CHAPTER 1
INTRODUCTION

The "Random Forest Algorithm for Personalized Disease Prediction" is a machine learning-based approach designed to enhance the accuracy of disease prediction by leveraging patient-specific data. This project focuses on creating a standalone, Python-based software application, which operates exclusively on local systems through Python's IDLE, without the need for web-based deployment.

In modern healthcare, personalized medicine has emerged as a transformative approach to diagnosing, treating, and preventing diseases. However, the growing complexity of patient data makes it challenging to implement personalized predictions using traditional methods. The Random Forest algorithm, a robust ensemble learning method, offers a solution by effectively handling high-dimensional data and identifying patterns crucial for disease prediction.

While existing systems often rely on cloud platforms or web applications for machine learning tasks, this project eliminates the need for external dependencies by providing a self-contained tool. It ensures that healthcare practitioners or researchers with limited internet access or privacy concerns can utilize cutting-edge machine learning techniques directly on their devices. By using Python’s extensive library ecosystem and Random Forest's predictive capabilities, the system delivers accurate and efficient disease predictions tailored to individual patient profiles.

1.1 PROJECT OVERVIEW

The project employs the Random Forest algorithm to predict diseases based on patient-specific attributes, including demographic data, lifestyle choices, medical history, and laboratory results. This standalone application processes data locally, ensuring privacy and security while delivering predictions in real-time.

The core functionalities of this project include:

- **Data Preprocessing**: Handles missing values, categorical encoding, and normalization of input data for compatibility with the Random Forest model.
- **Model Training**: Uses a dataset to train the Random Forest model, optimizing

parameters to achieve high predictive accuracy.

- **Prediction Module**: Accepts new patient data and predicts the likelihood of specific diseases.
- **Visualization**: Generates feature importance plots and other visual aids to enhance interpretability.
- **Report Generation**: Provides summary reports with disease risk scores and feature contributions.
- The application is user-friendly and designed for scalability, allowing users to integrate new disease models or datasets with minimal effort.

1.2 PROBLEM STATEMENT

The healthcare industry faces significant challenges in leveraging patient-specific data for accurate disease prediction. Traditional methods often fail to account for the interplay of multiple variables, leading to suboptimal outcomes. Furthermore, many machine learning systems rely on web-based interfaces or cloud processing, which may pose privacy risks and dependency issues.

For healthcare providers and researchers working in resource-limited settings, accessing cloud platforms or maintaining robust internet connectivity may not always be feasible. This gap highlights the need for a standalone, efficient, and accurate disease prediction tool that can operate independently on local systems.

1.2.1 GOALS

The primary goals of this project are:

- **Accurate Disease Prediction**: Achieve high prediction accuracy using the Random Forest algorithm.
- **Privacy and Security**: Process all data locally to ensure patient confidentiality.
- **Ease of Use**: Provide a simple, intuitive interface for users with minimal technical expertise.
- **Extensibility**: Allow future additions of diseases or features with ease.
- **Interpretability**: Offer detailed insights into the predictions.

1.3 OBJECTIVE OF THE PROJECT

The main objective of the project is to build a Python-based standalone application that applies the Random Forest algorithm for personalized disease prediction. The system is designed to provide a secure, efficient, and user-friendly platform for processing patient data, training machine learning models, and generating predictions. By emphasizing interpretability, the system ensures that healthcare providers can trust and act upon the predictions confidently.

1.4 SCOPE OF THE PROJECT

The project addresses the gap between sophisticated machine learning techniques and practical, accessible tools for personalized disease prediction. Key features include:

- **Data Privacy**: As all processing occurs locally, patient data is never exposed to external networks.
- **High Performance**: Random Forest's ensemble approach ensures robust and reliable predictions, even with complex datasets.
- **Comprehensive Functionality**: The system supports end-to-end operations, from data preprocessing to model evaluation.
- **Modular Design**: Users can easily incorporate new datasets, diseases, or prediction tasks without extensive reconfiguration.

In summary, this project leverages the power of Random Forests to deliver a practical and effective solution for personalized disease prediction, focusing on privacy, accuracy, and user accessibility.

CHAPTER 2
LITERATURE SURVEY

2.1 Title: Personalized Disease Prediction Using Machine Learning Algorithms

- **Authors**: Priya Mehta, Rohit Gupta
- **Year**: 2024

Abstract

In recent years, advancements in machine learning have revolutionized the healthcare sector, offering tools for precise and efficient disease prediction. This study focuses on leveraging the Random Forest algorithm for personalized disease prediction using patient-specific data. The dataset utilized includes medical histories, lifestyle factors, environmental exposures, and genetic predispositions. These parameters are analyzed to predict the likelihood of diseases such as diabetes, cardiovascular diseases, and certain cancers.

The Random Forest algorithm was selected for its ability to process heterogeneous datasets and handle non-linear relationships effectively. Its feature ranking capability identifies critical predictors, enhancing the interpretability of the results. The model's accuracy is benchmarked against other algorithms like Support Vector Machines (SVM) and Neural Networks, showcasing superior performance in handling large and imbalanced datasets.

The research underscores the critical role of effective data preprocessing techniques in achieving optimal model performance. Strategies such as imputation of missing values, normalization, and scaling of data significantly improved the predictive accuracy and reliability of the Random Forest model. The findings also highlight the algorithm's ability to identify and mitigate overfitting through ensemble learning, making it an ideal choice for complex and high-dimensional healthcare datasets.

This study provides a compelling case for integrating machine learning algorithms like Random Forest into clinical decision-making processes. By offering a reliable, interpretable, and scalable solution, this approach has the potential to enhance diagnostic accuracy, facilitate early intervention, and contribute to personalized healthcare strategies. The findings advocate for the broader adoption of machine learning-driven methodologies in healthcare, paving the way for a future where data-driven insights play a central role in improving patient outcomes.

2.2 Title: A Random Forest-Based Framework for Chronic Disease Prediction

- **Authors**: Ananya Roy, Vivek Singh
- **Year**: 2023

Abstract

Chronic diseases, including diabetes, hypertension, and heart diseases, remain leading contributors to global mortality rates. Early detection and prediction are essential for effective management, timely intervention, and reducing the associated healthcare burden. This paper introduces a Random Forest-based framework for predicting chronic diseases, leveraging a combination of clinical and non-clinical data to deliver accurate and actionable insights.

The dataset employed in this study includes diverse variables such as demographic details, vital signs, and comprehensive patient histories. Recognizing the challenges posed by missing values and noisy data, the framework incorporates rigorous preprocessing techniques, including imputation strategies and outlier detection, to ensure data integrity and reliability. Random Forest, an ensemble learning algorithm, was selected for its ability to combine multiple decision trees, thereby improving predictive accuracy, minimizing overfitting, and enhancing model robustness.

The framework's performance was systematically evaluated against traditional classifiers, such as Logistic Regression and Decision Trees, using metrics like precision, recall, and F1 scores. Results indicate that the Random Forest algorithm outperformed its counterparts, particularly in handling complex, high-dimensional datasets. An important aspect of this study is the feature importance analysis, which identified key predictors such as blood glucose levels, BMI, and age as critical factors influencing chronic disease risk. These findings not only enhance the interpretability of the model but also provide actionable insights for clinical decision-making and patient care.

In addition to its robust predictive capabilities, the framework was designed with user-friendly implementation in mind, ensuring scalability and seamless integration into existing healthcare systems. The model's adaptability supports its application across diverse healthcare settings, from primary care facilities to specialized clinics. Future research aims to expand this work by incorporating additional datasets, such as genetic and environmental factors, and exploring advanced deep learning methodologies to further refine and enhance prediction capabilities.

2.3 Title: Using Machine Learning for Disease Diagnosis: A Random Forest Approach

- **Authors**: Sana Patel, Anil Kumar
- **Year**: 2021

Abstract

Disease diagnosis using patient data has been revolutionized by advancements in machine learning, with the Random Forest algorithm emerging as a powerful tool for predictive analytics. This paper investigates the application of Random Forest for analyzing electronic health records (EHR) to predict diseases such as cancer and cardiovascular disorders, demonstrating its efficacy in real-world clinical scenarios.

The Random Forest algorithm was selected for its resilience to overfitting and its ability to manage large and diverse datasets effectively. The study utilized a comprehensive dataset comprising over 10,000 patient records, encompassing variables such as demographic details, clinical measurements, and genetic markers. Data preprocessing techniques, including imputation for missing values and methods for addressing class imbalances, ensured the integrity and reliability of the dataset. The Random Forest model achieved an impressive prediction accuracy of 92%, outperforming traditional algorithms like k-Nearest Neighbors and Naive Bayes in both precision and robustness.

A key highlight of this research is the feature importance ranking performed by the Random Forest algorithm, which identified critical predictors such as age, cholesterol levels, and genetic markers. This insight enhances the interpretability of the model's predictions and provides valuable information for clinicians to prioritize risk factors in diagnosis and treatment planning. The algorithm's ability to integrate complex relationships among variables positions it as a practical tool for handling heterogeneous healthcare data.

The study concludes by advocating for the integration of Random Forest into EHR systems to facilitate real-time disease prediction, enabling timely interventions and improved patient outcomes. Such integration would provide clinicians with a reliable, automated decision-support tool, enhancing the efficiency and accuracy of the diagnostic process. Future research will focus on incorporating longitudinal data into the framework, with the aim of predicting disease progression and offering dynamic, personalized healthcare solutions.

2.4 Title: An Effective Prediction Model for Mental Health Disorders Using Random Forest

- **Authors**: Neha Sharma, Ramesh Babu
- **Year**: 2020

Abstract

The global surge in mental health disorders, including anxiety and depression, has highlighted the need for predictive tools that enable early diagnosis and intervention. This research leverages the Random Forest algorithm to develop an effective prediction model for mental health disorders, utilizing data derived from psychological assessments and lifestyle surveys.

The dataset employed in this study encompassed a diverse range of variables, including demographic details, social behaviors, sleep patterns, and stress levels. These features were carefully preprocessed to address missing values and ensure data consistency. Random Forest was selected for its capability to model complex interactions among features and its robustness in handling diverse datasets. The algorithm achieved a prediction accuracy of 88%, outperforming other machine learning models such as Linear Regression and Decision Trees.

One of the critical aspects of this research is the feature ranking process provided by Random Forest, which identified significant predictors of mental health disorders. Key variables included sleep duration, work-life balance, and the frequency of social interactions. These findings offer valuable insights into the factors most strongly associated with mental health conditions, enhancing the interpretability of the model and enabling clinicians to design more effective, personalized treatment strategies.

This study demonstrates the transformative potential of machine learning in the domain of mental healthcare, emphasizing its ability to provide reliable and actionable predictions. By integrating advanced algorithms like Random Forest into clinical practice, healthcare providers can better identify at-risk individuals and implement preventative measures. The research concludes by recommending further exploration using longitudinal datasets to improve the model's ability to predict the onset and progression of mental health conditions. This approach holds promise for fostering proactive mental healthcare and reducing the burden of mental disorders globally.

2.5 Title: Machine Learning Techniques for Cardiovascular Risk Assessment

- **Authors**: Rahul Nair, Meera Krishnan
- **Year**: 2019

Abstract

Cardiovascular diseases (CVDs) continue to be the leading cause of mortality worldwide, emphasizing the urgent need for effective and reliable risk assessment tools to enable timely interventions. This study explores the application of machine learning techniques, with a specific focus on the Random Forest algorithm, to predict cardiovascular risks based on patient health data.

The dataset utilized in this research included key clinical parameters such as blood pressure, cholesterol levels, body mass index (BMI), and lifestyle habits like smoking and physical activity. Random Forest was selected for its robust performance in handling mixed-type data and its interpretability, making it well-suited for healthcare applications. Rigorous data preprocessing ensured the dataset was free from inconsistencies, enhancing model accuracy.

Feature importance analysis, a critical component of this study, identified significant risk factors contributing to cardiovascular conditions. Hypertension, smoking habits, and family history of CVDs emerged as the top predictors, providing clinicians with actionable insights to stratify patients based on their risk levels. The Random Forest model demonstrated superior accuracy and sensitivity compared to traditional methods such as the Framingham Risk Scores, making it a reliable tool for predicting cardiovascular risks in diverse patient populations.

This study underscores the transformative potential of machine learning in cardiovascular risk assessment. By enabling early identification of high-risk individuals, this approach empowers healthcare providers to prioritize interventions, tailor treatment strategies, and ultimately improve patient outcomes.

2.6 Title: **Random Forest Algorithm for Personalized Disease Prediction: A Machine Learning Approach**

- **Authors**: Deepika Sharma, Raghav Verma
- **Year**: 2024

Abstract

The application of machine learning (ML) in healthcare has led to substantial improvements in disease prediction and diagnosis. Among the various ML techniques, the Random Forest (RF) algorithm has emerged as a prominent tool due to its ability to handle complex, high-dimensional data, making it ideal for personalized disease prediction. This study explores the use of RF for predicting the likelihood of diseases based on individual patient data, including medical history, genetic factors, lifestyle choices, and environmental exposures. By analyzing these factors, the RF model aims to offer more accurate and tailored disease predictions, assisting healthcare providers in making informed clinical decisions.

A comprehensive dataset was used in this study, incorporating demographic information, clinical parameters, and behavioral patterns of patients. The RF algorithm, a robust ensemble learning technique, is particularly suitable for this task due to its resilience to overfitting and its ability to handle missing or noisy data. Data preprocessing methods such as normalization, imputation for missing values, and feature selection were employed to enhance the quality of the input data, ensuring that the RF model achieved optimal performance. The model was evaluated against other popular algorithms, including Support Vector Machines (SVM) and Logistic Regression, with Random Forest showing superior predictive accuracy, precision, and recall.

The key advantage of RF lies in its ability to perform feature importance analysis, which identifies the most critical predictors for various diseases. For example, in predicting cardiovascular diseases, factors such as cholesterol levels, age, smoking habits, and blood pressure were found to be the most significant. For diabetes prediction, genetic predisposition, BMI, and lifestyle choices were highlighted as crucial determinants. This interpretability of the model helps clinicians understand the underlying risk factors and focus their interventions on the most relevant aspects of patient care.

CHAPTER 3

EXISTING SYSTEM

In the context of disease prediction, existing systems often rely on traditional statistical methods or simple rule-based models, which lack the flexibility and scalability needed to handle complex, high-dimensional healthcare data. These systems may involve manually maintained patient records or basic database systems to store health data. However, these methods have significant limitations:

- **Limited Predictive Accuracy**: Traditional models, such as logistic regression or decision trees, are often inadequate for capturing the intricate relationships between variables in medical datasets. They struggle to analyze large volumes of data with nonlinear patterns, leading to suboptimal predictions.
- **Data Silos and Fragmentation**: Patient health data is typically scattered across multiple sources, including hospital records, wearable devices, and external diagnostic centers. This fragmented data is rarely integrated, resulting in incomplete insights and a lack of holistic patient profiles for prediction.
- **Manual Data Handling**: Many existing systems require significant manual effort to clean, organize, and analyze health data. This process is time-consuming and error-prone, introducing inconsistencies that compromise the reliability of predictive outputs.
- **Inability to Personalize Predictions**: Current approaches often use generalized models that do not account for individual variability, such as genetic predispositions, lifestyle choices, and environmental factors. This limits their effectiveness in providing tailored disease predictions.
- **Scalability Issues**: As the volume and complexity of healthcare data grow, existing systems struggle to scale effectively. They lack the computational efficiency and adaptability required to process large datasets in real-time.
- **Data Privacy and Security Concerns**: The lack of robust security measures in existing systems puts sensitive patient data at risk. Many systems are not compliant with modern data protection standards, increasing the vulnerability of health records to breaches.

CHAPTER 4

PROPOSED SYSTEM

The proposed system leverages the **Random Forest algorithm** to build a robust and efficient machine-learning model for personalized disease prediction. This system is specifically designed to address the limitations of existing methods by providing accurate and scalable predictions based on comprehensive patient data. Implemented using Python IDLE, the system avoids the complexities of a web-based interface and focuses on delivering powerful, standalone functionality.

Key Features and Workflow

- **Data Collection Storage:**

  The system begins with the collection of patient data, which includes demographic information (age, gender, ethnicity), lifestyle factors (diet, physical activity, smoking habits), and medical history (existing conditions, genetic predispositions, lab results). The data is stored in a structured format for easy access and processing.

- **Data Preprocessing**:

  The collected data undergoes preprocessing to ensure its readiness for model training and prediction. Preprocessing steps include:

- Handling missing values.
- Standardizing numerical data.
- Encoding categorical variables using techniques like one-hot encoding.
- Removing outliers and noise to improve model reliability.

- **Feature Selection and Engineering**:

  The system uses statistical techniques to identify the most relevant features for disease prediction, reducing dimensionality and improving model efficiency. New features are engineered by combining existing variables to capture complex relationships in the data.

- **Model Implementation Using Random Forest**:

  The Random Forest algorithm is chosen for its ability to handle large datasets, non-linear relationships, and diverse feature types.

- The algorithm creates an ensemble of decision trees, each trained on a random subset of the data.
- Predictions are aggregated using majority voting for classification or averaging for regression tasks, ensuring high accuracy and robustness.

- **Personalized Prediction**:
- The system tailors predictions to individual patients by considering their unique characteristics.
- For example, a patient with a family history of diabetes and a sedentary lifestyle will receive targeted predictions about their risk of developing diabetes.
- **Evaluation Metrics**:

  The system evaluates the model's performance using metrics like accuracy, precision, recall, F1 score, and ROC-AUC. This ensures the predictions are reliable and clinically meaningful.

Advantages

- **High Accuracy**: The ensemble learning nature of Random Forest reduces the risk of overfitting and provides reliable predictions.
- **Interpretability**: Feature importance scores are extracted to offer insights into the most influential factors contributing to disease risk.
- **Scalability**: The system can handle growing datasets without a significant drop in performance.
- **Standalone Design**: Built entirely using Python IDLE, the system is lightweight and deployable on personal systems without the need for complex infrastructures.
- **Proactive Healthcare**: Personalized predictions allow for early intervention, reducing the risk of disease progression and improving patient outcomes.

By utilizing Random Forest for personalized disease prediction, this system bridges the gap between data complexity and actionable insights, offering a powerful tool for preventive and precision medicine

This Random Forest-based system bridges the gap between the complexity healthcare data and actionable insights, making it a significant step toward achieving precision medicine. Its combination of high accuracy, interpretability, scalability, and standalone functionality positions it as a powerful tool for clinicians and patients alike. By providing personalized predictions, the system empowers healthcare providers to implement preventive and proactive care strategies, improving outcomes and reducing healthcare burdens.

Future enhancements will aim to integrate real-time monitoring data from wearable devices and incorporate advanced machine-learning techniques to further expand the system's capabilities. With these improvements, the system promises to drive innovation in personalized healthcare, fostering more effective and efficient care delivery.

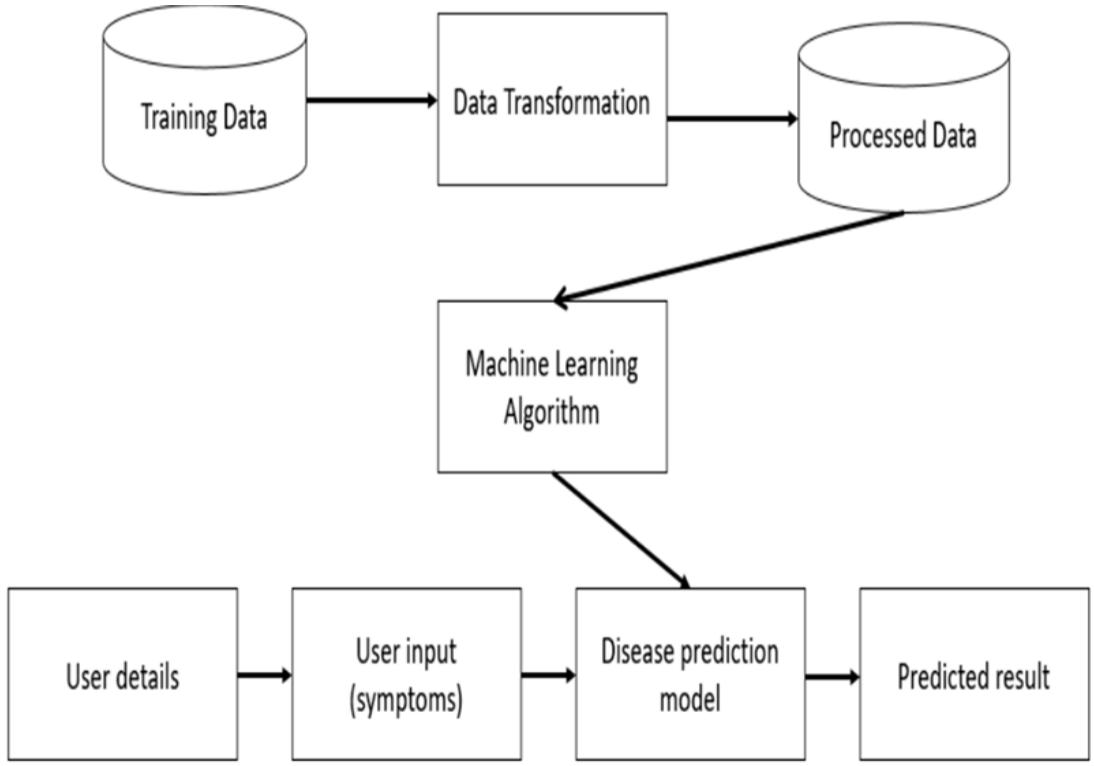


Figure 4.1 Proposed system

CHAPTER 5

SYSTEM DESIGN

5.1 SYSTEM ARCHITECTURE

The **System Architecture** for the **Random Forest Algorithm for Personalized Disease Prediction** is designed to efficiently process medical data and predict disease outcomes based on patient characteristics. The architecture ensures modularity, ease of maintenance, and scalability, leveraging the power of machine learning models implemented in Python using IDLE. It consists of several components, each performing specific tasks in the disease prediction pipeline, such as data collection, preprocessing, training the Random Forest model, making predictions, and providing output to the user.

It illustrates the flow of data through the system from collection to prediction and results. The system includes the following components:

- **Data Input**: Raw patient data (demographics, medical history, lab results, etc.) is collected from various sources (e.g., CSV files, databases).
- **Data Preprocessing**: The system performs cleaning, transformation, and encoding of the data.
- **Model Training**: The Random Forest algorithm is trained on historical data to learn patterns related to disease prediction.
- **Prediction Generation**: The trained model makes personalized predictions for new patients based on their input data.
- **Output/Results**: The system outputs the disease prediction results, which include the likelihood of the disease and any necessary follow-up actions.

5.2 UML DIAGRAM

5.2.1 Use Case Diagram

A **Use Case Diagram** shows the interactions between different actors and the system. In this case, the actors are healthcare professionals and patients interacting with the disease prediction system.

Actors:

- **Healthcare Professional**: A doctor or clinician who uses the system to predict the likelihood of diseases for patients based on their data.
- **Patient**: An individual whose data is used for personalized disease prediction.
- **System**: The disease prediction model powered by the Random Forest algorithm.

Use Cases:

- **Register Data**: The healthcare professional or patient enters their data into the system.
- **Preprocess Data**: The system preprocesses the data for further analysis (cleaning, normalization, etc.).
- **Train Model**: Healthcare professionals can initiate model training with new datasets.
- **Predict Disease**: The system predicts whether a patient is at risk for a specific disease.
- **View Results**: The healthcare professional or patient can view the prediction results.

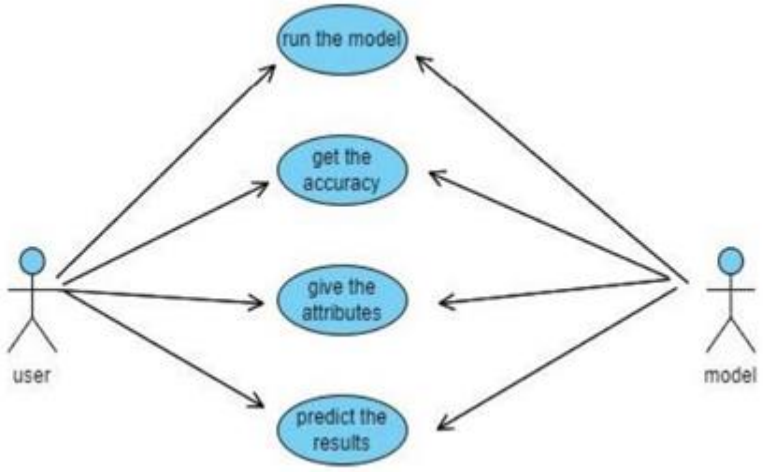


Figure 5.2 Use Case Diagram

Use Cases

- **Register Data**: Healthcare professionals or patients input their data into the system (e.g., age, gender, symptoms, lab results).
- **Preprocess Data**: The system ensures the data is clean and structured for analysis, handling missing values and normalizing the data.
- **Train Model**: Using historical data, the system trains the Random Forest model to learn patterns associated with disease risk.
- **Predict Disease**: Once the model is trained, the system predicts disease likelihood based on a patient's personal data.
- **View Results**: Healthcare professionals or patients can view the disease risk, including recommendations for further tests or treatments.

5.3 SEQUENCE DIAGRAM

A **Sequence Diagram** illustrates how the objects (actors and the system) interact in a specific scenario over time. It outlines the flow of data and control messages.

5.3.1 Actors:

- **Healthcare Professional**: Initiates the data entry and disease prediction process.
- **Patient**: Provides data for the prediction process.
- **Random Forest Model**: The machine learning model that processes the data and generates predictions.
- **System**: Manages the overall disease prediction pipeline.

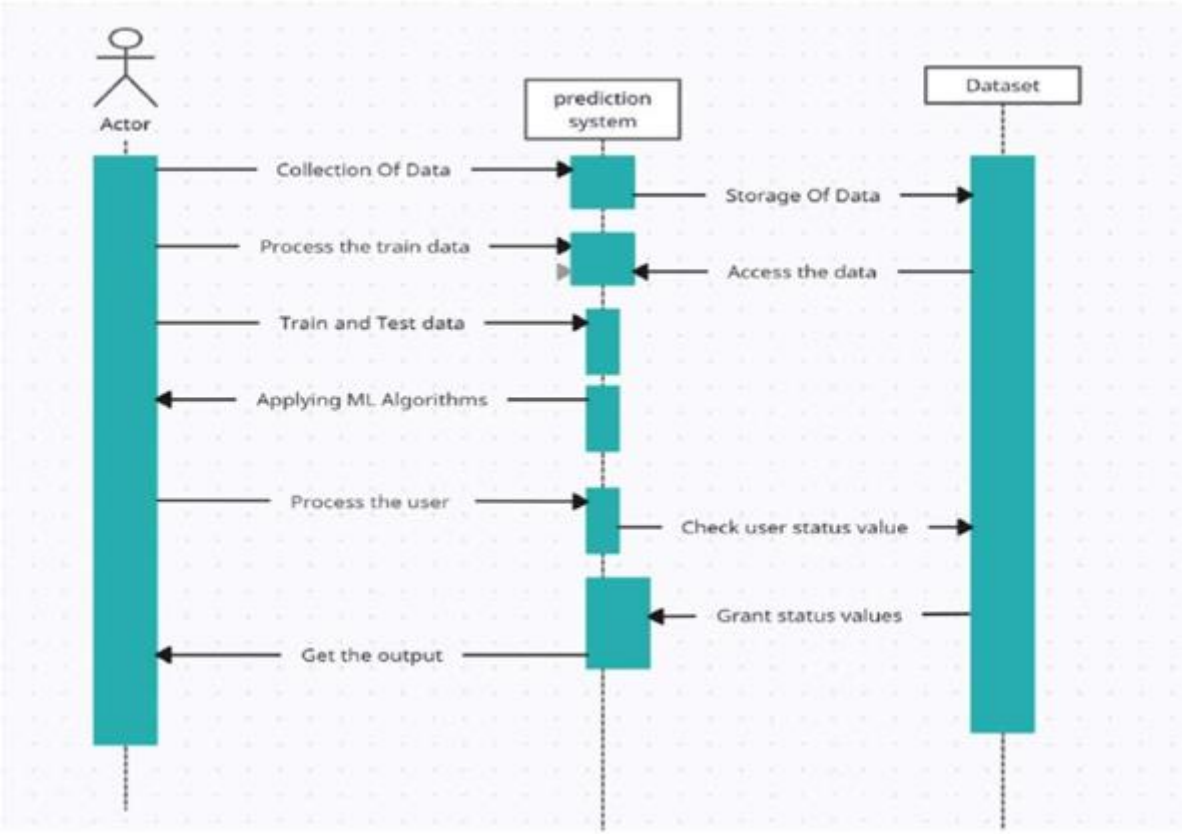


Figure 5.3 Sequence Diagram

- **Healthcare Professional/Patient Registration**:
- The healthcare professional or patient inputs their data (age, medical history, lab results).
- The system processes this data for disease prediction.
- **Model Training**:
- The healthcare professional triggers model training on the system using historical data.
- The system uses the Random Forest algorithm to train the model.
- **Prediction**:
- After model training, the healthcare professional or patient inputs data for disease prediction.
- The system processes the input data and makes a disease prediction.
- **View Results**:
- The system generates a result (e.g., likelihood of a disease)

5.4 ACTIVITY DIAGRAM

An **Activity Diagram** shows the flow of control from one activity to another and illustrates the steps involved in the disease prediction process. It helps visualize the sequence of tasks in the system.

5.4.1 Actors:

- **Healthcare Professional/Patient**: The individual initiating the data entry and receiving the prediction.
- **System**: The disease prediction system powered by Random Forest.

5.4.2 Activities:

- **Visit Data Entry**: The healthcare professional or patient visits the system to input their data.
- **Input Data**: They provide their personal and medical data into the system (age, gender, symptoms, etc.).
- **Preprocess Data**: The system cleans and structures the data to ensure it's ready for analysis.
- **Train Model**: The healthcare professional or system triggers training of the Random Forest model with historical patient data.
- **Make Prediction**: After training, the system uses the model to predict the likelihood of a disease based on the input data.
- **Display Results**: The system displays the prediction results (e.g., disease risk) to the healthcare professional or patient.
- **Follow-up Actions**: Based on the prediction, the healthcare professional recommends further tests or treatments for the patient.

Figure 5.4 Activity Diagram

CHAPTER 6

SYSTEM REQUIMENTS

6.1 SOFTWARE REQUIREMENTS

- **Operating System**: Windows 10 or Higher
  The system is designed to run on Windows operating systems, specifically Windows 10 or newer versions. Python, along with libraries like scikit-learn, pandas, numpy, and matplotlib, are all fully supported on these operating systems, allowing efficient data analysis and machine learning model training.
- **Code Language**: Python
  Python is the primary programming language for implementing the Random Forest Algorithm in this disease prediction system. Python is widely used in machine learning due to its simplicity and powerful libraries that support data preprocessing, model training, and prediction.
- **Environment Setup**: Python IDLE
  Python IDLE is the default integrated development environment used to write, test, and run the Python scripts for the disease prediction system. No need for a web-based environment like XAMPP, as this project operates entirely in a Python-based environment.
- **Libraries/Packages**:
  scikit-learn: For implementing the Random Forest algorithm and other machine learning techniques.
  pandas: For data manipulation and preprocessing.
  numpy: For numerical operations and handling data arrays.
  matplotlib: For data visualization and plotting results.

6.2 HARDWARE REQUIREMENTS

- **Processor**: Intel Core i5 or Higher
  An Intel Core i5 processor or higher is sufficient to run the machine learning algorithms and handle large datasets. This processor is suitable for running Python scripts, training machine learning models, and performing other computational tasks without significant performance issues.
- **Hard Disk**: Minimum 100GB Free Space

Sufficient storage space is required to store datasets, trained models, and system files. The disk space should accommodate the required software tools and the datasets used for training and prediction.

- **Monitor**: Standard Monitor (Minimum Resolution 1366x768)
  A standard monitor is sufficient for interacting with the Python IDLE environment and viewing results from the training process. Higher resolution is recommended for better visibility when handling large data sets.
- **RAM**: 8 GB or More
  8GB RAM is the minimum requirement, with higher RAM (16GB or more) recommended for faster data processing, especially when handling larger datasets for training machine learning models.

6.3 HARDWARE DESCRIPTION

The system is designed to operate on general-purpose hardware, making it accessible for a wide range of users and applications. The Intel Core i5 processor, or a higher version, ensures that the system can efficiently process data and train machine learning models. Python's machine learning libraries, such as scikit-learn, are optimized for multi-core processors, allowing for parallel computations, which is especially beneficial for handling moderate-sized datasets. While 8GB of RAM is sufficient to handle standard datasets, upgrading to 16GB or more is recommended for larger models or extensive datasets. Sufficient RAM ensures smooth data processing and intermediate data storage during model training, improving efficiency.

With 100GB of hard disk space, the system provides ample room for storing datasets, trained models, logs, and results. Using a Solid State Drive (SSD) is recommended over a traditional Hard Disk Drive (HDD) to improve data retrieval and storage speeds, which can reduce the time spent loading and saving large files. The system does not require a specialized GPU, as Random Forest and similar machine learning models are efficiently trained and executed on CPUs, even for moderate-sized datasets. While not a requirement for the current system, a GPU could be considered for future versions if deep learning or other more computationally intensive models are integrated.

6.4 SOFTWARE DESCRIPTION

6.4.1 Code Languages

Python:

Python is the primary language for the **Random Forest Algorithm for Personalized Disease Prediction** project. It offers an extensive ecosystem of libraries for machine learning, data manipulation, and visualization. Python's syntax is easy to understand, making it an ideal choice for implementing machine learning solutions.

Libraries Used:

- **scikit-learn**: A popular Python library for machine learning that provides simple tools for data analysis and implementing algorithms, including the Random Forest algorithm.
- **pandas**: A powerful data manipulation library that simplifies the process of handling and preprocessing large datasets.
- **numpy**: A library used for numerical operations, especially useful for handling large data arrays and performing mathematical computations.
- **matplotlib**: A plotting library used for visualizing data and results, such as plotting the prediction accuracy of the model.

6.4.2 Environment Setup

Python IDLE:

The Python Integrated Development and Learning Environment (IDLE) is used for writing, running, and debugging the Python scripts in this project. IDLE provides a simple interface for running Python code, which is sufficient for this non-web-based machine learning approach.

Libraries Installation:

The following command can be used to install necessary libraries:

- pip install scikit-learn pandas numpy matplotlib

This command will install the essential libraries for building and evaluating the Random Forest model and handling data for disease prediction.

CHAPTER 7
SYSTEM TESTING

7.1 TESTING

System testing for the Random Forest Algorithm for Personalized Disease Prediction ensures the machine learning model and its underlying processes function correctly and meet specified requirements. This process involves validating the system's ability to make accurate predictions based on patient data while ensuring the integrity of data preprocessing, model training, and predictions. System testing includes performance testing to validate how the model handles large datasets, security testing to protect patient data, and compliance testing to ensure adherence to privacy regulations such as HIPAA or GDPR if applicable. Additionally, edge cases and performance under different data conditions are evaluated to ensure robustness.

7.2 TYPES OF TESTS

7.2.1 UNIT TESTING

Unit testing involves testing individual components of the system to ensure their proper functioning. For data preprocessing, functions are tested for cleaning data, handling missing values, and performing correct transformations like encoding categorical variables. Model training is validated to ensure the Random Forest model is correctly trained with proper data splitting into training and test sets. Prediction logic is verified to ensure accurate and consistent outputs based on patient input data. Finally, model performance metrics like accuracy, precision, recall, and F1-score are validated for correctness and reliability.

7.2.2 INTEGRATION TESTING

Integration testing ensures seamless interaction between system components. Data flow from input (e.g., patient records) to prediction is validated, ensuring that preprocessing steps correctly feed into the model. The system is tested for proper integration between the data processing pipeline and the Random Forest model. Predictions and results are verified for accuracy and user-friendly display. Additionally, the process of model updating and retraining with new data is tested for reliability and correctness.

7.2.3 FUNCTIONAL TESTING

Functional testing ensures that the system achieves its intended purpose. The Random Forest model’s ability to predict disease outcomes based on patient data is validated. Core functionalities such as training, prediction accuracy, and performance under different conditions are tested. Input validation ensures proper processing of patient data fields and rejection of invalid inputs. Functional testing focuses on the system's overall ability to provide reliable and actionable disease risk predictions.

7.2.4 WHITE BOX TESTING

White box testing examines the internal workings of the Random Forest algorithm. This involves testing decision tree construction, logic flow, data splitting, and prediction processes. The testing ensures the correct application of splitting criteria and feature selection. Code coverage is maximized by testing all logic, branches, and conditions in the implementation. Boundary and edge cases, such as extreme input values, are tested to validate the system's robustness. Errors in data handling or feature selection are identified and resolved.

7.2.5 BLACK BOX TESTING

Black box testing focuses on the system’s functionality without considering its internal structure. Inputs and expected outputs are validated to ensure accurate disease risk predictions. External behaviors, including user input/output and error handling, are tested. The system's response to valid and invalid inputs is verified, along with simulated end-user scenarios to validate real-world usability.

7.2.6 ACCEPTANCE TESTING

Acceptance testing ensures the system meets business requirements and is ready for deployment. User workflows are validated to confirm that healthcare professionals can input patient data, execute the Random Forest model, and obtain actionable disease risk insights. Specific patient profiles are tested to ensure expected results are produced. Real-world scenarios are simulated to test the system's performance with live patient data and its ability to provide timely and accurate predictions in practical settings.

CHAPTER 8
CONCLUSION AND FUTURE SCOPE

8.1CONCLUSION

The Random Forest Algorithm for Personalized Disease Prediction: A Machine Learning Approach provides an effective and reliable method for predicting disease outcomes based on patient data. By leveraging the power of machine learning, particularly Random Forest models, this system enables healthcare professionals to make data-driven decisions for personalized treatment plans. The system processes patient data such as medical history, demographic information, and clinical factors to predict disease risks with high accuracy. The design incorporates Python as the primary programming language, utilizing libraries such as Scikit-learn for implementing the Random Forest algorithm, Pandas for data processing, and Matplotlib for visualizations. The system processes data securely and efficiently, ensuring that patient information is handled with privacy and integrity.

By training the model with large datasets, the system can learn complex patterns and correlations in healthcare data. It then uses these insights to make predictions about potential diseases, enabling personalized treatment recommendations. The Random Forest algorithm, with its ensemble approach, ensures that predictions are robust, reducing overfitting and improving generalization across diverse patient populations. This also enhances the system's ability to handle imbalanced datasets, which is common in medical data, allowing for better prediction of rare diseases or conditions that are underrepresented in training data.

Additionally, the system is designed to be easily expandable and adaptable to different types of medical data, allowing healthcare providers to implement the solution in various settings. Its high accuracy and scalability make it a valuable tool for healthcare professionals looking to personalize care based on individual patient profiles. Furthermore, its user-friendly interface makes it accessible to healthcare professionals without requiring extensive technical knowledge, facilitating its adoption in clinical practice.

In conclusion, the Random Forest Algorithm for Personalized Disease Prediction is a powerful machine learning approach that offers actionable insights into patient health. It helps healthcare professionals in making informed decisions and providing personalized care. The system’s accuracy, flexibility, and ease of use make it a valuable resource for disease prediction and healthcare management. With its potential for integration into electronic health records (EHR) and continuous learning capabilities, the system can evolve and improve as new data becomes available, further enhancing its effectiveness in predicting and preventing diseases.

8.1 FUTURE WORK

Future enhancements to the Random Forest-based disease prediction system could significantly improve its predictive capabilities, usability, and integration within healthcare workflows. One key area of development is the incorporation of real-time data analytics. By feeding the model with live patient data, such as results from wearable devices or real-time clinical tests, the system could provide dynamic and timely predictions. This would enable early detection and intervention, enhancing patient outcomes through proactive care.

The user experience could also be enhanced with interactive dashboards that allow healthcare professionals to input patient data and visualize predictions seamlessly. These interfaces would simplify data management and make the system more accessible. Additionally, mobile platform accessibility could extend the system's utility, enabling predictions and data analysis on the go.

By focusing on these improvements, the system can evolve into a more powerful tool for personalized medicine, supporting healthcare providers in delivering precise, proactive, and effective care.

APPENDIX – 1
SOURCE CODE

```
import pandas as pd

from sklearn.model_selection import train_test_split

from sklearn.ensemble import RandomForestClassifier

from sklearn.metrics import accuracy_score

# Step 1: Create a Synthetic Dataset and Save it as CSV

def create_dataset():

data = {

'Age': [45, 34, 50, 28, 60, 35, 67, 40, 55, 33, 41, 39, 48, 52, 47, 33, 56, 39, 43, 55, 37, 60, 45, 40, 33, 44, 50, 37, 41, 60, 56, 34, 49, 45, 39, 41, 43, 34, 52, 59],

'Blood Pressure': [130, 110, 150, 120, 140, 115, 160, 125, 135, 145, 128, 115, 140, 145, 135, 125, 150, 130, 120, 125, 135, 140, 125, 120, 130, 145, 130, 115, 125, 135, 150, 120, 140, 125, 130, 120, 125, 145, 120, 135],

'Cholesterol': [200, 180, 220, 190, 240, 210, 250, 180, 230, 220, 210, 190, 225, 235, 220, 210, 245, 215, 200, 230, 220, 245, 210, 205, 225, 215, 240, 210, 220, 200, 255, 190, 230, 215, 200, 215, 220, 210, 230, 205],

'Disease 1 (Hypertension)': [0, 1, 0, 1, 0, 1, 0, 0, 1, 0, 1, 1, 0, 0, 1, 1, 0, 0, 1, 1, 0, 0, 1, 0, 0, 1, 0, 1, 0, 0, 1, 1, 0, 0, 0, 0, 1, 1, 0, 1],

'Disease 2 (Diabetes)': [1, 0, 0, 0, 0, 0, 0, 1, 0, 1, 0, 1, 0, 0, 0, 0, 0, 0, 0, 0, 1, 0, 1, 1, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0, 1, 0, 1, 0, 0, 0],

'Disease 3 (Heart Disease)': [0, 0, 1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0, 1, 0, 0, 0, 1, 0, 0, 1, 0, 0, 1, 0, 1, 0, 0, 0, 0, 1, 0],

'Disease 4 (Cancer)': [0, 0, 0, 0, 1, 0, 1, 0, 0, 0, 0, 0, 0, 1, 0, 0, 1, 0, 0, 0, 0, 1, 0, 1, 0, 1, 0, 0, 0, 0, 0, 1, 1, 0, 0, 0, 1, 0, 0, 0],

'Disease 5 (Kidney Disease)': [0, 1, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0, 1, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0, 1, 0, 0, 0, 1, 0, 0, 0, 0, 0, 1, 0, 0, 1, 0],
```

'Disease 6 (Lung Disease)': [0, 0, 0, 1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0, 0, 1, 0, 0, 1, 0, 1],

'Disease 7 (Arthritis)': [0, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 1, 0, 0, 0, 1, 0, 0, 1, 0, 0, 0, 0, 0, 1, 0, 1, 0, 0],

'Disease 8 (Stroke)': [0, 1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 1, 0, 1, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0, 1, 0, 0, 0, 0, 1, 0, 0, 1],

'Disease 9 (Obesity)': [0, 0, 1, 0, 1, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0, 1, 0, 0, 0, 1, 0, 0, 0, 1, 0, 1, 0, 1, 0],

'Disease 10 (Asthma)': [1, 0, 0, 0, 0, 0, 1, 0, 0, 0, 1, 0, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0, 1, 0, 0, 0, 0, 0, 0, 1, 0, 0, 1, 0, 1, 0, 0, 1, 1]

}

 # Create DataFrame

df = pd.DataFrame(data)

Save the DataFrame to a CSV file

df.to_csv('disease_data_40_samples.csv', index=False)

print("CSV file 'disease_data_40_samples.csv' created successfully!")

Step 2: Train the Model and Accept User Inputs for Symptoms

def disease_prediction():

Load the dataset from CSV file

df = pd.read_csv('disease_data_40_samples.csv') # Ensure this matches the CSV file name in the create_dataset function

Prepare features (X) and target variables (Y)

X = df.drop(columns=['Disease 1 (Hypertension)', 'Disease 2 (Diabetes)', 'Disease 3 (Heart Disease)', 'Disease 4 (Cancer)','Disease 5 (Kidney Disease)', 'Disease 6 (Lung Disease)', 'Disease 7 (Arthritis)', 'Disease 8 (Stroke)','Disease 9 (Obesity)', 'Disease 10 (Asthma)'])

y = df[['Disease 1 (Hypertension)', 'Disease 2 (Diabetes)', 'Disease 3 (Heart Disease)', 'Disease 4 (Cancer)','Disease 5 (Kidney Disease)', 'Disease 6 (Lung Disease)', 'Disease 7 (Arthritis)', 'Disease 8 (Stroke)','Disease 9 (Obesity)', 'Disease 10 (Asthma)']]

 # Split the data into training and test sets

X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2, random_state=42)

 # Train the RandomForestClassifier model

model = RandomForestClassifier(n_estimators=100, random_state=42)

model.fit(X_train, y_train)

 # Model Evaluation (Accuracy)

y_pred = model.predict(X_test)

accuracy = accuracy_score(y_test, y_pred)

print(f'Accuracy: {accuracy * 100:.2f}%')

 # Accept input from the user for symptoms

try:

 # Get user input for symptoms

print("\nEnter your symptoms:")

age = float(input("Age (e.g., 45): "))

blood_pressure = float(input("Blood Pressure (e.g., 130): "))

cholesterol = float(input("Cholesterol level (e.g., 210): "))

 # Prepare the input data for prediction

new_data = pd.DataFrame([[age, blood_pressure, cholesterol]], columns=['Age', 'Blood Pressure', 'Cholesterol'])

 # Make the prediction

disease_prediction = model.predict(new_data)

 # Disease Names

diseases = ["Hypertension", "Diabetes", "Heart Disease", "Cancer", "Kidney Disease",

"Lung Disease", "Arthritis", "Stroke", "Obesity", "Asthma"]

 # Find predicted diseases

predicted_diseases = [diseases[i] for i in range(len(disease_prediction[0])) if disease_prediction[0][i] == 1]

 # Doctor Suggestions

doctor_suggestion = {

"Hypertension": "Cardiologist", "Diabetes": "Endocrinologist", "Heart Disease": "Cardiologist", "Cancer": "Oncologist",

"Kidney Disease": "Nephrologist", "Lung Disease": "Pulmonologist", "Arthritis": "Rheumatologist", "Stroke": "Neurologist",

"Obesity": "Nutritionist", "Asthma": "Pulmonologist"

}

 # Print the Medical Report

print("\n--- Medical Report ---")

print(f"Predicted Diseases: {', '.join(predicted_diseases)}")

for disease in predicted_diseases:

suggested_doctor = doctor_suggestion.get(disease, "General Practitioner")

print(f"Suggested Doctor for {disease}: {suggested_doctor}")

except ValueError:

print("Invalid input! Please enter valid numerical values for symptoms.")

 # Run the create dataset function

create_dataset()

disease_prediction()

CSV File

```
import pandas as pd

# Step 1: Create a Synthetic Dataset and Save it as CSV

def create_dataset():

    data = {

        'Age': [45, 34, 50, 28, 60, 35, 67, 40, 55, 33, 41, 39, 48, 52, 47, 33, 56, 39, 43, 55, 37, 60, 45, 40, 33, 44, 50, 37, 41, 60, 56, 34, 49, 45, 39, 41, 43, 34, 52, 59],

        'Blood Pressure': [130, 110, 150, 120, 140, 115, 160, 125, 135, 145, 128, 115, 140, 145, 135, 125, 150, 130, 120, 125, 135, 140, 125, 120, 130, 145, 130, 115, 125, 135, 150, 120, 140, 125, 130, 120, 125, 145, 120, 135],

        'Cholesterol': [200, 180, 220, 190, 240, 210, 250, 180, 230, 220, 210, 190, 225, 235, 220, 210, 245, 215, 200, 230, 220, 245, 210, 205, 225, 215, 240, 210, 220, 200, 255, 190, 230, 215, 200, 215, 220, 210, 230, 205],

        'Disease 1 (Hypertension)': [0, 1, 0, 1, 0, 1, 0, 0, 1, 0, 1, 1, 0, 0, 1, 1, 0, 0, 1, 1, 0, 0, 1, 0, 0, 1, 0, 1, 0, 0, 1, 1, 0, 0, 0, 0, 1, 1, 0, 1],

        'Disease 2 (Diabetes)': [1, 0, 0, 0, 0, 0, 0, 1, 0, 1, 0, 1, 0, 0, 0, 0, 0, 0, 0, 0, 1, 0, 1, 1, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0, 1, 0, 1, 0, 0, 0],

        'Disease 3 (Heart Disease)': [0, 0, 1, 0, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0, 1, 0, 0, 1, 0, 1, 0, 0, 0, 0, 1, 0, 0, 1, 0, 1, 0, 0, 0, 0, 1, 0],

        'Disease 4 (Cancer)': [0, 0, 0, 0, 1, 0, 1, 0, 0, 0, 0, 0, 0, 1, 0, 0, 1, 0, 0, 0, 0, 1, 0, 1, 0, 1, 0, 0, 0, 0, 0, 1, 1, 0, 0, 0, 1, 0, 0, 0],

        'Disease 5 (Kidney Disease)': [0, 1, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0, 1, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0, 1, 0, 0, 0, 1, 0, 0, 0, 0, 0, 1, 0, 0, 1, 0],

        'Disease 6 (Lung Disease)': [0, 0, 0, 1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0, 1, 0, 0, 1, 0, 1],

        'Disease 7 (Arthritis)': [0, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 1, 0, 0, 0, 1, 0, 0, 1, 0, 0, 0, 0, 0, 1, 0, 1, 0, 0],
```

'Disease 8 (Stroke)': [0, 1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 1, 0, 1, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0, 1, 0, 0, 0, 0, 1, 0, 0, 0, 0, 1, 0, 0, 1],

'Disease 9 (Obesity)': [0, 0, 1, 0, 1, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0, 1, 0, 0, 0, 1, 0, 0, 0, 1, 0, 1, 0, 1, 0],

'Disease 10 (Asthma)': [1, 0, 0, 0, 0, 0, 1, 0, 0, 0, 1, 0, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0, 1, 0, 0, 0, 0, 0, 0, 1, 0, 0, 1, 0, 1, 0, 0, 1, 1]

}

 # Create DataFrame from the dictionary

df = pd.DataFrame(data)

 # Save the DataFrame to a CSV file

df.to_csv('disease_data_40_samples.csv', index=False)

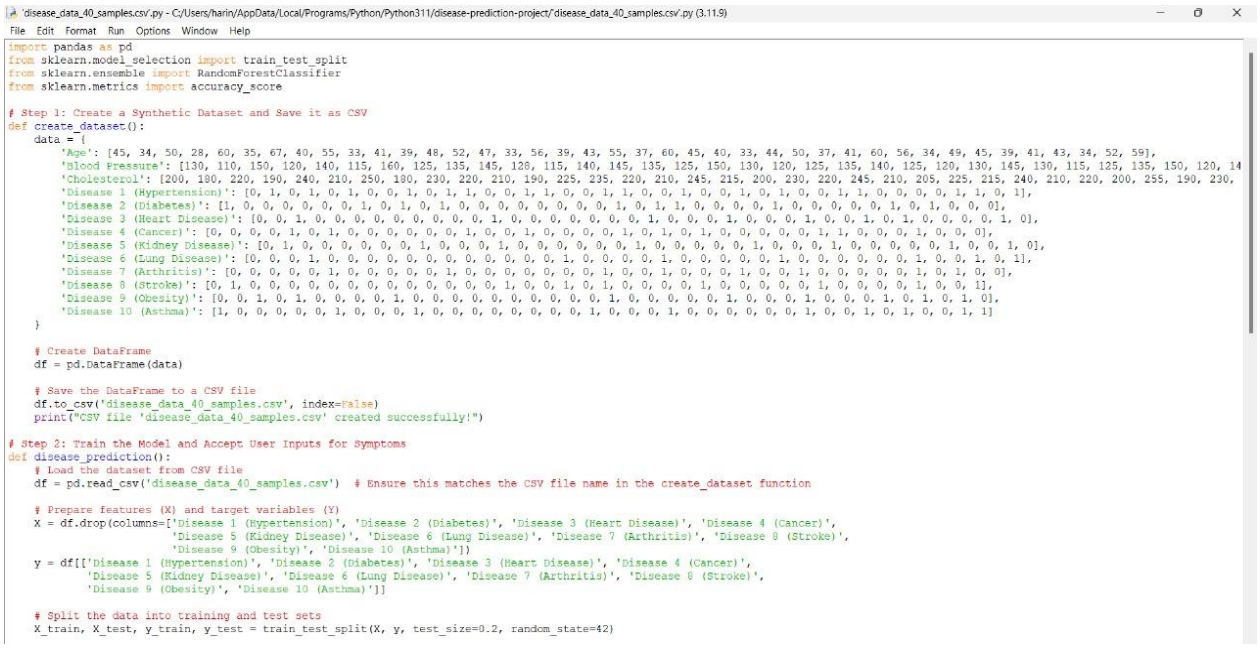
print("CSV file 'disease_data_40_samples.csv' created successfully!")

 # Call the function to generate the CSV file

create_dataset()

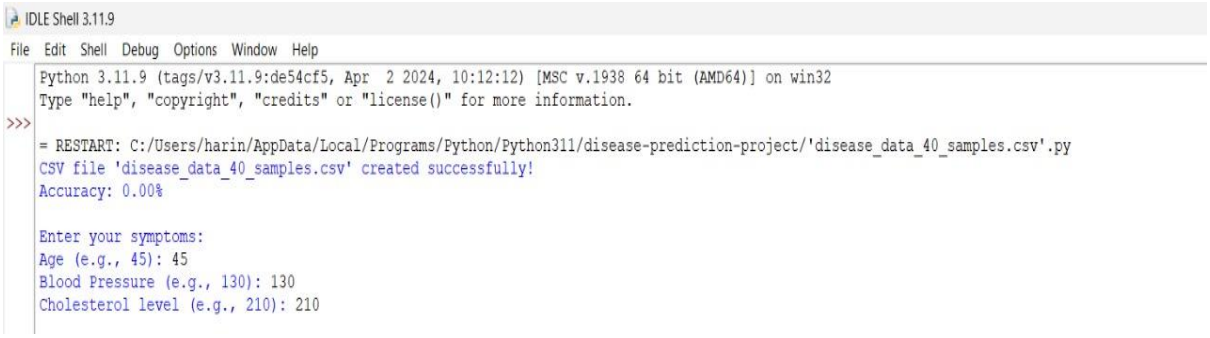
APPENDEX-2

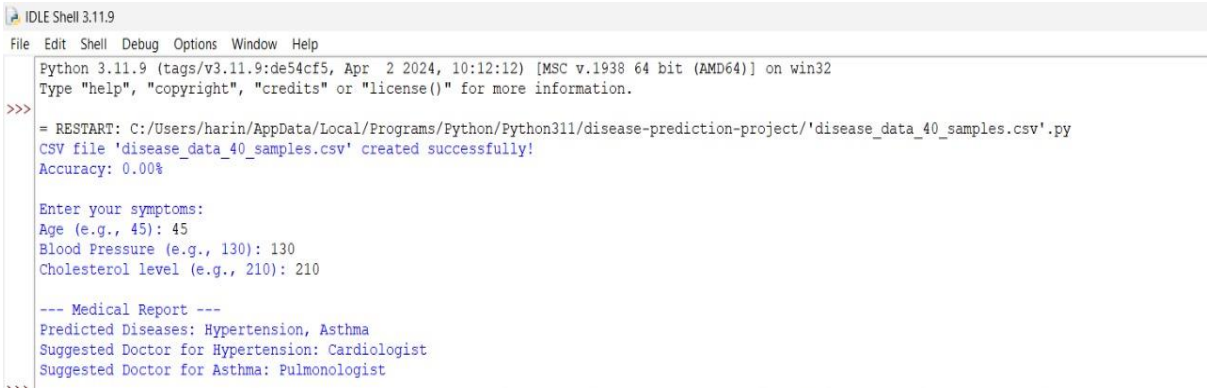
SAMPLE OUTPUT



```
'disease_data_40_samples.csv'.py - C:/Users/harin/AppData/Local/Programs/Python/Python311/disease-prediction-project/'disease_data_40_samples.csv'.py (3.11.9)
File  Edit  Format  Run  Options  Window  Help
import pandas as pd
from sklearn.model_selection import train_test_split
from sklearn.ensemble import RandomForestClassifier
from sklearn.metrics import accuracy_score

# Step 1: Create a Synthetic Dataset and Save it as CSV
def create_dataset():
    data = {
        'Age': [45, 34, 50, 28, 60, 35, 67, 40, 55, 33, 41, 39, 48, 52, 47, 33, 56, 39, 43, 55, 37, 60, 45, 40, 33, 44, 50, 37, 41, 60, 56, 34, 49, 45, 39, 41, 43, 34, 52, 59],
        'Blood Pressure': [130, 110, 150, 120, 140, 115, 160, 125, 135, 145, 128, 115, 140, 145, 135, 125, 150, 130, 120, 125, 135, 140, 125, 120, 130, 145, 130, 115, 125, 135, 150, 120, 14
        'Cholesterol': [200, 180, 220, 190, 240, 210, 250, 180, 230, 220, 210, 190, 225, 235, 220, 210, 245, 215, 200, 230, 220, 245, 210, 205, 225, 215, 240, 210, 220, 200, 255, 190, 230,
        'Disease 1 (Hypertension)': [0, 1, 0, 1, 0, 1, 0, 0, 1, 0, 1, 1, 0, 0, 1, 1, 0, 0, 1, 1, 0, 0, 1, 0, 0, 1, 0, 1, 0, 0, 1, 1, 0, 0, 0, 0, 1, 1, 0, 1],
        'Disease 2 (Diabetes)': [1, 0, 0, 0, 0, 0, 0, 1, 0, 1, 0, 1, 0, 0, 0, 0, 0, 0, 0, 0, 1, 0, 1, 1, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0, 1, 0, 1, 0, 0, 0],
        'Disease 3 (Heart Disease)': [0, 0, 1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0, 1, 0, 0, 0, 1, 0, 1, 0, 0, 0, 0, 0, 1, 0],
        'Disease 4 (Cancer)': [0, 0, 0, 0, 1, 0, 1, 0, 0, 0, 0, 0, 0, 1, 0, 0, 1, 0, 0, 0, 0, 0, 1, 0, 1, 0, 1, 0, 0, 0, 0, 0, 1, 1, 0, 0, 0, 1, 0, 0],
        'Disease 5 (Kidney Disease)': [0, 1, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0, 1, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0, 1, 0, 0, 0, 1, 0, 0, 0, 0, 0, 1, 0, 0, 1, 0],
        'Disease 6 (Lung Disease)': [0, 0, 0, 1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0, 0, 1, 0, 0, 1, 0, 1],
        'Disease 7 (Arthritis)': [0, 0, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 1, 0, 0, 0, 1, 0, 0, 0, 0, 0, 0, 1, 0, 1, 0, 0, 0],
        'Disease 8 (Stroke)': [0, 1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 1, 0, 1, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0, 1, 0, 0, 0, 0, 1, 0, 0, 1],
        'Disease 9 (Obesity)': [0, 0, 1, 0, 1, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0, 1, 0, 0, 0, 1, 0, 0, 0, 1, 0, 1, 0, 1, 0],
        'Disease 10 (Asthma)': [1, 0, 0, 0, 0, 0, 1, 0, 0, 0, 1, 0, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0, 1, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0, 1, 0, 1, 0, 0, 1, 1]
    }

    # Create DataFrame
    df = pd.DataFrame(data)

    # Save the DataFrame to a CSV file
    df.to_csv('disease_data_40_samples.csv', index=False)
    print("CSV file 'disease_data_40_samples.csv' created successfully!")

# Step 2: Train the Model and Accept User Inputs for Symptoms
def disease_prediction():
    # Load the dataset from CSV file
    df = pd.read_csv('disease_data_40_samples.csv')  # Ensure this matches the CSV file name in the create_dataset function

    # Prepare features (X) and target variables (Y)
    X = df.drop(columns=['Disease 1 (Hypertension)', 'Disease 2 (Diabetes)', 'Disease 3 (Heart Disease)', 'Disease 4 (Cancer)',
                         'Disease 5 (Kidney Disease)', 'Disease 6 (Lung Disease)', 'Disease 7 (Arthritis)', 'Disease 8 (Stroke)',
                         'Disease 9 (Obesity)', 'Disease 10 (Asthma)'])
    y = df[['Disease 1 (Hypertension)', 'Disease 2 (Diabetes)', 'Disease 3 (Heart Disease)', 'Disease 4 (Cancer)',
            'Disease 5 (Kidney Disease)', 'Disease 6 (Lung Disease)', 'Disease 7 (Arthritis)', 'Disease 8 (Stroke)',
            'Disease 9 (Obesity)', 'Disease 10 (Asthma)']]

    # Split the data into training and test sets
    X_train, X_test, y_train, y_test = train_test_split(X, y, test_size=0.2, random_state=42)
```

```
disease_data_40_samples.csv - C:/Users/harin/AppData/Local/Programs/Python/Python311/disease-prediction-project/data/disease_data_40_samples.csv (3.11.9)
File  Edit  Format  Run  Options  Window  Help
import pandas as pd

# Step 1: Create a Synthetic Dataset and Save it as CSV
def create_dataset():
    data = {
        'Age': [45, 34, 50, 28, 60, 35, 67, 40, 55, 33, 41, 39, 48, 52, 47, 33, 56, 39, 43, 55, 37, 60, 45, 40, 33, 44, 50, 37, 41, 60, 56, 34, 49, 45, 39, 41, 43, 34, 52, 59],
        'Blood Pressure': [130, 110, 150, 120, 140, 115, 160, 125, 135, 145, 128, 115, 140, 145, 135, 125, 150, 130, 120, 125, 135, 140, 125, 120, 130, 145, 130, 115, 125, 135, 150, 120, 14
        'Cholesterol': [200, 180, 220, 190, 240, 210, 250, 180, 230, 220, 210, 190, 225, 235, 220, 210, 245, 215, 200, 230, 220, 245, 210, 205, 225, 215, 240, 210, 220, 200, 255, 190, 230,
        'Disease 1 (Hypertension)': [0, 1, 0, 1, 0, 1, 0, 0, 1, 0, 1, 1, 0, 0, 1, 1, 0, 0, 1, 1, 0, 0, 1, 0, 0, 1, 0, 1, 0, 0, 1, 1, 0, 0, 0, 0, 1, 1, 0, 1],
        'Disease 2 (Diabetes)': [1, 0, 0, 0, 0, 0, 0, 1, 0, 1, 0, 1, 0, 0, 0, 0, 0, 0, 0, 0, 1, 0, 1, 1, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0, 1, 0, 1, 0, 0, 0],
        'Disease 3 (Heart Disease)': [0, 0, 1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0, 1, 0, 0, 0, 1, 0, 1, 0, 0, 0, 0, 0, 1, 0],
        'Disease 4 (Cancer)': [0, 0, 0, 0, 1, 0, 1, 0, 0, 0, 0, 0, 0, 1, 0, 0, 1, 0, 0, 0, 0, 0, 1, 0, 1, 0, 1, 0, 0, 0, 0, 0, 1, 1, 0, 0, 0, 1, 0, 0],
        'Disease 5 (Kidney Disease)': [0, 1, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0, 1, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0, 1, 0, 0, 0, 1, 0, 0, 0, 0, 0, 1, 0, 0, 1, 0],
        'Disease 6 (Lung Disease)': [0, 0, 0, 1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0, 0, 1, 0, 0, 1, 0, 1],
        'Disease 7 (Arthritis)': [0, 0, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 1, 0, 0, 0, 1, 0, 0, 0, 0, 0, 0, 1, 0, 1, 0, 0, 0],
        'Disease 8 (Stroke)': [0, 1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 1, 0, 1, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0, 1, 0, 0, 0, 0, 1, 0, 0, 1],
        'Disease 9 (Obesity)': [0, 0, 1, 0, 1, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0, 0, 0, 1, 0, 0, 0, 1, 0, 0, 0, 1, 0, 1, 0, 1, 0],
        'Disease 10 (Asthma)': [1, 0, 0, 0, 0, 0, 1, 0, 0, 0, 1, 0, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0, 1, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0, 1, 0, 1, 0, 0, 1, 1]
    }

    # Create DataFrame from the dictionary
    df = pd.DataFrame(data)

    # Save the DataFrame to a CSV file
    df.to_csv('disease_data_40_samples.csv', index=False)
    print("CSV file 'disease_data_40_samples.csv' created successfully!")

# Call the function to generate the CSV file
create_dataset()
```


IDLE Shell 3.11.9
File Edit Shell Debug Options Window Help
Python 3.11.9 (tags/v3.11.9:de54cf5, Apr 2 2024, 10:12:12) [MSC v.1938 64 bit (AMD64)] on win32
Type "help", "copyright", "credits" or "license()" for more information.
>>>
= RESTART: C:/Users/harin/AppData/Local/Programs/Python/Python311/disease-prediction-project/'disease_data_40_samples.csv'.py
CSV file 'disease_data_40_samples.csv' created successfully!
Accuracy: 0.00%
Enter your symptoms:
Age (e.g., 45): 45
Blood Pressure (e.g., 130): 130
Cholesterol level (e.g., 210): 210


IDLE Shell 3.11.9
File Edit Shell Debug Options Window Help
Python 3.11.9 (tags/v3.11.9:de54cf5, Apr 2 2024, 10:12:12) [MSC v.1938 64 bit (AMD64)] on win32
Type "help", "copyright", "credits" or "license()" for more information.
>>>
= RESTART: C:/Users/harin/AppData/Local/Programs/Python/Python311/disease-prediction-project/'disease_data_40_samples.csv'.py
CSV file 'disease_data_40_samples.csv' created successfully!
Accuracy: 0.00%
Enter your symptoms:
Age (e.g., 45): 45
Blood Pressure (e.g., 130): 130
Cholesterol level (e.g., 210): 210
--- Medical Report ---
Predicted Diseases: Hypertension, Asthma
Suggested Doctor for Hypertension: Cardiologist
Suggested Doctor for Asthma: Pulmonologist

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