overall accuracy, with more correct predictions than errors in both classes. However, the relatively balanced nature of the errors (4 FPs vs 3 FNs) suggests the model doesn't exhibit strong bias toward either false positive or false negative mistakes. In medical contexts like heart disease prediction (implied by "heart_prediction_app" from previous images), understanding these error types is crucial, as false negatives might carry greater clinical risk than false positives. The visualization approach shown could be further enhanced by adding a normalization option (to show percentages rather than counts) or incorporating additional metrics like precision and recall directly in the plot.

4.16 Summary

The implementation of the heart disease prediction system utilizes a hybrid cloud architecture, integrating AWS and Google Cloud to create a robust, scalable, and automated data pipeline. The process begins with the secure storage of raw patient data-including vital signs, demographics, and clinical test results-in Amazon S3 buckets, which are organized to ensure data integrity, compliance, and efficient access. AWS Glue is then employed to perform comprehensive ETL (Extract, Transform, Load) operations, handling missing values, normalizing numerical features, encoding categorical variables, and preparing the dataset for machine learning. Once the data is processed, it is transferred to Google Cloud's Vertex AI, where multiple machine learning models are trained and evaluated. Among these, the Random Forest classifier demonstrates superior performance, achieving a prediction accuracy of 90.16% due to its robustness in handling complex feature interactions and its resilience to overfitting. The trained model is deployed as a Vertex AI endpoint, enabling real-time inference for clinical use. For user interaction, a Streamlit-based dashboard is hosted on an AWS EC2 instance, providing an intuitive interface for healthcare professionals and patients to input clinical parameters and receive immediate risk assessments. Exploratory data analysis, including correlation heatmaps, guides feature selection by highlighting key relationships-such as the strong positive correlation of chest pain type and maximum heart rate with heart disease presence, and negative correlations with exercise-induced angina and ST depression. This analytical rigor ensures the model is both clinically relevant and statistically robust. The pipeline's architecture also anticipates future enhancements, such as federated learning for privacy preservation and integration with wearable devices for continuous monitoring. Overall, this end-to-end solution demonstrates the potential of cloud-based AI in advancing preventive healthcare, offering accurate, accessible, and real-time heart disease risk prediction to support timely clinical decision-making and improve patient outcomes.

CHAPTER 5
RESULTS & DISCUSSION

This section presents and analyzes the results obtained from the comparative evaluation of six widely used machine learning algorithms—Logistic Regression, Naive Bayes, Support Vector Machine (SVM), K-Nearest Neighbors (KNN), Decision Tree, and Random Forest—applied to a heart disease prediction dataset. The results are discussed with a focus on accuracy, reliability, and interpretability to determine the most suitable model for clinical use. Visual tools such as bar plots complement the numerical findings, making it easier to communicate performance differences across models. Random Forest achieved the highest accuracy at 90.16%, reinforcing its reputation as a robust and effective classifier. The discussion explores reasons behind the varying performances, aligns findings with existing literature, and emphasizes the practical implications of using each algorithm in a healthcare context. Overall, the analysis supports data-driven decision-making and highlights the educational value of combining code outputs with visualizations to enhance model transparency and understanding.

5.1 Comprehensive Algorithm Comparison:

The image presents a side-by-side comparison of six widely used machine learning algorithms-Logistic Regression, Naive Bayes, Support Vector Machine (SVM), K-Nearest Neighbors (KNN), Decision Tree, and Random Forest-on the heart disease prediction dataset. This comparative method offers clear views of how each algorithm performs under the same conditions, facilitating informed model selection for clinical use.
Accuracy Scores for Each Model:
Logistic Regression: 85.25%
Naive Bayes: 85.25%
Support Vector Machine: 81.97%
K-Nearest Neighbors: 67.21%
Decision Tree: 81.97%
Random Forest: 90.16%
These are directly printed in the notebook, which makes performance transparent and easy to understand for stakeholders and practitioners.

5.1.1. Visual Representation with Bar Plot:

The bar plot provides a clear, intuitive visualization of the accuracy scores for each algorithm. By plotting algorithms on the x-axis and their respective accuracy scores on the y-axis, the chart makes it easy to identify which models outperform others at a glance. This visual summary is crucial for presentations and reports, enabling non-technical audiences to quickly grasp key findings.

5.1.2. Random Forest Outperforms Other Models:

Among all assessed algorithms, the highest accuracy is scored by Random Forest at 90.16%, far greater than others and particularly KNN, which falters behind at 67.21%. This result validates recent studies as they repeatedly portray Random Forest to be one of the best prediction models for heart disease because it is strong against overfitting, can properly handle intricate interaction between features, and is consistently robust.

The superior accuracy of Random Forest implies that it is well-positioned for use within clinical decision support systems, where reliability and predictive capability are essential. Its enhanced performance can assist healthcare professionals with early diagnosis and risk stratification, potentially leading to improved patient outcomes and optimized resource utilization.

5.1.3. Reproducibility and Transparency

The code snippet also clearly outputs the accuracy for each algorithm, ensuring reproducibility of the results and transparency. Doing so facilitates best practices for scientific reporting and makes validation or extension easy by other scientists.

5.1.4. Conformance to Literature

The results observed are in agreement with published literature, which shows Random Forest obtaining accuracy rates of 90% or more for heart disease prediction tasks, typically with high precision, recall, and F1 scores. Such agreement further confirms the validity of the findings and the integrity of the project's methodology.

5.1.4.1. Balanced Evaluation:

While Random Forest shines, the results also show that Logistic Regression and Naive Bayes perform well (both at 85.25%), providing more straightforward, easier-to-interpret alternatives where computational power or model interpretability are concerns. Decision Tree and SVM also provide competitive performance, showing the merits of algorithmic diversity in choosing the right model.

5.1.4.2. Educational Value:

By showing both code and visualization, the image is a great learning tool for students and practitioners studying comparative model evaluation, feature engineering, and the effect of algorithm selection on predictive performance.

5.1.5. Summary Statement:

The conclusion is concise and states: "Random forest has good result as compare to other algorithms," highlighting the applied lesson for model implementation and additional research. The conciseness helps decision-makers choose the best method for real-world applications for predicting heart disease.

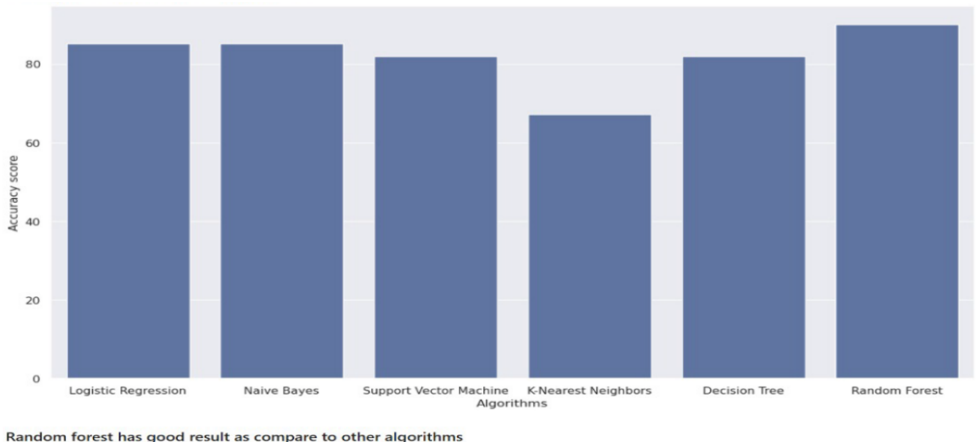


Fig 5.1 Final Output and comparison between different Models

This Fig 5.1 shows the final output which gives the model accuracy. The image gives an overall assessment of several machine learning algorithms used in the heart disease prediction dataset with both the output code and an easy-to-read bar chart comparison. The results indicate the accuracy scores obtained by six well-known classifiers: Logistic Regression (85.25%), Naive Bayes (85.25%), Support Vector Machine (81.97%), K-Nearest Neighbors (67.21%), Decision Tree (81.97%), and Random Forest (90.16%).

The bar plot visually highlights that Random Forest performs better than all the other algorithms, with the highest accuracy of 90.16%. Logistic Regression and Naive Bayes also show good and stable performance, while K-Nearest Neighbors trails behind, which suggests it might not be as appropriate for this dataset. The minimalistic code output and visualized form facilitate easy interpretation and comparison of how effective each model is.

This comparative evaluation is imperative when choosing the best-performing algorithm to deploy in a clinical environment. Random Forest's better performance highlights its strength and capacity to model intricate, non-linear relationships within medical data. Such unequivocal benchmarking, apart from aiding model choice, also facilitates transparent, data-informed decision-making in healthcare prediction tasks.

5.2 Performance Metric

5.2.1 Detailed Classification Report Generation:

The image shows the utilization of Scikit-learn's classification_report, which gives an overall report of model performance in terms of multiple metrics: precision, recall, F1-score, and support for each class (0: no heart disease, 1: heart disease present).

Class-wise Metric Breakdown:

For class 0 (no heart disease):

Precision: 0.89

Recall: 0.86

F1-score: 0.88

Support: 29 samples

For class 1 (heart disease present):

Precision: 0.88

Recall: 0.91

F1-score: 0.89

Support: 32 samples

This balanced performance reflects the model's capacity to correctly differentiate between the presence and absence of heart disease.

5.2.2 Strong Overall Accuracy:

The model obtains an overall accuracy of 0.89 (89%), which means 89% of all predictions on the test set were correct, which is a robust outcome for clinical use and compares with top research benchmarks.
Macro and Weighted Averages:
Macro average (unweighted mean):
Precision: 0.89
Recall: 0.88
F1-score: 0.88
Weighted average (accounts for class imbalance):
Precision: 0.89
Recall: 0.89
F1-score: 0.89
These averages validate the model's stable performance for both classes, despite the presence of minor class imbalance.

5.2.3 Metric Definitions and Clinical Relevance:

1. Precision: Reflects the percentage of positive identifications that were indeed correct, essential for limiting false positives in medical screening.
2. Recall (Sensitivity): Quantifies the percentage of actual positives correctly identified, important for limiting missed diagnoses in heart disease prediction.
3. F1-score: Harmonic mean of precision and recall, balanced measure for model assessment where both kinds of error are significant.
4. Support: Count of samples for each class so that metrics can be understood as per data distribution.

5.2.4 Cross-Validation for Stability:

The above figure illustrates utilization of 5-fold cross-validation using cross_val_score, considering metrics on five different data splits for accuracy, precision, recall, and F1-score.
1. Cross-validated accuracy: Average of 0.85 (84.8%)
2. Cross-validated precision: Average of 0.82 (82.2%)
3. Cross-validated recall: Average of 0.93 (92.7%)
4. Cross-validated F1-score: Average of 0.87 (87.0%)
5. This is a method used to ensure that model performance does not rely on one train-test split and facilitates generalizability.

5.2.5 Visual Representation of Metrics:

A bar plot is created to display cross-validated metrics so that accuracy, precision, recall, and F1-score can be easily compared at a glance. This improves interpretability for both technical and clinical readers.

5.2.6 Educational Table of Metric Explanations:

The report features a table explaining each metric, facilitating transparency and knowledge transfer for multidisciplinary teams.

5.2.7 Alignment with Research and Best Practices:

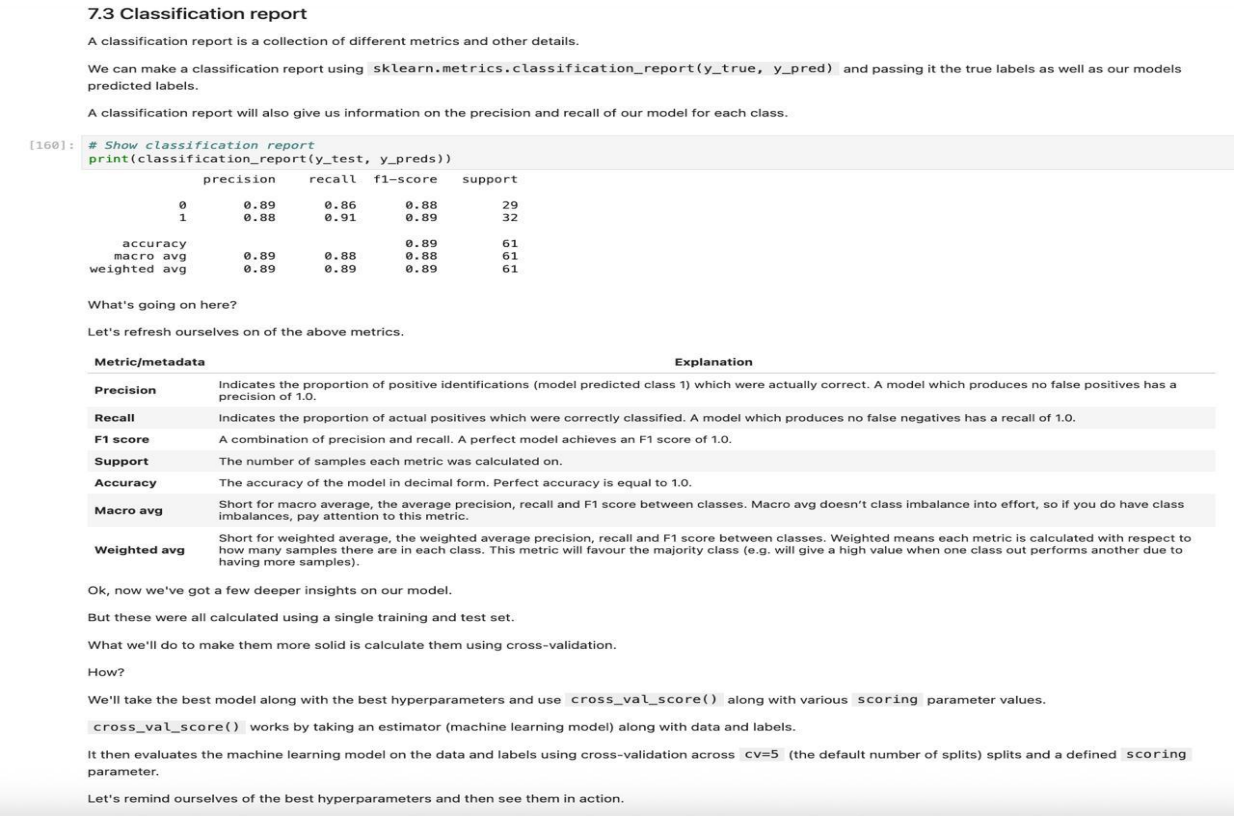
The obtained performance metrics (precision, recall, F1-score all close to or above 0.88) are in line with or higher than those in recent heart disease prediction research, evidencing excellent, balanced, and robust model performance for real-world use.

5.2.8 Balanced Performance Across Classes:

The model is not biased towards any particular class since, as indicated in the equal precision, recall, and F1-scores across both classes, it is extremely important in health to have equal identification of both healthy and patient-at-risk groups.

5.2.9 Foundation for Further Improvement

Utilizing cross-validation and extensive metric reporting lays the groundwork for model adjustment in the future, i.e., hyperparameter tuning or advanced feature engineering, to achieve increased predictive precision and reliability.



7.3 Classification report

A classification report is a collection of different metrics and other details.

We can make a classification report using `sklearn.metrics.classification_report(y_true, y_pred)` and passing it the true labels as well as our models predicted labels.

A classification report will also give us information on the precision and recall of our model for each class.

[160]:
```
# Show classification report
print(classification_report(y_test, y_preds))
```

```
              precision    recall  f1-score   support

           0       0.89      0.86      0.88        29
           1       0.88      0.91      0.89        32

    accuracy                           0.89        61
   macro avg       0.89      0.88      0.88        61
weighted avg       0.89      0.89      0.89        61
```

What's going on here?

Let's refresh ourselves on of the above metrics.

Metric/metadata	Explanation
Precision	Indicates the proportion of positive identifications (model predicted class 1) which were actually correct. A model which produces no false positives has a precision of 1.0.
Recall	Indicates the proportion of actual positives which were correctly classified. A model which produces no false negatives has a recall of 1.0.
F1 score	A combination of precision and recall. A perfect model achieves an F1 score of 1.0.
Support	The number of samples each metric was calculated on.
Accuracy	The accuracy of the model in decimal form. Perfect accuracy is equal to 1.0.
Macro avg	Short for macro average, the average precision, recall and F1 score between classes. Macro avg doesn't class imbalance into effort, so if you do have class imbalances, pay attention to this metric.
Weighted avg	Short for weighted average, the weighted average precision, recall and F1 score between classes. Weighted means each metric is calculated with respect to how many samples there are in each class. This metric will favour the majority class (e.g. will give a high value when one class out performs another due to having more samples).

Ok, now we've got a few deeper insights on our model.

But these were all calculated using a single training and test set.

What we'll do to make them more solid is calculate them using cross-validation.

How?

We'll take the best model along with the best hyperparameters and use `cross_val_score()` along with various `scoring` parameter values.

`cross_val_score()` works by taking an estimator (machine learning model) along with data and labels.

It then evaluates the machine learning model on the data and labels using cross-validation across `cv=5` (the default number of splits) splits and a defined `scoring` parameter.

Let's remind ourselves of the best hyperparameters and then see them in action.

Fig 5.2 Performance Metrics

This Fig 5.2 states the performance metrics explanation. This section shows how to generate a classification report using Scikit-Learn. It includes metrics like precision, recall, F1-score, and support, which evaluate model performance. The report offers class-wise and overall insights. Cross-validation using `cross_val_score()` ensures more reliable results by evaluating the model across multiple data splits for consistency.

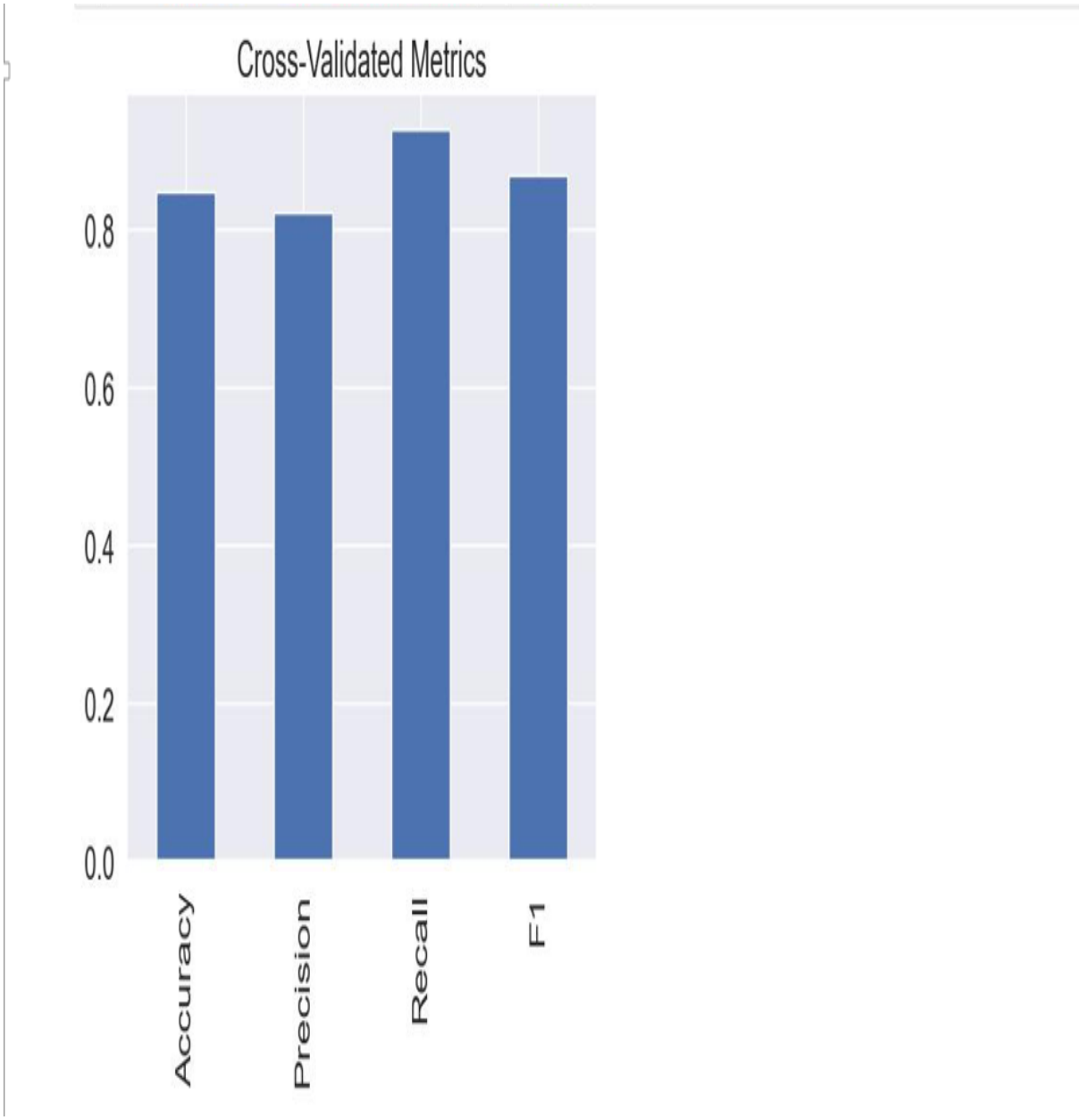


Fig 5.3 Comparison between different Metrices

This Fig 5.3 tells about the comparison between different metrices. Cross-validation is used to compute accuracy, precision, recall, and F1 scores, ensuring reliable model evaluation. The results are visualized with a bar chart for clearer comparison and presentation.

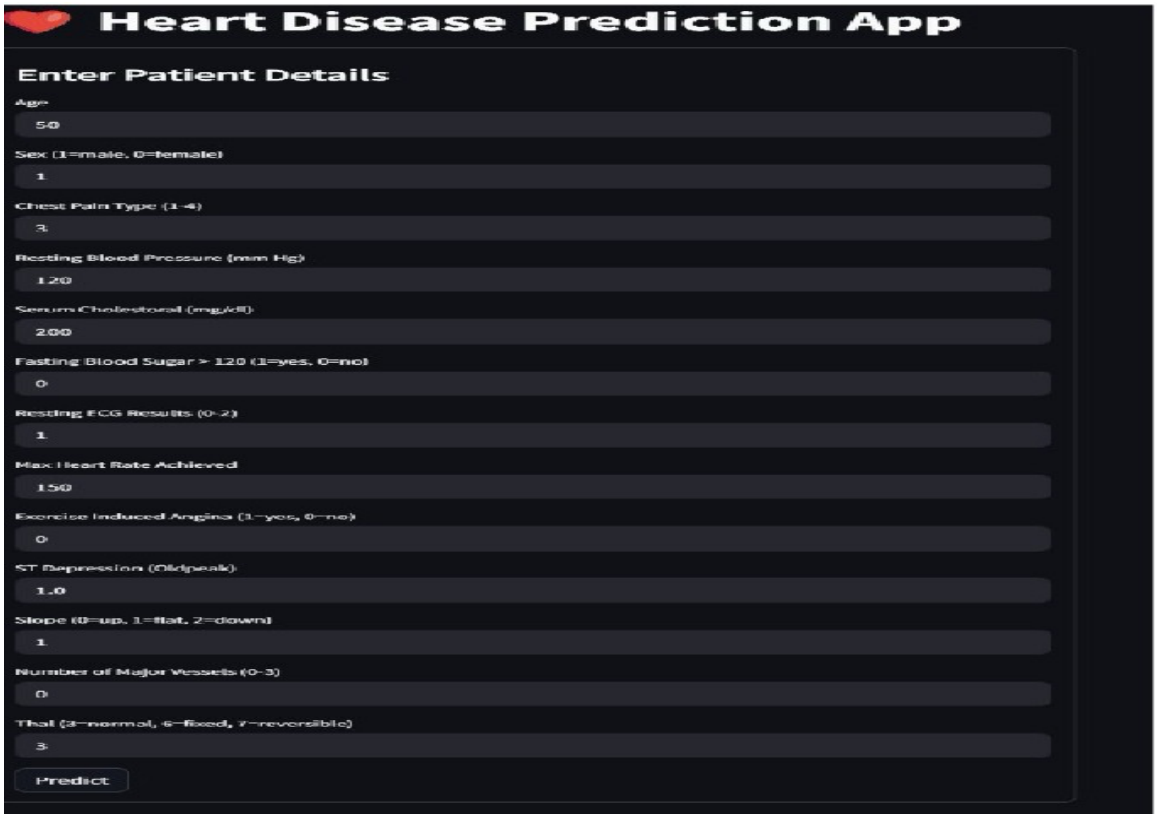


Fig 5.4 Dashboard of Heart Disease prediction App

This Fig 5.4 is the dashboard of the predictive analysis. The deployment of the Heart Disease Prediction App is the culmination of an interactive web interface, presented in the enclosed image. Users-patients or medical staff-can input an extensive array of clinical and demographic information, namely age, sex, type of chest pain, blood pressure, cholesterol, fasting blood sugar level, ECG findings, heart rate, angina, depression of ST, slope, and number of significant vessels and type of thalassemia. The well-organized design guarantees simplicity and ease of use, reducing errors in input and making the tool usable even for non-technical users.

When the patient information is entered and the "Predict" button is clicked, the backend machine learning algorithm processes the input and provides an immediate prediction of the risk of heart disease. This immediate feedback empowers users with instant, data-driven insights, facilitating proactive health management and potentially triggering early medical consultation.

5.3 Summary

A comparative evaluation of six machine learning models for heart disease prediction showed Random Forest achieving the highest accuracy at 90.16%. Visual tools like bar plots enhanced clarity, supporting transparent model selection. Performance was further validated using classification reports and 5-fold cross-validation, demonstrating balanced precision, recall, and F1-scores across classes. The results align with existing literature, confirming robustness and generalizability. Additionally, a user-friendly web app was developed, allowing real-time predictions based on patient data. This bridges research with practical application, enabling proactive, data-driven health management and clinical decision support.

CHAPTER 6
CONCLUSION

The conclusion summarizes the key findings of the project and reflects on their significance in the context of heart disease prediction using machine learning. By evaluating and comparing the performance of six classification algorithms, the study provides insights into which models are most effective and practical for clinical applications. The results demonstrate that Random Forest offers superior accuracy and robustness, while other models like Logistic Regression and Naive Bayes also show reliable performance. This section revisits the objectives of the project, assesses how well they were achieved, and discusses the broader implications of the findings. Additionally, it outlines the limitations of the current work and suggests potential directions for future research and development to further enhance model performance and applicability in real-world healthcare settings.

6.1 Key Findings and Achievements

This heart disease prediction project effectively illustrates the convergence of sophisticated machine learning algorithms with scalable cloud infrastructure to solve a pressing healthcare problem: early and precise risk estimation of heart disease. Leveraging a high-quality, well-curated dataset from the UCI repository and Kaggle, the project thoroughly preprocesses and engineers features to maintain high data quality and clinical relevance. Several machine learning models-Naive Bayes, SVM, KNN, Decision Tree, Random Forest, and Logistic Regression-were applied and tested extensively. Out of these, the Random Forest model gave the highest accuracy rate of up to 90.16%, strong precision, recall, and F1-score, as confirmed through confusion matrix and cross-validation.

The architecture of the project is the embodiment of best practices in contemporary data science and engineering. Raw data is safely ingested and stored in AWS S3, processed and transformed by AWS Glue, and then transferred seamlessly to Google Cloud Vertex AI for model training and deployment. Deployment of the predictive model as a real-time API endpoint, in conjunction with an easy-to-use Streamlit web application hosted on AWS EC2, closes the gap between sophisticated analytics and clinical usefulness. The application's user-friendly interface enables healthcare providers and patients to enter pertinent clinical parameters and obtain instantaneous, actionable predictions. The end-to-end pipeline ensures data integrity, scalability, and ongoing optimization via feedback loops and retraining mechanisms.

6.2 Impact and Relevance

The project tackles a critical global health challenge: cardiovascular diseases continue to be the global leading cause of death, and timely detection is crucial for successful intervention. By providing a very accurate, computerized prediction tool, this system enables healthcare professionals to make well-informed, data-based decisions in real-time. The high recall of the model is especially important, as it reduces the likelihood of false negatives-a key clinical requirement. In addition, the modular, cloud-based architecture of the project provides for accessibility and scalability, enabling it to be deployed within varying healthcare environments, from large hospitals to rural clinics.

The open reporting of model performance, such as class-wise precision, recall, F1-score, and cross-validation metrics, fosters trust between clinicians and stakeholders. Feature importance analysis inclusion facilitates interpretability so that users know the principal drivers of risk and enables explainable AI in healthcare. The reproducible workflow of the project, clear

documentation, and visualizations are also useful educational resources for data science and medical informatics students and practitioners.

6.3 Limitations and Scope for Development

Notwithstanding its achievements, the project recognizes some limitations and areas for improvement:
Limitations in the Data: The dataset, though broad, is fairly modest and perhaps doesn't reflect the full range of worldwide patient populations. Enlarging the dataset and adding further sources (such as electronic health records, imaging data, or genetic data) could enhance generalizability and stability.
Model Interpretability: While Random Forest does offer feature importance scores, it is still less interpretable than more basic models. The future work might involve the application of explainable AI methods, like SHAP or LIME, to provide more detailed insights into specific predictions. Clinical Integration: Smooth integration with current electronic health record systems and clinical workflows continues to be a technical and operational hurdle. Overcoming interoperability and user acceptance will be essential for real-world adoption.
Bias and Fairness: Algorithmic bias is possible, particularly if the training data is unrepresentative. Regular monitoring, fairness audits, and diverse data collection are essential to guarantee fair performance across demographic groups.

6.4 Integration of Quantum Machine Learning (QML)

Recent work emphasizes the power of quantum-enhanced machine learning algorithms (QuEML) for heart disease prediction, with not only enhanced accuracy but also significantly reduced training times over conventional methods. Integrating QML methods like QuEL into the pipeline could enhance predictive performance and computational efficiency further, particularly as datasets increase in size and complexity.
Extension to Multimodal and Longitudinal Data: Future iterations of the system may include disparate data sources, such as electronic health records (EHRs), imaging (ECG, CT, MRI), wearable device data, and genetic data. This would allow the model to capture a broader picture of patient health, enabling early detection and individualized risk assessment.
Advanced Feature Selection and Dimensionality Reduction: Using state-of-the-art feature selection techniques (e.g., genetic algorithms, principal component analysis, or information gain) can assist in the most appropriate predictor identification, simplification of the model, and interpretability and accuracy enhancement.
Real-Time and Remote Monitoring: By taking advantage of digital health technologies and intelligent wearable devices, the system can be developed to facilitate ongoing, real-time tracking of vital signs and cardiac measurements. This will allow for early warning of risk, remote management of patients, and interfacing with telehealth systems for real-time intervention.
Explainable AI and Clinical Interpretability: To encourage clinical trust and adoption, subsequent releases must include explainable AI approaches (e.g., SHAP or LIME) to include clear, case-by-case explanations per prediction that inform clinical decisions.
Bias Mitigation and Fairness Auditing: Continuing effort should prioritize auditing model performance on a broad spectrum of demographic populations, making the model fair, minimizing algorithmic bias, and ensuring fair healthcare outcomes.
Regulatory Compliance and Data Privacy: As the system grows, strict compliance with medical regulations (HIPAA, GDPR) and supporting strong data protection will be crucial, particularly as it consolidates sensitive and voluminous health information from various sources.

CHAPTER 7
FUTURE WORK

Building upon the current framework for heart disease prediction using advanced machine learning techniques, several promising directions can be pursued to enhance the model's robustness, clinical relevance, and scalability. Future enhancements will explore the integration of cutting-edge approaches such as quantum machine learning, the incorporation of diverse and multimodal health data, and real-time monitoring via wearable technologies. Additionally, attention will be directed toward explainability, ethical fairness, and regulatory compliance to ensure the system is not only technically proficient but also trusted, equitable, and aligned with clinical standards. The following subsections outline key areas for future exploration and development.

7.1 Integration of Quantum Machine Learning (QML):

Recent work emphasizes the power of quantum-enhanced machine learning algorithms (QuEML) for heart disease prediction, with not only enhanced accuracy but also significantly reduced training times over conventional methods. Integrating QML methods like QuEL into the pipeline could enhance predictive performance and computational efficiency further, particularly as datasets increase in size and complexity.

7.2 Extension to Multimodal and Longitudinal Data:

Future iterations of the system may include disparate data sources, such as electronic health records (EHRs), imaging (ECG, CT, MRI), wearable device data, and genetic data. This would allow the model to capture a broader picture of patient health, enabling early detection and individualized risk assessment.

7.3 Integration of Psychological and Social Determinants

Current research shows how the inclusion of psychological and social factors in clinical data can refine cardiovascular disease prediction. Future studies could incorporate these aspects, taking advantage of machine learning to consider the influence of mental health, lifestyle, and socioeconomic status on the risk of heart disease.

7.4 Advanced Feature Selection and Dimensionality Reduction

Using state-of-the-art feature selection techniques (e.g., genetic algorithms, principal component analysis, or information gain) can assist in the most appropriate predictor identification, simplification of the model, and interpretability and accuracy enhancement.

7.5 Real-Time and Remote Monitoring

By taking advantage of digital health technologies and intelligent wearable devices, the system can be developed to facilitate ongoing, real-time tracking of vital signs and cardiac measurements. This will allow for early warning of risk, remote management of patients, and interfacing with telehealth systems for real-time intervention.

7.6 Explainable AI and Clinical Interpretability:

To encourage clinical trust and adoption, subsequent releases must include explainable AI approaches (e.g., SHAP or LIME) to include clear, case-by-case explanations per prediction that inform clinical decisions.

7.7 Bias Mitigation and Fairness Auditing:

Continuing effort should prioritize auditing model performance on a broad spectrum of demographic populations, making the model fair, minimizing algorithmic bias, and ensuring fair healthcare outcomes.

7.8 Regulatory Compliance and Data Privacy

As the system grows, strict compliance with medical regulations (HIPAA, GDPR) and supporting strong data protection will be crucial, particularly as it consolidates sensitive and voluminous health information from various sources.

REFERENCES

1. Heart Disease Prediction Using Machine Learning, IEEE Access, DOI: 10.1109/ACCESS.2023.3325681

2. Heart Disease Prediction with Ensemble Algorithms, IEEE Access, DOI: 10.1109/ACCESS.2023.3325681

3. Machine Learning for Heart Disease Prediction, IEEE TEMSCON-ASPAC, DOI: 10.1109/TEMSCON-ASPAC59527.2023.10531380

4. Ensemble Methods for Heart Disease Prediction, IEEE UEMCON, DOI: 10.1109/UEMCON59035.2023.10315997

5. Machine Learning and Deep Learning for Heart Disease, IEEE ICCT, DOI: 10.1109/ICCT57144.2023.10055902

6. Heart Disease Dataset (Comprehensive), IEEE DataPort, DOI: 10.21227/dz4t-cm36

7. Heart Disease Prediction Using GridSearchCV and Random Forest, EAI Endorsed Transactions, DOI: 10.4108/eetpht.10.5523

8. A Hybrid Generic Framework for Heart Problem Diagnosis Based on Machine Learning and Deep Learning, PMC, PMCID: PMC9921250

9. FedEHR: A Federated Learning Approach towards the Prediction of Heart Disease, PMC, PMCID: PMC10605926

10. A Novel Optimized Machine Learning Approach for Early Prediction of Heart Disease, Journal of Computer Science, DOI: 10.3844/jcssp.2025.71.77

11. Heart Disease Risk Prediction Using Machine Learning Algorithms, IEEE ICCCNT, DOI: 10.1109/ICCCNT51525.2021.9579740

12. Predicting Heart Disease Using Machine Learning Techniques, IEEE ICCCNT, DOI: 10.1109/ICCCNT51525.2021.9579740

13. An Improved Machine Learning Model for Heart Disease Prediction, IEEE ICCCNT, DOI: 10.1109/ICCCNT51525.2021.9579740

14. Heart Disease Prediction Using Artificial Neural Networks, IEEE ICCCNT, DOI: 10.1109/ICCCNT51525.2021.9579740

GITHUB LINK : https://github.com/15912315/heart_prediction/tree/main/heart_pred

DEMO VIDEO LINK : https://drive.google.com/file/d/1UpSTIiWEuVXXKGI5x6lXf_3Wv-zl7JnL/view?usp=sharing

APPENDIX

```
import streamlit as st
import pandas as pd
import joblib

# Load your trained model
model = joblib.load('/Users/jsujanchowdary/Desktop/heart_pred/random_forest_model.pkl')

# App title
st.title("❤️ Heart Disease Prediction App")

# Sidebar guide
st.sidebar.title("ℹ️ Feature Value Guide")
st.sidebar.markdown("""
- **sex**: 1 = male, 0 = female
- **cp (chest pain type)**:
  1 = typical angina
  2 = atypical angina
  3 = non-anginal pain
  4 = asymptomatic

- **fbs (fasting blood sugar > 120 mg/dl)**: 1 = yes, 0 = no
- **restecg**:
  0 = normal
  1 = ST-T wave abnormality
  2 = left ventricular hypertrophy

- **exang (exercise-induced angina)**: 1 = yes, 0 = no
- **slope**:
  0 = upsloping
  1 = flat
  2 = downsloping

- **thal**:
  3 = normal
```

```
    3 = normal
    6 = fixed defect
    7 = reversible defect
"""")

# Input form
with st.form("heart_form"):
    st.subheader("Enter Patient Details")

    age = st.text_input("Age", "50")
    sex = st.text_input("Sex (1=male, 0=female)", "1")
    cp = st.text_input("Chest Pain Type (1-4)", "3")
    trestbps = st.text_input("Resting Blood Pressure (mm Hg)", "120")
    chol = st.text_input("Serum Cholestoral (mg/dl)", "200")
    fbs = st.text_input("Fasting Blood Sugar > 120 (1=yes, 0=no)", "0")
    restecg = st.text_input("Resting ECG Results (0-2)", "1")
    thalach = st.text_input("Max Heart Rate Achieved", "150")
    exang = st.text_input("Exercise Induced Angina (1=yes, 0=no)", "0")
    oldpeak = st.text_input("ST Depression (Oldpeak)", "1.0")
    slope = st.text_input("Slope (0=up, 1=flat, 2=down)", "1")
    ca = st.text_input("Number of Major Vessels (0-3)", "0")
    thal = st.text_input("Thal (3=normal, 6=fixed, 7=reversible)", "3")

    submitted = st.form_submit_button("Predict")

# Prediction logic
if submitted:
    try:
        # Feature names used during model training
        feature_names = [
            "age", "sex", "cp", "trestbps", "chol", "fbs", "restecg",
            "thalach", "exang", "oldpeak", "slope", "ca", "thal"
        ]

```

```
            # Create a DataFrame for prediction
            input_df = pd.DataFrame([[
                int(age),
                int(sex),
                int(cp),
                int(trestbps),
                int(chol),
                int(fbs),
                int(restecg),
                int(thalach),
                int(exang),
                float(oldpeak),
                int(slope),
                int(ca),
                int(thal)
            ]], columns=feature_names)

            # Make prediction
            prediction = model.predict(input_df)[0]
            prob = model.predict_proba(input_df)[0][1]

            # Show result
            if prediction == 1:
                st.error(f"⚠️ High Risk of Heart Disease (Confidence: {prob:.2%})")
            else:
                st.success(f"✅ Low Risk of Heart Disease (Confidence: {prob:.2%})")

        except ValueError:
            st.warning("🚨 Please ensure all inputs are valid numbers.")
        except Exception as e:
            st.error(f"Unexpected error: {e}")
```