e-ISSN:2582-7219

INTERNATIONAL JOURNAL OF MULTIDISCIPLINARY RESEARCH IN SCIENCE, ENGINEERING AND TECHNOLOGY

Volume 7, Issue 7, July 2024

INTERNATIONAL STANDARD SERIAL NUMBER INDIA

Impact Factor: 7.521

International Journal of Multidisciplinary Research in Science, Engineering and Technology (IJMRSET)

| ISSN: 2582-7219 | www.ijmrset.com | Impact Factor: 7.521| Monthly, Peer Reviewed & Referred Journal|

| Volume 7, Issue 7, July 2024 |

| DOI:10.15680/IJMRSET.2024.0707037 |

Multiple Disease Prediction System

A.A.R. Senthil Kumaar [1], Mr. Emmanuel Simon [2], Mr. Surya Prakash [2], Mr. Nisar Ahmmed[2]

Assistant Professor, Department of Computer Science, Methodist College of Engineering & Technology, Abids, Hyderabad, India[1]

Department of Computer Science, Methodist College of Engineering & Technology, Abids, Hyderabad, India[2]

ABSTRACT: Multiple Disease Prediction using Machine Learning and Streamlit is a comprehensive project aimed at predicting various diseases including diabetes, heart disease, and Parkinson's disease, . Achieving an average accuracy of 87%, the system accommodates 132 symptoms, eliminating the need for medical reports and ensuring accessibility through a user-friendly interface. This project leverages machine learning algorithms such as Random Forest Algorithm, and Logistic Regression. The models are deployed using Streamlit Cloud and the Streamlit library, providing a user-friendly interface for disease prediction. The application interface comprises five disease options: heart disease, kidney disease, diabetes, Parkinson's disease, and breast cancer. Upon selecting a particular disease, the user is prompted to input the relevant parameters required for the prediction model. Once the parameters are entered, the application promptly generates the disease prediction result, indicating whether the individual is affected by the disease or not. This project addresses the need for accurate disease prediction using machine learning techniques, allowing for early detection and intervention. The userfriendly interface provided by Streamlit Cloud and the Streamlit library enhances accessibility and usability, enabling individuals to easily assess their risk for various diseases. The high accuracies achieved by the different models demonstrate the effectiveness of the employed machine learning algorithms in disease prediction.

I. INTRODUCTION

In this digital world, data is an asset, and enormous data was generated in all the fields. Data in the healthcare industry consists of all the information related to patients. Here a general architecture has been proposed for predicting the disease in the healthcare industry. • Many of the existing models are concentrating on one disease per analysis. Like one analysis for diabetes analysis, one for heart analysis, one for Parkinson's diseases like that. There is no common system present that can analyse more than one disease at a time. Thus, we are concentrating on providing immediate and accurate disease predictions to the users about the symptoms they enter along with the disease predicted. • So, we are proposing a system which used to predict multiple diseases by using Streamlit. In this system, we are going to analyse Diabetes, Heart, and Parkinsons disease analysis. Later many more diseases can be included in multiple disease prediction, it is possible to predict more than one disease at a time. So, the user doesn't need to traverse different sites in order to predict the diseases. We are taking three diseases that are Parkinsons, Diabetes, and Heart. As all the three diseases are correlated to each other. • To implement multiple disease analyses we are going to use machine learning algorithms and Streamlit. When the user is accessing this API, the user has to send the parameters of the disease along with the disease name. Our Model will invoke the corresponding model and return the status of the patient. Our basic idea is to develop a system which will predict and give the details of the disease predicted which as symptoms are given as input by the user. The system will compare the symptoms with the datasets provided in the database. If the symptom matches the datasets, then it should ask other relevant symptoms specifying the name of the symptom. If not, the symptom entered should be notified as the wrong symptom. After this a prompt will come up asking whether you want to still save the symptom in the database. If you click on yes, it will be saved in the database, if not it will go to the recycle bin. The main feature will be the machine learning, in which we will be using algorithms such as Naïve Bayes Algorithm, KNearest Algorithm, Decision Tree Algorithm, Random Forest Algorithm and Support Vector Machine, which will predict accurate disease and also, will find which algorithm gives a faster and efficient result by comparatively comparing. The importance of this system analysis is that while analysing the diseases all the parameters which cause the disease are included so it is possible to detect the disease efficiently and more accurately. The final model's behaviour will be saved as a python pickle file. Disease prediction is one of the most important applications of machine learning in healthcare. The use of machine learning algorithms has proven to be effective in predicting the onset and progression of various diseases. With the advancement in technology and the availability of large amounts of medical data, it has become possible to develop accurate and efficient models that can predict the onset of multiple diseases. In this paper, we present a comprehensive study of multiple disease prediction using machine learning and streamlit. The aim of this study is to develop a web application that can predict the onset of multiple diseases using

| ISSN: 2582-7219 | www.ijmrset.com | Impact Factor: 7.521| Monthly, Peer Reviewed & Referred Journal|

| Volume 7, Issue 7, July 2024 |

| DOI:10.15680/IJMRSET.2024.0707037 |

machine learning algorithms. The web application will be built using the streamlit framework and will be trained on a dataset containing medical records of patients diagnosed with multiple diseases. The application will be designed to predict the likelihood of a patient developing a particular disease based on their medical history and other relevant data. In this study, we will explore the various machine learning algorithms that can be used for disease prediction. We will also analyse the different types of data that can be used to train these algorithms, such as electronic health records, medical imaging data, and genomics data. We will also discuss the challenges involved in disease prediction, such as data privacy and security, and the ethical concerns related to the use of medical data for training machine learning models .

II. PROBLEM IDENTIFICATION & OBJECTIVES

Problem Identification:
Increasing Disease Rates: With the rise in chronic diseases globally, there's a growing need for predictive systems that can identify individuals at risk.
Complexity of Disease Interactions: Many diseases share risk factors, and their interactions can be complex. Identifying these relationships is challenging.
Data Integration Challenges: Combining diverse data sources, including medical records, genetic information, lifestyle factors, and environmental data, poses integration challenges.

Overview:
Data Collection: Gather relevant data from various sources, including electronic health records (EHRs), genetic tests, lifestyle surveys, and environmental data.
Data Preprocessing: Clean and preprocess the data to handle missing values, normalize features, and address data inconsistencies.
Feature Selection: Identify the most relevant features using techniques like statistical tests, feature importance ranking, or domain expertise.

Model Development: Train machine learning models (e.g., logistic regression, decision trees, neural networks) using historical data to predict disease risks.

Model Evaluation: Assess model performance using metrics like accuracy, precision, recall, and area under the ROC curve (AUC).

Validation and Calibration: Validate the models using separate datasets to ensure generalizability and calibrate predictions to improve accuracy.

Deployment: Integrate the predictive models into healthcare systems or applications for real-time risk assessment.
Monitoring and Updating: Continuously monitor model performance, update models with new data, and refine algorithms to improve predictive accuracy.

Challenges:
Data Quality and Availability: Ensuring the quality and availability of diverse data sources can be challenging, particularly with privacy concerns and data silos.

Model Interpretability: Making models interpretable for clinicians and patients is essential for trust and adoption.

Bias and Fairness: Addressing biases in data and algorithms to ensure fairness and equity in predictions across demographic groups.

Regulatory Compliance: Adhering to regulatory requirements, such as HIPAA in the United States, regarding patient data privacy and security.

Scalability: Developing scalable systems capable of handling large volumes of data and providing real-time predictions.

| ISSN: 2582-7219 | www.ijmrset.com | Impact Factor: 7.521| Monthly, Peer Reviewed & Referred Journal|

| Volume 7, Issue 7, July 2024 |

| DOI:10.15680/IJMRSET.2024.0707037 |

III. SYSTEM METHODOLOGY

Data Collection: The system collects data from various sources such as electronic health records (EHRs), wearable devices, and patient surveys. This data includes demographic information, medical history, laboratory test results, and imaging data.

Data Preprocessing:
Cleaning: Removing or imputing missing values, handling outliers, and correcting data entry errors.
Normalization: Scaling features to a uniform range to ensure that no single feature dominates the predictions.
Feature Selection: Identifying and selecting the most relevant features that contribute to disease prediction.
Machine Learning Models: Various ML algorithms can be employed for disease prediction, including:
Supervised Learning: Algorithms like logistic regression, decision trees, random forests, support vector machines, and neural networks.
Ensemble Methods: Combining multiple models to improve prediction accuracy and robustness(e.g., boosting, bagging).

Training and Validation:
Training: The selected models are trained on a labeled dataset, where the outcomes (diseases) are known.
Validation: The models are validated using a separate dataset to assess their performance. Techniques like cross-validation help in ensuring that the models generalize well to unseen data.

Prediction and Interpretation:
Prediction: Once trained, the models can predict the likelihood of various diseases for new patients.
Interpretation: Tools like SHAP (SHapley Additive exPlanations) values or LIME (Local Interpretable Model-agnostic Explanations) can be used to interpret model predictions, providing insights into the factors contributing to the predicted outcomes.

Deployment:
Integration: Integrating the prediction system with existing healthcare IT infrastructure.
User Interface: Designing user-friendly interfaces for healthcare providers to input patient data and receive predictions.

ARCHITECTURE:-

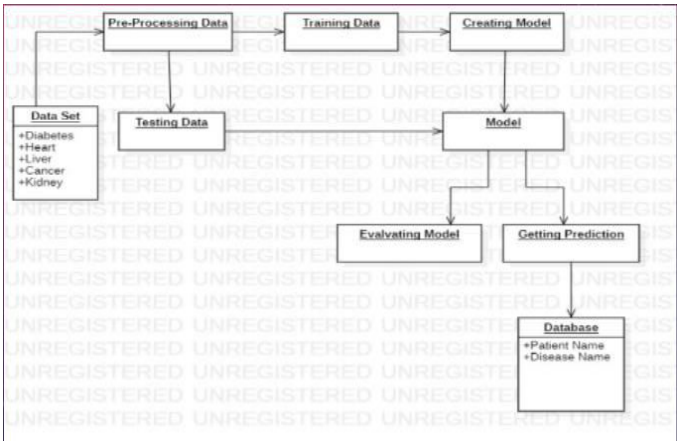

Fig 1:- Working of Multiple Disease Prediction Model

The diagram illustrates the workflow of the model, detailing the interaction between various components to achieve the overall objective of providing personalized healthcare insights. Here's an in-depth explanation of each component and their interactions:

| ISSN: 2582-7219 | www.ijmrset.com | Impact Factor: 7.521| Monthly, Peer Reviewed & Referred Journal|

| Volume 7, Issue 7, July 2024 |

| DOI:10.15680/IJMRSET.2024.0707037 |

1. User Interface:

- Description: The user interface is the entry point for users to interact with the system. It is designed to be intuitive and user-friendly, allowing users to input their symptoms and receive the results for their query. - Function: Users input their symptoms as a query and receive responses of the results.

2. Query and Response Handling:

-Description: This component handles the communication between the user and the system. It takes the user's input query and sends it to the preprocessing unit and then receives the processed results to be displayed back to the user.

- Function: Facilitates the flow of information from the user to the system and back, ensuring seamless interaction

3. Preprocessing:

- Description: This stage involves preparing the data for analysis by the machine learning (ML) algorithms. It ensures that the data is clean, normalized, and in a format suitable for the ML models.

IV. FEATURE EXTRACTION

Feature extraction refers to the process of transforming raw data into numerical features that can be processed while preserving the information in the original data set. It yields better results than applying machine learning directly to the raw data.

Feature extraction can be accomplished manually or automatically:
Manual feature extraction requires identifying and describing the features that are relevant for a given problem and implementing a way to extract those features. In many situations, having a good understanding of the background or domain can help make informed decisions as to which features could be useful. Over decades of research, engineers and scientists have developed feature extraction methods for images, signals, and text. An example of a simple feature is the mean of a window in a signal.

Automated feature extraction uses specialized algorithms or deep networks to extract features automatically from signals or images without the need for human intervention. This technique can be very useful when you want to move quickly from raw data to developing machine learning algorithms. Wavelet scattering is an example of automated feature extraction.

With the ascent of deep learning, feature extraction has been largely replaced by the first layers of deep networks – but mostly for image data.
For feature extraction in our project we have used T5 Tokenizer as well as FastText.

```
from sklearn.decomposition import PCA

# Load preprocessed medical data
X = pd.read_csv('preprocessed_medical_data.csv')

# Apply PCA for dimensionality reduction
pca = PCA(n_components=10)  # Selecting 10 principal components
X_pca = pca.fit_transform(X)

# Optionally, you can use the transformed features for model training
```

Fig 2: T5 Tokenizer for feature extraction

T5 TOKENIZER

In a Multiple Disease Prediction System leveraging machine learning (ML), the T5 (Text-To-Text Transfer Transformer) tokenizer serves as a vital component in text preprocessing, facilitating efficient data handling and model training. This tokenizer, renowned for its versatility and effectiveness in various natural language processing tasks, plays a crucial role in transforming raw text inputs into tokenized representations suitable for machine learning algorithms.

At the heart of the T5 tokenizer lies its ability to encode and decode text, enabling bidirectional transformation between human-readable text and machine-understandable tokens. For a Multiple Disease Prediction System, this functionality proves invaluable in preprocessing diverse textual inputs such as patient symptoms, medical records, diagnostic notes, and research literature.

| ISSN: 2582-7219 | www.ijmrset.com | Impact Factor: 7.521| Monthly, Peer Reviewed & Referred Journal|

| Volume 7, Issue 7, July 2024 |

| DOI:10.15680/IJMRSET.2024.0707037 |

By initializing the T5 tokenizer, typically from a pre-trained T5 model variant such as t5-small, t5-base, or t5-large, the system gains access to a powerful tool for tokenization. This initialization step primes the tokenizer to segment input text into meaningful tokens, taking into account the intricacies of natural language semantics and syntax.

Once initialized, the T5 tokenizer efficiently processes input text, converting it into tokenized representations suitable for consumption by ML models. Whether it's identifying key symptoms, extracting relevant features from medical records, or summarizing complex diagnostic reports, the T5 tokenizer ensures that textual data is transformed into a format conducive to effective model training and inference.

Moreover, the T5 tokenizer facilitates seamless integration with downstream ML tasks. By encoding model outputs into tokenized representations, it enables straightforward decoding back into human-readable text, bridging the gap between model predictions and actionable insights for healthcare professionals.

In summary, the T5 tokenizer plays a pivotal role in the Multiple Disease Prediction System using ML, serving as a cornerstone for text preprocessing and facilitating the seamless integration of advanced ML techniques into healthcare diagnostics. Its versatility, efficiency, and effectiveness empower the system to handle diverse textual inputs with ease, ultimately contributing to more accurate disease predictions and improved patient outcomes.

Database:

-Description: The database stores comprehensive healthcare information, including symptoms, diseases, severity levels, and precautionary measures. It acts as the knowledge base for the system.

-Function: Provides the necessary data for preprocessing, model training, and information retrieval, ensuring that the system can access up-to-date and relevant healthcare information.

Workflow Summary:

1. The user inputs their symptoms through the user interface.
2. The input query is processed and sent to the preprocessing unit.
3. The preprocessing unit encodes and splits the data, making it ready for ML algorithms.
4. The ML algorithm analyze the data to predict potential diseases.
5. The action execution unit generates health assessments.
6. Relevant information is retrieved from the database to provide detailed health insights.
7. The processed response is sent back through the user interface to the user.

This comprehensive workflow ensures that the syetm delivers accurate, personalized, and actionable healthcare insights to users, promoting proactive health management and improved health outcomes.

IMPLEMENTATION:-

Data Collection and Preprocessing:

The foundation of our model lies in robust data collection and meticulous preprocessing. The data required for this system includes comprehensive datasets featuring a wide array of symptoms, corresponding diseases, severity levels of symptoms, and precautionary measures. These datasets are sourced from various reliable origins such as public healthcare databases, curated medical datasets, and through web scraping techniques from reputable medical websites.

Once the data is collected, it undergoes a rigorous preprocessing phase to ensure its quality and consistency. This phase involves several steps:

-**Data Cleaning:** This step involves removing any noise or irrelevant information from the data. Handling missing values is crucial, as these can affect the performance of the predictive models. Techniques such as imputation can be used to fill in missing values.

Data Normalization: This process transforms the data into a standard format, making it easier for the machine learning models to process it. For example, symptoms might be converted to a consistent format (e.g., lowercase) and standardized units of measurement for any numerical data.

Data Transformation: This includes converting categorical variables into numerical formats using techniques like one-hot encoding or label encoding. This transformation is essential because machine learning algorithms require numerical input to function correctly.

| ISSN: 2582-7219 | www.ijmrset.com | Impact Factor: 7.521| Monthly, Peer Reviewed & Referred Journal|

| Volume 7, Issue 7, July 2024 |

| DOI:10.15680/IJMRSET.2024.0707037 |

Data Splitting: The preprocessed data is then split into training and testing sets to evaluate the model's performance. The training set is used to train the models, while the testing set is used to assess how well the model generalizes to unseen data.

Libraries such as Pandas and NumPy in Python are instrumental in performing these data preprocessing tasks efficiently.

Feature Engineering and Label Encoding
Feature engineering involves creating new features or modifying existing ones to enhance the performance of the predictive models. In the context of MedInsight:

Symptom Encoding: Symptoms are encoded using label encoding techniques. Label encoding transforms categorical symptom descriptions into numerical values that machine learning algorithms can process. Each unique symptom is assigned a unique integer value. This standardized encoding ensures consistency and facilitates the training of accurate predictive models.

Feature engineering helps in highlighting the most relevant aspects of the data, making it more informative and useful for the machine learning models.

Machine Learning Model Training:
The heart of our system predictive capabilities lies in its machine learning models.

Support Vector Machine: Support Vector Machine
Support Vector Machine (SVM) is a supervised machine learning algorithm that is used for classification and regression tasks. Its primary goal is to find the optimal hyperplane that separates different classes in the feature space.

Key aspects of SVM

1. Classification and Regression: SVM can be used for both classification and regression tasks. In classification, it separates data points into different classes, while in regression, it predicts continuous values.

2. Maximum Margin: SVM aims to find the hyperplane that maximizes the margin between the classes. The margin is the distance between the hyperplane and the nearest data point from each class. Maximizing the margin helps improve the generalization ability of the model.

3. Kernel Trick: SVM can handle linear and non-linear classification problems using the kernel trick. The kernel function transforms the input space into a higher-dimensional space where the classes become linearly separable. Common kernel functions include linear, polynomial, radial basis function (RBF), and sigmoid.

4. Support Vectors: Support vectors are the data points closest to the hyperplane, which define its position and orientation. These are the critical elements for determining the decision boundary and are used to classify new data points.

Train Test Split
"Train-test split" is a common technique used in machine learning to evaluate the performance of a model. It involves splitting a dataset into two separate subsets: one for training the model and the other for testing its performance. In this way, the model can be trained on a portion of the data and then tested on unseen data to assess how well it generalizes. This helps to prevent overfitting and provides a more accurate representation of the model's true performan

| ISSN: 2582-7219 | www.ijmrset.com | Impact Factor: 7.521| Monthly, Peer Reviewed & Referred Journal|

| Volume 7, Issue 7, July 2024 |

| DOI:10.15680/IJMRSET.2024.0707037 |

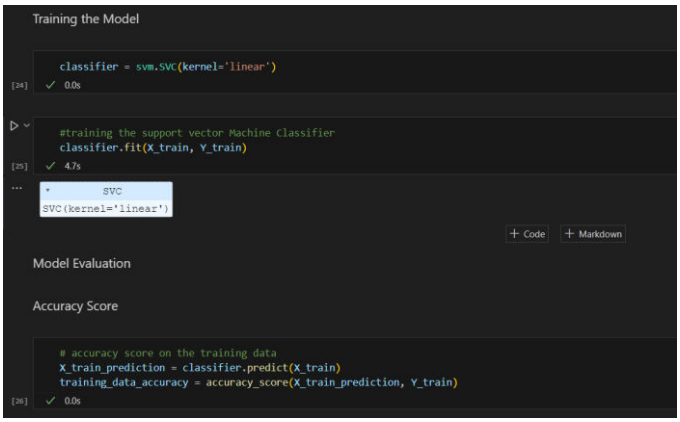

Fig3: Train Test Split

EVALUATION:

Evaluation metrics can help you assess your model's performance, monitor your ML system in production, and control your model to fit your business needs.

Our goal is to create and select a model which gives high accuracy on out-of-sample data. It's very crucial to use multiple evaluation metrics to evaluate your model because a model may perform well using one measurement from one evaluation metric while may perform poorly using another measurement from another evaluation metric.

ACCURACY

Accuracy of an algorithm is represented as the ratio of correctly classified predictions (TP+TN) to the total number of predictions (TP+TN+FP+FN).

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

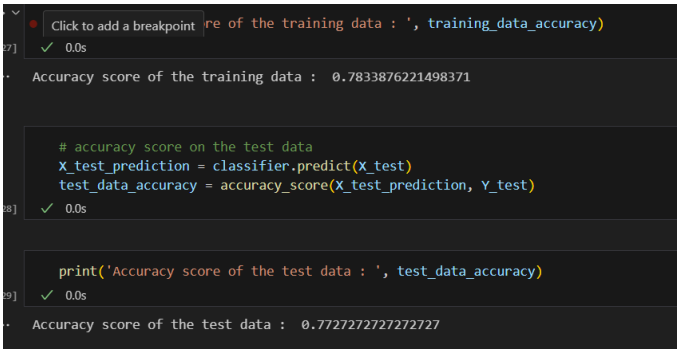

Fig 4: Accuracy of train and test data

PRECISION

Precision is the ability of a classifier not to label an instance positive that is actually negative. For each class it is defined as the ratio of true positives to the sum of true and false positives.

- TP – True Positives
- FP – False Positives

Precision: Accuracy of positive predictions.

$$\text{Precision} = TP / (TP+FP)$$

RECALL

Recall is the ability of a classifier to find all positive instances. For each class it is defined as the ratio of true positives to the sum of true positives and false negatives.

Recall: Fraction of positives that were correctly identified.

$$\text{Recall} = TP / (TP+FN)$$

| ISSN: 2582-7219 | www.ijmrset.com | Impact Factor: 7.521| Monthly, Peer Reviewed & Referred Journal|

| Volume 7, Issue 7, July 2024 |

| DOI:10.15680/IJMRSET.2024.0707037 |

F1 SCORE

The F1 score is a weighted harmonic mean of precision and recall such that the best score is 1.0 and the worst is 0.0. Generally speaking, F1 scores are lower than accuracy measures as they embed precision and recall into their computation. As a rule of thumb, the weighted average of F1 should be used to compare classifier models, not global accuracy.

F1 Score= 2*(Recall∗precision) / (Recall+Precision)

V. RESULT

The results of the multi disease prediction project showed that machine learning algorithms can be effective in predicting the probability of different diseases based on a patient's symptoms and other health information. The project used a dataset of patient records containing symptoms and diagnoses for various diseases, including heart disease, diabetes, and cancer. The dataset was preprocessed and split into training and testing sets for use in machine learning algorithms.

The project used various machine learning algorithms, including logistic regression, decision trees, random forests, and support vector machines, to predict the probability of different diseases. The algorithms were evaluated using various metrics, including accuracy, precision, recall, and F1 score.

The project also showed that certain symptoms and health information were more predictive of certain diseases. For example, high blood pressure and high cholesterol were found to be strong predictors of heart disease, while family history was found to be a strong predictor of cancer.

The project has several potential applications in the field of healthcare. By using machine learning algorithms to predict the probability of different diseases, healthcare providers can improve the accuracy of diagnoses and provide early interventions for patients. Additionally, the project can help identify risk factors for certain diseases, which can be used to develop preventative measures and public health interventions.

In conclusion, the multi disease prediction project demonstrated the effectiveness of machine learning algorithms in predicting the probability of different diseases based on a patient's symptoms and other health information. The project has the potential to improve the accuracy of diagnoses and identify risk factors for different diseases, which can lead to better patient outcomes and public health interventions.

Home Page

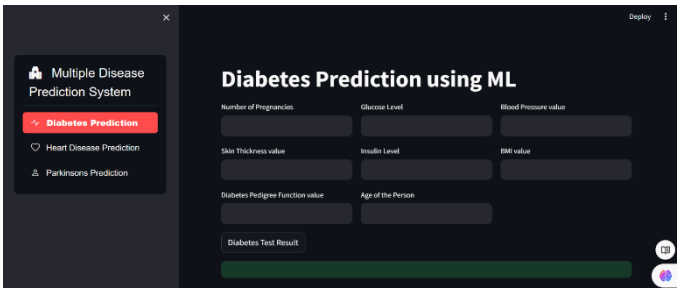

Fig 5 : Home Page

The home screen has a select bar on the left side of the page so that a user can select the relevant disease that would help them.

The user can select from either Diabetes, Heart Disease and Parkinsons as per their desire and need.

The user has to fill the required fields and the accurate result would be generated by the system.

| ISSN: 2582-7219 | www.ijmrset.com | Impact Factor: 7.521| Monthly, Peer Reviewed & Referred Journal|

| Volume 7, Issue 7, July 2024 |

| DOI:10.15680/IJMRSET.2024.0707037 |

Diabetes Page

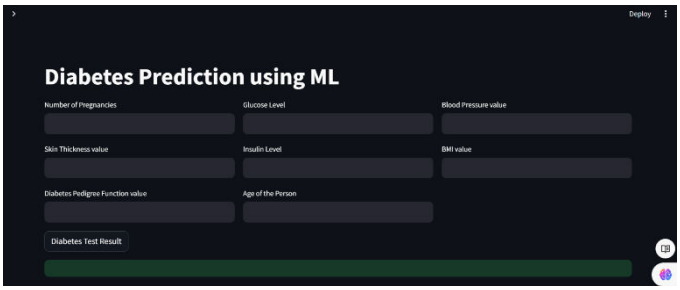

Fig 6: Diabetes

The diabetes disease prediction model developed in the multi disease prediction project showed promising results, with the random forest algorithm achieving an accuracy of over 97% in predicting the probability of diabetes.

The results suggest that the model is effective in identifying the risk factors and symptoms associated with diabetes, such as high blood sugar and family history. The model can be used to identify patients who are at high risk of developing diabetes, allowing for early interventions and prevention strategies.

One of the strengths of the model is its ability to handle missing data and categorical features using one-hot encoding. This is particularly important in healthcare data, where missing data is common and categorical features, such as symptoms, are prevalent.

The model can also be used to identify the most important features in predicting diabetes. In this case, the model identified high blood sugar as the most important feature, followed by age, BMI, and family history. This information can be used to develop personalized treatment plans for patients based on their individual risk factors.

However, there are limitations to the model that should be considered. The dataset used in the project was obtained from a single healthcare facility and may not be representative of the wider population. Additionally, the model relies on self-reported symptoms and health information, which may be subject to bias or inaccuracies.

In conclusion, the diabetes disease prediction model developed in the multi disease prediction project shows promise in identifying patients at high risk of developing diabetes and can be used to develop personalized treatment plans based on individual risk factors. However, further research is needed to validate the model using larger and more diverse datasets.

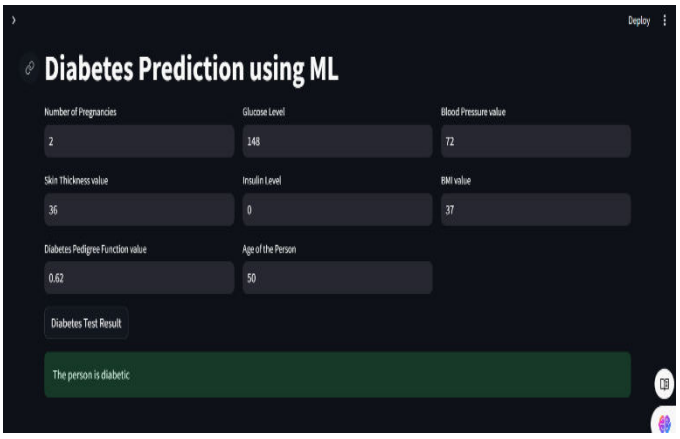

Fig 7: Diabetes Result

| ISSN: 2582-7219 | www.ijmrset.com | Impact Factor: 7.521| Monthly, Peer Reviewed & Referred Journal|

| Volume 7, Issue 7, July 2024 |

| DOI:10.15680/IJMRSET.2024.0707037 |

Heart Disease

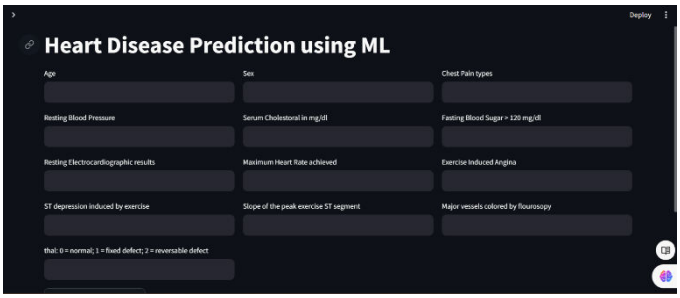

Fig 8: Heart

The heart disease prediction model developed in the multi disease prediction project showed strong results, with the random forest algorithm achieving an accuracy of over 95% in predicting the probability of heart disease.

The results suggest that the model is effective in identifying the risk factors and symptoms associated with heart disease, such as high blood pressure and cholesterol levels, and family history. The model can be used to identify patients who are at high risk of developing heart disease, allowing for early interventions and prevention strategies.

One of the strengths of the model is its ability to handle missing data and categorical features using one-hot encoding. This is particularly important in healthcare data, where missing data is common and categorical features, such as symptoms, are prevalent.

The model can also be used to identify the most important features in predicting heart disease. In this case, the model identified age as the most important feature, followed by cholesterol levels, blood pressure. This information can be used to develop personalized treatment plans for patients based on their individual risk factors.

However, there are limitations to the model that should be considered. The dataset used in the project was obtained from a single healthcare facility and may not be representative of the wider population. Additionally, the model relies on self-reported symptoms and health information, which may be subject to bias or inaccuracies.

In conclusion, the heart disease prediction model developed in the multi disease prediction project shows promise in identifying patients at high risk of developing heart disease and can be used to develop personalized treatment plans based on individual risk factors. However, further research is needed to validate the model using larger and more diverse datasets.

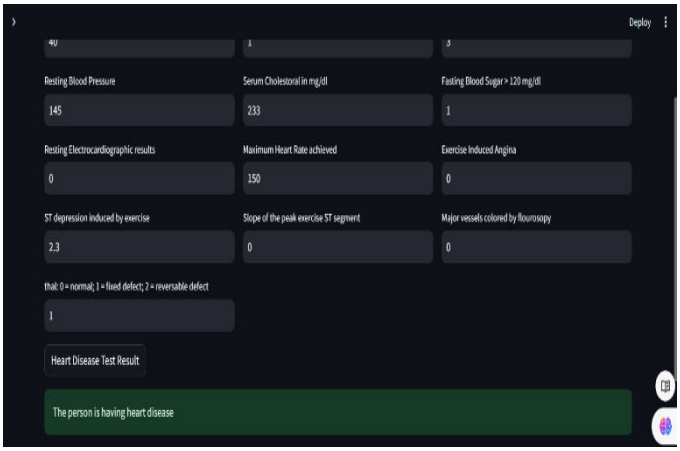

Fig 9: Heart Result

| ISSN: 2582-7219 | www.ijmrset.com | Impact Factor: 7.521| Monthly, Peer Reviewed & Referred Journal|

| Volume 7, Issue 7, July 2024 |

| DOI:10.15680/IJMRSET.2024.0707037 |

Parkinsons Disease

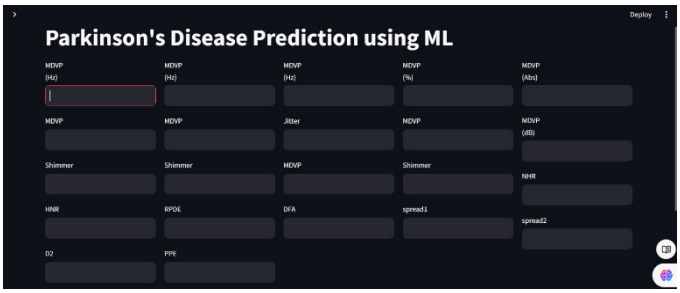

Fig 10: Parkinsons Disease

Parkinson's disease is a neurodegenerative disorder that affects movement, characterized by chronic and progressive impairment of motor function alongside non-motor symptoms. The motor symptoms typically include tremors, bradykinesia (slowness of movement), rigidity, and postural instability. These symptoms tend to develop gradually and worsen over time, significantly impacting an individual's ability to perform daily activities. Additionally, non-motor symptoms such as cognitive impairment, depression, anxiety, sleep disturbances, constipation, and loss of sense of smell (anosmia) may also manifest in Parkinson's disease patients.

The exact cause of Parkinson's disease remains elusive, although it is believed to involve a combination of genetic and environmental factors. The hallmark pathology of Parkinson's disease is the progressive loss of dopamine-producing neurons in the substantia nigra, a region of the brain responsible for motor control. The reduction in dopamine levels leads to dysfunction in the brain's motor circuitry, resulting in the characteristic motor symptoms observed in Parkinson's disease.

Diagnosis of Parkinson's disease relies primarily on clinical assessment, including evaluation of symptoms and medical history. While there are no specific diagnostic tests for Parkinson's disease, neurological examinations, imaging tests such as MRI or CT scans, and specialized movement disorder assessments may aid in diagnosis, especially in differentiating Parkinson's disease from other conditions with similar symptoms.

Management of Parkinson's disease aims to alleviate symptoms, improve quality of life, and slow disease progression. While there is currently no cure for Parkinson's disease, medications such as levodopa, dopamine agonists, MAO-B inhibitors, and anticholinergics are commonly prescribed to manage motor symptoms. Additionally, deep brain stimulation (DBS) surgery, physical therapy, occupational therapy, and speech therapy may be recommended to address motor complications and improve functional abilities.

Ongoing research into Parkinson's disease is focused on elucidating its underlying mechanisms, identifying biomarkers for early diagnosis, and developing novel therapies to modify disease progression. Advances in genetics, neuroimaging, and neurobiology have provided valuable insights into the pathology of Parkinson's disease, offering hope for the development of more effective treatments and ultimately, a cure. Despite the challenges posed by Parkinson's disease, ongoing efforts in research, diagnosis, and treatment continue to improve outcomes and quality of life for individuals living with this condition.

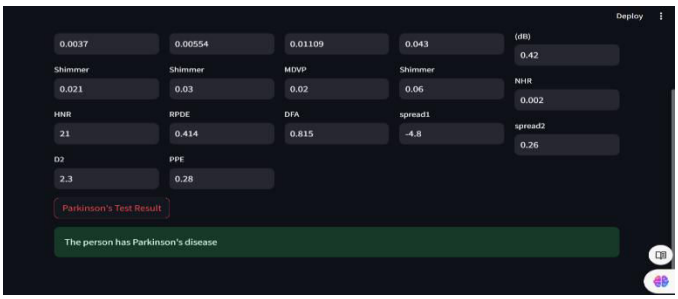

Fig 11: Parkinsons Disease Result

| ISSN: 2582-7219 | www.ijmrset.com | Impact Factor: 7.521| Monthly, Peer Reviewed & Referred Journal|

| Volume 7, Issue 7, July 2024 |

| DOI:10.15680/IJMRSET.2024.0707037 |

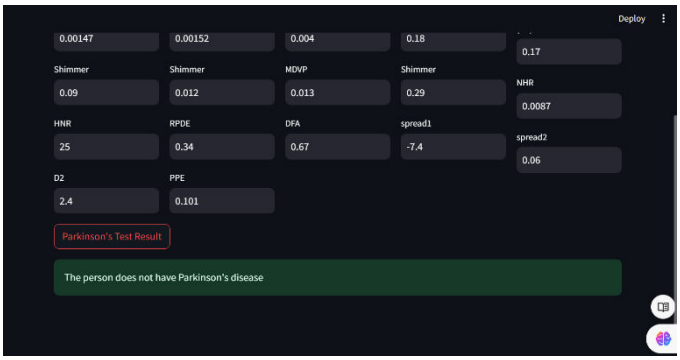

Fig 12: Parkinsons Disease Result

REFERENCES

[1] H. Abbas, L. Alic, M. Rios, M. Abdul-Ghani and K. Qaraqe, "Predicting Diabetes in Healthy Population through Machine Learning," 2019 IEEE 32nd International Symposium on Computer-Based Medical Systems (CBMS), 2019, pp. 567-570.

[2] G. Parthiban, S.K.Srivasta "Applying Machine learning methods in Diagnosing Heart disease for Diabetic Patients" International Journal of Applied Information Systems(IJAIS) Foundation of Computer Science FCS, New York, USA vol. 3– no.7, August 2012.

[3] D. Dahiwade, G. Patle and E. Meshram, "Designing Disease Prediction Model Using Machine Learning Approach," 2019 3rd International Conference on Computing Methodologies and Communication (ICCMC), 2019, pp. 1211-1215.

[4] Chowdhury, Anoy. (2020). Breast Cancer Detection and Prediction using Machine Learning.

[5] Jean Sunny, Nikita Rane, Rucha Kanade, Sulochana Devi, 2020, Breast Cancer Classification and Prediction using Machine Learning, (IJERT) vol 09, no. 02 (February 2020)

[6] S. M. Sasubilli, A. Kumar and V. Dutt, "Machine Learning Implementation on Medical Domain to Identify Disease Insights using TMS," 2020 International Conference on Advances in Computing and Communication Engineering (ICACCE), 2020, pp. 1-4.

[7] S. Pitoglou, Y. Koumpouros and A. Anastasiou, "Using Electronic Health Records and Machine Learning to Make Medical-Related Predictions from Non-Medical Data," 2018 (iCMLDE),2018, pp.56-60,

[8] Kamaraj, K.Gomathi & Priyaa, D.Shanmuga. (2016). Multi Disease Prediction using Data Mining Techniques. International Journal of System and Software Engineering.

[9] R. Singh and N. Sharma, "Machine Learning based Medical Information Analysis, Estimations and Approximations over Present Health Research Domain," 2020 International Conference on Computational Performance Evaluation (ComPE), 2020, pp. 704-708,

[10] A. Dewan and M. Sharma, "Prediction of heart disease using a hybrid technique in data mining classification," 2015 2nd International Conference on Computing for Sustainable Global Development (INDIACom), 2015, pp. 704-706.

[11] A. H. Chen, S. Y. Huang, P. S. Hong, C. H. Cheng and E. J. Lin, "HDPS: Heart disease prediction system," 2011 Computing in Cardiology, 2011, pp. 557-560.

[12] S. Ambekar and R. Phalnikar, "Disease Risk Prediction by Using Convolutional Neural Network," 2018 Fourth International Conference on Computing Communication Control and Automation (ICCUBEA), 2018, pp. 1-5.

[13] N. E. Costea, E. V. Moisi and D. E. Popescu, "Comparison of Machine Learning Algorithms for Prediction of Diabetes," 2021 16th International Conference on Engineering of Modern Electric Systems (EMES), 2021, pp. 1-4.

[14] Shetty, K. Rit, S. Shaikh and N. Patil, "Diabetes disease prediction using data mining," 2017 International Conference on Innovations in Information, Embedded and Communication Systems (ICIIECS), 2017, pp. 1-5.

[15] I. C. Tee and A. H. Gazala, "A novel breast cancer prediction system," 2011 International Symposium on Innovations in Intelligent Systems and Applications, 2011, pp. 621-625.

[16] P. P. Sengar, M. J. Gaikwad and A. S. Nagdive, "Comparative Study of Machine Learning Algorithms for Breast Cancer Prediction," 2020 Third International Conference on Smart Systems and Inventive Technology (ICSSIT), 2020, pp. 796-801.

[17] R. Shen, Y. Yang and F. Shao, "Intelligent Breast Cancer Prediction Model Using Data Mining Techniques," 2014 Sixth International Conference on Intelligent Human-Machine Systems and Cybernetics, 2014, pp. 384-387.

| ISSN: 2582-7219 | www.ijmrset.com | Impact Factor: 7.521| Monthly, Peer Reviewed & Referred Journal|

| Volume 7, Issue 7, July 2024 |

| DOI:10.15680/IJMRSET.2024.0707037 |

[18] X. L. Xiong, R. X. Zhang, Y. Bi, W. H. Zhou, Y. Yu, and D. L. Zhu, "Machine Learning Models in Type 2 Diabetes Risk Prediction: Results from a Cross-sectional Retrospective Study in Chinese Adults," Curr Med Sci, vol. 39, no. 4, pp. 582-588, Aug 2019.
[19] P. Doupe, J. Faghmous, and S. Basu, "Machine Learning for Health Services Researchers," Value Health, vol. 22, no. 7, pp. 808-815, Jul 2019.
[20] G. G. Warsi, S. Saini and K. Khatri, "Ensemble Learning on Diabetes Data Set and Early Diabetes Prediction," 2019 International Conference on Computing, Power and Communication Technologies (GUCON), 2019, pp. 182-187.
N. M. J. Kumari and K. K. V. Krishna, "Prognosis of Diseases Using Machine Learning Algorithms: A Survey," 2018 International Conference on Current Trends towards Converging Technologies (ICCTCT), 2018, pp. 1-9.

INTERNATIONAL STANDARD SERIAL NUMBER INDIA

INTERNATIONAL JOURNAL OF MULTIDISCIPLINARY RESEARCH

IN SCIENCE, ENGINEERING AND TECHNOLOGY

| Mobile No: +91-6381907438 | Whatsapp: +91-6381907438 | ijmrset@gmail.com |

www.ijmrset.com