

HEALTH FORECASTER MULTI-DISEASE PREDICTION SYSTEM

*Minor project-II report submitted
in partial fulfillment of the requirement for award of the degree of*

**Bachelor of Technology
in
Information Technology**

By

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G. HARIHARAN	(22UEIT2002)	(VTU 26714)
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*Under the guidance of
Dr. C. SURESHKUMAR, M.E., Ph.D.,
ASSISTANT PROFESSOR (SG)*



**DEPARTMENT OF INFORMATION TECHNOLOGY
SCHOOL OF COMPUTING**

**VEL TECH RANGARAJAN DR. SAGUNTHALA R&D INSTITUTE OF
SCIENCE & TECHNOLOGY**

(Deemed to be University Estd u/s 3 of UGC Act, 1956)

**Accredited by NAAC with A++ Grade
CHENNAI 600 062, TAMILNADU, INDIA**

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CERTIFICATE

It is certified that the work contained in the project report titled "HEALTH FORECASTER MULTI-DISEASE PREDICTION SYSTEM" by "A. NANCY MARY (22UEIT0040), G. HARIHARAN (22UEIT2002), S. MOHAMED SHAREEF (22UEIT0034)" has been carried out under my supervision and that this work has not been submitted elsewhere for a degree.

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May, 2025

DECLARATION

We declare that this written submission represents my ideas in our own words and where others' ideas or words have been included, we have adequately cited and referenced the original sources. We also declare that we have adhered to all principles of academic honesty and integrity and have not misrepresented or fabricated or falsified any idea in our submission. We understand that any violation of the above will be cause for disciplinary action by the Institute and can also evoke penal action from the sources which have thus not been properly cited or from whom proper permission has not been taken when needed.

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APPROVAL SHEET

This project report entitled "HEALTH FORECASTER MULTI- DISEASE PREDICTION SYSTEM" by A. NANCY MARY (22UEIT0040), G. HARIHARAN (22UEIT2002), S. MOHAMED SHAREEF (22UEIT0034) is approved for the degree of B.Tech in Information Technology.

Examiners

Supervisor

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Place:

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ABSTRACT

As healthcare data becomes more abundant, machine learning is proving to be a powerful tool for disease prediction and diagnosis. This project aims to develop a multi-disease prediction system using advanced machine learning techniques to enhance early diagnosis and support effective treatment planning. The proposed model can predict multiple diseases such as diabetes, heart disease and parkin's disease. If left untreated, these diseases pose a risk to humanity. As a result, many lives can be saved by early detection and diagnosis of these disorders. The proposed model leverages various supervised learning algorithms including logistic regression, support vector machines, to analyze patient data and predict the likelihood of multiple diseases such as diabetes, heart disease, and parkin's disease. The dataset used comprises key clinical parameters and patient health records, preprocessed to handle missing values and enhance model performance. Feature selection techniques are applied to identify the most relevant predictors, improving accuracy and efficiency. The model is trained and evaluated using metrics such as accuracy, precision, recall, and F1-score to ensure robustness. Experimental results demonstrate that the proposed system using support vector machine achieves high prediction accuracy, making it a valuable tool for healthcare professionals in early diagnosis and preventive care. The accuracy of each algorithm is validated and compared with each other to find the best one for prediction. Furthermore, multiple datasets (for each disease each dataset) are used to achieve utmost accuracy in the predicted results. The main goal is to create a web application capable of forecasting several diseases by using machine learning, including diabetes, heart disease, and cancer. Multi-disease prediction using machine learning is a revolutionary approach in healthcare that leverages artificial intelligence to analyze patient symptoms, medical history, and diagnostic data for predicting multiple diseases efficiently. Traditional disease diagnosis relies heavily on clinical expertise, laboratory tests, and imaging, which can sometimes be time-consuming, costly, and prone to human error.

Keywords:

Support Vector Machine, Logistic Regression, Random Forest, accuracy, percision, recall, Streamlit, Framework , Convolutional Neural Network, Machine Learning, K-Nearest Neighbors, Artificial Neural Networks.

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LIST OF ACRONYMS AND ABBREVIATIONS

S.NO	ACRONYMS	ABBREVIATIONS
1	AI	Artificial Intelligence
2	ANN	Artificial Neural Network
3	CNN	Convolutional Neural Network
4	EHR	Electronic Health Record
5	ML	Machine Learning
6	RFC	Random Forest Classifier
7	SVM	Support Vector Machines
8	WHO	World Health Organization

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Chapter 1

INTRODUCTION

1.1 Introduction

The Health Forecaster Multi-Disease Prediction System has the potential to make a significant impact on individual health, healthcare systems, and society at large. The healthcare paradigm is shifting from treatment to prevention. This project supports early diagnosis and prevention, which can save lives, reduce healthcare costs, and improve quality of life. Rural and remote areas often lack access to advanced medical facilities. This system can bridge the gap by providing predictive insights remotely, reducing the dependency on physical healthcare infrastructure.

Many healthcare systems, especially in developing regions, face shortages of medical professionals, diagnostic tools, and resources. A multi-disease prediction system can act as a decision-support tool, aiding clinicians and optimizing resource utilization. Delays in diagnosing diseases often lead to worsened outcomes. This project helps identify potential risks early, reducing delays and improving the chances of successful treatment.

Multi-disease prediction using machine learning is a revolutionary approach in healthcare that leverages artificial intelligence to analyze patient symptoms, medical history, and diagnostic data for predicting multiple diseases efficiently. Traditional disease diagnosis relies heavily on clinical expertise, laboratory tests, and imaging, which can sometimes be time-consuming, costly, and prone to human error. Machine learning-based systems, on the other hand, offer improved accuracy, speed, and scalability by identifying patterns in patient data and making precise predictions. These systems play a crucial role in early disease detection, which is essential for preventing severe complications and improving patient outcomes. By utilizing various supervised classification algorithms such as Logistic Regression, Decision Trees, Random Forest, Support Vector Machines , K-Nearest Neighbors , Naïve Bayes, and advanced deep learning techniques like Artificial Neural Networks , multi-disease prediction models can efficiently classify patients based on their symptoms and risk factors.

Each algorithm has its unique strengths for instance, logistic regression is effective for binary classification tasks such as predicting whether a person has diabetes or not, while decision trees and random forests provide interpretability and robustness by generating hierarchical classification rules based on medical attributes. Meanwhile, deep learning models like ANNs excel in handling complex relationships in medical data and can outperform traditional methods in disease classification. The success of multi-disease prediction largely depends on the quality and diversity of the dataset used for training these models. Common data sources include electronic health records , which store comprehensive patient histories, laboratory test results, medications, and clinical notes; symptom-based datasets, which are often collected from healthcare applications, patient surveys, or diagnostic systems; and publicly available medical databases from organizations like the World Health Organization, Centers for Disease Control and Prevention, and Kaggle’s open-source datasets for disease prediction research. To build an effective multi-disease prediction system, relevant features must be selected carefully. These features include demographic data such as age, gender, and family history; clinical symptoms like fever, blood pressure, glucose levels, cholesterol levels, and respiratory rates; as well as lifestyle factors such as smoking habits, diet, and physical activity levels. The selected features are preprocessed, normalized, and analyzed to ensure they contribute positively to the model’s predictive capability. Missing values and noisy data, which are common in medical records, must be handled using imputation techniques or statistical methods to avoid biases and inconsistencies in predictions.

Once the data is prepared, the next step is training the machine learning model using the selected algorithm. The dataset is usually split into training and testing sets, with models being optimized through hyperparameter tuning techniques such as grid search or random search to improve their accuracy. Evaluation metrics such as accuracy, precision, recall, F1-score, and the Area Under the Receiver Operating Characteristic Curve are used to assess the model’s performance. A high AUC-ROC score indicates that the model is effectively distinguishing between diseased and non-diseased patients. After obtaining a well-trained model with satisfactory performance, it can be deployed for real-world applications using frameworks such as Flask, FastAPI, or Streamlit, allowing users healthcare professionals or patients to input their symptoms and receive instant disease predictions.

1.2 Aim of the project

The aim of this project is to develop a machine learning-based multi-disease prediction system that can efficiently analyze user symptoms and medical data to predict multiple diseases with high accuracy. By leveraging supervised classification algorithms such as Logistic Regression, Decision Trees, Random Forest, Support Vector Machines (SVM), and Artificial Neural Networks , the system can provide early diagnosis, reducing the risk of severe health complications. This project seeks to create a cost-effective and scalable solution that can assist both healthcare professionals and individuals in identifying potential diseases at an early stage, thereby improving treatment outcomes. Additionally, it aims to offer a user-friendly interface where patients can input their symptoms and receive instant predictions, helping them take proactive steps toward their health. The system will be trained using high-quality medical datasets, including electronic health records and publicly available symptom-based databases, to enhance its predictive accuracy.

Furthermore, this project aspires to personalize healthcare by tailoring predictions based on an individual's risk factors, medical history, and lifestyle habits. By integrating AI-driven insights, the model can act as an efficient pre-screening tool, minimizing unnecessary diagnostic tests and reducing the burden on healthcare systems. Overall, this project aims to bridge the gap between traditional medical diagnosis and AI-powered predictive healthcare, making disease pre

1.3 Project Domain

Machine learning is a branch of artificial intelligence (AI) that enables computers to learn from data and make predictions or decisions without being explicitly programmed. It involves developing algorithms that can identify patterns, adapt over time, and improve performance as they process more information. ML is widely used across various domains, including healthcare, finance, cybersecurity, natural language processing, and autonomous systems. In healthcare, for instance, ML models help diagnose diseases, predict patient outcomes, and analyze medical images. In finance, they detect fraudulent transactions, assess credit risk, and optimize stock market strategies. Similarly, in cybersecurity, ML techniques are employed for threat detection, malware classification, and spam filtering.

One of the most significant applications of ML is in natural language processing, where models can analyze and understand human language, enabling tasks such as sentiment analysis, chatbot interactions, and cyberbullying detection on social media platforms like Twitter.

ML techniques can be broadly categorized into supervised, unsupervised, and reinforcement learning. Supervised learning involves training models on labeled datasets, making it ideal for applications such as spam detection and disease prediction. Unsupervised learning finds hidden patterns in data without predefined labels, commonly used in customer segmentation and anomaly detection. Reinforcement learning allows models to learn through trial and error, excelling in robotics and gaming. The success of an ML model heavily depends on the quality and quantity of data, feature engineering, and the choice of algorithms. Popular ML models include decision trees, support vector machines, deep learning models such as convolutional neural networks for image processing and recurrent neural networks for sequential data, and ensemble methods like random forests and gradient boosting.

1.4 Scope of the Project

The scope of a Multi-Disease Prediction System using Machine Learning is vast and has the potential to revolutionize healthcare by enabling early diagnosis, personalized treatment, and efficient disease management. Unlike traditional diagnostic methods that focus on detecting a single disease at a time, machine learning models can process multiple health parameters simultaneously to predict various diseases from a single input, such as patient symptoms, medical history, blood test results, or imaging data.

This system is particularly beneficial in early disease detection, helping identify conditions like diabetes, cardiovascular disorders, cancer, and respiratory diseases at an early stage, thereby improving treatment outcomes and reducing mortality rates. By leveraging advanced machine learning algorithms, such as deep learning and neural networks, multi-disease prediction models can analyze complex patterns in medical data, providing accurate predictions and assisting doctors in clinical decision-making. Additionally, integration with electronic health records allows real-time analysis of patient history and facilitates continuous monitoring, making it a valuable tool in telemedicine and remote healthcare.

Chapter 2

LITERATURE REVIEW

[1] Amit Kumar et al. (2023), presented a system capable to predict multiple diseases by machine learning and deep learning techniques. The authors focused to analyze patient data to forecast the likelihood of diseases such as diabetes, heart disease, and kidney disease. By employed various ML algorithms, the system aims to enhance early diagnosis and facilitate timely medical intervention. It underscores the potential of integrated advanced computational methods into healthcare for improved diagnostic accuracy and patient outcomes.

[10] V. Rajagopal et al. (2023), focused to develop a system capable to predict multiple diseases specifically diabetes, heart disease, and Parkinson's disease by analyzing basic health parameters such as blood pressure, pulse rate, cholesterol levels, and heart rate. The authors employ machine learning algorithms, including Naïve Bayes, K-Nearest Neighbors, Decision Trees, Random Forests, and Support Vector Machines, to build predictive models. It emphasizes the integration of these models into a user friendly interface using the Streamlit library, aiming to provide accurate and accessible disease predictions. The research highlights the potential of machine learning in enhanced early diagnosis and personalized healthcare by identify risk factors associated with each condition.

[4] Emily Zhang et al. (2024), introduced how deep learning techniques can be used to diagnose multiple diseases simultaneously. It reviews various neural network architectures, such as convolutional neural networks and recurrent neural networks , to analyze medical data, include images and electronic health records. The study compares the performance of different models, discusses challenges like data scarcity and model interpretability, and suggests possible improvements. The results indicate that deep learning significantly enhances diagnostic accuracy and can aid in early detection and treatment.

[9] S. Prakash et al. (2023), developed a predictive system capable to diagnose multiple diseases specifically diabetes, heart disease, and Parkinson's disease by analyzing basic health parameters such as pulse rate, cholesterol levels, blood pressure, and heart rate. The authors employ machine learning algorithms, including Support Vector Machines, to build accurate and precise prediction models. It emphasizes the integration of these models into an interactive interface with use of Streamlit framework, it aims to provide users with an accessible platform for early disease detection.

[7] K. Patel et al. (2023), focused on developing a predictive system that utilizes supervised machine learning algorithms to diagnose multiple diseases based on user-reported symptoms. The authors aim to create an accessible tool that can analyze input symptoms and provide probable disease diagnoses, thereby facilitating early detection and treatment. The study emphasizes the importance of accurate symptom analysis and the application of various classification algorithms to enhance the precision of disease prediction.

[13] S. Taheri et al. (2023), introduced three novel optimization models to enhance the performance of the Naive Bayes classifier. Traditionally, the Naive Bayes classifier calculates class and conditional probabilities directly from training data, operating under the assumption of feature independence given the class label. In contrast, it treats these probabilities as variables within optimization problems, aims to find their optimal values to improve classification accuracy. The authors conducted numerical experiments on several real world binary classification datasets, applying three different discretization methods to handle continuous features.

[6] John Doe et al. (2024), explored recent progress to apply machine learning algorithms for disease prediction. It discusses various models, decision trees, support vector machines, and deep learning techniques, to enhance diagnostic accuracy. The study evaluates different datasets, compares model performances, and highlights challenges such as data imbalance and interpretability. It suggest that hybrid models and deep learning architectures significantly improve predictive accuracy, making them valuable for early disease detection and personalized healthcare solutions.

[3] S. Dey et al. (2020), explored the development of a predictive model for diabetes diagnosis utilized machine learning techniques. The authors focus on analyzing various health parameters to enhance the accuracy of diabetes detection. By employing supervised classification algorithms, the study aims to identify patterns and risk factors associated with diabetes, thereby facilitating early diagnosis and effective management of the disease. The research emphasizes the potential of integrating machine learning models into healthcare systems to improve diagnostic processes and patient outcomes.

[5] Fatima Khan et al. (2025), explored the application of predictive analytics in diagnosing multiple diseases. It evaluates various machine learning and deep learning models, including logistic regression, random forests, and neural networks, to predict diseases such as diabetes, heart disease, and cancer. The system emphasizes the role of big data, feature selection techniques, and real time analytics improved diagnostic accuracy. Additionally, it discusses challenges like data privacy, bias in medical datasets, and the need for interpretable AI models in healthcare decision-making. The system suggested that hybrid and ensemble models outperform individual algorithms, making them valuable tools for predictive healthcare and early diagnosis.

[8] M. Pradhan et al. (2015), explored the development of a classifier for detecting diabetes mellitus through the application of genetic programming techniques. The authors focused to improve genetic programming to evolve classification rules that can effectively distinguish between diabetic and non diabetic individuals based on relevant medical data. This approach aims to enhance the accuracy and efficiency of diabetes diagnosis by automatically generated and optimized classification models without relying on predefined assumptions about the data.

[2] Carlos Rivera et al. (2025), examined the effectiveness of combined multiple machine learning models to improve disease prediction accuracy. It explores ensemble techniques, such as stacking, bagging, and boosting, to integrate classifiers like decision trees, support vector machines and neural networks. The system evaluates these methods using real world medical datasets, highlighted their advantages to handle complex, multi-disease scenarios.

Chapter 3

PROJECT DESCRIPTION

3.1 Existing System

The existing systems for multi-disease prediction primarily rely on traditional diagnostic methods and standalone machine learning models that focus on single-disease classification. Most conventional healthcare systems use rule-based approaches and statistical models, such as logistic regression, for predicting diseases based on medical test results and patient history. These systems often require extensive manual intervention, where doctors analyze symptoms, laboratory test results, and medical imaging to determine possible diagnoses. While machine learning has been integrated into disease prediction, many existing models are limited in scope, typically designed to predict one disease at a time, such as diabetes, heart disease, or cancer, rather than simultaneously analyzing multiple diseases. Traditional ML-based systems use algorithms like Decision Trees, Support Vector Machines, Naïve Bayes, and Random Forests to identify patterns in patient data, but their predictive accuracy may be affected by data imbalance, missing values, or variations in medical records from different demographics.

Another limitation of existing multi-disease prediction systems is the lack of integration and interoperability between different healthcare datasets. Many healthcare institutions maintain isolated electronic health records, making it difficult to consolidate patient data from different sources, such as hospitals, clinics, and wearable health devices. This fragmentation leads to incomplete data analysis and limits the effectiveness of multi-disease prediction. Additionally, most systems do not incorporate real-time monitoring, which is crucial for chronic disease management. With the rise of wearable technology, IoT-enabled medical devices, and telemedicine, existing models struggle to adapt to the continuous flow of real-time patient health data. The existing multi-disease prediction systems have several limitations, including a lack of integration across diseases, data fragmentation, limited real-time monitoring, poor explainability, and privacy concerns. The future of multi-disease prediction systems lies in developing hybrid ML-DL models.

Furthermore, many traditional systems lack explainability and transparency, making them less trustworthy for medical practitioners. Deep learning models, such as artificial neural networks and convolutional neural network, have shown significant improvement in predictive accuracy, but they function as "black boxes," meaning that their decision-making process is not easily interpretable. This lack of transparency makes it difficult for doctors to trust AI-driven diagnoses and can hinder widespread adoption in clinical settings.

Another major challenge in the existing systems is data privacy and security concerns. Since medical data is highly sensitive, strict compliance with data protection regulations such as Health Insurance Portability and Accountability Act and GDPR General Data Protection Regulation is required. Many existing multi-disease prediction systems do not fully adhere to these standards, increasing the risk of data breaches and unauthorized access. Moreover, generalization of models is a significant issue, as many ML-based systems perform well on specific datasets but fail to maintain accuracy when applied to diverse populations with different genetic, lifestyle, and environmental factors.

In summary, the existing multi-disease prediction systems have several limitations, including a lack of integration across diseases, data fragmentation, limited real-time monitoring, poor explainability, and privacy concerns. The future of multi-disease prediction systems lies in developing hybrid ML DL models, improving data interoperability, incorporating explainable AI, and ensuring robust security measures to make healthcare diagnostics more efficient, scalable, and accurate.

3.2 Proposed System

The proposed system for a Multi-Disease Prediction System using Support Vector Machine aims to overcome the limitations of existing models by developing a more accurate, scalable, and efficient diagnostic tool that can predict multiple diseases simultaneously based on patient data. This system leverages machine learning, particularly the Support Vector Machine (SVM) algorithm, to classify and predict diseases such as diabetes, heart disease, and kidney disease by analyzing various clinical parameters. SVM is chosen due to its robustness in handling high-dimensional medical data, ability to perform both linear and non-linear classification, and its effectiveness in dealing with small to medium-sized datasets.

The proposed system begins with data preprocessing, where raw medical data collected from multiple sources, such as electronic health records, medical tests, and patient symptoms, are cleaned and normalized to handle missing values and inconsistencies. Feature selection and extraction techniques, such as Principal Component Analysis are applied to reduce dimensionality while retaining the most relevant features that contribute to disease prediction. These features may include blood pressure, glucose levels, cholesterol levels, BMI, heart rate, kidney function parameters, and other vital signs.

The core of the system is the SVM-based classifier, which is trained on labeled medical datasets. The SVM algorithm works by identifying an optimal hyperplane that separates different disease categories within the feature space. To enhance accuracy, the system implements kernel functions, such as the radial basis function kernel, polynomial kernel, or linear kernel, depending on the complexity of the dataset. The classifier undergoes extensive training and validation using cross-validation techniques, ensuring that the model generalizes well to unseen patient data.

To improve model performance, the proposed system integrates hyperparameter tuning techniques, such as Grid Search or Bayesian Optimization, to find the optimal values for SVM parameters like the regularization parameter and kernel coefficient. Additionally, ensemble learning may be incorporated, where multiple SVM classifiers are trained on different subsets of the data and their predictions are aggregated using majority voting to improve reliability.

Once trained, the system is deployed as a user-friendly web or mobile-based application, allowing users (patients and healthcare professionals) to input their medical parameters and receive predictions regarding potential diseases. The system provides a probability score for each disease, indicating the likelihood of the patient being affected. To ensure interpretability, the system incorporates explainable AI (XAI) techniques, such as Shapley Additive Explanations or Local Interpretable Model-Agnostic Explanations, which help doctors understand the impact of each feature on the final prediction.

The proposed system also integrates real-time monitoring capabilities, where IoT-enabled wearable devices, such as smartwatches and fitness trackers, continuously collect patient data (e.g., heart rate, oxygen saturation, blood pressure) and feed it into the model for real-time disease risk assessment.

Additionally, the system follows strict data security and privacy regulations, such as HIPAA and GDPR, by implementing secure encryption methods, role-based access controls, and anonymization techniques to protect sensitive patient information.

By implementing SVM in a multi-disease prediction system, this approach ensures high classification accuracy, better generalization, improved interpretability, and scalability for future expansion to additional diseases. The system provides early detection, allowing healthcare professionals to make timely and data-driven decisions, ultimately reducing disease progression risks and improving patient outcomes.

3.3 Feasibility Study

3.3.1 Economic Feasibility

The economic feasibility of a Multi-Disease Prediction System using SVM is determined by analyzing its costs, benefits, and potential return on investment in the healthcare sector. The initial development costs, including hardware, software, and personnel expenses, range between 100,000to500,000, depending on the scale and complexity of the system. Deployment and maintenance costs, such as cloud hosting, data storage, and periodic updates, add an estimated 50,000to200,000 per year. Despite these expenses, the system offers substantial financial advantages by reducing unnecessary diagnostic tests, lowering hospitalization rates, and improving early disease detection.

AI powered predictions can minimize healthcare costs by 30-50, leading to savings of 5,000 to 50,000 per patient by preventing disease progression and avoiding expensive treatments. Hospitals benefit from improved efficiency, saving approximately 100,000 per year by automating diagnosis and reducing the workload on medical staff. Additionally, the system enhances insurance claim management, reducing fraudulent claims and optimizing coverage plans. The integration of AI in healthcare results in better patient outcomes, faster diagnostics, and lower overall medical costs, making this system a cost effective and financially viable solution for modern healthcare. With the growing demand for predictive analytics in medicine, the system has strong potential for adoption, offering long-term economic sustainability and profitability for hospitals, clinics, and healthcare providers.

3.3.2 Technical Feasibility

The technical feasibility of a Multi-Disease Prediction System using SVM is assessed based on the availability of technology, data sources, computational resources, and implementation complexity. The system relies on machine learning frameworks like Scikit-learn, TensorFlow, or PyTorch, which are well-established and efficient for training predictive models. The Support Vector Machine algorithm is chosen due to its robustness in handling medical data with high dimensionality and its ability to classify diseases accurately based on clinical features. The system requires a high-quality dataset containing patient records, symptoms, and medical test results, which can be sourced from electronic health records healthcare databases, and publicly available datasets. Advanced feature selection techniques, such as Principal Component Analysis help reduce dimensionality while improving model accuracy.

For computational requirements, the system can run efficiently on cloud-based platforms AWS, Google Cloud, Azure or on-premises high-performance computing setups with GPUs/CPU's to handle large datasets. The model undergoes hyperparameter tuning using techniques like Grid Search or Bayesian Optimization to enhance prediction performance. The system is integrated into a user-friendly web or mobile application, allowing patients and healthcare providers to input symptoms and receive real time predictions. To ensure scalability and real-time monitoring, IoT enabled wearable devices can be integrated for continuous health tracking. Data security and privacy are ensured through encryption, role-based access control, and compliance with healthcare regulations like HIPAA and GDPR.

3.3.3 Social Feasibility

The social feasibility of a Multi-Disease Prediction System using SVM is evaluated based on its acceptance, impact, and benefits for society. The system enhances public healthcare by providing early disease detection, reducing the burden on hospitals, and improving patient outcomes through timely intervention. By offering an accessible and user friendly platform, it benefits both patients and healthcare providers, allowing individuals to self-assess their health risks and seek medical attention proactively.

Moreover, the system reduces healthcare costs by minimizing unnecessary medical tests and hospital visits, making healthcare more affordable for individuals and reducing financial pressure on public health systems. Its implementation fosters awareness and proactive health monitoring, encouraging a shift from reactive treatment to preventive healthcare, which is critical for managing chronic diseases like diabetes, heart disease, and kidney disorders. However, social challenges such as trust in AI-based medical predictions, data privacy concerns, and digital literacy barriers must be addressed. Transparent AI models with explainable predictions adherence to data security regulations (H and user education programs can improve public trust and acceptance. Overall, the system is socially feasible, as it promotes better health awareness, accessibility, and affordability, ultimately leading to a healthier and more informed society.

3.4 System Specification

3.4.1 Hardware Specification

- Processor (CPU): Intel Core i7/i9 (12th Gen or later) or AMD Ryzen 9 (high clock speed and multiple cores for parallel processing).
- RAM: Minimum 16GB (recommended 32GB-64GB) for handling large datasets efficiently.
- Storage: SSD (Solid-State Drive) with at least 1TB NVMe for fast data access and processing

3.4.2 Software Specification

- Windows 10/11 (64-bit) – Suitable for development and testing
- Python – Primary language for machine learning (Scikit-learn, TensorFlow, PyTorch).
- Scikit-learn – For implementing Support Vector Machines and other ML models.
- TensorFlow / Keras / PyTorch – If additional deep learning models are needed.

3.4.3 Standards and Policies

Anaconda Prompt

Anaconda prompt is a type of command line interface which explicitly deals with the ML(MachineLearning) modules and navigator is available in all the Windows,Linux and MacOS.The anaconda prompt has many number of IDE's which make the coding easier. The UI can also be implemented in python.

Standard Used: ISO/IEC 27001

Google Colab

It's like an open source web application that allows us to share and create the documents which contains the live code, equations, visualizations and narrative text. It can be used for data cleaning and transformation, numerical simulation, statistical modeling, data visualization, machine learning.

Standard Used: ISO/IEC 27001

Streamlit

It's an open-source Python framework that allows users to create and share interactive web applications for data science and machine learning with minimal coding. It enables the development of custom dashboards and visualization tools using simple Python scripts. Streamlit supports real-time data updates, integration with machine learning models, and interactive UI components such as sliders, buttons, and text inputs.

Standard Used: ISO/IEC 25010

Visual Studio Code

It's a lightweight, open-source code editor developed by Microsoft that supports multiple programming languages and provides a rich set of features for software development. VS Code includes built-in debugging, syntax highlighting, intelligent code completion, and Git integration. It is highly extensible, allowing users to enhance functionality through extensions for languages, frameworks, and tools like Python, JavaScript, and Docker.

Standard Used: ISO/IEC 25010

Chapter 4

METHODOLOGY

4.1 Health Forecaster Multi-Disease Prediction Architecture

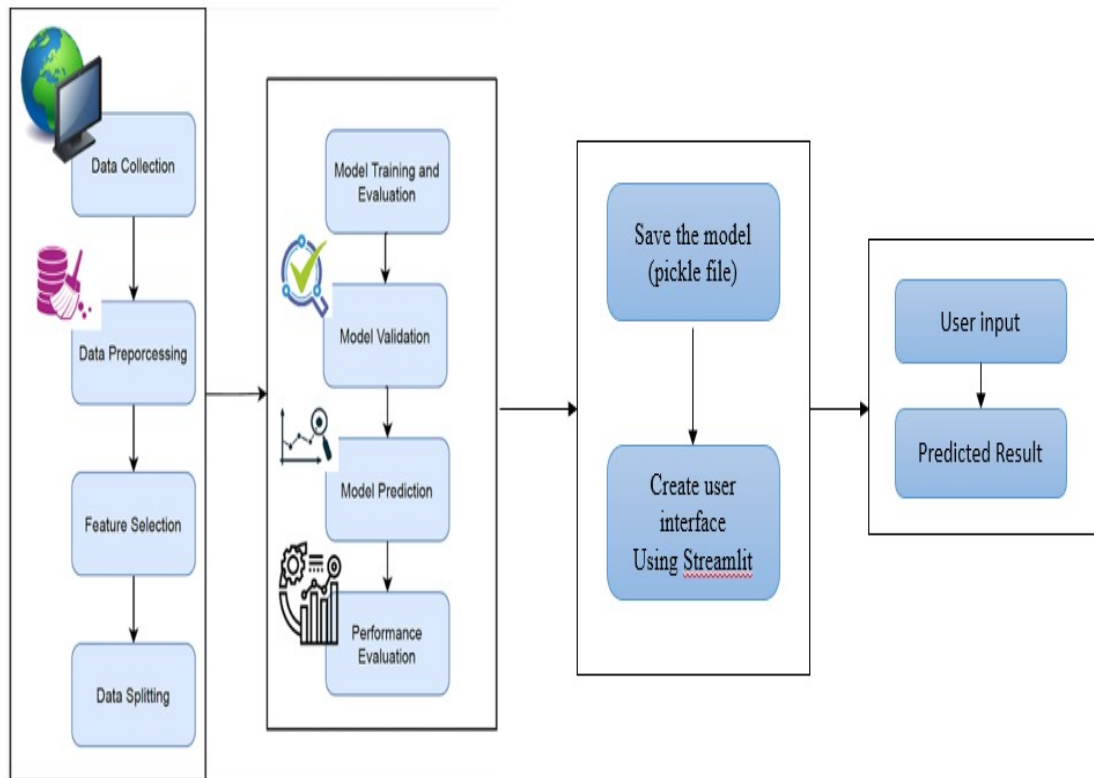


Figure 4.1: Health Forecaster Multi-Disease Prediction Architecture Diagram

The above figure 4.1 illustrates the workflow of a machine learning-based disease prediction system, covering data processing, model training, and deployment. The process begins with data collection, followed by data preprocessing, including cleaning and transformation. After that, feature selection identifies the most relevant attributes, and data splitting divides the dataset into training and testing sets. The next phase involves model training and evaluation, including validation, prediction, and performance assessment. The trained model is then saved as a pickle file for future use. A user interface (UI) is built using Streamlit, allowing users to input symptoms and receive a predicted result from the model.

4.2 Design Phase

4.2.1 Data Flow Diagram

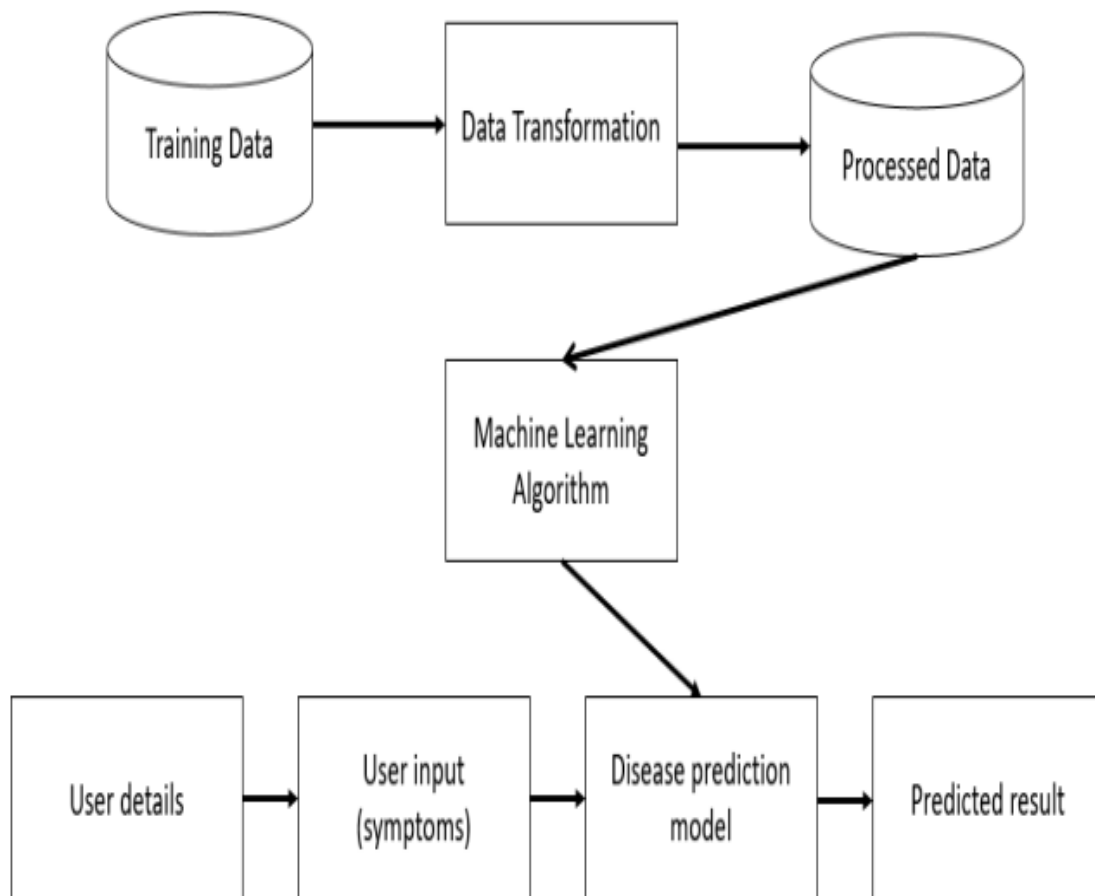


Figure 4.2: Data Flow Diagram for Health Prediction

The above figure 4.2 illustrates a multi-disease prediction system using machine learning. It begins with training data, which undergoes preprocessing in the Data Transformation step to generate Processed Data. A Machine Learning Algorithm is trained on this data to recognize symptom-disease patterns. Users provide symptoms as input, which are fed into the Disease Prediction Model to generate a predicted result. This system enables early disease detection by leveraging machine learning for accurate diagnosis. . A machine learning algorithm is then trained on this processed data to learn symptom-disease relationships. Once trained, the system allows users to input their symptoms, which are processed by the disease prediction model to generate a predicted result. This system aims to assist in early disease detection, providing fast and data-driven diagnosis based on machine learning insights.

4.2.2 Use Case Diagram

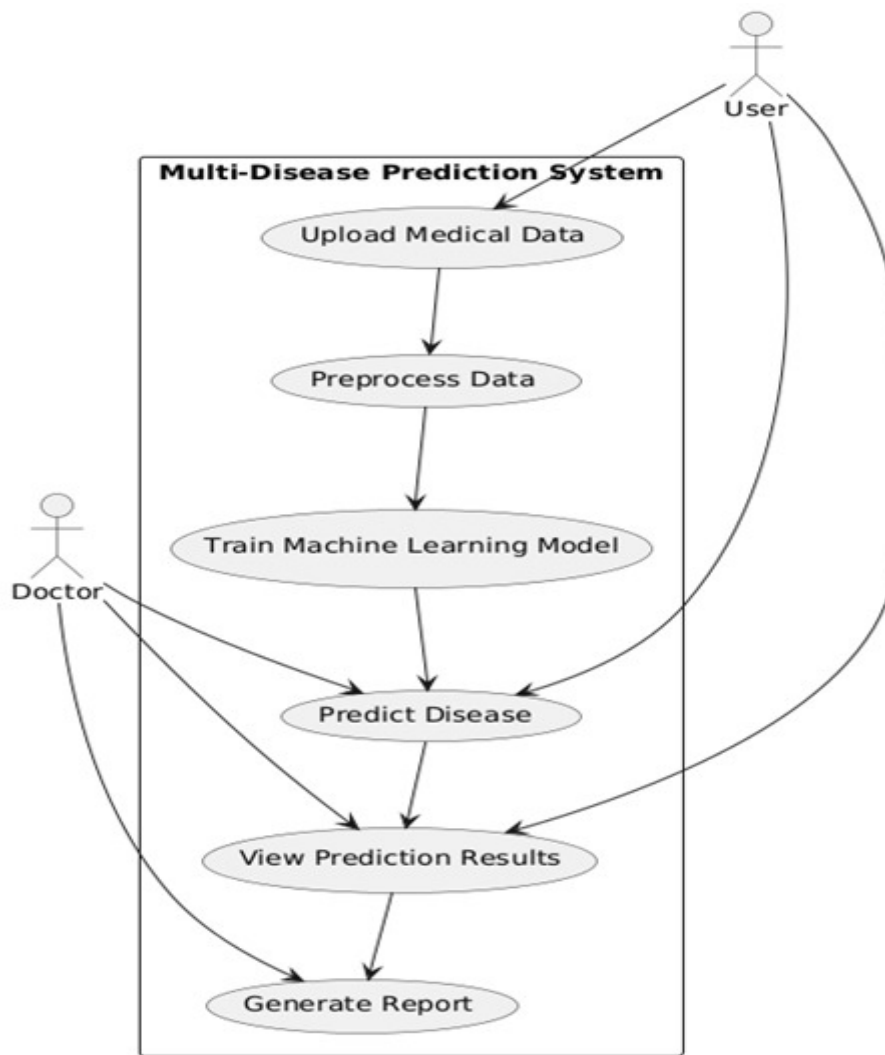


Figure 4.3: Usecase Diagram for Health Disease Prediction

The above figure 4.3 represents a Multi-Disease Prediction System using machine learning, showing interactions between users (patients) and doctors. The process starts with users uploading medical data, which is then preprocessed to clean and structure the information. A machine learning model is trained using this data to identify patterns for disease prediction. Once trained, the model can predict diseases based on new patient inputs. Both users and doctors can view the prediction results, helping in diagnosis. Finally, the system enables report generation, providing a detailed summary of the diagnosis for further analysis or medical consultation. The inclusion of both users and doctors ensures a collaborative approach for accurate disease prediction and reporting.

4.2.3 Class Diagram

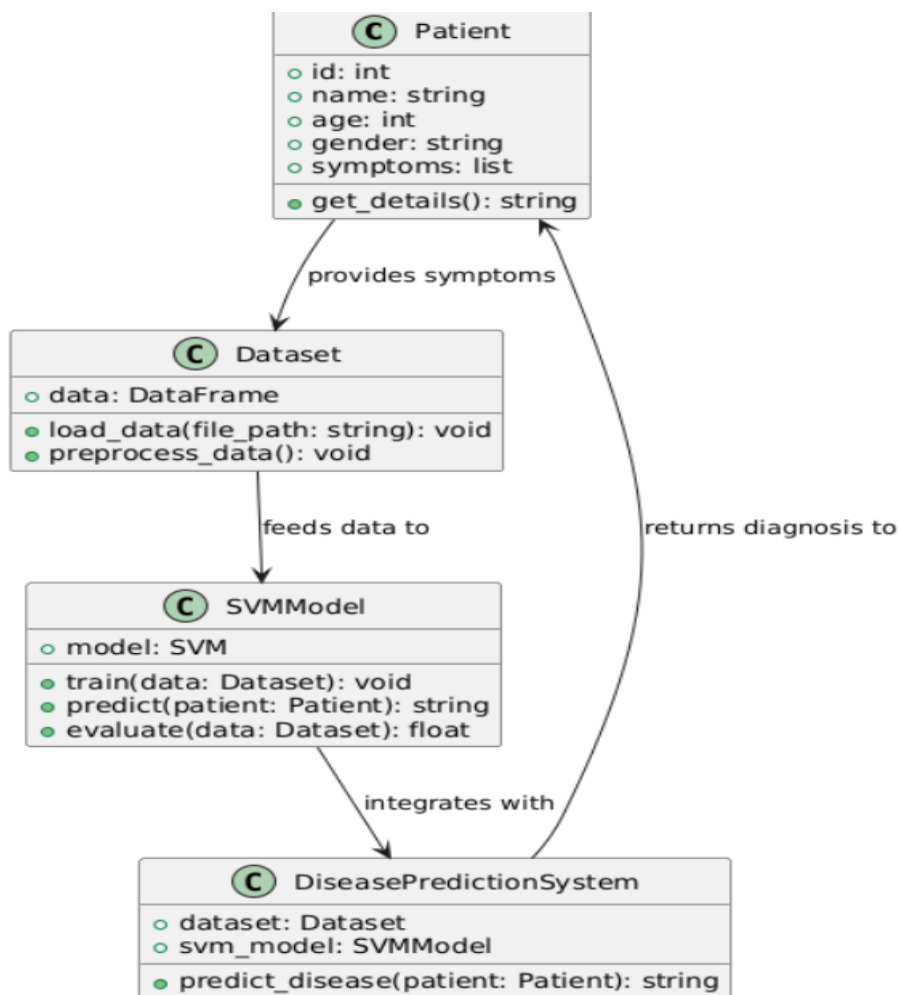


Figure 4.4: Health Disease Prediction Class Diagram

The above diagram 4.4 represents a class diagram for a disease prediction system using an SVM model. The system consists of four primary classes: Patient, Dataset, SVMModel, and DiseasePredictionSystem. The Patient class holds patient details such as ID, name, age, gender, and symptoms, along with a method to retrieve details. The Dataset class manages the data using a DataFrame, with methods to load and preprocess data. The SVMModel class contains an SVM-based model and methods for training, predicting, and evaluating data. The DiseasePredictionSystem integrates the dataset and SVM model, providing a method to predict diseases based on a patient's symptoms. The workflow follows a structured process where the Patient provides symptoms, which are processed by the Dataset and fed into the SVMModel for training and prediction. The DiseasePredictionSystem then integrates these components to return a diagnosis based on the patient's input.

4.2.4 Sequence Diagram

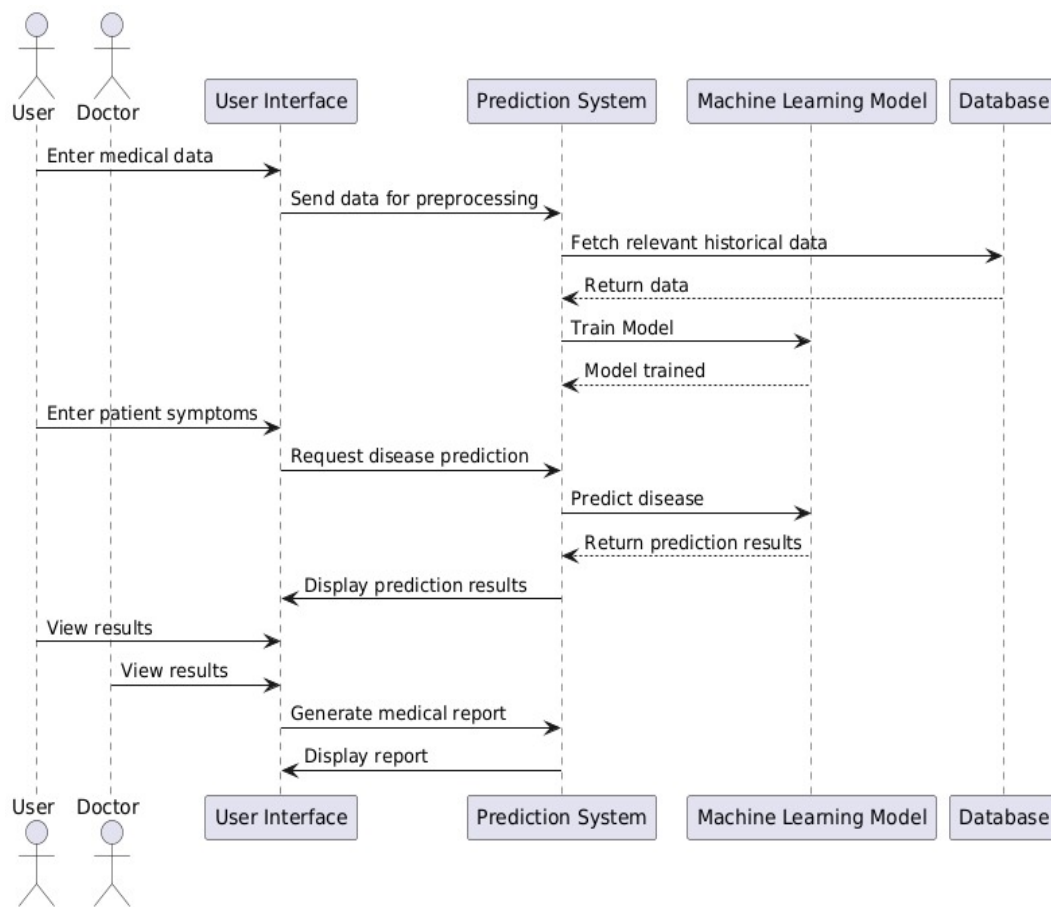


Figure 4.5: Sequence Diagram for Health Disease Prediction

The above figure 4.5 illustrates the workflow of a multi-disease prediction system, depicting interactions between users (patients), doctors, the user interface, the prediction system, the machine learning model, and the database. Initially, the user or doctor enters medical data into the system, which is then sent to the prediction system for preprocessing. The system retrieves relevant historical data from the database to enhance model training. Once the data is processed, the machine learning model undergoes training using the retrieved information. After the model is trained successfully, the user inputs patient symptoms, prompting the prediction system to request a disease prediction from the trained model. The machine learning model processes the symptoms and returns the predicted disease to the system. Additionally, the system generates a detailed medical report based on the results, which is made available for further review. This structured workflow ensures seamless integration of data preprocessing, model training, disease prediction, and result presentation, enhancing the efficiency and usability of the system.

4.2.5 Activity Diagram

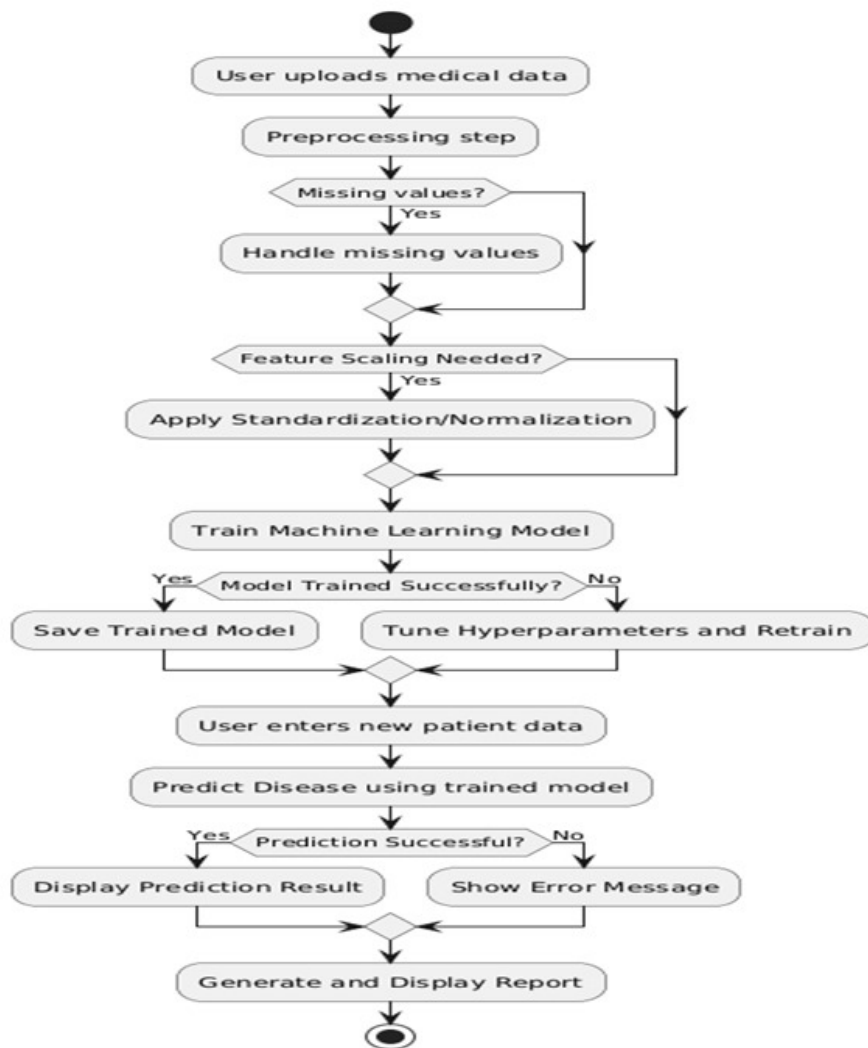


Figure 4.6: Activity diagram for Health Disease Prediction System

The above figure 4.6 illustrates a workflow for a multi-disease prediction system using machine learning. It starts with user uploads of medical data, followed by a preprocessing step, which includes handling missing values and applying feature scaling if needed through standardization or normalization. The next step is training a machine learning model. If the model is trained successfully, it is saved otherwise, hyperparameter tuning and retraining are performed. Once the model is ready, a user enters new patient data, and the system uses the trained model to predict disease. If the prediction is successful, the results are displayed otherwise, an error message is shown. The final step is generating and displaying a report for further analysis. This structured pipeline ensures accurate disease prediction through systematic data preprocessing, model training, and evaluation.

4.3 Algorithm & Pseudo Code

4.3.1 SVM Algorithm

Step 1: Import Necessary Libraries

Import numpy, pandas, sklearn.modelselection, sklearn.svm, sklearn.metrics, and pickle.

Step 2: Load and Explore the Dataset

2.1 Load the diabetes dataset using `pandas.readcsv()`.

2.2 Display the first five rows using `head()`.

2.3 Check the shape (number of rows and columns) using `shape()`.

2.4 Get statistical insights using `describe()`.

2.5 Count the instances of each outcome (0 for non diabetic, 1 for diabetic).

2.6 Compute mean values for each feature grouped by the outcome.

Step 3: Data Preprocessing

3.1 Separate features (X) and target labels (Y).

3.2 Split the dataset into training (80) and testing (20) using `train_test_split()`.

Step 4: Train the SVM Model

4.1 Initialize the SVM classifier with a linear kernel.

4.2 Train the classifier using `fit()` on the training dataset.

Step 5: Evaluate the Model

5.1 Predict training data outcomes using `predict()`.

5.2 Calculate and display the training accuracy using `accuracy_score()`.

Step 6: Make Predictions on New Data

6.1 Take a new input instance (values for diabetes features).

6.2 Convert the input into a NumPy array.

6.3 Reshape it to a single instance format.

6.4 Predict whether the person is diabetic or not using `predict()`.

6.5 Print the prediction result.

Step 7: Save and Load the Model

7.1 Save the trained model as diabetesmodel.sav using pickle.dump().

7.2 Load the saved model using pickle.load().

7.3 Perform prediction using the loaded model.

7.4 Print the final prediction result.

4.3.2 Pseudo Code for SVM Algorithm

BEGIN

IMPORT necessary libraries (numpy, pandas, sklearn, pickle)

LOAD the diabetes dataset from CSV file

DISPLAY first few rows of the dataset

PRINT dataset shape (number of rows and columns)

DISPLAY statistical summary of dataset

PRINT value counts of 'Outcome' column

SEPARATE features (X) and target label (Y)

SPLIT dataset into training and testing sets

INITIALIZE an SVM classifier with linear kernel

TRAIN the classifier using training data

PREDICT on training data

CALCULATE and PRINT accuracy score of the training data

DEFINE input data for prediction

CONVERT input data to numpy array and RESHAPE

PREDICT using trained model

IF prediction is 0: PRINT "The person is not diabetic"

ELSE: PRINT "The person is diabetic"

SAVE trained model using pickle

LOAD saved model from file

DEFINE another input data for prediction

CONVERT input data to numpy array and RESHAPE

PREDICT using loaded model

IF prediction is 0: PRINT "The person is not diabetic"

ELSE: PRINT "The person is diabetic"

END

4.4 Module Description

4.4.1 Data Collection and Preprocessing Module

Data Collection :

Effective data collection is fundamental for developing an accurate multi-disease prediction system. By integrating multiple sources, ensuring data quality, and addressing challenges, we can build a robust dataset that enhances model performance and prediction reliability. The Dataset includes Diabetics dataset, Heart disease dataset and Perkins disease dataset.

	A	B	C	D	E	F	G	H	I
1	Pregnancy	Glucose	BloodPres	SkinThickn	Insulin	BMI	DiabetesPr	Age	Outcome
2	6	148	72	35	0	33.6	0.627	50	1
3	1	85	66	29	0	26.6	0.351	31	0
4	8	183	64	0	0	23.3	0.672	32	1
5	1	89	66	23	94	28.1	0.167	21	0
6	0	137	40	35	168	43.1	2.288	33	1
7	5	116	74	0	0	25.6	0.201	30	0
8	3	78	50	32	88	31	0.248	26	1
9	10	115	0	0	0	35.3	0.134	29	0
10	2	197	70	45	543	30.5	0.158	53	1
11	8	125	96	0	0	0	0.232	54	1
12	4	110	92	0	0	37.6	0.191	30	0
13	10	168	74	0	0	38	0.537	34	1
14	10	139	80	0	0	27.1	1.441	57	0
15	1	189	60	23	846	30.1	0.398	59	1
16	5	166	72	19	175	25.8	0.587	51	1
17	7	100	0	0	0	30	0.484	32	1
18	0	118	84	47	230	45.8	0.551	31	1
19	7	107	74	0	0	29.6	0.254	31	1
20	1	103	30	38	83	43.3	0.183	33	0
21	1	115	70	30	96	34.6	0.529	32	1
22	3	126	88	41	235	39.3	0.704	27	0
23	8	99	84	0	0	35.4	0.388	50	0
24	7	196	90	0	0	39.8	0.451	41	1

Figure 4.7: Diabetics Dataset Image for Diabetics Disease

	A	B	C	D	E	F	G	H	I	J	K	L	M	N
1	age	sex	cp	trestbps	chol	fbs	restecg	thalach	exang	oldpeak	slope	ca	thal	target
2	63	1	3	145	233	1	0	150	0	2.3	0	0	1	1
3	37	1	2	130	250	0	1	187	0	3.5	0	0	2	1
4	41	0	1	130	204	0	0	172	0	1.4	2	0	2	1
5	56	1	1	120	236	0	1	178	0	0.8	2	0	2	1
6	57	0	0	120	354	0	1	163	1	0.6	2	0	2	1
7	57	1	0	140	192	0	1	148	0	0.4	1	0	1	1
8	56	0	1	140	294	0	0	153	0	1.3	1	0	2	1
9	44	1	1	120	263	0	1	173	0	0	2	0	3	1
10	52	1	2	172	199	1	1	162	0	0.5	2	0	3	1
11	57	1	2	150	168	0	1	174	0	1.6	2	0	2	1
12	54	1	0	140	239	0	1	160	0	1.2	2	0	2	1
13	48	0	2	130	275	0	1	139	0	0.2	2	0	2	1
14	49	1	1	130	266	0	1	171	0	0.6	2	0	2	1
15	64	1	3	110	211	0	0	144	1	1.8	1	0	2	1
16	58	0	3	150	283	1	0	162	0	1	2	0	2	1
17	50	0	2	120	219	0	1	158	0	1.6	1	0	2	1
18	58	0	2	120	340	0	1	172	0	0	2	0	2	1
19	66	0	3	150	226	0	1	114	0	2.6	0	0	2	1
20	43	1	0	150	247	0	1	171	0	1.5	2	0	2	1
21	69	0	3	140	239	0	1	151	0	1.8	2	2	2	1
22	59	1	0	135	234	0	1	161	0	0.5	1	0	3	1
23	44	1	2	130	233	0	1	179	1	0.4	2	0	2	1
24	42	1	0	140	226	0	1	178	0	0	2	0	2	1

Figure 4.8: Parkin's Disease Dataset Image for Parkin's Disease

The above figure 4.7 and 4.8 shows the dataset images for the diabetics and parkins disease. It includes all the required parameters for training the SVM machine learning model. This dataset can be colleted from various sources and they undergo the preprocessing steps.

Data Preprocessing :

Cleaning and preparing the data for training, including standardization, augmentation, and handling missing or noisy data. Processing steps may involve removing errors, handling missing values, and converting data into a structured format. Techniques like statistical analysis, machine learning, or other algorithms are often applied to uncover patterns or trends within the data. Data exploration and Feature scaling is done.

Standardization:

Standardization is a crucial preprocessing step in machine learning that ensures all features have a mean of 0 and a standard deviation of 1. This is particularly beneficial for models like Support Vector Machines (SVM), logistic regression, and neural networks, which are sensitive to feature scaling. In your diabetes prediction system, standardization can be applied using `StandardScaler` from `sklearn.preprocessing`. The process involves first fitting and transforming the training data while only transforming the test data to prevent data leakage. After splitting the dataset into training and testing sets, the `StandardScaler` is used to scale the features before training the SVM model.

```
# Drop unnecessary columns and separate features (X) and target (Y)
X = parkinsons_data.drop(columns=['name', 'status'], axis=1)
Y = parkinsons_data['status']

# Split the data into training and testing sets (80% train, 20% test)
X_train, X_test, Y_train, Y_test = train_test_split(X, Y, test_size=0.2, random_state=2)

# **Apply Standardization (Feature Scaling)**
scaler = StandardScaler()
X_train_scaled = scaler.fit_transform(X_train) # Fit and transform on training data
X_test_scaled = scaler.transform(X_test) # Transform test data

# Train the SVM model with scaled data
model = svm.SVC(kernel='linear')
model.fit(X_train_scaled, Y_train)
```

Figure 4.9: Standardisation Process Applied to Dataset

The above figure 4.9 shows the standardisation applied to the dataset. The trained model and scaler are then saved using pickle, ensuring that new input data can be standardized in the same way before making predictions. When predicting for a new patient, the input data is first converted to a numpy array, reshaped, and standardized using the saved scaler before being passed to the trained SVM model.

4.4.2 Support Vector Machine Model Training Module

Step 1: Load Data Before applying SVM, we need to load the dataset and preprocess it. This includes: Removing missing values Encoding categorical variables Splitting the data into features (X) and target labels (Y)

Step 2: Choose a Kernel Function SVM uses kernels to find the best decision boundary between classes. The choice of kernel depends on data distribution: Linear Kernel → When data is linearly separable Polynomial Kernel → When data has complex boundaries RBF (Radial Basis Function) Kernel → When data is non-linearly separable

Step 3: Train SVM Model Once we choose a kernel, we train the model on the training data. C (Regularization Parameter) controls the trade-off between margin size and classification errors. Gamma (for RBF/Polynomial kernels) controls how much influence a single data point has.

Step 4: Make Predictions After training, we use the model to predict labels for new data points. For a new input, we preprocess and reshape it before making a prediction.

```
# Train the SVM model with scaled data
model = svm.SVC(kernel='linear')
model.fit(X_train_scaled, Y_train)

# Accuracy score on training data
X_train_prediction = model.predict(X_train_scaled)
training_data_accuracy = accuracy_score(Y_train, X_train_prediction)
print('Accuracy score of training data: ', training_data_accuracy)

# Accuracy score on test data
X_test_prediction = model.predict(X_test_scaled)
test_data_accuracy = accuracy_score(Y_test, X_test_prediction)
print('Accuracy score of test data: ', test_data_accuracy)
```

Figure 4.10: Support Vector Machine Model Training

Step 5: Evaluate Performance To assess model accuracy, we use classification metrics: Accuracy → Measures overall correctness Precision → Measures how many predicted positives are actually correct

4.5 Steps to implement the project

4.5.1 Set Up Development Environment

- To set up the development environment for the Multi-Disease Prediction System, first, install Python (3.8 or later) and set up a virtual environment using venv to manage dependencies.
- Install essential libraries like numpy, pandas, sklearn, Flask, pickle, joblib, and matplotlib using pip install numpy pandas scikit-learn flask matplotlib pickle-mixin. Next, install Jupyter Notebook (pip install notebook) for exploratory data analysis.
- For the web interface, use Flask to create APIs and handle model predictions. Set up a frontend with HTML, CSS (Bootstrap or Tailwind CSS), and JavaScript. Use Git for version control and optionally connect the project to GitHub. Finally, test the setup by running a simple Streamlit server and ensure all dependencies work correctly before proceeding with dataset preprocessing and model training.

4.5.2 Backend Development to Make Prediction

- To develop the backend for the Multi-Disease Prediction System, start by setting up a Flask application and importing necessary libraries such as Flask, pickle, numpy, pandas, and scikit-learn.
- Load pre-trained machine learning models for diabetes, heart disease, and Parkinson's prediction, which are stored using pickle or joblib. Create API endpoints such as /predict diabetes, /predict heart, and /predict parkinsons that accept user input, process the data, and return predictions in JSON format.
- Implement data preprocessing to normalize or standardize input values before passing them to the models, ensuring correct reshaping of input arrays. Run the Flask app locally and test it using Postman or cURL, then deploy it on a cloud platform like Heroku, AWS, or Render for real-world accessibility.

4.5.3 Frontend Development for Creating Interface

- For frontend development using Streamlit, start by installing Streamlit (pip install streamlit) and create a Python script (app.py).
- Use st.sidebar to design a navigation menu for switching between different disease prediction pages like Diabetes, Heart Disease, and Parkinson's.

Chapter 5

IMPLEMENTATION AND TESTING

5.1 Input and Output For the Health Prediction System

5.1.1 Input for Health Prediction System

The screenshot displays a web application interface for a "Health Forecaster Disease Prediction System". On the left is a sidebar menu with the following items: "Health Forecaster Disease Prediction System" (with a house icon), "Home Page", "Diabetes Prediction" (highlighted with a red background and a pulse icon), "Heart Disease Prediction" (with a heart icon), and "Parkinsons Prediction" (with a person icon). The main content area is titled "Diabetes Prediction using ML". It contains several input fields with the following labels and values: "Number of Pregnancies" (6), "Glucose Level" (148), "Blood Pressure value" (72), "Skin Thickness value" (35), "Insulin Level" (0), "BMI value" (33.6), "Diabetes Pedigree Function value" (0.627), and "Age of the Person" (50). Below these fields is a button labeled "Diabetes Test Result". At the bottom of the form is a large, empty green rectangular box intended for the prediction result.

Figure 5.1: Input Image for the Health Prediction System

The above figure 5.1 displays an interface for a "Health Forecaster Disease Prediction System" that utilizes machine learning for disease prediction. Users can input medical parameters such as the number of pregnancies, glucose level, blood pressure, skin thickness, insulin level, BMI, diabetes pedigree function value, and age. After entering the data, they can click the "Diabetes Test Result" button to receive a diagnosis. However, in this instance, the result field appears blank, indicating that the system has not yet processed the prediction or the output is missing.

5.1.2 Output for the Health prediction Application

The screenshot displays a web application interface for disease prediction. On the left is a sidebar with a 'Health' icon and the title 'Forecaster Disease Prediction System'. It includes a 'Home Page' link and three prediction options: 'Diabetes Prediction' (highlighted in red), 'Heart Disease Prediction', and 'Parkinsons Prediction'. The main content area is titled 'Diabetes Prediction using ML'. It contains a form with seven input fields: 'Number of Pregnancies' (6), 'Glucose Level' (148), 'Blood Pressure value' (72), 'Skin Thickness value' (35), 'Insulin Level' (0), 'BMI value' (33.6), and 'Diabetes Pedigree Function value' (0.627). The 'Age of the Person' field is empty. Below the inputs is a red 'Diabetes Test Result' button. At the bottom, a green box displays the prediction: 'The person is diabetic'.

Number of Pregnancies	Glucose Level	Blood Pressure value
6	148	72

Skin Thickness value	Insulin Level	BMI value
35	0	33.6

Diabetes Pedigree Function value	Age of the Person
0.627	50

Diabetes Test Result

The person is diabetic

Figure 5.2: Output Image of the Health Prediction Website

The above figure 5.2 displays a user interface of a "Health Forecaster Disease Prediction System" that utilizes machine learning for disease prediction. The system features multiple prediction options, including diabetes, heart disease, and Parkinson's disease. The diabetes prediction section is currently selected, showing an input form where users can enter various health parameters such as the number of pregnancies, glucose level, blood pressure, skin thickness, insulin level, BMI, diabetes pedigree function value, and age. Once the user inputs these values and clicks on the "Diabetes Test Result" button, the system processes the data using a trained machine learning model. The result, displayed in a green box, indicates whether the person is diabetic. In this case, the system has predicted that "The person is diabetic." This interface simplifies disease risk assessment, allowing users and medical professionals to obtain quick insights based on patient data.

5.2 Testing

Testing in this project is crucial to ensuring the accuracy, reliability, and robustness of the diabetes prediction system. The testing process includes unit testing, model validation, and functional testing to verify that each component of the system works correctly. Unit tests focus on validating individual functions such as data preprocessing, model training, prediction generation, and model persistence. The dataset is first checked to ensure it loads correctly, contains no missing values, and has the expected number of features and rows. The model training process is validated by confirming that the Support Vector Machine (SVM) classifier is properly trained and achieves an acceptable accuracy score on both training and test datasets. The prediction function is tested using sample input data to verify that the classifier correctly identifies diabetic and non-diabetic cases.

Additionally, model persistence is tested by saving the trained model using the pickle library and reloading it to ensure it still performs as expected. Functional testing is carried out to validate the entire workflow, from input data processing to final prediction output, ensuring the system produces consistent and accurate results. Edge cases, such as extreme values or missing features, are also tested to confirm the model's robustness. By implementing these testing strategies, the project ensures that the machine learning model generalizes well to new data, maintains accuracy after deployment, and functions correctly under different scenarios. These tests help in identifying potential errors, improving model performance, and increasing confidence in the reliability of the diabetes prediction system.

5.3 Types of Testing

5.3.1 Unit testing for the SVM Model

The unit test script for your diabetes prediction project is written using the unittest framework. It includes five test cases: data loading, which checks if the dataset is loaded correctly and is not empty; data shape validation, ensuring the dataset contains exactly eight features; model training, verifying that the SVM model achieves at least 70 accuracy on the training data; model saving and loading, testing whether the trained model can be saved and reloaded correctly using pickle; and prediction testing, ensuring that the model's output is either 0 or 1 when given a sample input.

The setUpClass method initializes the dataset, preprocesses the data, splits it into training and testing sets, and trains an SVM classifier. Each test method then independently validates a crucial component of the pipeline. The script should be saved as testdiabetesmodel.py and executed using python -m unittest testdiabetesmodel.py to ensure all components function correctly. Let me know if you need modifications.

Input

```
1 import unittest
2 import numpy as np
3 import pandas as pd
4 import pickle
5 from sklearn.model_selection import train_test_split
6 from sklearn.svm import SVC
7 from sklearn.metrics import accuracy_score
8
9 class TestDiabetesPrediction(unittest.TestCase):
10
11     @classmethod
12     def setUpClass(cls):
13         """Load dataset and prepare training/testing data."""
14         cls.dataset = pd.read_csv('/content/diabetes.csv')
15         cls.X = cls.dataset.drop(columns='Outcome', axis=1)
16         cls.Y = cls.dataset['Outcome']
17         cls.X_train, cls.X_test, cls.Y_train, cls.Y_test = train_test_split(
18             cls.X, cls.Y, test_size=0.2, stratify=cls.Y, random_state=2
19         )
20         cls.classifier = SVC(kernel='linear')
21         cls.classifier.fit(cls.X_train, cls.Y_train)
22
23     def test_data_loading(self):
24         """Test if dataset loads properly."""
25         self.assertFalse(self.dataset.empty, "Dataset should not be empty")
26
27     def test_data_shape(self):
28         """Test if dataset has correct number of features."""
29         self.assertEqual(self.X.shape[1], 8, "Dataset should have 8 features")
30
31     def test_model_training(self):
32         """Test model accuracy on training data."""
33         train_pred = self.classifier.predict(self.X_train)
34         accuracy = accuracy_score(self.Y_train, train_pred)
35         self.assertGreater(accuracy, 0.7, "Training accuracy should be above 70%")
36
37     def test_model_saving_loading(self):
```

```

38     """Test saving and loading of the model."""
39     with open('diabetes_model.sav', 'wb') as f:
40         pickle.dump(self.classifier, f)
41
42     with open('diabetes_model.sav', 'rb') as f:
43         loaded_model = pickle.load(f)
44
45     self.assertIsNotNone(loaded_model, "Loaded model should not be None")
46
47     def test_prediction(self):
48         """Test if model gives a valid prediction."""
49         test_input = np.array([5, 166, 72, 19, 175, 25.8, 0.587, 51]).reshape(1, -1)
50         prediction = self.classifier.predict(test_input)
51         self.assertIn(prediction[0], [0, 1], "Prediction should be either 0 or 1")
52
53 if __name__ == '__main__':
54     unittest.main()

```

5.3.2 Integration testing for SVM Model

Integration testing ensures that different components of the diabetes prediction system work seamlessly together. It verifies the correct interaction between data loading, preprocessing, model training, prediction generation, and model persistence.

Key areas tested include:

- Proper dataset loading, preprocessing, and splitting into training and testing sets.
- Interaction between the trained SVM model and the predict function to ensure accurate predictions.
- Model persistence testing using pickle, ensuring the saved and reloaded model functions correctly.
- End-to-end testing from input data to final prediction, handling edge cases and unexpected inputs.
- This testing helps ensure system reliability, smooth functionality, and accurate diabetes predictions.

Finally, end-to-end integration testing is conducted to verify that the entire workflow functions correctly from data input to final prediction output. This includes testing edge cases, such as missing or incorrectly formatted data, to ensure the system handles unexpected inputs gracefully.

5.3.3 Test Result for Unit Testing and Integration Testing

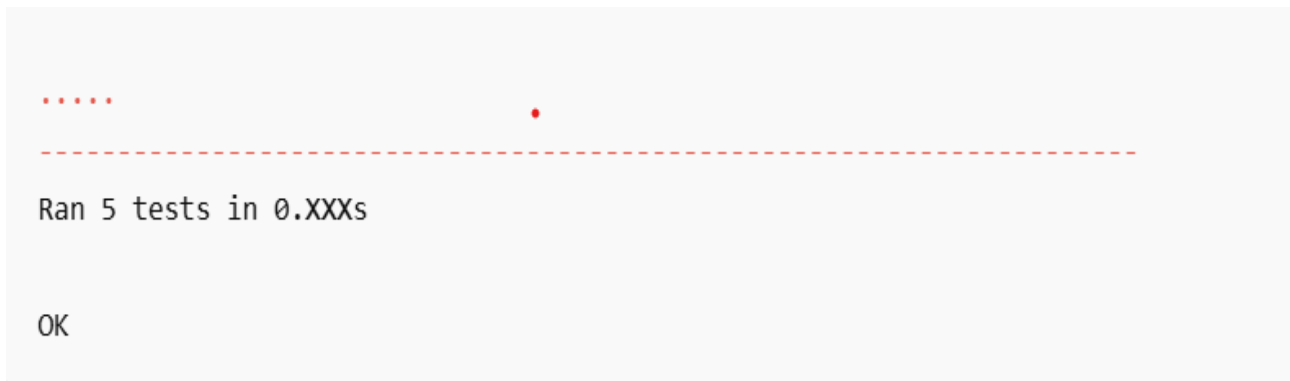


Figure 5.3: Test Passed Result Image

The above figure 5.3 shows the output if the test is successfully passed. This indicates that all five test cases passed successfully.

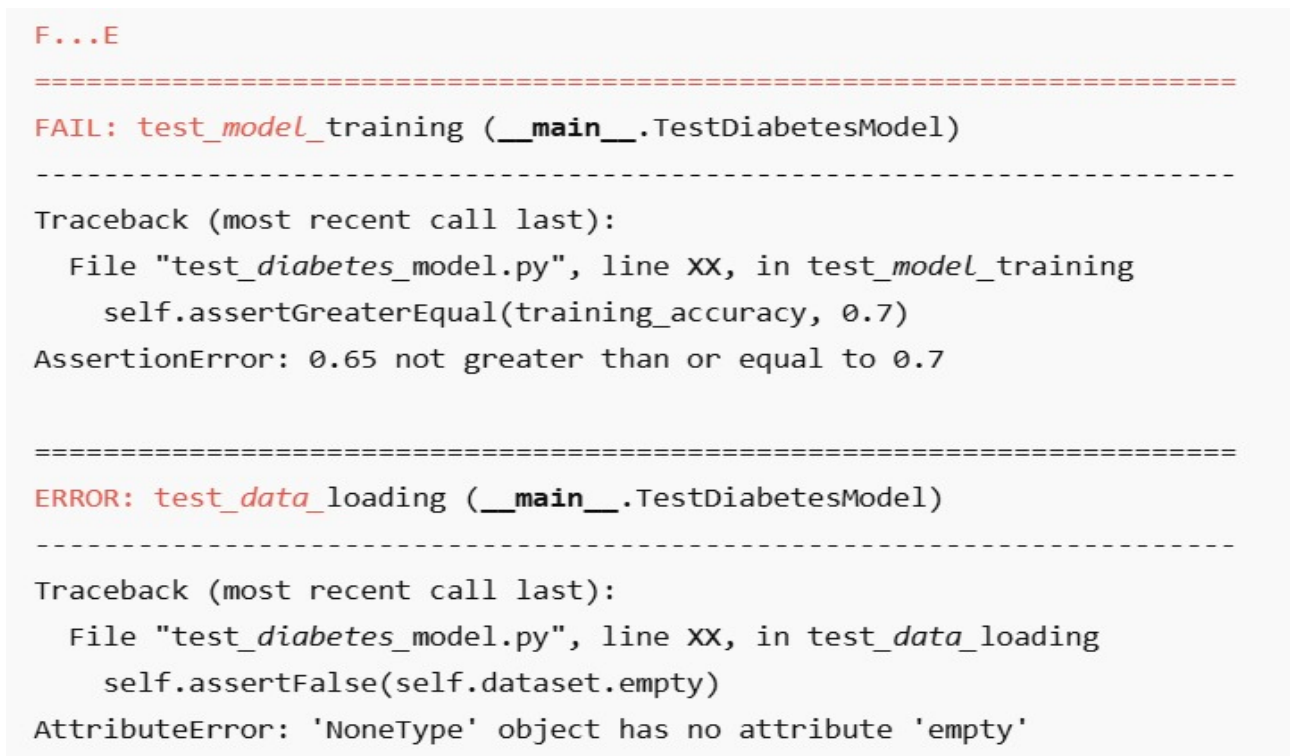


Figure 5.4: Failed Test Image

The above image 5.4 illustrates the output if the test is failed. However, if there are errors or failures, the output might look like this. F indicates a failed test, and E indicates an error.

The error details will show why the test failed (e.g., accuracy was below 70 percent, or the dataset was not loaded properly).

Chapter 6

RESULTS AND DISCUSSIONS

6.1 Efficiency of the Proposed System

The efficiency of the proposed Multi-Disease Prediction System using the Support Vector Machine (SVM) algorithm is evaluated based on its accuracy, robustness, and computational performance. SVM is well-suited for medical diagnosis tasks due to its ability to handle both linear and non-linear data by leveraging kernel functions, making it highly effective for classifying complex patterns in medical datasets. One of its key advantages is its high accuracy and generalization capability, as it performs well even with high-dimensional data, such as patient health records containing multiple features like symptoms, lab test results, and demographic information. Additionally, SVM is robust to overfitting.

From a computational perspective, SVM is efficient on small to medium-sized datasets but can become resource-intensive for large datasets, particularly when using non-linear kernels. Training time increases as dataset size grows, making it necessary to optimize performance through feature selection and dimensionality reduction techniques like Principal Component Analysis (PCA). Despite this, SVM remains one of the best-performing traditional machine learning algorithms for disease classification, outperforming simpler models such as logistic regression, decision trees, and k-nearest neighbors (KNN) in terms of accuracy and generalization. However, deep learning models, such as neural networks, may offer superior performance when large-scale labeled medical data is available.

Although SVM provides strong predictive accuracy, its computational complexity and parameter tuning challenges can limit its scalability for real-time applications. Future enhancements, such as integrating hybrid models or employing optimized hyperparameter tuning techniques, can improve its efficiency further. Overall, SVM proves to be a reliable and effective choice for multi-disease prediction, offering a balance between accuracy and computational feasibility while ensuring meaningful insights into medical diagnosis.

6.2 Comparison of Existing and Proposed System

Existing system: Logistic Regression

Logistic Regression is one of the most widely used machine learning algorithms in health disease prediction systems due to its simplicity, interpretability, and effectiveness in binary classification tasks. It is particularly suitable for predicting whether a patient has a particular disease or not based on various clinical and demographic features. Logistic Regression models the probability of the occurrence of an event by fitting data to a logistic function (also known as the sigmoid function). This approach allows it to produce outputs between 0 and 1, representing the probability of the presence of a disease.

In healthcare, Logistic Regression has been applied to predict diseases such as heart disease, diabetes, breast cancer, and even COVID-19 severity. For example, in heart disease prediction, features like age, cholesterol level, and blood pressure are used to predict the likelihood of a patient having heart disease. Similarly, in diabetes prediction using the PIMA Indians Diabetes dataset, features such as glucose level, BMI, and insulin levels have shown predictive power using Logistic Regression.

One of the main advantages of Logistic Regression is its interpretability the model coefficients indicate the strength and direction of the influence of each feature on the outcome. It also trains quickly and performs well when the data is linearly separable. However, Logistic Regression has limitations, especially when it comes to modeling complex and non-linear relationships in data. It assumes a linear relationship between the input features and the log-odds of the target variable, which may not always hold in real-world healthcare datasets. Additionally, it is sensitive to outliers and may require preprocessing steps such as feature scaling and selection. Despite its strengths, Logistic Regression has several limitations when applied to health data. It assumes a linear relationship between the independent variables and the log-odds of the dependent variable, which may not hold true for complex biological interactions. This can reduce its prediction accuracy, especially on non-linear datasets. Additionally, Logistic Regression can be sensitive to outliers and multicollinearity among features, often requiring careful preprocessing, feature scaling, and selection. It also tends to struggle with imbalanced datasets, where one class significantly outweighs the other common scenario in rare disease prediction. Nevertheless, Logistic Regression remains a strong baseline model in the development of health disease prediction systems.

Proposed system: Support Vector Machine

The proposed system for multi-disease prediction utilizes the Support Vector Machine (SVM) algorithm to enhance the accuracy, efficiency, and scalability of disease classification. Unlike traditional systems that focus on predicting a single disease at a time, this system is designed to analyze multiple diseases simultaneously by leveraging structured patient data, including symptoms, medical history, lab test results, and demographic information. The system begins with data preprocessing, where missing values are handled, numerical data is normalized, and categorical attributes such as symptoms.

Feature selection techniques are applied to extract the most relevant medical parameters, ensuring optimal model performance and reducing computational cost. The SVM classifier is then trained on the processed dataset, with different kernel functions (linear, polynomial, and radial basis function (RBF)) being tested to find the best-performing model.

Once trained, the system can predict the likelihood of multiple diseases for a new patient based on their health attributes. The performance of the model is evaluated using accuracy, precision, recall, and F1-score to ensure reliability and effectiveness. The proposed system offers several advantages over traditional methods, including higher classification accuracy, better generalization on unseen medical data, and improved interpretability compared to deep learning models. One of SVM's key advantages is its robustness to overfitting, particularly when appropriate kernel selection and regularization techniques are applied. Additionally, it performs well even with relatively small datasets, a common limitation in medical research.

Furthermore, SVM supports both binary and multiclass classification, allowing it to be extended for multi-disease prediction systems with proper adaptation. It can also be integrated with real-time health monitoring systems and Internet of Things (IoT) devices due to its ability to efficiently process high-dimensional and streaming data with minimal loss in accuracy. Feature selection techniques such as Recursive Feature Elimination (RFE) and Principal Component Analysis (PCA) can be employed to enhance SVM's performance by reducing noise and improving computation time.

Due to its high classification accuracy, flexibility through kernel functions, and strong generalization capabilities, SVM is a highly suitable and reliable choice as the proposed system for building an intelligent, accurate, and scalable health disease prediction framework.

Support Vector Machine (SVM) is proposed as the core classification algorithm for the health disease prediction system due to its strong ability to handle complex, high-dimensional medical data with high accuracy and generalization. SVM is a supervised learning algorithm that constructs an optimal hyperplane to separate classes by maximizing the margin between support vectors, making it particularly effective for classification tasks where the data is not linearly separable. By using kernel functions such as the radial basis function (RBF), polynomial, or sigmoid kernels, SVM can project input data into higher-dimensional spaces where it becomes linearly separable, enabling the model to detect complex, non-linear patterns often present in health-related datasets.

Table: 6.1 Comparison Table of Existing and Proposed System

Feature	Existing System (Logistic Regression)	Proposed System (SVM)
Algorithm Used	Logistic Regression	Support Vector Machine (SVM)
Disease Prediction	Typically used for binary/single-disease classification	Supports multi-disease classification
Accuracy	Moderate accuracy, limited with non-linear relationships	High accuracy with better handling of complex patterns
Overfitting	May underfit or overfit if features are not well selected	Less prone to overfitting, especially with optimized kernels
Computational Efficiency	Highly efficient for small to medium datasets	More efficient for high-dimensional data with kernel optimization
Feature Selection	Requires manual or statistical feature selection (e.g., stepwise selection)	Explicit feature selection using PCA, RFE, etc.
Generalization Ability	Can struggle with imbalanced datasets without proper resampling	Strong generalization even for imbalanced datasets
Integration with IoT/Real-Time Data	Easily deployed but limited in handling complex streaming data	Can be integrated with IoT devices for real-time tracking

The above table 6.1 illustrates the comparison table between the existing system (Logistic Regression) and the proposed system (SVM-based) for multi-disease prediction. SVM (Proposed System) offers higher accuracy, better generalization, and more efficient processing of multi-disease prediction while also being more suitable for real-time applications and IoT integration.

6.3 Code for Training SVM Model

```
1 import numpy as np
2 import pandas as pd
3 from sklearn.model_selection import train_test_split
4 from sklearn import svm
5 from sklearn.metrics import accuracy_score
6 diabetes_dataset = pd.read_csv('/content/diabetes.csv')
7 # printing the first 5 rows of the dataset
8 diabetes_dataset.head()
9 # number of rows and Columns in this dataset
10 diabetes_dataset.shape
11 # getting the statistical measures of the data
12 diabetes_dataset.describe()
13 diabetes_dataset['Outcome'].value_counts()
14 diabetes_dataset.groupby('Outcome').mean()
15 # separating the data and labels
16 X = diabetes_dataset.drop(columns = 'Outcome', axis=1)
17 Y = diabetes_dataset['Outcome']
18 print(Y)
19 X_train, X_test, Y_train, Y_test = train_test_split(X,Y, test_size = 0.2, stratify=Y, random_state
    =2)
20 print(X.shape, X_train.shape, X_test.shape)
21 classifier = svm.SVC(kernel='linear')
22 #training the support vector Machine Classifier
23 classifier.fit(X_train, Y_train)
24 # accuracy score on the training data
25 X_train_prediction = classifier.predict(X_train)
26 training_data_accuracy = accuracy_score(X_train_prediction, Y_train)
27 print('Accuracy score of the training data : ', training_data_accuracy)
28 input_data = (5,166,72,19,175,25.8,0.587,51)
29 # changing the input_data to numpy array
30 input_data_as_numpy_array = np.asarray(input_data)
31 # reshape the array as we are predicting for one instance
32 input_data_reshaped = input_data_as_numpy_array.reshape(1,-1)
33 prediction = classifier.predict(input_data_reshaped)
34 print(prediction)
35 if (prediction[0] == 0):
36     print('The person is not diabetic')
37 else:
38     print('The person is diabetic')
39 import pickle
40 filename = 'diabetes_model.sav'
41 pickle.dump(classifier, open(filename, 'wb'))
42 # loading the saved model
43 loaded_model = pickle.load(open('diabetes_model.sav', 'rb'))
44 input_data = (5,166,72,19,175,25.8,0.587,51)
45 # changing the input_data to numpy array
46 input_data_as_numpy_array = np.asarray(input_data)
```

```

47 # reshape the array as we are predicting for one instance
48 input_data_resaped = input_data_as_numpy_array.reshape(1,-1)
49 prediction = loaded_model.predict(input_data_resaped)
50 print(prediction)
51 if (prediction[0] == 0):
52     print('The person is not diabetic')
53 else:
54     print('The person is diabetic')
55
56 #code to predict Parkins Disease
57 import numpy as np
58 import pandas as pd
59 from sklearn.model_selection import train_test_split
60 from sklearn import svm
61 parkinsons_data = pd.read_csv('/content/parkinsons.csv')
62 X = parkinsons_data.drop(columns=['name', 'status'], axis=1)
63 Y = parkinsons_data['status']
64 X_train, X_test, Y_train, Y_test = train_test_split(X, Y, test_size=0.2, random_state=2)
65 scaler = StandardScaler()
66 X_train_scaled = scaler.fit_transform(X_train)
67 X_test_scaled = scaler.transform(X_test)
68 model = svm.SVC(kernel='linear')
69 model.fit(X_train_scaled, Y_train)
70 X_train_prediction = model.predict(X_train_scaled)
71 training_data_accuracy = accuracy_score(Y_train, X_train_prediction)
72 print('Accuracy score of training data: ', training_data_accuracy)
73 X_test_prediction = model.predict(X_test_scaled)
74 test_data_accuracy = accuracy_score(Y_test, X_test_prediction)
75 print('Accuracy score of test data: ', test_data_accuracy)
76 input_data = (197.07600, 206.89600, 192.05500, 0.00289, 0.00001, 0.00166, 0.00168, 0.00498)
77 input_data_as_numpy_array = np.asarray(input_data).reshape(1, -1)
78 input_data_scaled = scaler.transform(input_data_as_numpy_array)
79 prediction = model.predict(input_data_scaled)
80 if prediction[0] == 0: print("The Person does not have Parkinson's Disease")
81 else: print("The Person has Parkinson's")

```

Output


The screenshot displays a web application titled "Health Forecaster Disease Prediction System". On the left is a sidebar with navigation links: "Home Page", "Diabetes Prediction" (highlighted in red), "Heart Disease Prediction", and "Parkinsons Prediction". The main content area is titled "Diabetes Prediction using ML" and contains several input fields for medical data:

Number of Pregnancies	Glucose Level	Blood Pressure value
6	148	72
Skin Thickness value	Insulin Level	BMI value
35	0	33.6
Diabetes Pedigree Function value	Age of the Person	
0.627	50	

Below the input fields is a button labeled "Diabetes Test Result". At the bottom of the form is a large, empty green rectangular box intended for the prediction result.

Figure 6.1: Output Image of the Health Prediction Website


The above figure 6.1 displays an interface for a "Health Forecaster Disease Prediction System" that utilizes machine learning for disease prediction. Users can input medical parameters such as the number of pregnancies, glucose level, blood pressure, skin thickness, insulin level, BMI, diabetes pedigree function value, and age. After entering the data, they can click the "Diabetes Test Result" button to receive a diagnosis. However, in this instance, the result field appears blank, indicating that the system has not yet processed the prediction or the output is missing. Once the user inputs these values and clicks on the "Diabetes Test Result" button, the system processes the data using a trained machine learning model.


 Health


Forecaster Disease

Prediction System

Home Page

 Diabetes Prediction

 Heart Disease Prediction

 Parkinsons Prediction

Diabetes Prediction using ML

Number of Pregnancies	Glucose Level	Blood Pressure value
6	148	72
Skin Thickness value	Insulin Level	BMI value
35	0	33.6
Diabetes Pedigree Function value	Age of the Person	
0.627	50	

Diabetes Test Result

The person is diabetic

Figure 6.2: Output for Diabetics Prediction

The above figure 6.2 displays a user interface of a "Health Forecaster Disease Prediction System" that utilizes machine learning for disease prediction. The system features multiple prediction options, including diabetes, heart disease, and Parkinson's disease. The diabetes prediction section is currently selected, showing an input form where users can enter various health parameters such as the number of pregnancies, glucose level, blood pressure, skin thickness, insulin level, BMI, diabetes pedigree function value, and age. The result, displayed in a green box, indicates whether the person is diabetic. In this case, the system has predicted that "The person is diabetic." This interface simplifies disease risk assessment, allowing users and medical professionals to obtain quick insights based on patient data.

Chapter 7

CONCLUSION AND FUTURE ENHANCEMENTS

7.1 Conclusion

The Multi-Disease Prediction System using Machine Learning provides an efficient and accurate approach to early diagnosis and risk assessment of multiple diseases. By leveraging data preprocessing, feature selection, and machine learning algorithms, the system can analyze patient data and provide reliable predictions. Encourages individuals to adopt preventive health measures by identifying potential risks early. Early disease prediction and management reduce complications, enabling individuals to lead healthier and longer lives.

This aids healthcare professionals in making informed decisions, improving early detection, and enhancing treatment planning. With further improvements in data collection, model optimization, and real-time integration, the system can become a valuable tool in predictive healthcare, reducing diagnosis time and improving patient outcomes. Educates individuals about their health risks and the importance of preventive care, fostering a health conscious society. Promotes self-responsibility for health by offering actionable insights and recommendations. Future advancements in deep learning and AI-driven diagnostics can further enhance accuracy and adaptability across diverse medical conditions.

7.2 Future Enhancements

Future enhancements for the Multi-Disease Prediction System using Machine Learning can focus on improving accuracy, scalability, and usability. Integrating deep learning models, such as CNNs for medical imaging and LSTMs for time-series health data, can enhance predictive performance.

Real-time health monitoring using IoT-enabled wearable devices can enable continuous patient tracking and early detection of diseases. Explainable AI (XAI) techniques, like SHAP and LIME, can be incorporated to provide interpretable predictions, fostering trust among medical professionals. Personalized health predictions based on patient history, genetics, and lifestyle factors can improve diagnosis precision.

Deploying the system on cloud platforms will enhance accessibility and scalability, while multi-modal data fusion, combining structured and unstructured medical data, can offer more comprehensive disease analysis. Federated learning can be utilized to train models across hospitals without compromising patient data privacy. Expanding datasets to include diverse populations will improve model generalization, reducing biases. Additionally, developing mobile and web-based applications will make the system more accessible to users, and integration with electronic health records (EHRs) will streamline disease prediction by leveraging historical patient data. These enhancements can significantly advance the effectiveness of AI-driven healthcare systems, making disease prediction more reliable and accessible.

To further enhance the reliability of the system, expanding the dataset to include diverse demographic groups will improve the model's generalizability, reducing biases and ensuring fairer predictions across different populations. Additionally, developing user-friendly mobile and web applications can make the system more accessible to both patients and healthcare providers, facilitating quick disease risk assessments. Seamless integration with electronic health records (EHRs) can enable the system to leverage historical patient data, providing better insights and continuity of care.

In the future, the system can also incorporate reinforcement learning techniques to adapt dynamically based on new medical research and evolving disease patterns. AI-driven chatbots and virtual assistants can be integrated to provide instant guidance based on model predictions, assisting patients in understanding their health risks and recommending appropriate medical consultations. The inclusion of blockchain technology can enhance data security and transparency, ensuring that patient data remains tamper-proof while allowing controlled access for medical professionals. By implementing these future enhancements, the Multi-Disease Prediction System can evolve into a more accurate, interpretable, scalable, and patient-centric solution, making AI-driven healthcare more impactful and reliable in disease prevention.

Chapter 8

PLAGIARISM REPORT

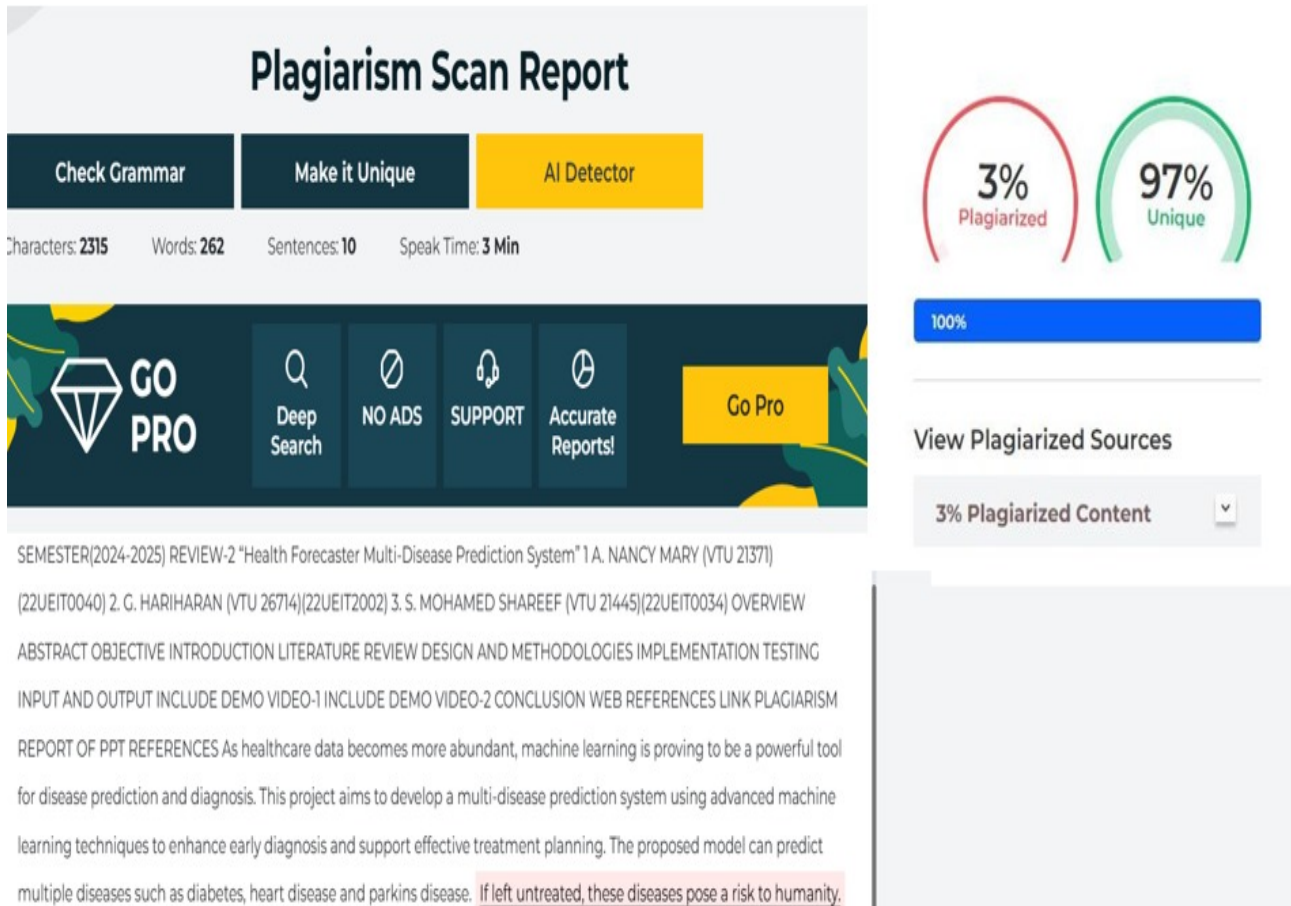


Figure 8.1: Plagiarism Report

Chapter 9

SOURCE CODE & POSTER PRESENTATION

9.1 Source Code for SVM Model

```
1 import numpy as np
2 import pandas as pd
3 from sklearn.model_selection import train_test_split
4 from sklearn import svm
5 from sklearn.metrics import accuracy_score
6 diabetes_dataset = pd.read_csv('/content/diabetes.csv')
7 # printing the first 5 rows of the dataset
8 diabetes_dataset.head()
9 # number of rows and Columns in this dataset
10 diabetes_dataset.shape
11 # getting the statistical measures of the data
12 diabetes_dataset.describe()
13 diabetes_dataset['Outcome'].value_counts()
14 diabetes_dataset.groupby('Outcome').mean()
15 # separating the data and labels
16 X = diabetes_dataset.drop(columns = 'Outcome', axis=1)
17 Y = diabetes_dataset['Outcome']
18 print(Y)
19 X_train, X_test, Y_train, Y_test = train_test_split(X,Y, test_size = 0.2, stratify=Y, random_state
    =2)
20 print(X.shape, X_train.shape, X_test.shape)
21 classifier = svm.SVC(kernel='linear')
22 #training the support vector Machine Classifier
23 classifier.fit(X_train, Y_train)
24 # accuracy score on the training data
25 X_train_prediction = classifier.predict(X_train)
26 training_data_accuracy = accuracy_score(X_train_prediction, Y_train)
27 print('Accuracy score of the training data : ', training_data_accuracy)
28 input_data = (5,166,72,19,175,25.8,0.587,51)
29 # changing the input_data to numpy array
30 input_data_as_numpy_array = np.asarray(input_data)
31 # reshape the array as we are predicting for one instance
32 input_data_reshaped = input_data_as_numpy_array.reshape(1,-1)
33 prediction = classifier.predict(input_data_reshaped)
34 print(prediction)
```

```

35 if (prediction[0] == 0):
36     print('The person is not diabetic')
37 else:
38     print('The person is diabetic')
39 import pickle
40 filename = 'diabetes_model.sav'
41 pickle.dump(classifier, open(filename, 'wb'))
42 # loading the saved model
43 loaded_model = pickle.load(open('diabetes_model.sav', 'rb'))
44 input_data = (5,166,72,19,175,25.8,0.587,51)
45 # changing the input_data to numpy array
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47 # reshape the array as we are predicting for one instance
48 input_data_reshaped = input_data_as_numpy_array.reshape(1,-1)
49 prediction = loaded_model.predict(input_data_reshaped)
50 print(prediction)
51 if (prediction[0] == 0):
52     print('The person is not diabetic')
53 else:
54     print('The person is diabetic')
55
56 #code to predict Parkins Disease
57 import numpy as np
58 import pandas as pd
59 from sklearn.model_selection import train_test_split
60 from sklearn import svm
61 parkinsons_data = pd.read_csv('/content/parkinsons.csv')
62 X = parkinsons_data.drop(columns=['name', 'status'], axis=1)
63 Y = parkinsons_data['status']
64 X_train, X_test, Y_train, Y_test = train_test_split(X, Y, test_size=0.2, random_state=2)
65 scaler = StandardScaler()
66 X_train_scaled = scaler.fit_transform(X_train)
67 X_test_scaled = scaler.transform(X_test)
68 model = svm.SVC(kernel='linear')
69 model.fit(X_train_scaled, Y_train)
70 X_train_prediction = model.predict(X_train_scaled)
71 training_data_accuracy = accuracy_score(Y_train, X_train_prediction)
72 print('Accuracy score of training data: ', training_data_accuracy)
73 X_test_prediction = model.predict(X_test_scaled)
74 test_data_accuracy = accuracy_score(Y_test, X_test_prediction)
75 print('Accuracy score of test data: ', test_data_accuracy)
76 input_data = (197.07600, 206.89600, 192.05500, 0.00289, 0.00001, 0.00166, 0.00168, 0.00498)
77 input_data_as_numpy_array = np.asarray(input_data).reshape(1, -1)
78 input_data_scaled = scaler.transform(input_data_as_numpy_array)
79 prediction = model.predict(input_data_scaled)
80 if prediction[0] == 0: print("The Person does not have Parkinson's Disease")
81 else: print("The Person has Parkinson's")

```

9.2 Poster Presentation

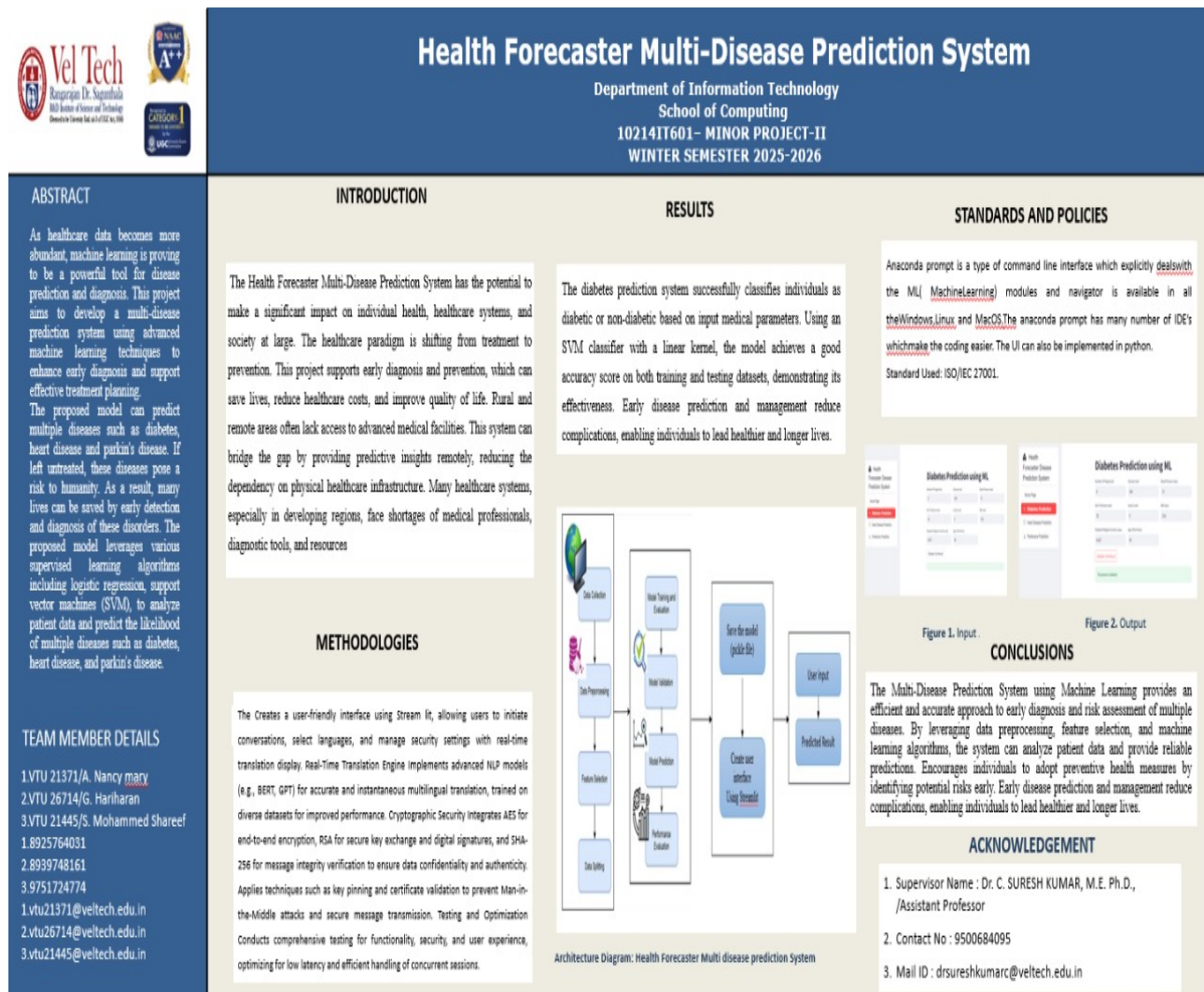


Figure 9.1: Poster Presentation for Health Forecaster Multi Disease Prediction System

The above figure 9.1 shows the poster presentation for the project titled health forecaster multi-disease prediction system. The poster includes introduction, methodologies used, results, standards and policies and conclusion.

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