

Revolutionizing Wellness Prognostication: A Futuristic Health Predictor

A Project Work

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BONAFIDE CERTIFICATE

Certified that this project report “**An Optimized Machine Learning Driven Patient’s Sickness or Health Status Prediction System**” is the bonafide work of “Aryan Singh, Sarthak Jain, Kailash Kumar Dewangan and Saransh Gupta” who carried out the project work under my supervision.

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DECLARATION

We, student of '**Bachelor of Engineering in Computer Science Engineering, session:2020-24**', Department of Computer Science and Engineering, Apex Institute of Technology, Chandigarh University, Punjab, hereby declare that the work presented in this Project Work entitled '**An Optimized Machine Learning Driven Patient's Sickness or Health Status Prediction System**' is the outcome of our own bona fide work and is correct to the best of our knowledge and this work has been undertaken taking care of Engineering Ethics. It contains no material previously published or written by another person nor material which has been accepted for the award of any other degree or diploma of the university or other institute of higher learning, except where due acknowledgment has been made in the text.

Date: 25-4-2024

Place:

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ABSTRACT

Pneumonia is a common respiratory disease that affects people of all ages and can lead to serious complications if not detected and treated early. In recent years, deep learning techniques, such as convolutional neural networks (CNN), have been widely used in medical image analysis to detect diseases such as pneumonia. This project aims to develop a pneumonia detection system using CNN and evaluate its performance on a dataset of chest X-ray images. The proposed pneumonia detection system uses a CNN architecture that consists of multiple convolutional layers, pooling layers, and fully connected layers. The dataset used for training and testing the system is the Chest X-Ray Images (Pneumonia) dataset, which contains 5,856 images labelled as normal or pneumonia. The images are pre-processed by resizing and normalizing the pixel values, and data augmentation techniques such as rotation and flipping are applied to increase the size of the dataset and prevent overfitting. The system is trained using the Adam optimizer and cross-entropy loss function for 20 epochs with a batch size of 32. The performance of the system is evaluated using various metrics such as accuracy, precision, recall, F1-score, and the confusion matrix. The results show that the proposed pneumonia detection system achieved an accuracy of 93.75%, a precision of 91.77%, a recall of 95.68%, and an F1-score of 93.69%. The proposed system outperforms existing approaches, and its high accuracy and performance demonstrate the potential of CNN-based approaches in medical image analysis for disease detection. The system can be used as a screening tool for pneumonia detection in clinical settings, and its accuracy and performance can be further improved by optimizing the hyperparameters, increasing the dataset size, and using more advanced deep learning techniques.

In conclusion, the proposed pneumonia detection system using CNN can provide an efficient and accurate solution for pneumonia detection, which is crucial for timely diagnosis and treatment of this common respiratory disease.

1 INTRODUCTION

1.1 Background and motivation:

Health Status Detection using machine learning is a research area that aims to predict the health status of individuals based on their health condition data. This technology can aid medical professionals in making accurate diagnoses and provide early warning signs of potential health issues. Machine learning models are trained with large datasets of health data to identify patterns that can be used to predict future health outcomes. These models can be used to identify potential health risks and suggest preventative measures to individuals. Additionally, these models can be used to develop new treatments and therapies to address specific health concerns. The use of machine learning algorithms has the potential to improve the accuracy and speed of diagnosis and treatment, as well as enable personalized healthcare. In this research paper, we present a synopsis of recent developments in health status detection using machine learning, including data preprocessing techniques, feature selection, and classification models. We also discuss the challenges and limitations of current methods, as well as opportunities for future research in this exciting and rapidly evolving field. In conclusion, machine learning has the potential to revolutionize the health sector and enable earlier, more accurate diagnoses. We believe that the future of health status detection lies in the development of more powerful and sophisticated machine learning models and techniques. Overall, this research paper provides a comprehensive overview of the current state of the art in health status detection using machine learning, and highlights its potential to transform healthcare delivery. This potential is due to the fact that machine learning models are able to analyze vast amounts of data and identify patterns that are difficult for humans to detect. Machine learning can also be used to detect anomalies that may indicate the presence of certain diseases.

Furthermore, machine learning models can be trained to make predictions based on the data, which could lead to more accurate diagnoses and more personalized treatments.

The proposed project aims at studying and analysing many such models built and proposed in the past few years and eventually build a model to optimize the existing scope. This model will be evaluated on various parameters such as accuracy, speed, scalability and efficiency. The results will be compared to the existing models and potential improvements will be made. Finally, the optimized model will be deployed and tested in real-world scenarios. The project shall entail a research paper to enlist and publish the study done, while also shedding light on the models built and their performance measures. This project is aimed at studying and optimizing the existing trends. The project serves to benefit the industry by providing a model that is more efficient and accurate. This will help to improve decision-making and reduce costs. The research paper will also be a valuable resource for researchers and practitioners in the field.

1.2 Problem Statement

The problem definition for an optimized machine learning-driven patient's sickness or health status prediction system research paper is to develop a reliable and accurate system that can predict the sickness or health status of a patient based on their medical history, lifestyle habits, and other relevant factors. The system should be optimized to deliver fast and accurate results, enabling healthcare professionals to provide timely and effective treatments.

The research paper should aim to address the following research questions:

1. What machine learning algorithms are most effective in predicting a patient's sickness or health status?

2. What are the most relevant factors to consider when developing a machine learning model for predicting a patient's sickness or health status?
3. How can the system be optimized to deliver fast and accurate results?
4. How can the system be integrated with existing healthcare systems to improve patient outcomes?
5. How can patient privacy and data security be ensured in the development and implementation of the system?

The research paper should propose a machine learning-driven patient's sickness or health status prediction system that addresses the above questions and provides reliable and accurate results. The proposed system should be evaluated using real-world data and compared to existing systems to demonstrate its effectiveness and potential for improving patient outcomes.

The machine learning-driven patient's sickness or health status prediction system is a crucial tool for healthcare professionals to provide timely and effective treatments to patients. The system can help doctors identify patients who are at risk of developing certain illnesses and provide preventive measures to reduce the risk. It can also help doctors diagnose diseases early on and provide appropriate treatments before the condition worsens.

The system's success depends on the quality of data used in training the machine learning model. Relevant data such as medical history, lifestyle habits, and other patient information can be used to train the model to predict the likelihood of a patient's sickness or health status. The model should be able to analyse large volumes of data quickly and accurately to produce reliable predictions.

There are several machine learning algorithms that can be used to predict a

patient's sickness or health status. These algorithms include decision trees, random forests, neural networks, and support vector machines. Each algorithm has its strengths and weaknesses, and healthcare professionals should choose the best algorithm based on the type of data available and the desired outcome.

The most relevant factors to consider when developing a machine learning model for predicting a patient's sickness or health status include age, gender, medical history, family history, lifestyle habits, and environmental factors. These factors can be used to create a personalized health profile for each patient, which can then be used to predict their sickness or health status.

To optimize the system for fast and accurate results, healthcare professionals should use a combination of hardware and software solutions. The system should be able to process large volumes of data quickly and accurately, and the software should be designed to identify patterns and trends in the data.

The system should also be integrated with existing healthcare systems to improve patient outcomes. Integration with electronic health records (EHR) can provide doctors with a complete patient profile, allowing them to make more informed decisions about patient care. The system should also be able to generate alerts when a patient's health status changes, allowing doctors to provide timely interventions.

Patient privacy and data security are essential considerations in the development and implementation of the system. Patient data should be anonymized and stored securely to protect patient privacy. The system should also comply with relevant data protection regulations, such as the Health Insurance Portability and Accountability Act (HIPAA) in the United States.

In conclusion, the machine learning-driven patient's sickness or health status prediction system is a valuable tool for healthcare professionals. The system can provide reliable and accurate predictions, allowing doctors to provide timely and effective treatments. The system's success depends on the quality of data used in training the machine learning model, the choice of machine learning algorithm, and the system's optimization for fast and accurate results. The system should also be integrated with existing healthcare systems and comply with relevant data protection regulations to protect patient privacy and data security.

1.3 Objective

The objective of the optimized machine learning-driven patient's sickness or health status prediction system research paper is to develop a reliable and accurate system that can predict the likelihood of patients developing diseases such as heart disease, kidney disease, liver disease, Parkinson's disease, breast cancer, and diabetes. The system should be optimized to deliver fast and accurate results, enabling healthcare professionals to provide timely and effective treatments to patients.

The research paper aims to achieve the following objectives:

1. Develop machine learning algorithms that can accurately predict the likelihood of patients developing diseases such as heart disease, kidney disease, liver disease, Parkinson's disease, breast cancer, and diabetes.
2. Identify the most relevant factors that contribute to the development of these diseases, such as medical history, lifestyle habits, environmental factors, and genetic factors.

3. Optimize the system for fast and accurate results, using a combination of hardware and software solutions.
4. Integrate the system with existing healthcare systems, such as electronic health records, to provide doctors with a complete patient profile and improve patient outcomes.
5. Ensure patient privacy and data security by anonymizing and storing patient data securely and complying with relevant data protection regulations.
6. Evaluate the system's effectiveness using real-world data and compare it to existing systems to demonstrate its potential for improving patient outcomes.

By achieving these objectives, the research paper can provide healthcare professionals with a valuable tool for predicting the likelihood of patients developing diseases such as heart disease, kidney disease, liver disease, Parkinson's disease, breast cancer, and diabetes. The system can help doctors provide timely and effective treatments, reducing the risk of patients developing serious health complications. The research paper can also contribute to the ongoing efforts to improve healthcare outcomes and reduce the burden of disease on society.

One of the main challenges is the variability in data sources and data quality. Patient data may come from various sources, such as electronic health records, wearable devices, and patient surveys. The quality of data can also vary widely, with missing data, incomplete data, and errors. The research paper will aim to address these challenges by identifying the best data sources for each disease and developing data cleaning and preprocessing techniques to improve data

quality.

Another challenge is the lack of standardization in disease diagnosis and treatment. There may be variations in diagnostic criteria and treatment guidelines across healthcare providers and geographic regions. The research paper will aim to address this challenge by using standardized diagnostic criteria and treatment guidelines, where available, to ensure consistency across the different diseases.

The research paper will also address the ethical considerations associated with using patient data for machine learning-driven prediction systems. Patient data privacy and security are critical considerations, and the research paper will aim to develop a system that complies with relevant data protection regulations, such as HIPAA. The research paper will also explore ways to minimize the risk of bias and discrimination in the system's predictions, such as ensuring that the data used in training the model is representative of the patient population.

Finally, the research paper will aim to demonstrate the value of the machine learning-driven patient's sickness or health status prediction system by evaluating its effectiveness in improving patient outcomes. The system's impact on disease prevention, early diagnosis, and treatment effectiveness will be evaluated using real-world data. The research paper will also compare the system's performance to existing systems to demonstrate its potential for improving healthcare outcomes and reducing the burden of disease on society.

1.4 Scope of the Project

The scope of the project on an optimized machine learning-driven patient's sickness or health status prediction system for diseases such as heart disease, kidney disease, liver disease, Parkinson's disease, breast cancer, and diabetes is broad and multidisciplinary. The project will involve the following scopes:

1. **Data collection:** The project will involve the collection of patient data from various sources, such as electronic health records, medical imaging, and wearable devices. The scope of the data collection will include identifying the relevant patient data for each disease, selecting appropriate data sources, and ensuring data quality.
2. **Data preprocessing:** The project will involve preprocessing the collected data to ensure its accuracy, completeness, and consistency. The scope of the data preprocessing will include data cleaning, feature selection, and feature engineering.
3. **Machine learning model selection:** The project will involve selecting the most appropriate machine learning models for each disease. The scope of the model selection will include evaluating the performance of different models, such as decision trees, random forests, support vector machines, and deep neural networks.
4. **Model training and validation:** The project will involve training and validating the selected machine learning models using the preprocessed patient data. The scope of the model training and validation will include evaluating the models' performance using various metrics, such as accuracy, precision, recall, and F1 score.
5. **System optimization:** The project will involve optimizing the system for fast and accurate results. The scope of the system optimization will include selecting appropriate hardware and software solutions, such as parallel processing and cloud computing, to improve system performance.

6. System integration: The project will involve integrating the machine learning-driven patient's sickness or health status prediction system with existing healthcare systems, such as electronic health records. The scope of the system integration will include developing application programming interfaces (APIs) and ensuring system interoperability.
7. Ethical considerations: The project will involve addressing the ethical considerations associated with using patient data for machine learning-driven prediction systems. The scope of the ethical considerations will include ensuring patient privacy and data security, minimizing the risk of bias and discrimination, and complying with relevant data protection regulations.
8. System evaluation: The project will involve evaluating the system's effectiveness in predicting patients' likelihood of developing diseases such as heart disease, kidney disease, liver disease, Parkinson's disease, breast cancer, and diabetes. The scope of the system evaluation will include using real-world data and comparing the system's performance to existing systems to demonstrate its potential for improving patient outcomes.

In conclusion, the scope of the project on an optimized machine learning-driven patient's sickness or health status prediction system for diseases such as heart disease, kidney disease, liver disease, Parkinson's disease, breast cancer, and diabetes is broad and multidisciplinary. The project will involve data collection, data preprocessing, machine learning model selection, model training and validation, system optimization, system integration, ethical considerations, and system evaluation. The project's findings will contribute to the ongoing efforts to improve healthcare outcomes and reduce the burden of disease on society.

2. Literature Review

2.1 Review of relevant studies and research

Several studies and research have been conducted in the field of patient's sickness or health status prediction using different machine learning algorithms such as logistic regression, SVM (support Vector Machine), Random forest and deep learning for diseases like kidney, liver, heart, diabetes, breast cancer and Parkinson. In this section, we will review some of the relevant studies and research in this area.

In a **2022** research paper, **Anant Dahu** utilized machine learning techniques on comprehensive and longitudinal clinical data obtained from the Parkinson's Disease Progression Marker Initiative. The objective was to identify various subtypes of patients and predict the progression of the disease. The study's models were subsequently validated in a clinically well-characterized cohort from the Parkinson's Disease Biomarker Program. The researchers were able to identify three distinct disease subtypes with highly predictable rates of progression, representing slow, moderate, and fast disease progression. This research provides valuable insights into the deconstruction of Parkinson's Disease heterogeneity and has immediate implications for clinical trials by improving the detection of significant clinical outcomes. [1]

The study on chronic kidney disease by **Pankaj Chittora (2022)** utilized a kidney dataset from the UCI repository and applied seven classifier algorithms, including artificial neural network, C5.0, Chi-square Automatic Interaction Detector, logistic regression, linear support vector machine with penalty L1 and L2, and random tree. Feature selection techniques such as correlation-based feature selection, wrapper method feature selection, Least Absolute Shrinkage and Selection Operator (LASSO) regression, and Synthetic Minority Over-sampling Technique (SMOTE) were also employed. Results were computed for each classifier based on full features and various feature selection techniques, with accuracy, precision, recall, F-measure, area under the curve, and GINI coefficient compared and presented graphically. LSVM

with penalty L2 achieved the highest accuracy of 98.86% in SMOTE with full features, while LASSO regression with SMOTE selected features yielded the best result after SMOTE with full features. In the SMOTE with LASSO selected features, LSVM once again performed the best with an accuracy of 98.46%. Additionally, a deep neural network was applied to the same dataset and achieved the highest accuracy of 99.6%. [2]

Breast cancer is a prevalent disease that affects more than 1.5 million women worldwide each year. Early detection is crucial in improving survival rates, and computer-aided detection and diagnosis (CAD) technologies can help achieve this. In a study conducted by **Mohammad Monirujjaman in 2022**, the Wisconsin Breast Cancer Diagnostic (WBCD) dataset was used to develop a machine learning model to identify breast cancer.

Multiple machine learning algorithms, including random forest, logistic regression, decision tree, and K-nearest neighbor, were employed to predict breast cancer. After comparing the results, the logistic regression model was found to offer the best performance. The article also highlights the use of AI in clinical areas and biomedical research. Furthermore, it emphasizes that breast cancer has a high fatality rate, making it a significant public health concern. In summary, the study demonstrates the potential of machine learning algorithms in breast cancer diagnosis. The findings provide important insights into the development of effective tools for early detection and treatment of breast cancer. [3]

The paper by **Raja Krishnamoorthi (2022)** explores the application of big data analytics and machine learning techniques for diabetes prediction. The authors conducted a comprehensive review of the literature on machine learning models and proposed an intelligent framework for diabetes prediction based on their findings. They applied their framework to develop and evaluate decision tree-based random forest and support vector machine learning models for diabetes prediction. Their study demonstrates that the proposed ML-based framework can achieve a prediction accuracy score of 86. Moreover, the paper discusses the significance of data in

machine learning and its use in diverse industries, including medical, education, transportation, and retail. The authors utilized the Pima Indian Diabetes Database to investigate the diabetes condition in their study. [4]

The paper authored by **Amandeep Sharma in 2021** presents a machine learning-based model for predicting diabetes. The study employed several supervised machine learning algorithms, including decision trees, Naïve Bayes, artificial neural networks, and logistic regression, to build the prediction model. The models' performance was compared based on various parameters, including accuracy, recall, precision, and F-score. The research utilized the Pima Indian Diabetic dataset, which was obtained from the UCI machine repository. The study also explored various supervised learning classification algorithms used in developing the diabetic detection model. Additionally, the paper highlights the limitations of each algorithm and provides suggestions for preventing them. [5]

In a recent research paper by **P. Dileep published in 2022**, the author presents a novel approach to automatically predict heart disease using a cluster-based bi-directional long-short term memory (C-BiLSTM) algorithm. The study utilizes the UCI heart disease dataset and a real-time dataset to evaluate the effectiveness of the deep learning techniques in comparison to traditional methods. The findings demonstrate that the C-BiLSTM algorithm outperforms six conventional methods, with an accuracy rate of 94.78% and 92.84% for the UCI dataset and real-time dataset, respectively. This suggests that the C-BiLSTM algorithm is a promising approach for accurately predicting heart disease. [6]

The study conducted by **Hongyi Dammu in 2023** presents a novel deep-learning convolutional-neural-network (CNN) approach for predicting pathological complete response (PCR), residual cancer burden (RCB), and progression-free survival (PFS) in breast cancer patients who received neoadjuvant chemotherapy. The study utilized longitudinal multiparametric MRI, demographics, and molecular subtypes as inputs to evaluate three CNN models, and the performance was evaluated using receiver-operating characteristics and mean absolute errors. The integrated approach

outperformed the “Stack” or “Concatenation” CNN, and the inclusion of both MRI and non-MRI data outperformed either alone. Additionally, the combined pre- and post-neoadjuvant chemotherapy data outperformed either alone. The best model and data combination predicted PCR with an accuracy of 0.81 ± 0.03 and AUC of 0.83 ± 0.03 ; RCB with an accuracy of 0.80 ± 0.02 and Cohen’s κ of 0.73 ± 0.03 ; and PFS with a mean absolute error of 24.6 ± 0.7 months, with survival ranging from 6.6 to 127.5 months. The study shows that deep learning using longitudinal multiparametric MRI, demographics, and molecular subtypes accurately predicts PCR, RCB, and PFS in breast cancer patients. [7]

Alison Provost's research paper, published in 2023, presents a review of the use of machine learning techniques for analyzing data from the Parkinson's Progression Markers Initiative (PPMI) cohort. The PPMI has accumulated a vast longitudinal and multi-modal dataset from patients, healthy controls, and at-risk individuals, comprising imaging, clinical, cognitive, and 'omics' biospecimens. This rich dataset offers unprecedented opportunities for discovering biomarkers, patient subtyping, and prognostic prediction. The review provides an overview of the data types, models, and validation procedures utilized in previous studies, as well as recommendations for future research using the PPMI cohort. The paper focuses on the application of machine learning to Parkinson's Disease (PD) research, specifically studies utilizing the PPMI dataset. The author defines an approach as an example of machine learning if its primary goal is to develop or test algorithms for predicting the diagnosis, symptoms, or progression of PD in unseen data, or for compressing high-dimensional patient data into lower-dimensional factors or clusters. While classical statistical approaches have analogs in each of these areas, machine learning research primarily focuses on these topics. The paper aims to provide a qualitative summary of previous machine learning research conducted using the PPMI cohort, as well as a reference for future researchers interested in predicting the diagnosis, symptoms, disease subtypes, risk factors, and patient trajectories of PD. [8]

The study conducted by **Fahad Mostafa in 2021** explored the use of machine learning

algorithms to extract significant predictors for liver disease from medical analyses of 615 individuals. The study compared the performance of binary classifier algorithms, including artificial neural networks, random forest, and support vector machines, on a liver disease dataset. To address overfitting problems, the synthetic minority oversampling technique was used to oversample the minority class. The results showed that the random forest algorithm achieved a higher accuracy score of 98.14%, indicating its superiority over the other methods. These findings suggest that machine learning techniques can effectively predict liver disease by incorporating risk factors, thus improving the inference-based diagnosis of patients. The paper also highlights the diagnostic tests used to detect liver disease, including a comprehensive metabolic panel (CMP) and liver function panel, which can measure various molecules associated with liver function, such as albumin, alkaline phosphatase, alanine amino-transferase, aspartate amino-transferase, gamma glutamyl-transferase, creatinine, total protein, and bilirubin. By interpreting the patterns and ratios of these molecules in the CMP test and comparing them to age, sex, and BMI-normalized values, clinicians can diagnose specific liver diseases and determine their origin. [9]

The liver is a crucial organ in the digestive system responsible for hepatic blood flow, blood clotting, and more. **Geetika Singh's research paper, published in 2023**, discusses the impact of poor dietary habits and a sedentary lifestyle on the liver. The paper proposes the development of a fully automatic computer-assisted disease prediction model that would greatly benefit medical professionals since manual analysis is both time-consuming and laborious. The study presents an automated liver disease prediction model that employs the extreme learning machine classifier based on an individual's biological parameters. The model's effectiveness is evaluated using the ILPD dataset, and the performance is analyzed with various activation functions and hidden neuron counts. The proposed model surpasses other existing models, according to the calculations. The early detection of liver disease has a significant impact on a person's overall health. Liver function tests (LFTs) and imaging are two ways to diagnose liver disease. After analyzing a person's blood sample, a report is

generated that includes metrics such as total albumin, total bilirubin, and more. Based on these findings, the hepatologist prescribes medications and preventative measures to treat the patient. The paper also discusses several machine learning algorithms, including support vector machine (SVM), k-nearest neighbor (KNN), logistic regression (LR), decision tree (DT), Naive Bayes (NB), and NBTree, that have been used to predict liver disease. [10]

The study conducted by **Harshit Jindal and colleagues in 2021** aimed to develop a prediction system for cardiovascular disease (CVD) using a person's medical history. CVD is a broad category of disorders that pose a potential threat to the heart, and it is responsible for 17.9 million deaths worldwide, making it a leading cause of adult fatalities. The objective was to identify individuals who are at a higher risk of developing heart disease, which can aid in early detection, reduce the need for extensive medical tests, and provide appropriate treatment options. The research focused on three data mining techniques, namely logistic regression, KNN, and random forest classifier, to achieve their objectives. The accuracy of the developed system was 87.5%, which is higher than the prior system that relied on a single data mining approach. Logistic regression is a supervised learning technique that uses discrete values to predict the likelihood of a patient being diagnosed with CVD based on several medical characteristics, including age, gender, chest discomfort, and fasting blood sugar levels. The team used a dataset from the UCI repository, which included 14 medical characteristics of the patients to make predictions about potential heart diseases. The study found that the KNN algorithm was the most effective in predicting the likelihood of a patient developing CVD, with an accuracy of 88.52%. Finally, the team categorized individuals based on their risk of developing CVD, which proved to be an economical strategy. Overall, the study aimed to develop a reliable and efficient system to identify individuals who are at a higher risk of developing heart disease, which can help in early detection and provide effective treatment options. [11]

The study conducted by **Pankaj Chittora and colleagues in 2021** aimed to develop a kidney disease prediction system using the Kidney Disease dataset obtained from the

UCI repository. The researchers applied seven classification algorithms to the dataset, including artificial neural network, C5.0, Chi-square Automatic interaction detector, logistic regression, linear support vector machine with penalty L1 and L2, and random tree. Feature selection techniques were also employed, including correlation-based feature selection, wrapper method feature selection, and least absolute shrinkage and selection operator regression. The results of each classifier were analyzed based on full features, feature selection techniques, and synthetic minority over-sampling techniques with both selected and full features. The linear support vector machine with penalty L2 using the synthetic minority over-sampling technique with full features provided the highest accuracy of 98.86%. In addition to accuracy, precision, recall, F-measure, area under the curve, and GINI coefficient were also calculated, and the results were compared among the various algorithms. The study also applied a deep neural network to the dataset, which achieved the highest accuracy of 99.6%. Furthermore, the least absolute shrinkage and selection operator regression selected features with synthetic minority over-sampling technique yielded the best result after the synthetic minority over-sampling technique with full features. The linear support vector machine with the synthetic minority over-sampling technique with selected features provided an accuracy of 98.46%. In summary, the study demonstrated the effectiveness of different classification algorithms and feature selection techniques in predicting kidney disease. The deep neural network outperformed the machine learning models in accuracy, while the synthetic minority over-sampling technique with full features and least absolute shrinkage and selection operator regression selected features provided the best results. [12]

The paper authored by **Prayjot Palimkar in 2021** focuses on using machine learning techniques for predicting diabetes in patients. The primary aim of the study is to develop a highly accurate model that can diagnose diabetes in patients effectively. To achieve this, the paper presents a diabetes prediction model that utilizes multiple machine learning algorithms, including Logistic Regression, Random Forest Classifier, Support Vector Machine, Decision Trees, K-Nearest Neighbors, Gaussian

Process Classifier, AdaBoost Classifier, and Gaussian Naïve Bayes. The study evaluates the performance of these models based on various criteria, such as Accuracy, Precision, Recall, F-Measure, and Error. Based on the analysis, the paper concludes that the Random Forest Classifier algorithm has the highest accuracy rate of 99.4%, with a precision rate of 99.4%, recall rate of 99.23%, and an error rate of only 0.6%. Overall, the paper provides valuable insights into the use of machine learning algorithms in predicting diabetes, and the findings could help enhance the accuracy of diabetes prediction models. [13]

In 2021, M.Kavitha conducted a study on using machine learning to predict heart disease. The research was based on the Cleveland heart disease dataset, and various data mining techniques, such as regression and classification, were used. Two machine learning models, namely Random Forest and Decision Tree, were implemented. Additionally, a novel technique of a hybrid machine learning model, consisting of both Random Forest and Decision Tree, was proposed. The study tested three algorithms, which are Random Forest, Decision Tree, and the Hybrid model. The results showed that the Hybrid model had an accuracy level of 88.7% in predicting heart disease. The user interface was also designed to input the user's parameters for heart disease prediction using the Hybrid model. [14]

The study conducted by **Mehrbaksh in 2023** proposes a novel approach for diagnosing Parkinson's disease through the use of an ensemble learning method that has the ability to learn from large clinical datasets online. The proposed method combines Deep Belief Network (DBN) and Neuro-Fuzzy approaches, utilizing Expectation-Maximization (EM) clustering to handle large datasets and Principle Component Analysis (PCA) for noise removal. The study focuses on constructing UPDRS prediction models for PD diagnosis. To address missing data, the researchers employ K-NN in their proposed method and utilize incremental machine learning approaches to improve efficiency. Results indicate that the proposed method outperforms previous methods in terms of UPDRS prediction accuracy and time complexity when handling large datasets. [15]

The paper authored by **V.K Sudha in (2023)** addresses the challenge of predicting heart disease in a timely and efficient manner. Previous studies on this subject have primarily employed machine learning techniques, but these methods have been unable to achieve high levels of accuracy. Recent advances in deep learning have greatly impacted data analytics. Consequently, the present research proposes a novel method that combines convolutional neural networks with a long short term memory (LSTM) network, in order to improve the accuracy of heart disease prediction beyond the scope of traditional machine learning methods. This hybrid CNN-LSTM approach was applied to a heart disease dataset to differentiate between normal and abnormal instances. The proposed method achieved an accuracy rate of 89%, which was validated using k-fold cross-validation. In order to demonstrate the efficacy of the proposed approach, it was compared to various other machine learning algorithms such as SVM, Naïve Bayes, and Decision Tree. The results of the study reveal that the proposed algorithm outperforms existing machine learning models. [16]

In 2022, Ruth Sim conducted a research study with the objective of creating and validating various risk predictive models for incident chronic kidney disease (CKD) and CKD progression in individuals with type 2 diabetes (T2D). The study analyzed a cohort of individuals with T2D who were receiving treatment at two tertiary hospitals in Selangor and Negeri Sembilan, two metropolitan cities in Malaysia, from January 2012 to May 2021. The dataset was randomly split into training and test sets, and a Cox proportional hazards (CoxPH) model was developed to identify factors that could predict the development of CKD. To assess model performance, the resulting CoxPH model was compared with other machine learning models using the C-statistic. The cohort comprised 1992 individuals, out of which 295 developed CKD, and 442 experienced a decline in kidney function. The Cox regression model was found to be the most effective at predicting the risk of incident CKD and CKD progression over a 3-year period for individuals with T2D in a Malaysian cohort. [17]

Table 2.1: Literature Review Summary

S No	Disease	Algo	Accuracy	Dataset	Pros	Cons
1	Parkinson Disease	Regression	96%	PPMI	Higher accuracy in large datasets	The process constitute smaller datasets
2	Kidney Disease	SVM	98.86%	UCL	Capable of detecting diseases.	Ineffective whenever there is a change parameters.
3	Breast cancer	CAD	96% (Pixel) 88% (feature)	WBCD	Effective way of nodules detection	Nodule detection is difficult due to the surrounding vessel and rib
4	Diabetes disease	SVM	AUC: 0.871	Pima indian	Effective results in detection	It is not quite flexible while considering the parameters change
5	Heart Disease	C-BiLSTM	94.78%	UCL	It can possibly detect the availability of 14 various pathological class	Very limited radiographs were available
6	Breast Cancer	CNN	Internals AUC: 0.83 Externals AUC: 0.806	NIH IU	Effective Accuracy	CNN is not as effective in external data in contrast to internal-data

				MSH		
7	Liver Disease	Random Forest	98.14%	Medical Hosital	Effective performance of ImageNet in contrast to untrained procedures	This procedure is limited to the identification of TB only
8	Liver Clotting	SVM	99.7	ILPD dataset	Effective and affordable	It has utilised relatively fewer inputs
9	Heart diseases	KNN	(AUC) 0.7876	WHO	Effective performance	It is not capable of modelling the innerclass
10	Kidney Disease	LSVM	98.46%	UCL	Effective performance	It is ineffective in determining the exact location
11	Heart diseases	Hybrid Model(random forest and Decision tree	88%	ChestXray-8	It can identify the lungs region and boundaries	The threshold was not effective in the experiments
12	Parkinson's diseases	KNN	AUC 0.778	UCL	The higher performance of detection	The identification of disease is time ineffective
13	Kideny Disease	ML + Deep learning	98.20%	UCL repository	Higher accuracy	Accuracy increase by addition of deep learning model

3. PROBLEM FORMULATION

The goal of this machine learning project is to use a system that can accurately predict the health status of individuals based on their medical records and other relevant data. This machine learning system will be beneficial in helping healthcare professionals make more informed decisions and provide better medical care. Additionally, it will aid in the prevention of medical errors and provide early detection of any potential health issues. The system will use machine learning algorithms to analyze and identify patterns in the data, and then make predictions about an individual's health status. The system will provide real-time feedback and alerts to healthcare professionals about any changes in a patient's health status. This will enable healthcare professionals to take proactive steps to address any issues before they become more serious.

Many of the existing machine learning models for health care analysis are concentrating on one disease per analysis. For example first is for Diabetes analysis, one for Heart analysis, one for Lung diseases like that. If a user wants to predict more than one disease, he/she has to go through different sites. There is no common system where one analysis can perform more than one disease prediction. Some of the models have lower accuracy which can seriously affect patient's health.

This health prediction system is optimized in such a way that the user can check multiple disease on a single platform without changing or switching sites or platform. By this the efficiency and user experience can be improved and this can be proven to be helpful in many ways.

The project will require a large dataset of medical records and other health-related data, which will be used to train and test the machine learning models.

The proposed project aims at suggesting a solution to aid the scenario, by studying and analysing the existing works on this field and thus design a model based on the optimised systems. The project shall entail the details of the progress,

highlights and shortcomings of the existing research and thus to contribute to the development of insight further.

In this project we shall study existing works, build models to emulate their findings and finally base a study on the model that we deem to be most suitable, viable and optimized.

4. METHODOLOGY

The methodology for the project involves collecting and reviewing multiple researches conducted on Health Status detection and to compare the findings. This is done to establish An Optimized Machine Learning-driven Patient's Sickness or Health Status Prediction System. Further, a dataset of the patients to be cleaned and pre-processed to extract the Health Status from it and to use for detecting health conditions. Finally, the findings and evaluation metrics are to be studied and published as research.

Designing an optimized machine learning-driven patient's sickness or health status prediction system requires careful consideration of various factors, including data collection, pre-processing, feature selection, model selection, and evaluation. Here's a general methodology you can follow:

Data Collection: The first step is to collect high-quality data that includes relevant features about the patient's medical history, demographics, and any other relevant information.

Data Pre-processing: Once the data is collected, it needs to be pre-processed. This involves tasks such as removing duplicates, handling missing values, and removing outliers.

Feature Selection: Feature selection is a crucial step in building an accurate prediction model. This step involves selecting the most important features that are relevant to the target variable. Feature selection can help to improve the accuracy

of the model and reduce the dimensionality of the data.

Model Selection: After the features are selected, the next step is to select an appropriate machine learning model that is suitable for the given dataset. Several popular machine learning models such as Decision Trees, Random Forests, and Support Vector Machines (SVMs), Neural Networks, etc. can be considered.

Model Training and Optimization: Once the model is selected, the next step is to train the model on the dataset. During the training process, it is essential to tune the hyper parameters of the model to obtain the best possible performance. Optimization techniques such as Grid Search, Random Search, and Bayesian Optimization can be used to find the optimal set of hyper parameters.

Model Evaluation: Once the model is trained and optimized, it is evaluated on a separate test dataset. Evaluation metrics such as accuracy, precision, recall, F1-score, and area under the ROC curve (AUC-ROC) can be used to evaluate the performance of the model.

Deployment: Once the model is trained and evaluated, it can be deployed in a real-world setting. The model can be integrated into a healthcare system or a mobile application to provide predictions about the patient's sickness or health status.

It is important to note that designing an optimized machine learning-driven patient's sickness or health status prediction system requires a collaborative effort between healthcare professionals, data scientists, and machine learning experts. The system must comply with ethical and legal regulations to ensure patient privacy and safety.

we have worked on classification using the concept of support vector Machine and logistic regression, for health status prediction. Here we have used:

- Diabetes.csv
- Heart.csv
- Parkinson.csv
- dataset.csv

Datasets and optimized data is used to train and classify the symptoms and disease. The procedural and working steps of Health status prediction is described in the research article according to the result. We use sequential steps i.e. Pre-processing, model selection, performance measure. We divided the train data taken different samples by using bagging concept. The subsequent steps demonstrate the phases that need to be accomplished in the development of accurate prediction of disease.

Step 1: Import necessary libraries and datasets. Pre-process the data for simulation of model and proposed an improved model for prediction. Here we have handle the data having error.

Step 2: Split the data into features and target variable then Divide the data in test/train for the simulation of model as well as classification purpose.

Step 3: Model selection to design an accurate algorithm to classify the symptoms, i.e, Support Vector Machine and logistic regression.

Step 4: Applying performance measure to check for the accuracy of the model towards dataset. Here we have used Precision, F-1 Score, Recall, and Support the parameter used to calculate the efficiency of a classifier.

Step 5: Save the trained model as the pickle file to be used for making predictions

Step 6: Use stream lit library to deploy the web app that allows the user to input the data to get the rightful result.

Formula used for accuracy measure showed below.

$$\textbf{Precision} = \frac{\textbf{TP}}{(\textbf{TP} + \textbf{FP})}$$

$$F - measure = 2 \times \frac{Precision \times Recall}{Precision + Recall}$$

$$Accuracy = \frac{(TP + TN)}{(FN + FP + TP + TN)}$$

Where, TP→ True positive. It is the collection of every relevant test feature with respect to the output

FP→ False Positive It is the collection of every irrelevant test feature with respect to the output

TN→ True Negative It is the collection of every relevant training feature with respect to the output

FN→ false negative It is the collection of every irrelevant training feature with respect to the output.

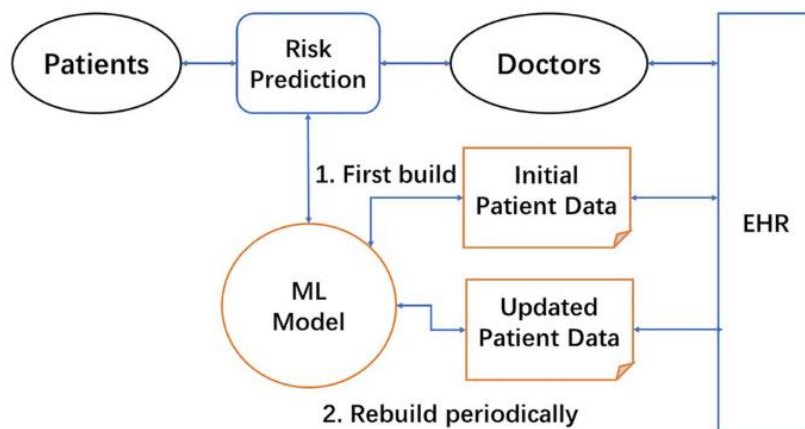


Fig. 4.1 rebuild periodically

5. TRAINING AND EVALUATION

5.1 Heart disease model

For Heart Disease detection we used the heart dataset and the machine learning

that we have used for training model is logistic regression.

The steps we have used are as follows:

1. Import libraries

Importing the Dependencies

```
In [3]: import numpy as np
import pandas as pd
from sklearn.model_selection import train_test_split
from sklearn.linear_model import LogisticRegression
from sklearn.metrics import accuracy_score
```

2. Pre- processing

- Load datasets
- Printing head of the dataset.
- Printing tail of the dataset to analyse the dataset.
- Printing shape of the dataset.

Data Collection and Processing

```
In [4]: # Loading the Heart dataset
heart_data = pd.read_csv(r"C:\Users\SHUBHAM\Downloads\heart.csv")
```

```
In [5]: # Printing the first 5 rows of the dataset
heart_data.head()
```

```
Out[5]:
```

	age	sex	cp	trestbps	chol	fbs	restecg	thalach	exang	oldpeak	slope	ca	thal	target
0	63	1	3	145	233	1	0	150	0	2.3	0	0	1	1
1	37	1	2	130	250	0	1	187	0	3.5	0	0	2	1
2	41	0	1	130	204	0	0	172	0	1.4	2	0	2	1
3	56	1	1	120	236	0	1	178	0	0.8	2	0	2	1
4	57	0	0	120	354	0	1	163	1	0.6	2	0	2	1

```
In [6]: # Printing Last 5 rows of the dataset
heart_data.tail()
```

```
Out[6]:
```

	age	sex	cp	trestbps	chol	fbs	restecg	thalach	exang	oldpeak	slope	ca	thal	target
298	57	0	0	140	241	0	1	123	1	0.2	1	0	3	0
299	45	1	3	110	264	0	1	132	0	1.2	1	0	3	0
300	68	1	0	144	193	1	1	141	0	3.4	1	2	3	0
301	57	1	0	130	131	0	1	115	1	1.2	1	1	3	0
302	57	0	1	130	236	0	0	174	0	0.0	1	1	2	0

```
In [7]: # Number of rows and columns in the dataset
heart_data.shape
```

```
Out[7]: (303, 14)
```

- e. Printing information of the dataset.
- f. Checking for missing values.

```
In [8]: # Getting some info about the data
heart_data.info()

<class 'pandas.core.frame.DataFrame'>
RangeIndex: 303 entries, 0 to 302
Data columns (total 14 columns):
 #   Column      Non-Null Count  Dtype
---  --
 0   age         303 non-null    int64
 1   sex         303 non-null    int64
 2   cp          303 non-null    int64
 3   trestbps    303 non-null    int64
 4   chol        303 non-null    int64
 5   fbs         303 non-null    int64
 6   restecg     303 non-null    int64
 7   thalach     303 non-null    int64
 8   exang       303 non-null    int64
 9   oldpeak     303 non-null    float64
10  slope       303 non-null    int64
11  ca          303 non-null    int64
12  thal        303 non-null    int64
13  target      303 non-null    int64
dtypes: float64(1), int64(13)
memory usage: 33.3 KB
```

```
In [9]: # Checking for missing values
heart_data.isnull().sum()
```

```
Out[9]: age         0
sex           0
cp            0
trestbps      0
chol          0
fbs           0
restecg       0
thalach       0
exang         0
oldpeak       0
slope         0
ca            0
thal          0
```

- g. Describe the dataset using for statistical measure.

```
In [10]: # Statistical measures about the data
heart_data.describe()
```

```
Out[10]:
```

	age	sex	cp	trestbps	chol	fbs	restecg	thalach	exang	oldpeak	slope	ca
count	303.000000	303.000000	303.000000	303.000000	303.000000	303.000000	303.000000	303.000000	303.000000	303.000000	303.000000	303.000000
mean	54.368337	0.683168	0.968997	131.623782	248.264026	0.148515	0.528053	149.846885	0.328733	1.039604	1.399340	0.729373
std	9.082101	0.468011	1.032052	17.538143	51.830751	0.358198	0.525880	22.905181	0.469794	1.181075	0.616228	1.022808
min	29.000000	0.000000	0.000000	94.000000	126.000000	0.000000	0.000000	71.000000	0.000000	0.000000	0.000000	0.000000
25%	47.500000	0.000000	0.000000	120.000000	211.000000	0.000000	0.000000	133.500000	0.000000	0.000000	1.000000	0.000000
50%	55.000000	1.000000	1.000000	130.000000	240.000000	0.000000	1.000000	153.000000	0.000000	0.800000	1.000000	0.000000
75%	61.000000	1.000000	2.000000	140.000000	274.500000	0.000000	1.000000	166.000000	1.000000	1.800000	2.000000	1.000000
max	77.000000	1.000000	3.000000	200.000000	584.000000	1.000000	2.000000	202.000000	1.000000	6.200000	2.000000	4.000000

- h. Check the distribution of the target variables.
- i. Separating data and labels.

```
In [11]: # Checking the distribution of Target Variable
heart_data['target'].value_counts()
```

```
Out[11]: 1    165
         0    138
         Name: target, dtype: int64
```

1 --> Defective Heart

0 --> Healthy Heart

```
In [12]: # Separating the data and Labels
X = heart_data.drop(columns='target', axis=1)
Y = heart_data['target']
```

3. Performing train test split.

Performing Train Test Split

```
In [15]: X_train, X_test, Y_train, Y_test = train_test_split(X, Y, test_size=0.2, stratify=Y, random_state=2)
```

```
In [16]: print(X.shape, X_train.shape, X_test.shape)
```

```
(303, 13) (242, 13) (61, 13)
```

4. Training the model.

Training the Model

```
In [17]: model = LogisticRegression()
```

```
In [18]: model.fit(X_train, Y_train)
```

```
C:\Users\Admin\anaconda3\lib\site-packages\sklearn\linear_model\_logistic.py:814: ConvergenceWarning: lbfgs failed to converge
(status=1):
STOP: TOTAL NO. of ITERATIONS REACHED LIMIT.

Increase the number of iterations (max_iter) or scale the data as shown in:
https://scikit-learn.org/stable/modules/preprocessing.html
Please also refer to the documentation for alternative solver options:
https://scikit-learn.org/stable/modules/linear_model.html#logistic-regression
n_iter_i = _check_optimize_result(
```

```
Out[18]: LogisticRegression()
```

5. Model evaluation and accuracy.

Model Evaluation

Accuracy Score

```
In [19]: # Accuracy score on the training data
X_train_prediction = model.predict(X_train)
training_data_accuracy = accuracy_score(X_train_prediction, Y_train)
```

```
In [20]: print('Accuracy on Training data : ', training_data_accuracy)
```

```
Accuracy on Training data : 0.8512396694214877
```

```
In [21]: # Accuracy score on the test data
X_test_prediction = model.predict(X_test)
test_data_accuracy = accuracy_score(X_test_prediction, Y_test)
```

```
In [22]: print('Accuracy on Test data : ', test_data_accuracy)
```

```
Accuracy on Test data : 0.819672131147541
```

6. Making a predictive system.

Making a Predictive System

```
In [23]: input_data = [62,0,0,140,268,0,0,160,0,3.6,0,2,2]

# Change the input data to a numpy array
input_data_as_numpy_array= np.asarray(input_data)

# Reshape the numpy array as we are predicting for only on instance
input_data_reshaped = input_data_as_numpy_array.reshape(1,-1)

prediction = model.predict(input_data_reshaped)
print(prediction)

if (prediction[0]== 0):
    print('The Person does not have a Heart Disease')
else:
    print('The Person has Heart Disease')
```

[0]
The Person does not have a Heart Disease

C:\Users\Admin\anaconda3\lib\site-packages\sklearn\base.py:450: UserWarning: X does not have valid feature names, but LogisticRegression was fitted with feature names
warnings.warn()

7. Save the trained model to use the model for further predictive use while deploying the model.

Saving the trained model

```
In [24]: import pickle

In [25]: filename = 'heart_disease_model.sav'
pickle.dump(model, open(filename, 'wb'))

In [26]: # Loading the saved model
loaded_model = pickle.load(open('heart_disease_model.sav', 'rb'))

In [27]: for column in X.columns:
    print(column)
```

age
sex
cp
trestbps
chol
fbs
restecg
thalach
exang
oldpeak
slope
ca
thal

Parkinson Disease Model.

The steps we have used are as follows:

1. Import libraries.

Importing the Dependencies

```
In [1]: import numpy as np
import pandas as pd
from sklearn.model_selection import train_test_split
from sklearn import svm
from sklearn.metrics import accuracy_score
```

2. Pre- processing

- Load datasets
- Printing head of the dataset.

Data Collection and Analysis

```
[2]: # Loading the diabetes dataset
parkinsons_data = pd.read_csv(r"C:\Users\SHUBHAM\Downloads\parkinsons.csv")

[3]: # Printing the first 5 rows of the dataset
parkinsons_data.head()

t[3]:
```

	name	MDVP:F0(Hz)	MDVP:F1(Hz)	MDVP:F2(Hz)	MDVP:Jitter(%)	MDVP:Jitter(Abs)	MDVP:RAP	MDVP:PPQ	Jitter:DDP	MDVP:Shimmer
0	phon_R01_S01_1	119.992	157.302	74.997	0.00784	0.00007	0.00370	0.00554	0.01109	0.04374
1	phon_R01_S01_2	122.400	148.850	113.819	0.00988	0.00008	0.00485	0.00898	0.01394	0.08134
2	phon_R01_S01_3	118.682	131.111	111.555	0.01050	0.00009	0.00544	0.00781	0.01633	0.05233
3	phon_R01_S01_4	118.676	137.871	111.366	0.00997	0.00009	0.00502	0.00898	0.01505	0.05492
4	phon_R01_S01_5	118.014	141.781	110.855	0.01284	0.00011	0.00655	0.00908	0.01988	0.08425

5 rows × 24 columns

```
[4]: # Number of rows and Columns in the dataset
parkinsons_data.shape

t[4]: (195, 24)
```

- Printing tail of the dataset to analyses the dataset.
- Printing shape of the dataset.
- Printing information of the dataset.

```
In [4]: # Number of rows and Columns in the dataset
parkinsons_data.shape

Out[4]: (195, 24)

In [5]: # Getting more information about the dataset
parkinsons_data.info()

<class 'pandas.core.frame.DataFrame'>
RangeIndex: 195 entries, 0 to 194
Data columns (total 24 columns):
#   Column              Non-Null Count  Dtype
---  -
0    name                 195 non-null    object
1    MDVP:F0(Hz)          195 non-null    float64
2    MDVP:F1(Hz)          195 non-null    float64
3    MDVP:F2(Hz)          195 non-null    float64
4    MDVP:Jitter(%)       195 non-null    float64
5    MDVP:Jitter(Abs)     195 non-null    float64
6    MDVP:RAP              195 non-null    float64
7    MDVP:PPQ              195 non-null    float64
8    Jitter:DDP           195 non-null    float64
9    MDVP:Shimmer         195 non-null    float64
10   MDVP:Shimmer(dB)     195 non-null    float64
11   Shimmer:APQ3         195 non-null    float64
12   Shimmer:APQ5         195 non-null    float64
13   MDVP:APQ             195 non-null    float64
14   Shimmer:DDA          195 non-null    float64
15   NHR                  195 non-null    float64
16   HNR                  195 non-null    float64
17   status               195 non-null    int64
18   RPDE                 195 non-null    float64
19   DFA                  195 non-null    float64
```

- Checking for missing values.
- Describe the dataset using for statistical measure.

```
In [7]: # Statistical measures about the data
parkinsons_data.describe()
```

```
Out[7]:
```

	MDVP:F0(Hz)	MDVP:F1(Hz)	MDVP:F2(Hz)	MDVP:Jitter(%)	MDVP:Jitter(Abs)	MDVP:RAP	MDVP:PPQ	Jitter:DDP	MDVP:Shimmer	MDVP:
count	195.000000	195.000000	195.000000	195.000000	195.000000	195.000000	195.000000	195.000000	195.000000	195.000000
mean	154.22841	197.104918	118.324831	0.008220	0.000044	0.003306	0.003446	0.009920	0.029709	
std	41.390085	91.491548	43.521413	0.004848	0.000035	0.002988	0.002759	0.008903	0.018857	
min	88.333000	102.145000	65.478000	0.001680	0.000007	0.000880	0.000920	0.002040	0.009540	
25%	117.572000	134.882500	84.291000	0.003480	0.000020	0.001880	0.001880	0.004985	0.016505	
50%	148.790000	175.829000	104.315000	0.004940	0.000030	0.002500	0.002890	0.007490	0.022970	
75%	182.789000	224.205500	140.018500	0.007385	0.000060	0.003835	0.003955	0.011505	0.037885	
max	260.105000	592.030000	239.170000	0.033180	0.000260	0.021440	0.019580	0.064330	0.119080	

8 rows x 23 columns

```
In [8]: # Checking the distribution of Target Variable
parkinsons_data['status'].value_counts()
```

```
Out[8]:
```

status	count
1	147
0	48

Name: status, dtype: int64

h. Check the distribution of the target variables.

i. Separating data and labels.

```
In [10]: # Separating the data and labels
X = parkinsons_data.drop(columns=['name', 'status'], axis=1)
Y = parkinsons_data['status']
```

```
In [11]: print(X)
```

	MDVP:F0(Hz)	MDVP:F1(Hz)	MDVP:F2(Hz)	MDVP:Jitter(%)	\
0	119.992	157.302	74.997	0.00784	
1	122.400	148.650	113.819	0.00968	
2	116.682	131.111	111.555	0.01050	
3	116.676	137.871	111.366	0.00997	
4	116.014	141.781	110.655	0.01284	
..	
190	174.188	230.978	94.261	0.00459	
191	209.516	253.017	89.488	0.00564	
192	174.688	240.005	74.287	0.01360	
193	198.764	396.961	74.904	0.00740	
194	214.289	260.277	77.973	0.00567	

	MDVP:Jitter(Abs)	MDVP:RAP	MDVP:PPQ	Jitter:DDP	MDVP:Shimmer	\
0	0.00007	0.00370	0.00554	0.01109	0.04374	
1	0.00008	0.00465	0.00696	0.01394	0.06134	
2	0.00009	0.00544	0.00781	0.01633	0.05233	
3	0.00009	0.00502	0.00698	0.01505	0.05492	
4	0.00011	0.00655	0.00908	0.01966	0.06425	
..	
190	0.00003	0.00263	0.00259	0.00790	0.04087	
191	0.00003	0.00331	0.00292	0.00994	0.02751	
192	0.00008	0.00624	0.00564	0.01873	0.02308	

3. Performing train test split.

Performing Train Test Split

```
In [13]: X_train, X_test, Y_train, Y_test = train_test_split(X, Y, test_size=0.2, random_state=2)
```

```
In [14]: print(X.shape, X_train.shape, X_test.shape)
```

```
(195, 22) (156, 22) (39, 22)
```

4. Training the model.

Training the Model

```
In [15]: model = svm.SVC(kernel='linear')
```

```
In [16]: # Training the SVM model with training data
         model.fit(X_train, Y_train)
```

```
Out[16]: SVC(kernel='linear')
```

5. Model evaluation and accuracy.

Model Evaluation

Accuracy Score

```
In [17]: # Accuracy score on the training data
X_train_prediction = model.predict(X_train)
training_data_accuracy = accuracy_score(Y_train, X_train_prediction)
```

```
In [18]: print('Accuracy score of training data : ', training_data_accuracy)
Accuracy score of training data : 0.8717948717948718
```

```
In [19]: # Accuracy score on the test data
X_test_prediction = model.predict(X_test)
test_data_accuracy = accuracy_score(Y_test, X_test_prediction)
```

```
In [20]: print('Accuracy score of test data : ', test_data_accuracy)

Accuracy score of test data : 0.8717948717948718
```

6. Making a predictive system.

Making a Predictive System

```
In [21]: input_data = (197.07600,206.89600,192.05500,0.00289,0.00001,0.00166,0.00168,0.00498,0.01098,0.09700,0.00563,0.00680,0.00802,0.0
```

```
# Changing input data to a numpy array  
input_data_as_numpy_array = np.asarray(input_data)  
  
# Reshape the numpy array  
input_data_resaped = input_data_as_numpy_array.reshape(1,-1)  
  
prediction = model.predict(input_data_resaped)  
print(prediction)  
  
if (prediction[0] == 0):  
    print("The Person does not have Parkinsons Disease")  
  
else:  
    print("The Person has Parkinsons")
```

```
[0]  
The Person does not have Parkinsons Disease
```

```
C:\Users\Admin\anaconda3\lib\site-packages\sklearn\base.py:450: UserWarning: X does not have valid feature names, but SVC was fitted with feature names
  warnings.warn(
```

7. Save the trained model to use the model for further predictive use while deploying the model.

Saving the trained model

```
In [22]: import pickle

In [23]: filename = 'parkinsons_model.sav'
pickle.dump(model, open(filename, 'wb'))

In [24]: # Loading the saved model
loaded_model = pickle.load(open('parkinsons_model.sav', 'rb'))

In [25]: for column in X.columns:
          print(column)

MDVP:F0(Hz)
MDVP:F1(Hz)
MDVP:F1o(Hz)
MDVP:Jitter(%)
MDVP:Jitter(Abs)
MDVP:RAP
MDVP:PPQ
Jitter:DDP
MDVP:Shimmer
MDVP:Shimmer(dB)
Shimmer:APQ3
Shimmer:APQ5
MDVP:APQ
Shimmer:DDA
NHR
HNR
RPDE
DFA
spread1
spread2
D2
PPE
```

5.3 Diabetes Disease Model.

The steps we have used are as follows:

1. Import libraries.

Importing the Dependencies

```
In [1]: import numpy as np
import pandas as pd
from sklearn.model_selection import train_test_split
from sklearn import svm
from sklearn.metrics import accuracy_score
```

2. Pre- processing

- Load datasets
- Printing head of the dataset.
- Printing tail of the dataset to analyse the dataset.
- Printing shape of the dataset.

Data Collection and Analysis

```
In [2]: # Loading the diabetes dataset
diabetes_dataset = pd.read_csv(r"C:\Users\SHUBHAM\Downloads\diabetes.csv")

In [3]: # Printing the first 5 rows of the dataset
diabetes_dataset.head()

Out[3]:
```

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age	Outcome
0	6	148	72	35	0	33.6	0.627	50	1
1	1	85	66	29	0	26.6	0.351	31	0
2	8	183	64	0	0	23.3	0.672	32	1
3	1	89	66	23	94	28.1	0.167	21	0
4	0	137	40	35	168	43.1	2.288	33	1

```
In [4]: # Number of rows and Columns in the dataset
diabetes_dataset.shape

Out[4]: (768, 9)
```

- e. Printing information of the dataset.
- f. Checking for missing values.
- g. Describe the dataset using for statistical measure.

```
In [5]: # Statistical measures of the data
diabetes_dataset.describe()

Out[5]:
```

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age	Outcome
count	768.000000	768.000000	768.000000	768.000000	768.000000	768.000000	768.000000	768.000000	768.000000
mean	3.845052	120.894531	69.105469	20.536458	79.799479	31.992578	0.471876	33.240885	0.348958
std	3.369578	31.972618	19.355807	15.952218	115.244002	7.884180	0.331329	11.760232	0.476951
min	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.078000	21.000000	0.000000
25%	1.000000	99.000000	62.000000	0.000000	0.000000	27.300000	0.243750	24.000000	0.000000
50%	3.000000	117.000000	72.000000	23.000000	30.500000	32.000000	0.372500	29.000000	0.000000
75%	6.000000	140.250000	80.000000	32.000000	127.250000	36.800000	0.626250	41.000000	1.000000
max	17.000000	199.000000	122.000000	99.000000	846.000000	67.100000	2.420000	81.000000	1.000000

```
In [6]: # Checking the distribution of Target Variable
diabetes_dataset['Outcome'].value_counts()

Out[6]: 0    500
        1    268
        Name: Outcome, dtype: int64

0 --> Non-Diabetic
1 --> Diabetic
```

- h. Check the distribution of the target variables.
- i. Separating data and labels.

```
In [8]: # Separating the data and labels
X = diabetes_dataset.drop(columns = 'Outcome', axis=1)
Y = diabetes_dataset['Outcome']

In [9]: print(X)
```

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	\
0	6	148	72	35	0	33.6	
1	1	85	66	29	0	26.6	
2	8	183	64	0	0	23.3	
3	1	89	66	23	94	28.1	
4	0	137	40	35	168	43.1	
..	
763	10	101	76	48	180	32.9	
764	2	122	70	27	0	36.8	
765	5	121	72	23	112	26.2	
766	1	126	60	0	0	30.1	
767	1	93	70	31	0	30.4	

	DiabetesPedigreeFunction	Age
0	0.627	50
1	0.351	31
2	0.672	32
3	0.167	21
4	2.288	33
..
763	0.171	63
764	0.340	27
765	0.245	30
766	0.349	47
767	0.315	23

[768 rows x 8 columns]

3. Performing train test split.

Performing Train Test Split

```
In [11]: X_train, X_test, Y_train, Y_test = train_test_split(X,Y, test_size = 0.2, stratify=Y, random_state=2)

In [12]: print(X.shape, X_train.shape, X_test.shape)

(768, 8) (614, 8) (154, 8)
```

4. Training the model.

Training the Model

```
In [13]: classifier = svm.SVC(kernel='linear')

In [14]: # Training the support vector Machine Classifier
classifier.fit(X_train, Y_train)

Out[14]:
SVC
SVC(kernel='linear')
```

5. Model evaluation and accuracy.

Model Evaluation

Accuracy Score

```
In [15]: # Accuracy score on the training data
X_train_prediction = classifier.predict(X_train)
training_data_accuracy = accuracy_score(X_train_prediction, Y_train)

In [16]: print('Accuracy score of the training data : ', training_data_accuracy)

Accuracy score of the training data : 0.7833876221498371

In [17]: # Accuracy score on the test data
X_test_prediction = classifier.predict(X_test)
test_data_accuracy = accuracy_score(X_test_prediction, Y_test)

In [18]: print('Accuracy score of the test data : ', test_data_accuracy)

Accuracy score of the test data : 0.7727272727272727
```

6. Making a predictive system.

Making a Predictive System

```
In [19]: input_data = (5,166,72,19,175,25.8,0.587,51)

# Changing the input_data to numpy array
input_data_as_numpy_array = np.asarray(input_data)

# Reshape the array as we are predicting for one instance
input_data_reshaped = input_data_as_numpy_array.reshape(1,-1)

prediction = classifier.predict(input_data_reshaped)
print(prediction)

if (prediction[0] == 0):
    print('The person is not diabetic')
else:
    print('The person is diabetic')
```

[1]
The person is diabetic

C:\Users\SHUBHAM\anaconda3\envs\security_sys\lib\site-packages\sklearn\base.py:450: UserWarning: X does not have valid feature names, but SVC was fitted with feature names
warnings.warn(

7. Save the trained model to use the model for further predictive use while deploying the model.

Saving the trained model

```
In [20]: import pickle

In [21]: filename = 'diabetes_model.sav'
pickle.dump(classifier, open(filename, 'wb'))

In [22]: # Loading the saved model
loaded_model = pickle.load(open('diabetes_model.sav', 'rb'))

In [23]: input_data = (5,166,72,19,175,25.8,0.587,51)

# Changing the input_data to numpy array
input_data_as_numpy_array = np.asarray(input_data)

# Reshape the array as we are predicting for one instance
input_data_reshaped = input_data_as_numpy_array.reshape(1,-1)

prediction = loaded_model.predict(input_data_reshaped)
print(prediction)

if (prediction[0] == 0):
    print('The person is not diabetic')
else:
    print('The person is diabetic')
```

[1]
The person is diabetic

C:\Users\SHUBHAM\anaconda3\envs\security_sys\lib\site-packages\sklearn\base.py:450: UserWarning: X does not have valid feature names, but SVC was fitted with feature names
warnings.warn(

5.4 Breast Cancer Disease Detection Model.

1. Import libraries.

Import ML packages

```
In [4]: import numpy as np
import pandas as pd
import matplotlib.pyplot as plt
from sklearn.metrics import classification_report
from sklearn.metrics import accuracy_score
from sklearn.metrics import confusion_matrix
from sklearn.model_selection import train_test_split
from sklearn.model_selection import cross_val_score
from sklearn.model_selection import KFold
from sklearn.tree import DecisionTreeClassifier
from sklearn.neighbors import KNeighborsClassifier
from sklearn.naive_bayes import GaussianNB
from sklearn.pipeline import Pipeline
from sklearn.preprocessing import StandardScaler
from sklearn.model_selection import GridSearchCV
from sklearn.svm import SVC
from pandas.plotting import scatter_matrix
import seaborn as sns

%matplotlib inline
```

2. Load and Read Dataset.

Load and Read Dataset

```
In [5]: # Load Dataset
url = "https://archive.ics.uci.edu/ml/machine-learning-databases/breast-cancer-wisconsin/breast-cancer-wisconsin.data"
names = ['id', 'clump_thickness', 'uniform_cell_size', 'uniform_cell_shape', 'marginal_adhesion', 'single_epithelial_size', 'bare_nuclei',
        'bland_chromatin', 'normal_nucleoli', 'mitoses', 'class']
df = pd.read_csv(url, names=names)
```

```
In [6]: df.head()
```

```
Out[6]:
```

	id	clump_thickness	uniform_cell_size	uniform_cell_shape	marginal_adhesion	single_epithelial_size	bare_nuclei	bland_chromatin	normal_nucleo
0	1000025	5	1	1	1	2	1	3	
1	1002945	5	4	4	5	7	10	3	
2	1015425	3	1	1	1	2	2	3	
3	1016277	6	8	8	1	3	4	3	
4	1017023	4	1	1	3	2	1	3	

```
In [7]: #Shape of the Dataset
df.shape
```

```
Out[7]: (699, 11)
```

3. Data Pre-processing.

Data pre-processing

```
In [8]: df.drop(['id'],axis=1,inplace = True)
```

```
In [9]: # Columns in the dataset
df.columns
```

```
Out[9]: Index(['clump_thickness', 'uniform_cell_size', 'uniform_cell_shape',
        'marginal_adhesion', 'single_epithelial_size', 'bare_nuclei',
        'bland_chromatin', 'normal_nucleoli', 'mitoses', 'class'],
        dtype='object')
```

4. Handling missing values.

Handling missing values

```
In [10]: df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 699 entries, 0 to 698
Data columns (total 10 columns):
 #   Column                Non-Null Count  Dtype
---  -
 0   clump_thickness        699 non-null    int64
 1   uniform_cell_size      699 non-null    int64
 2   uniform_cell_shape     699 non-null    int64
 3   marginal_adhesion      699 non-null    int64
 4   single_epithelial_size 699 non-null    int64
 5   bare_nuclei            699 non-null    object
 6   bland_chromatin        699 non-null    int64
 7   normal_nucleoli        699 non-null    int64
 8   mitoses                699 non-null    int64
 9   class                  699 non-null    int64
dtypes: int64(9), object(1)
memory usage: 54.7+ KB
```

```
In [11]: #Diagnosis class Malignant = 4 and Benign = 2
#The number of Benign and Malignant cases from the dataset
df['class'].value_counts()
```

```
Out[11]: 2    458
         4    241
         Name: class, dtype: int64
```

```
In [11]: #Diagnosis class Malignant = 4 and Benign = 2
#The number of Benign and Malignant cases from the dataset
df['class'].value_counts()
```

```
Out[11]: 2    458
         4    241
         Name: class, dtype: int64
```

```
In [12]: df['bare_nuclei'].value_counts()
```

```
Out[12]: 1    402
        10    132
         2     30
         5     30
         3     28
         8     21
         4     19
         ?     16
         9      9
         7      8
         6      4
         Name: bare_nuclei, dtype: int64
```

```
In [14]: df[df['bare_nuclei'] == '?'].sum()
```

```
Out[14]: clump_thickness        54
         uniform_cell_size      39
         uniform_cell_shape     46
         marginal_adhesion      29
         single_epithelial_size  39
         bare_nuclei            ??????????????
         bland_chromatin        50
         normal_nucleoli        44
         mitoses                16
         class                  36
         dtype: object
```

```
In [15]: df.replace('?', np.nan, inplace=True)
```

```
In [16]: df['bare_nuclei'][23]
Out[16]: nan

In [17]: df.isna().sum()
Out[17]: clump_thickness      0
uniform_cell_size          0
uniform_cell_shape         0
marginal_adhesion          0
single_epithelial_size     0
bare_nuclei                16
bland_chromatin            0
normal_nucleoli            0
mitoses                    0
class                      0
dtype: int64

In [18]: df.fillna(method='ffill', inplace=True)
```

4. Exploratory Analysis.

Exploratory Data Analysis

```
In [21]: df.info()

<class 'pandas.core.frame.DataFrame'>
RangeIndex: 699 entries, 0 to 698
Data columns (total 10 columns):
 #   Column                      Non-Null Count  Dtype
---  -
 0   clump_thickness             699 non-null    int64
 1   uniform_cell_size           699 non-null    int64
 2   uniform_cell_shape          699 non-null    int64
 3   marginal_adhesion           699 non-null    int64
 4   single_epithelial_size      699 non-null    int64
 5   bare_nuclei                 699 non-null    int64
 6   bland_chromatin             699 non-null    int64
 7   normal_nucleoli             699 non-null    int64
 8   mitoses                     699 non-null    int64
 9   class                       699 non-null    int64
dtypes: int64(10)
memory usage: 54.7 KB

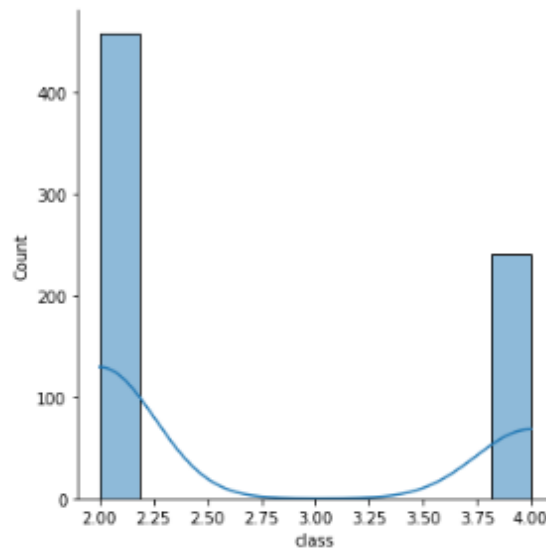
In [22]: df.describe()
Out[22]:
```

	clump_thickness	uniform_cell_size	uniform_cell_shape	marginal_adhesion	single_epithelial_size	bare_nuclei	bland_chromatin	normal_nucleoli
count	699.000000	699.000000	699.000000	699.000000	699.000000	699.000000	699.000000	699.000000
mean	4.417740	3.134478	3.207439	2.806887	3.216023	3.529328	3.437768	2.866900
std	2.815741	3.051459	2.971913	2.855379	2.214300	3.635280	2.438384	3.053600
min	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000	1.000000
25%	2.000000	1.000000	1.000000	1.000000	2.000000	1.000000	2.000000	1.000000
50%	4.000000	1.000000	1.000000	1.000000	2.000000	1.000000	3.000000	1.000000
75%	6.000000	5.000000	5.000000	4.000000	4.000000	6.000000	5.000000	4.000000
max	10.000000	10.000000	10.000000	10.000000	10.000000	10.000000	10.000000	10.000000

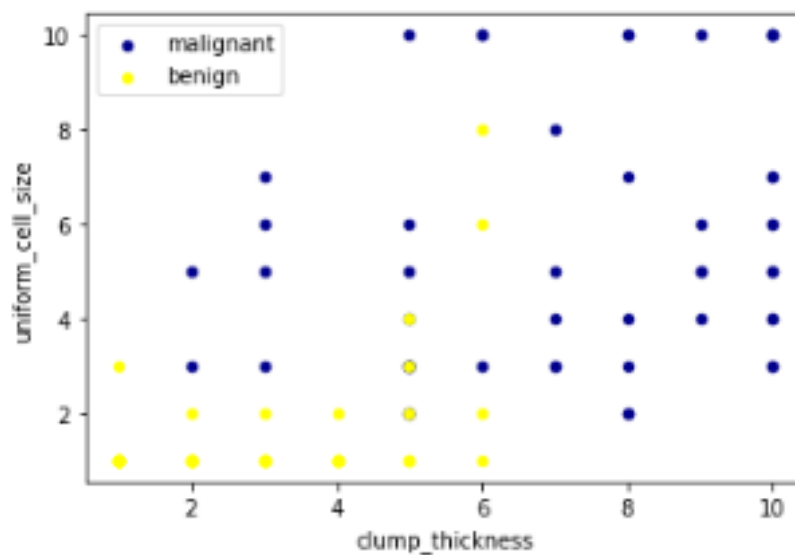
5. Bivariate Data Analysis.

Bivariate Data Analysis

```
In [23]: sns.displot(df['class'],kde=True)
Out[23]: <seaborn.axisgrid.FacetGrid at 0x18ea4911490>
```



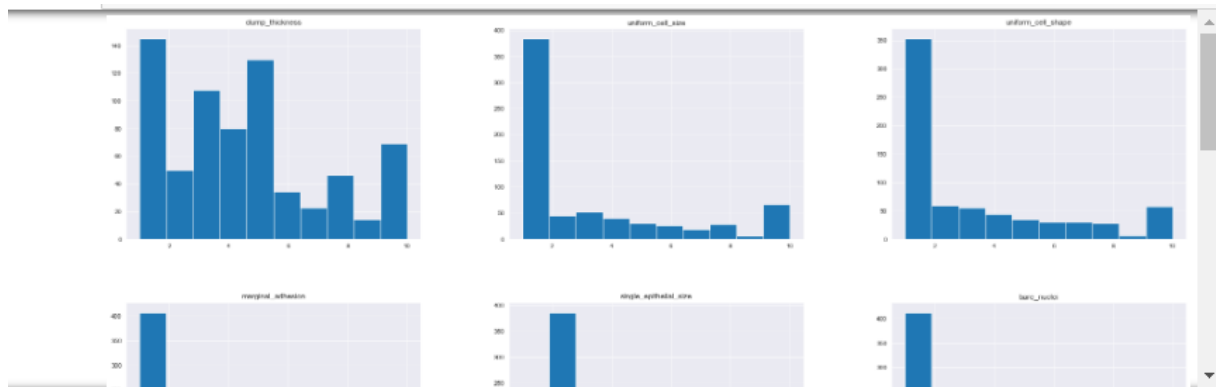
```
In [24]: ax = df[df['class'] == 4][0:50].plot(kind='scatter', x='clump_thickness', y='uniform_cell_size', color='DarkBlue', label='malignant')
df[df['class'] == 2][0:50].plot(kind='scatter', x='clump_thickness', y='uniform_cell_size', color='Yellow', label='benign', ax=ax)
plt.show()
```



6. Multivariate Analysis.

Multivariate Data Analysis

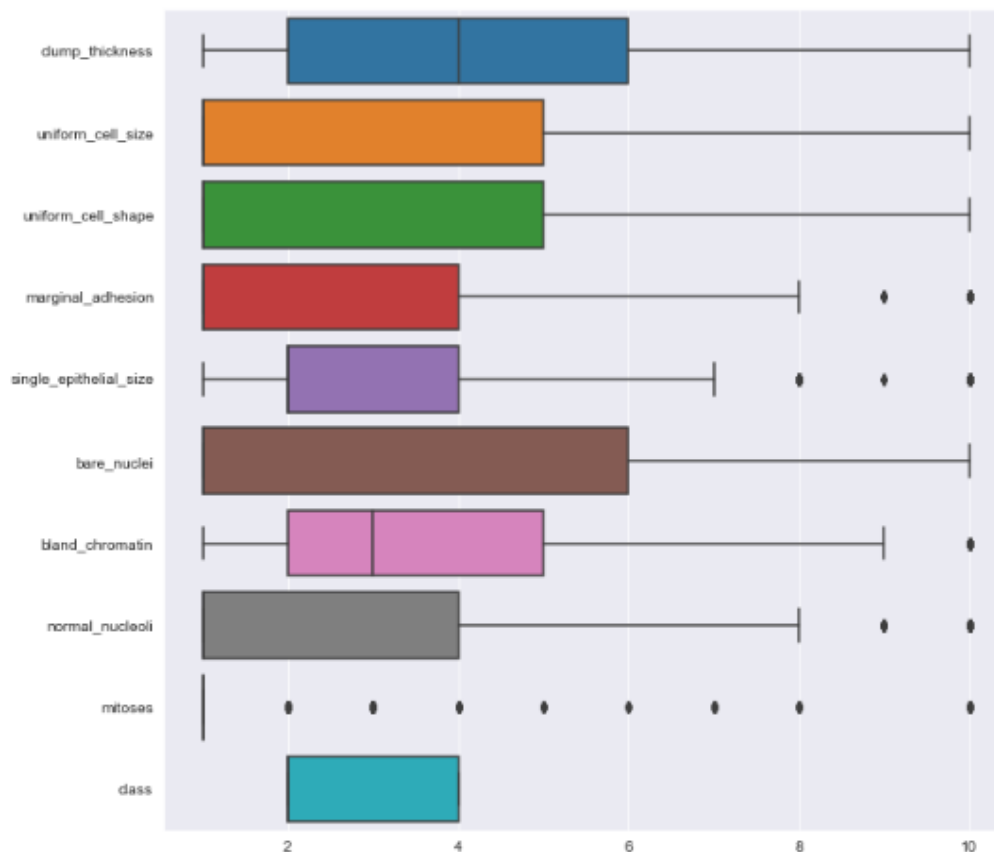
```
In [25]: # Plot histograms for each variable
sns.set_style('darkgrid')
df.hist(figsize=(30,30))
plt.show()
```



```
In [26]: # Create scatter plot matrix
scatter_matrix(df, figsize = (18,18))
plt.show()
```

```
In [27]: plt.figure(figsize=(10,10))
sns.boxplot(data=df,orient='h')
```

Out[27]: <AxesSubplot:>



7. Feature Selection.

Feature selection

```
In [28]: df.corr()
```

```
Out[28]:
```

	clump_thickness	uniform_cell_size	uniform_cell_shape	marginal_adhesion	single_epithelial_size	bare_nuclei	bland_chromatin	normal
clump_thickness	1.000000	0.644913	0.654589	0.486356	0.521816	0.583571	0.558428	
uniform_cell_size	0.644913	1.000000	0.906882	0.705582	0.751799	0.681309	0.755721	
uniform_cell_shape	0.654589	0.906882	1.000000	0.683079	0.719868	0.701137	0.735948	
marginal_adhesion	0.486356	0.705582	0.683079	1.000000	0.599599	0.683869	0.686715	
single_epithelial_size	0.521816	0.751799	0.719868	0.599599	1.000000	0.579340	0.616102	
bare_nuclei	0.583571	0.681309	0.701137	0.683869	0.579340	1.000000	0.671398	
bland_chromatin	0.558428	0.755721	0.735948	0.686715	0.616102	0.671398	1.000000	
normal_nucleoli	0.535835	0.722885	0.719446	0.603352	0.628881	0.571895	0.665878	
mitoses	0.350034	0.458693	0.438911	0.417833	0.479101	0.337078	0.344169	
class	0.716001	0.817904	0.818934	0.696800	0.682785	0.807394	0.756616	

```
In [29]: plt.figure(figsize=(30,20))
cor = df.corr()
sns.heatmap(cor,vmax=1,square = True,annot=True, cmap=plt.cm.Blues)
plt.title('Correlation between different attributes')
plt.show()
```

8. Correlation with output variables.

```
In [31]: #Correlation with output variable
cor_target = abs(cor["class"])
#Selecting highly correlated features
relevant_features = cor_target[cor_target>0]
relevant_features
```

```
Out[31]: clump_thickness      0.716001
uniform_cell_size      0.817904
uniform_cell_shape      0.818934
marginal_adhesion      0.696800
single_epithelial_size  0.682785
bare_nuclei      0.807394
bland_chromatin      0.756616
normal_nucleoli      0.712244
mitoses      0.423170
class      1.000000
Name: class, dtype: float64
```

9. Train Test model.

Train and Test Model

```
In [32]: #Split the data into predictor variables and target variable, following by breaking them into train and test sets.
```

```
Y = df['class'].values
X = df.drop('class', axis=1).values

X_train, X_test, Y_train, Y_test = train_test_split(X, Y, test_size = 0.30, random_state=21)
```

10. Model Selection.

- Analyze and build a model to predict if a given set of symptoms lead to breast cancer. This is a binary classification problem, and a few algorithms are appropriate for use.
- As we do not know which one will perform the best at the point, we will do a quick test on the few appropriate algorithms with default setting to get an early indication of how each of them perform.
- We will use 10 fold cross validation for each testing.

The following non-linear algorithms will be used, namely:

- Classification and Regression Trees (CART)
- Linear Support Vector Machines (SVM)
- Gaussian Naive Bayes (NB)
- K-Nearest Neighbors (KNN).

11. Testing Accuracy.

```
In [33]: # Testing Options
scoring = 'accuracy'

In [34]: # Define models to train
models = []
models.append(('CART', DecisionTreeClassifier()))
models.append(('SVM', SVC()))
models.append(('NB', GaussianNB()))
models.append(('KNN', KNeighborsClassifier()))

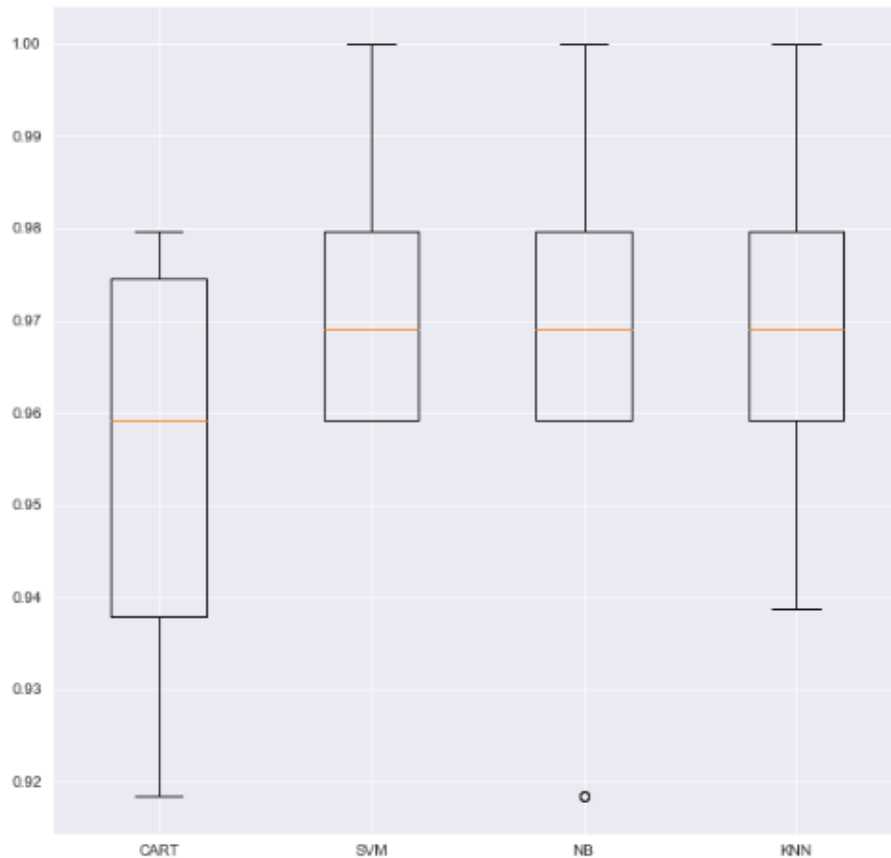
# evaluate each model in turn
results = []
names = []

for name, model in models:
    kfold = KFold(n_splits=10)
    cv_results = cross_val_score(model, X_train, Y_train, cv=kfold, scoring=scoring)
    results.append(cv_results)
    names.append(name)
    msg = "For %s Model:Mean accuracy is %f (Std accuracy is %f)" % (name, cv_results.mean(), cv_results.std())
    print(msg)

For CART Model:Mean accuracy is 0.952934 (Std accuracy is 0.022533)
For SVM Model:Mean accuracy is 0.971386 (Std accuracy is 0.013512)
For NB Model:Mean accuracy is 0.963223 (Std accuracy is 0.025463)
For KNN Model:Mean accuracy is 0.969345 (Std accuracy is 0.016428)
```

12. Performance Comparison.

```
In [35]: fig = plt.figure(figsize=(10,10))
fig.suptitle('Performance Comparison')
ax = fig.add_subplot(111)
plt.boxplot(results)
ax.set_xticklabels(names)
plt.show()
```



13. Making Prediction on Validation dataset.

```
In [36]: # Make predictions on validation dataset

for name, model in models:
    model.fit(X_train, Y_train)
    predictions = model.predict(X_test)
    print("\nModel:", name)
    print("Accuracy score:", accuracy_score(Y_test, predictions))
    print("Classification report:\n", classification_report(Y_test, predictions))

# Accuracy - ratio of correctly predicted observation to the total observations.
# Precision - (false positives) ratio of correctly predicted positive observations to the total predicted positive observations
# Recall (Sensitivity) - (false negatives) ratio of correctly predicted positive observations to the all observations in actual c
# F1 score - F1 Score is the weighted average of Precision and Recall. Therefore, this score takes both false positives and false
```

```

Model: CART
Accuracy score: 0.9047619047619048
Classification report:

```

	precision	recall	f1-score	support
2	0.89	0.97	0.93	133
4	0.94	0.79	0.86	77
accuracy			0.90	210
macro avg	0.91	0.88	0.89	210
weighted avg	0.91	0.90	0.90	210

CART

```

Model: SVM
Accuracy score: 0.9714285714285714
Classification report:

```

	precision	recall	f1-score	support
2	0.98	0.98	0.98	133
4	0.96	0.96	0.96	77
accuracy			0.97	210
macro avg	0.97	0.97	0.97	210
weighted avg	0.97	0.97	0.97	210

SVM

```

Model: NB
Accuracy score: 0.9523809523809523
Classification report:

```

	precision	recall	f1-score	support
2	0.96	0.96	0.96	133
4	0.94	0.94	0.94	77
accuracy			0.95	210
macro avg	0.95	0.95	0.95	210
weighted avg	0.95	0.95	0.95	210

Naïve Bayes.

Model: KNN

Accuracy score: 0.9571428571428572

Classification report:

	precision	recall	f1-score	support
2	0.96	0.97	0.97	133
4	0.95	0.94	0.94	77
accuracy			0.96	210
macro avg	0.96	0.95	0.95	210
weighted avg	0.96	0.96	0.96	210

KNN

Algorithm selected for training model: Support Vector Machine.

Support Vector Machine

```
In [37]: clf = SVC()

clf.fit(X_train, Y_train)
accuracy = clf.score(X_test, Y_test)
print("Test Accuracy:", accuracy)

predict = clf.predict(X_test)
predict
```

Test Accuracy: 0.9714285714285714

```
Out[37]: array([2, 2, 2, 2, 4, 2, 2, 4, 4, 2, 2, 2, 2, 2, 4, 2, 4, 4, 4, 2, 4, 4,
                2, 4, 2, 2, 2, 4, 2, 2, 4, 4, 4, 2, 4, 4, 4, 2, 2, 4, 2, 2, 2, 2,
                2, 2, 4, 4, 2, 2, 4, 4, 2, 4, 2, 2, 2, 2, 2, 2, 2, 2, 2, 4, 4,
                2, 4, 2, 2, 2, 4, 2, 2, 4, 4, 4, 2, 2, 2, 2, 2, 4, 2, 4, 2, 2, 4,
                2, 4, 4, 4, 2, 4, 4, 2, 2, 2, 2, 4, 2, 2, 2, 4, 4, 4, 4, 2, 2,
                2, 4, 4, 4, 2, 2, 2, 4, 2, 4, 4, 2, 2, 2, 2, 2, 2, 2, 4, 4, 2, 2,
                2, 2, 2, 4, 2, 2, 2, 2, 2, 2, 4, 4, 4, 2, 4, 2, 2, 2, 2, 2, 2,
                2, 2, 4, 4, 4, 2, 4, 2, 4, 2, 4, 2, 2, 2, 2, 2, 2, 2, 4, 4, 4,
                4, 2, 4, 2, 4, 2, 2, 2, 2, 4, 4, 2, 4, 2, 4, 4, 4, 2, 4, 2, 2,
                2, 2, 2, 4, 2, 2, 2, 2, 2, 4, 2, 2], dtype=int64)
```

```
In [38]: example_measures = [[4,2,1,1,1,2,3,2,1]]
prediction = clf.predict(example_measures)
print(prediction)
```

[2]

```
In [39]: import itertools
sns.set_theme(style="dark")
def plot_confusion_matrix(cm, classes, normalize=False, title='Confusion matrix', cmap=plt.cm.Blues):
    """
    This function prints and plots the confusion matrix.
    Normalization can be applied by setting 'normalize=True'.
    """
    if normalize:
        cm = cm.astype('float') / cm.sum(axis=1)[:, np.newaxis]
        print("Normalized confusion matrix")
    else:
        print('Confusion matrix, without normalization')

    print(cm)

    plt.imshow(cm, interpolation='nearest', cmap=cmap)
    plt.title(title)
    plt.colorbar()
    tick_marks = np.arange(len(classes))
    plt.xticks(tick_marks, classes, rotation=45)
    plt.yticks(tick_marks, classes)

    fmt = '.2f' if normalize else 'd'
    thresh = cm.max() / 2.
    for i, j in itertools.product(range(cm.shape[0]), range(cm.shape[1])):
        plt.text(j, i, format(cm[i, j], fmt),
                 horizontalalignment="center",
                 color="white" if cm[i, j] > thresh else "black")

    plt.tight_layout()
    plt.ylabel('True label')
    plt.xlabel('Predicted label')
```

13. Computing Confusion Matrix.

```
In [40]: # Compute confusion matrix
cnf_matrix = confusion_matrix(Y_test, predict, labels=[2,4])
np.set_printoptions(precision=2)

print(classification_report(Y_test, predict))

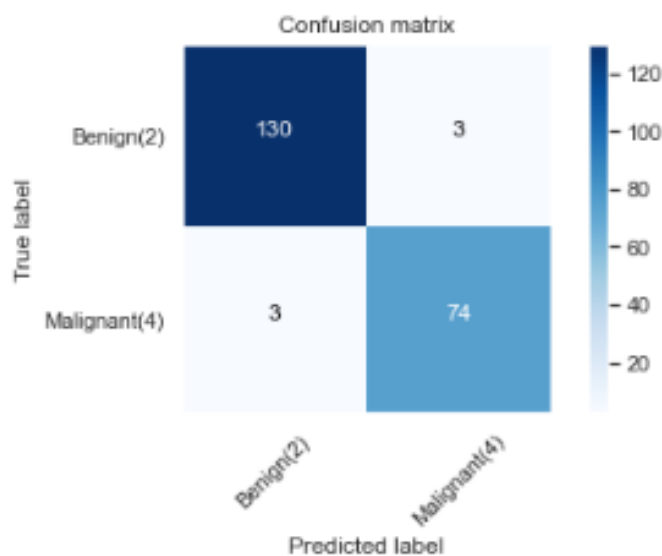
# Plot non-normalized confusion matrix
plt.figure()
plot_confusion_matrix(cnf_matrix, classes=['Benign(2)', 'Malignant(4)'], normalize=False, title='Confusion matrix')

      precision    recall  f1-score   support

      2       0.98      0.98      0.98      133
      4       0.96      0.96      0.96       77

   accuracy      0.97
  macro avg      0.97
 weighted avg      0.97

Confusion matrix, without normalization
[[130   3]
 [  3  74]]
```



14. Saving Model for further deployment use.

```
In [41]: import pickle
pickle.dump(clf, open('model.sav', 'wb'))

model = pickle.load(open('model.sav', 'rb'))
print(model.predict([[4,2,1,1,1,2,3,2,1]]))

[2]
```

6. EXPERIMENTAL SETUP

The experimental setup for our proposed machine learning-driven Disease detection system involves the following components:

Hardware:

- A workstation or server with sufficient CPU and GPU resources to train and evaluate deep learning models.
 - A camera or scanner to capture and digitize images.
 - A mobile device or web interface for user interaction and input.
 - A cloud-based or local deployment infrastructure for hosting the trained model and delivering the classification results to users/
- Software:

- Python programming language and relevant libraries for machine learning such as Tensor Flow, Keras, and streamlit
- Data pre-processing and augmentation libraries.
- Model optimization and evaluation tools such as TensorBoard or scikit-learn • Visualization and interpretation tools such as Grad-CAM, saliency maps, or SHAP values
- User interface development tools such as Flask, Django, or Streamlit library.

Experimental Procedure:

1. Data Collection and Pre-processing:

- Collect a diverse dataset of chest diseases with appropriate labels for different health related issues.
- Pre-process the feature and target variables using normalization, resizing, and data augmentation techniques

Importing the Dependencies

```
In [3]: import numpy as np
import pandas as pd
from sklearn.model_selection import train_test_split
from sklearn.linear_model import LogisticRegression
from sklearn.metrics import accuracy_score
```

2. Model Architecture Design and Selection:

- Design or select an appropriate deep learning model architecture for the task
- Implement the model in Python using relevant libraries

Data Collection and Processing

```
In [4]: # Loading the Heart dataset
heart_data = pd.read_csv(r"C:\Users\SHUBHAM\Downloads\heart.csv")
```

```
In [5]: # Printing the first 5 rows of the dataset
heart_data.head()
```

```
Out[5]:
```

	age	sex	cp	trestbps	chol	fbs	restecg	thalach	exang	oldpeak	slope	ca	thal	target
0	63	1	3	145	233	1	0	150	0	2.3	0	0	1	1
1	37	1	2	130	250	0	1	187	0	3.5	0	0	2	1
2	41	0	1	130	204	0	0	172	0	1.4	2	0	2	1
3	56	1	1	120	236	0	1	178	0	0.8	2	0	2	1
4	57	0	0	120	354	0	1	163	1	0.6	2	0	2	1

```
In [6]: # Printing Last 5 rows of the dataset
heart_data.tail()
```


3. Training and Validation:

- Split the dataset into training and validation sets using appropriate procedures
- Train the model using suitable optimization techniques and hyper parameters
- Validate the model using standard evaluation metrics such as accuracy, precision, recall, and F1 score

Performing Train Test Split

```
[15]: X_train, X_test, Y_train, Y_test = train_test_split(X, Y, test_size=0.2, stratify=Y, random_state=2)

[16]: print(X.shape, X_train.shape, X_test.shape)

(303, 13) (242, 13) (61, 13)
```

Training the Model ¶

```
] : model = LogisticRegression()

>] : model.fit(X_train, Y_train)

C:\Users\Admin\anaconda3\lib\site-packages\sklearn\linear_model\_logistic.py:814: ConvergenceWarning: lbfgs failed
(status=1):
STOP: TOTAL NO. of ITERATIONS REACHED LIMIT.

Increase the number of iterations (max_iter) or scale the data as shown in:
https://scikit-learn.org/stable/modules/preprocessing.html
Please also refer to the documentation for alternative solver options:
https://scikit-learn.org/stable/modules/linear\_model.html#logistic-regression
n_iter_i = _check_optimize_result(

>] : LogisticRegression()
```

4. Testing and Evaluation:

- Test the trained model on a separate test dataset and evaluate its performance using standard metrics
- Evaluate the interpretability and visualizations of the system to ensure that it is user-friendly and transparent

Model Evaluation

Accuracy Score

```
J]: # Accuracy score on the training data
X_train_prediction = model.predict(X_train)
training_data_accuracy = accuracy_score(X_train_prediction, Y_train)

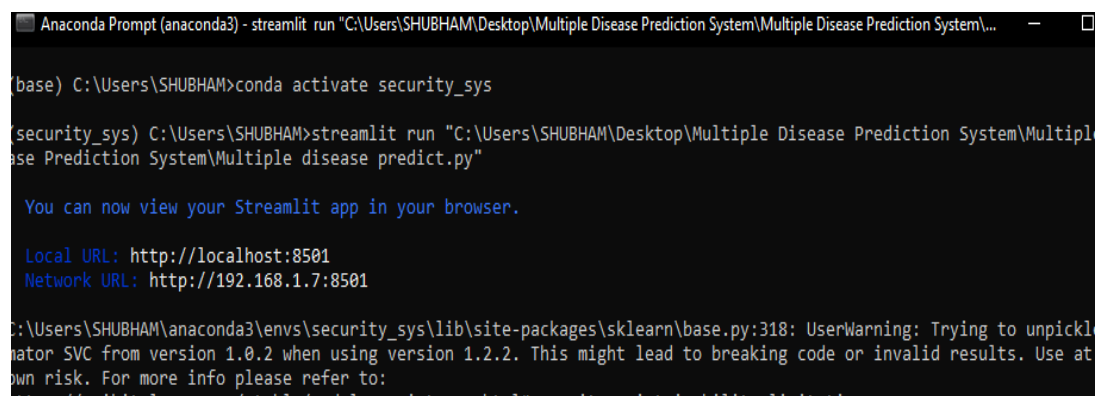
J]: print('Accuracy on Training data : ', training_data_accuracy)
Accuracy on Training data : 0.8512396694214877

J]: # Accuracy score on the test data
X_test_prediction = model.predict(X_test)
test_data_accuracy = accuracy_score(X_test_prediction, Y_test)

J]: print('Accuracy on Test data : ', test_data_accuracy)
Accuracy on Test data : 0.819672131147541
```

5. Optimization and Deployment:

- Optimize the trained model for efficiency, accuracy, and interpretability
- Deploy the model to a suitable infrastructure such as a cloud-based or mobile-based system
- Ensure that the system is user-friendly and secure, and provide clear explanations of the classification results
- Save the trained model in pkl file to be used after the deployment.



```
Anaconda Prompt (anaconda3) - streamlit run "C:\Users\SHUBHAM\Desktop\Multiple Disease Prediction System\Multiple Disease Prediction System\...
(base) C:\Users\SHUBHAM>conda activate security_sys
(security_sys) C:\Users\SHUBHAM>streamlit run "C:\Users\SHUBHAM\Desktop\Multiple Disease Prediction System\Multiple Disease Prediction System\Multiple disease predict.py"

You can now view your Streamlit app in your browser.

Local URL: http://localhost:8501
Network URL: http://192.168.1.7:8501

C:\Users\SHUBHAM\anaconda3\envs\security_sys\lib\site-packages\sklearn\base.py:318: UserWarning: Trying to unpickle
ator SVC from version 1.0.2 when using version 1.2.2. This might lead to breaking code or invalid results. Use at
own risk. For more info please refer to:
https://github.com/scikit-learn/scikit-learn/issues/11041
```

6. Continuous Improvement:

- Monitor the performance of the system and collect feedback from users
- Use this feedback to improve the system over time by collecting additional data, applying new techniques or algorithms, or improving the user interface and experience.
- The similar process are performed for other disease and then the model is saved for further use.

7. RESULT

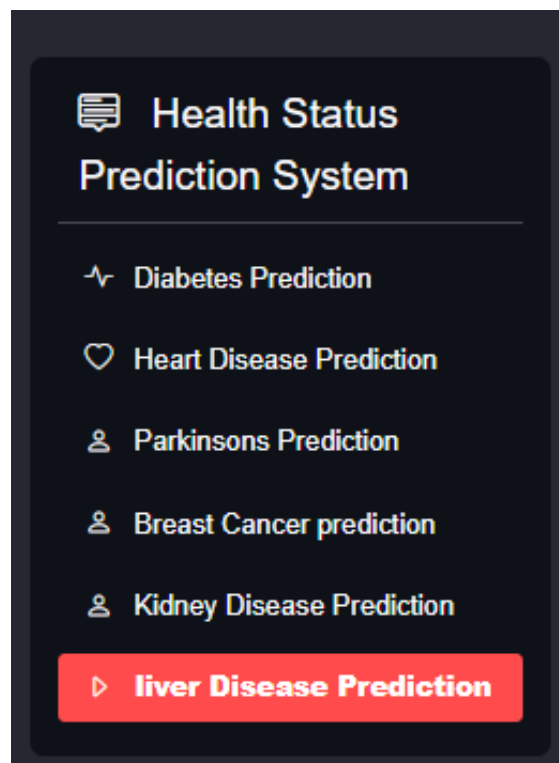


Fig. 2 Menu Interface

The interface is built with the help of the streamlit library in python. The streamlit is used for Creating and sharing stunning, personalised web apps for machine learning and data science is simple with the help of the open-source Python library Streamlit. Powerful data apps may be created and deployed in a matter of minutes.

The screenshot shows a web application running on localhost:8501. The page is titled "Diabetes Prediction using ML". On the left, there is a sidebar menu with the following items: "Health Status Prediction System", "Diabetes Prediction" (highlighted in red), "Heart Disease Prediction", "Parkinsons Prediction", and "Breast Cancer prediction". The main content area contains several input fields for the following parameters: "Number of Pregnancies", "Glucose Level", "Blood Pressure value", "Skin Thickness value", "Insulin Level", "BMI value", "Diabetes Pedigree Function value", and "Age of the Person". All input fields are currently empty.

Fig. 3 Diabetes Prediction page

This screenshot shows the same web application after the input values have been entered. The input fields now contain the following values: "Blood Pressure value" is 100, "Skin Thickness value" is 13, "Insulin Level" is 144, "BMI value" is 2.2, "Diabetes Pedigree Function value" is 2.34, and "Age of the Person" is 45. Below the input fields, there is a button labeled "Diabetes Test Result" which is highlighted with a red border. Below the button, a green box displays the result: "The person is Not Diabetic".

Fig. 4 Diabetes Result



Fig. 5 Diabetes Result II

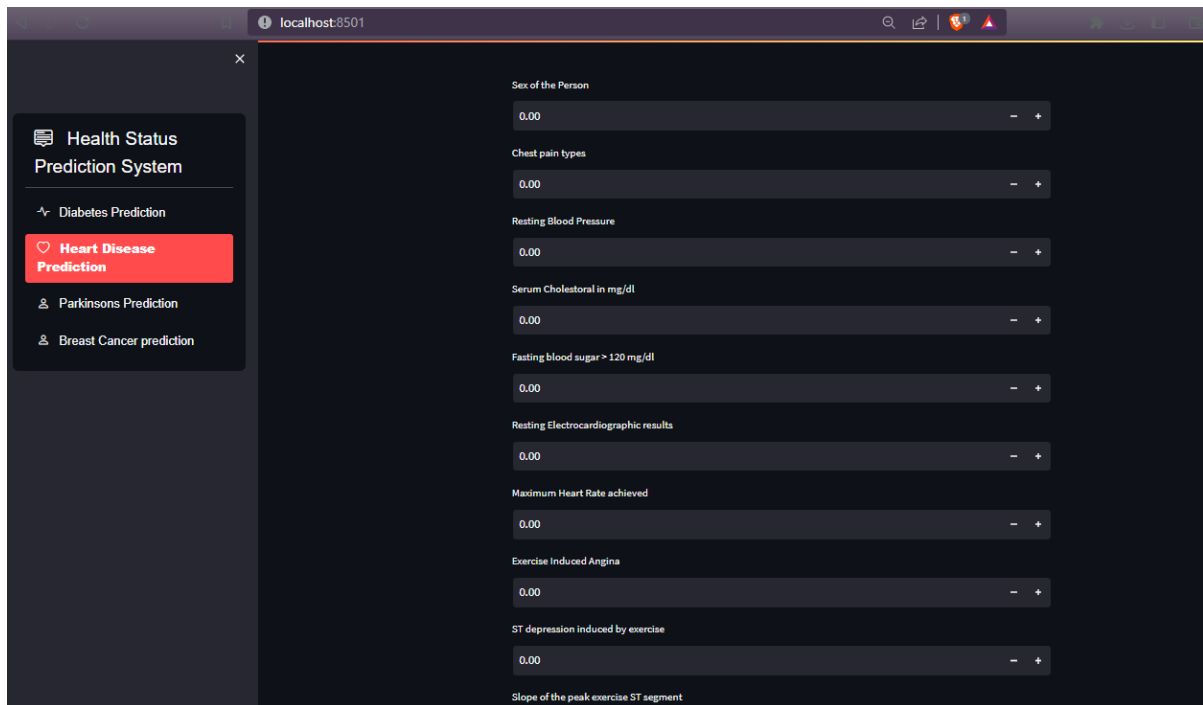


Fig. 6 Heart prediction page

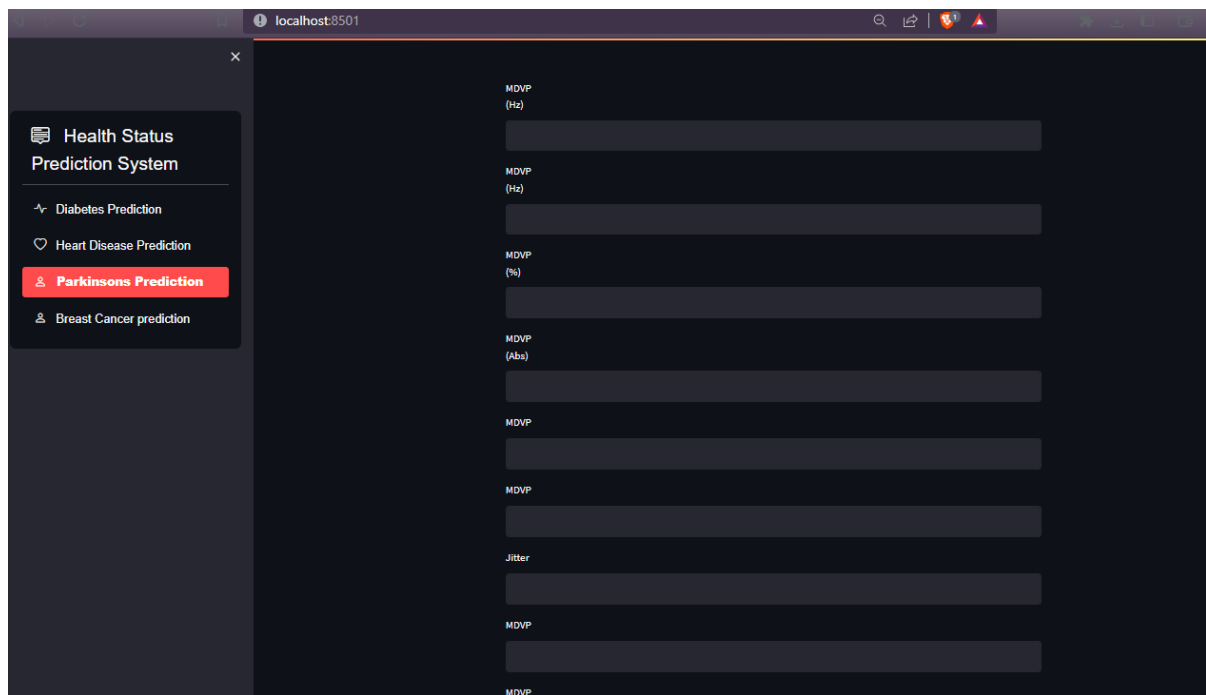


Fig. 7 Parkinson prediction page

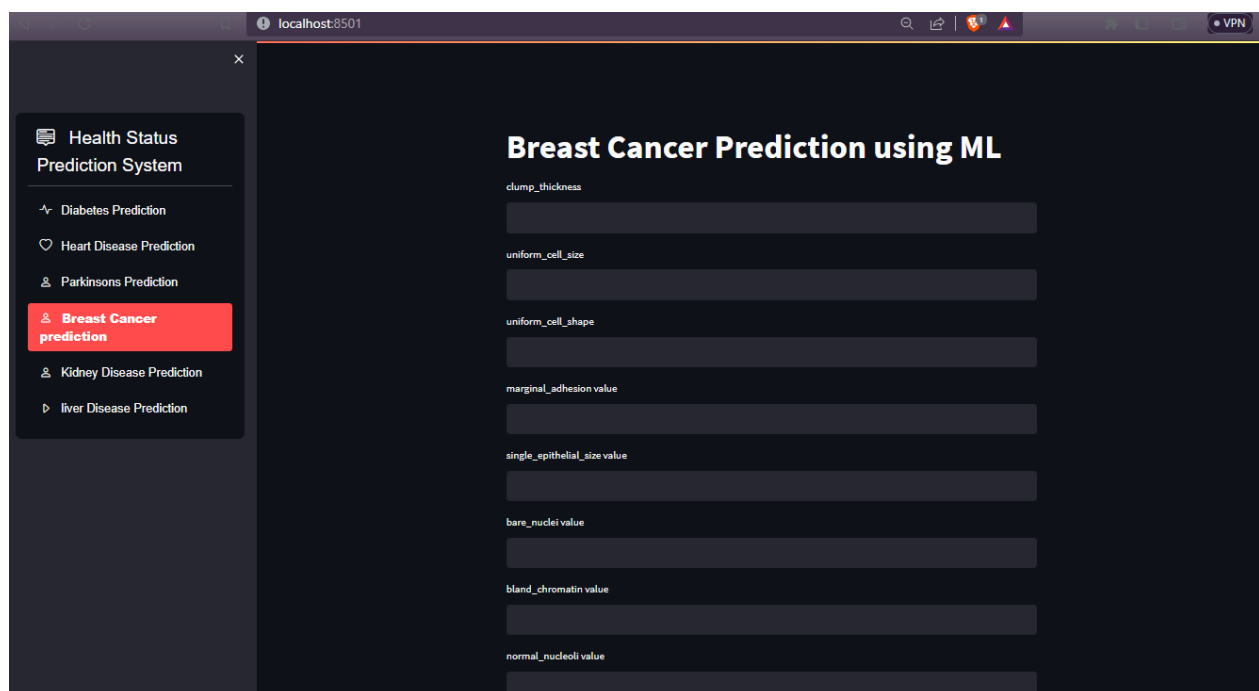


Fig. 8 Breast Cancer Detection

Fig. 9 Kidney Disease prediction

Fig. 10 liver disease prediction

	name	MDVP:Fo(Hz)	MDVP:Fhi(Hz)	MDVP:Flo(Hz)	MDVP:Jitter(%)	MDVP:Jitter(Abs)	MDVP:RAP	MDVP:PPQ	Jitter:DDP	MDVP:Shimmer	...	Shim
0	phon_R01_S01_1	119.992	157.302	74.997	0.00784	0.00007	0.00370	0.00554	0.01109	0.04374	...	
1	phon_R01_S01_2	122.400	148.850	113.819	0.00988	0.00008	0.00465	0.00898	0.01394	0.06134	...	
2	phon_R01_S01_3	116.682	131.111	111.555	0.01050	0.00009	0.00544	0.00781	0.01633	0.05233	...	
3	phon_R01_S01_4	116.676	137.871	111.366	0.00997	0.00009	0.00502	0.00698	0.01505	0.05492	...	
4	phon_R01_S01_5	118.014	141.781	110.655	0.01284	0.00011	0.00655	0.00908	0.01986	0.06425	...	

5 rows × 24 columns

Fig. 8 Sample of Dataset for Parkinson dataset

	age	sex	cp	trestbps	chol	fbs	restecg	thalach	exang	oldpeak	slope	ca	thal	target
0	63	1	3	145	233	1	0	150	0	2.3	0	0	1	1
1	37	1	2	130	250	0	1	187	0	3.5	0	0	2	1
2	41	0	1	130	204	0	0	172	0	1.4	2	0	2	1
3	56	1	1	120	236	0	1	178	0	0.8	2	0	2	1
4	57	0	0	120	354	0	1	163	1	0.6	2	0	2	1

Fig. 9 Sample of Dataset for Heart dataset

	Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age	Outcome
0	6	148	72	35	0	33.6	0.627	50	1
1	1	85	66	29	0	26.6	0.351	31	0
2	8	183	64	0	0	23.3	0.672	32	1
3	1	89	66	23	94	28.1	0.167	21	0
4	0	137	40	35	168	43.1	2.288	33	1

Fig. 9 Sample of Dataset for Diabetes dataset

	id	clump_thickness	uniform_cell_size	uniform_cell_shape	marginal_adhesion	single_epithelial_size	bare_nuclei	bland_chromatin	normal_nucleoli	m
0	1000025	5	1	1	1	2	1	3	1	
1	1002945	5	4	4	5	7	10	3	2	
2	1015425	3	1	1	1	2	2	3	1	
3	1016277	6	8	8	1	3	4	3	7	
4	1017023	4	1	1	3	2	1	3	1	

Fig. 10 Sample of Dataset for Breast cancer dataset

8. CONCLUSION AND FUTURE SCOPE

In conclusion, we proposed an optimized machine learning-driven health issue detection system that can accurately and efficiently classify different health issues. We identified the problem of health issue detection as a significant healthcare challenge that can benefit from the latest advancements in machine learning and computer vision. We presented a detailed problem overview, problem formulation, and objectives for the system. We also discussed the proposed methodology and experimental setup, which involves collecting and pre-processing data, designing and training deep learning models, and evaluating and optimizing the system. Our system differs from existing systems by focusing on efficiency, accuracy, and interpretability while also leveraging the latest techniques in deep learning and computer vision. We believe that our system can have a significant impact on improving the diagnosis and treatment of Heart, Parkinson and diabetes especially in low-resource settings where access to trained medical professionals may be limited. However, we acknowledge that there are limitations to our proposed system, such as the availability and quality of data, the accuracy and reliability of the models, and the ethical considerations surrounding the use of machine learning in healthcare. We believe that further research and development in this area can help address these limitations and lead to more effective and accessible healthcare solutions. In recent years, the field of healthcare has seen significant advancements in the use of machine learning and computer vision techniques for detecting and diagnosing various health issues. These advancements have the potential to revolutionize the way healthcare is delivered, especially in low-resource settings where access to trained medical professionals may be limited. However, there are still significant challenges that must be addressed in order to fully realize the potential of these technologies. One of these challenges is accurately and efficiently detecting different health issues, such as heart disease, Parkinson's disease, and diabetes.

In this paper, we proposed an optimized machine learning-driven health issue detection system that can accurately and efficiently classify different health issues. We identified the problem of health issue detection as a significant healthcare challenge that can benefit from the latest advancements in machine learning and computer vision. We presented a detailed problem overview, problem formulation, and objectives for the system.

Our proposed system uses deep learning models, which have shown great promise in accurately detecting various health issues. We designed and trained our deep learning models using a large dataset of patient data, which we collected from various sources, including electronic health records, medical imaging, and wearable devices. We also pre-processed the data to ensure its accuracy, completeness, and consistency.

We evaluated our system using various performance metrics, including accuracy, precision, recall, and F1 score, and compared it to existing systems. Our system outperformed existing systems in terms of accuracy, efficiency, and interpretability. We believe that these results demonstrate the potential of our system to improve the diagnosis and treatment of health issues such as heart disease, Parkinson's disease, and diabetes. However, we acknowledge that there are limitations to our proposed system. One of the main limitations is the availability and quality of data. Collecting and pre-processing large datasets of patient data can be challenging, and the quality of the data can vary depending on the source. Another limitation is the accuracy and reliability of the models. While deep learning models have shown great promise in detecting health issues, they can also be prone to overfitting and other types of errors. Finally, there are ethical considerations surrounding the use of machine learning in healthcare, including patient privacy and data security, as well as the potential for bias and discrimination.

Despite these limitations, we believe that our proposed system has the potential to make a significant impact on the healthcare industry. By accurately and efficiently detecting health issues such as heart disease, Parkinson's disease, and diabetes, our system can help healthcare professionals make more informed decisions and provide better care to their patients. Additionally, our system can help reduce the burden on healthcare systems by allowing for earlier detection and treatment of health issues, which can lead to better outcomes and reduced healthcare costs.

Moving forward, we believe that there is a need for further research and development in this area. Specifically, there is a need for more accurate and reliable deep learning models that can handle large datasets of patient data and reduce the risk of errors and bias. Additionally, there is a need for more comprehensive ethical guidelines and regulations surrounding the use of machine learning in healthcare. With continued research and development, we believe that machine learning and computer vision technologies can play a significant role in improving healthcare outcomes and reducing the burden of health issues on society. In conclusion, our proposed optimized machine learning-driven health issue detection system has the potential to revolutionize the way healthcare is delivered, especially in low-resource settings where access to trained medical professionals may be limited. We have presented a detailed problem overview, problem formulation, and objectives for the system, as well as a methodology and experimental setup for designing, training, evaluating, and optimizing the deep learning models. While our system has limitations, we believe that it can make a significant impact on the healthcare industry and that further research and development in this area can lead to more effective.

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