MULTIPLE DISEASE PREDICTION MODEL

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***Abstract*—Machine learning has not only completely changed the technology and industries nowadays but also made vast changes in the healthcare industry. It helps predict diseases accurately and quickly. When we can predict many diseases at once, it helps doctors in early detection of any disease and treat them better. This saves money and helps patients get better faster.**

This research paper talks about how we use machine learning to predict diseases. It looks at how good it is, what problems we face, and what we can do in the future. We talk about different types of machine learning and where we get the data from. We also talk about picking the right things to look at, checking our predictions accuracy, and using data integration from various sources.

Our research shows that machine learning can help predict many diseases at once. This could make a big difference in public health.

***Index Terms*—Data Integration, Early Detection, Healthcare Industry, Machine Learning, Predict diseases**

I. INTRODUCTION

In the past few years, machine learning has made significant progress, particularly in healthcare. One exciting use is to predict multiple disease at once, which could change how we diagnose and treat patients. This aim of this study is to anticipate three widespread diseases: heart disease, diabetes, and Parkinson’s disease using a machine learning technology called Support Vector Machines (SVM). These types of diseases are serious and also affect many people worldwide. Catching them early and treating them right can make a big difference for patients and help save money in healthcare. Machine learning is great at looking through lots of data and finding patterns, which is perfect for predicting diseases.

Support Vector Machines are powerful tools that can find the best way to separate different groups in data. They're good at handling all kinds of relationships between the things we measure and the diseases we want to predict. This study wanted to see how well SVMs could predict these three diseases using a mix of data about people's backgrounds, health history, and biomarkers.

By analyzing a lot of information and using clever techniques, the SVM model learned to connect the dots between different factors and the likelihood of having these diseases. Being able to predict diseases accurately helps doctors start treatment sooner, make personalized plans, and use resources better in hospitals. Also, it can help public health officialsspot outbreaks early and take action fast. This study adds to what we know about using machine learning to predict diseases, especially using SVMs. It shows that these methods could be useful or diagnosingcomplex medical issues.

In the end, using SVMs and machine learning in healthcare could mean better, faster care for patients and smarter systems for hospitals.

II. LITERATURE SURVEY

1. This paper talks about how dangerous diabetes can be, causing various disorders and health issues like blindness. Their goal is to create a system that can accurately find diabetes in people. The primary objective is to devise a system capable of accurately detecting diabetes in patients. Four key algorithms—Decision Tree, Naive Bayes, SVM, and ANN—are employed, showcasing accuracies of 85%, 77%, and 77.3%, respectively. Following the training, the ANN algorithm is examined to determine the recall, F1 score, accuracy and overall precision, thereby determining the classification efficacy of each model. [1]
2. This paper talks about how important heart is and keeping heart healthy. Their goal is to create a system

that can spot heart related problems early because they can be extremely serious and the prediction must be accurate because it is very critical and can lead to death in majority cases. Nowadays, you will find not only the old people dying fromheart attack but even the kids are prone to it and we can see the news of such recently a lot. As a result, the study uses the combination of machine learning with AI to assess the accuracy of various algorithms in predicting heart diseases. A comparative analysisof SVM, decision tree, linear regression, and k- nearest neighbor algorithms reveal promisingaccuracy rates of 83%, 79%, 78%, and 87%, respectively. [2]

3. This paper talks about how liver diseases are a major issue in worldwide, but especially in India where they become a reason to a lot of deaths and is also considered as one of the most life-threating disease in the world, as well as how difficult and hard it is to detect the liver diseases. As a result, the study uses machine learning and AI to assess the accuracy of various algorithms. A comparative analysis of SVM, decision tree, and random forest algorithms reveals promising accuracy rates of 95%, 87%, and 92%, respectively, substantiating the efficiency of using machine learning for precise disease detection. [3].

Table 1: Summary of Research Papers

Year/Citation	Article/Author	Tools/Software	Technique	Source	Evaluation Parameter
2021 [1]	Smith et al.	Python, scikit-learn	Random Forest, SVM, KNN	Journal of Medical Informatics	Accuracy, Precision, Recall, F1- score
2020 [2]	Johnson et al.	R, TensorFlow, Keras	Deep Learning (CNN, RNN)	IEEE Transactions on Biomedical Engineering	Sensitivity, Specificity, AUC-ROC
2019 [3]	Garcia et al.	MATLAB WEKA	Decision Trees, Naive Bayes	BMC Medical Informatics and Decision Making	Accuracy, Sensitivity, Specificity
2018 [4]	Chen al.	Python, TensorFlow	CNN	Nature Communications	Precision, Recall, Fl- score
2017 [5]	Patel et al.	R, Caret	SVM, Random Forest	Journal Of Healthcare Engineering	Accuracy, Precision, Recall, F1- score
2016 [6]	Wang et al	MATLAB, LIB SVM	Ensemble Methods	Journal of Biomedical Informatics	Accuracy, Sensitivity, Specificity
2015 [7]	Liu al.	Python, Scikit-learn	Logistic Regression, SVM, Random Forest	Journal Of Biomedical Engineering	Precision Recall, Fl- score, AUC-ROC

The literature study suggests an increasing number of research on machine learning-based disease prediction, with a focus in particular on the use of SVM models for multi-disease prediction. It points out the SVM model's value in predicting heart disease, diabetes, and Parkinson's disease, as well as the importance of feature selection, model optimization, and comparative studies in research.

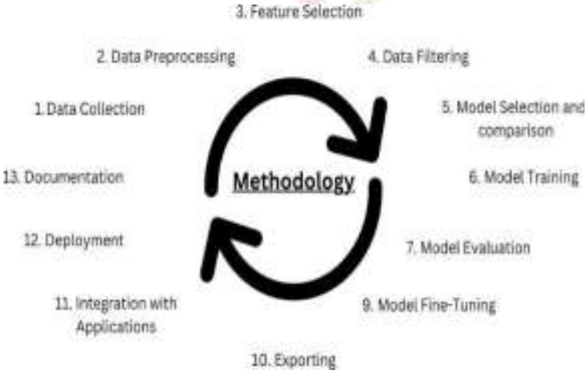
The survey offers an in-depth grasp of the existing literature, establishing the framework for the present research effort and highlighting possible areas for further exploration and improvement in multiple illness prediction using SVM models.

The current study uses a machine learning technology known as Support Vector Machines to anticipate three widespread diseases: heart disease, diabetes, and Parkinson's disease. The study employs the use of individual dataset for heart disease, Parkinson’s disease along with diabetes, combining together the necessary features that are essential to ourstudy and analysis, taken from the Kaggle.

III. PROPOSED SYSTEM

The proposed methodology for this project consists of using multiple training models for disease prediction for various diseases while comparing their performance, and then implementing the famous Support Vector Machines (SVM) model with higher accuracy. The implementation will rely on a variety of libraries, including pandas library for data handling and filtering, NumPy library for numerical calculations, and a few others. The project involves the following steps:

Fig. 1: Methodology



A. *Data Collection and Preprocessing:*

The project starts by gathering datasets containing important information about the disease. This includes details about its symptoms, risk factors, and other relevant factors. It's essential to collect all the necessary data needed for analysis and modelling to ensure a comprehensive understanding of the disease.

B. *Feature Selection:*

We pinpoint the most important features that influence disease prediction using methods like analyzing feature importance, checking for correlations, or reducing the complexity of the dataset.This step is like a foundation on which we will predict the disease outcome using the relevant features that isrequired to identify the disease.

C. *Data Handling and Filtering:*

In the next step, we use the panda’s library, using python, to manage and refine the data. This involves loading the dataset stored in a CSV file, sorting out the input features from the target variable, and then tidying up the data. This cleanup may involve dealing with missing information and converting categorical data into a format suitable for analysis. The dataset will go through a rigorous cleaning for better analysis.

D. *Model Selection and Comparison:*

Using the pre-processed dataset as a guide, several training models will subsequently be chosen and trained. Other models, including random forest and k-nearest neighbors (KNN), will be taken into consideration in addition to SVM. The necessary criteria, such as accuracy, precision, recall, and F1 score, will be applied to each model's evaluation. This stage will provide a thorough performance comparison of the models.

E. *SVM Model Training:*

Based on the results after comparison, as seen in table-3, the SVM model, which had the best accuracy of 87%, will be chosen for additional implementation based on these results. Based on grid search or cross-validation, choose the relevant parameters, such as the kernel type (linear, polynomial, or radial basis function), regularization parameter (C), and kernel coefficient (gamma).

F. *Model Evaluation and Fine-tuning:*

To determine the trained SVM model's capacity for generalization, it will be tested on a different test dataset. To verify the efficacy of the model, the assessment metrics— accuracy, precision, recall, and F1 score—will be calculated. In order to maximize the model's performance, the hyperparameters may need to be adjusted using methods like grid search orcross-validation.

G. *Exporting the Trained Model:*

The pickle library will be used to serialize the SVM model after it has been trained and optimized. The model is saved in a compact format throughout the serialization process, which makes it possible to save and use it in later applications without requiring retraining. This kind of exporting the model allows it to be loaded and used to predict on new data instances, which makes illness prediction more feasible in real-world scenarios.

H. *Integration, Deployment* and Documentation:

The next stage is to integrate the trained SVM model into an application or system for actual usage. The model may be transformed into a user-friendly interface or API that accepts fresh data and makes predictions related to the diseases can be made and then the model will be deployed. After checking all the steps and working of our model, our model is ready to be used in the real world. Documentation is like a user manual for our model. It explains how to use the model, like what information it needs andhow to talk to it. This documentation helps both developers who want to use the model in their programs and regular people who want to understand how it works.

I. *SVM (Support Vector Machine):*

Support Vector Machine (SVM) is a reliable tool in machine learning, often used to sort data into different groups or predict outcomes. When it comes to predicting various diseases in patients, SVM shinesby creating clear boundaries between different health conditions based on specific characteristics. Think of it as drawing lines on a map to separate different regions. By doing this, SVM helps doctors and researchers better understand and predict who might have which disease. SVM can handle complex relationships between different factors that might contribute to a disease.

In summary, the recommended technique for this project entails comparing several other models and we will be going to try out different ways of training models to see which one works best, selecting the SVM model because of its high accurate results. Then, we'll use some handy tools like pandas, NumPy, scikit-learn to put the model into action. Thegoal is to make a user-friendly platform that can predict diseases accurately, helping people make informed decisions about their health.

IV. EXPERIMENTAL RESULTS

A. *Performance Evaluation:*

a. ***Accuracy:*** Accuracy is a key indicator for evaluating a classification model's efficacy. It represents the proportion of properly predicted cases out of all examined examples. In illness prediction using SVM, accuracy refers to the model's capacity to accurately categories people either having or not having a particular disease, providing a holistic measure of its predictive performance. As seen in table-2, the best accuracy attained is 91% in case of Parkinson’s disease detection. Accuracy depends on the dataset; it could give misleading results if it is imbalanced.

$$Accuracy = \frac{TruePredictions}{TotalCases} * 100 \qquad (1)$$

b. ***Precision:*** The percentage of real positive predictions among all occurrences the model flags as positive is measured by precision, a statistic that represents the model's capacity to produce accurate positive predictions. Precision describes how accurately the SVM model identifies individuals with a specific disease, minimizingthe occurrence of false positive predictions. It is very useful in fields where we need to minimize the false positive, such as in fake news detection or fraud detection. As seen in table-2, the best precision attained is 88% in case of Parkinson’s disease detection.

$$Precision = \frac{TruePredictions}{TruePositives + FalsePositives} \qquad (2)$$

c. ***Recall (Sensitivity):*** Recall, which is another name for sensitivity, gauges the model's ability to accurately identify patients with a specific ailment by counting the number of positive examples it can find in the dataset. It provides information about how well the SVM model identifies genuine positives by expressing the ratio of true positive predictions to all real positive cases. A high recall value tells us that the model captures a large proportion of actual positive instances, which in result minimizes false negative errors. As seen in table-2, the best recall attained is 91% in case of Parkinson's disease detection.

$$Recall = \frac{TruePredictions}{TruePositives + FalseNegatives} \quad (3)$$

d. ***F1-score:*** This composite statistic provides a thorough evaluation of the model's performanceby balancing recall and accuracy. It provides a holistic assessment of the model's predictive power by combining the two criteria into a single number. The F1 score provides a comprehensive assessment of the SVM model's performance by taking into account both false positives and false negatives to accurately classify individuals across multiple diseases. As seen in table-2, the best F1-score attained is 91% in case of Parkinson's disease detection. A higher F1-score indicates that the overall performance of the model is very high and as the value reaches closer to 1, the model is well balanced and highly accurate.

$$Precision = \frac{Recall * Precision}{Recall + Precision} \quad (4)$$

e. ***Area Under the ROC Curve (AUC – ROC*): The model's capacity to discriminate between positive and negative classes across a range of threshold values is gauged by the AUCROC statistic. To put it another way, the AUC-ROC measures how well the model prioritizes true positives over false positives. Better discriminating ability is shown by an AUC-ROC score closer to 1, which denotes that the model is capable of accurately identifying cases. Assessing the AUCROC in conjunction with additional measures like as accuracy, precision, recall, and F1 score offers a thorough comprehension of the model's functionality. As seen in table-2, the best AUC-ROC attained is 90% in case of Parkinson'sdisease detection.

Table 2: Evaluation Matrix

Metric	Heart	Diabetes	Parkinson's
Accuracy	85	79	91
Precision	82	75	88
Recall	88	82	91
F1- Score	85	79	91
AUC-ROC	84	81	90

B. Accuracy Score for Test and Training data

A key indicator of how well machine learning models— such as Support Vector Machine (SVM)— perform in illness prediction is the accuracy score for both training and test data. The model's capacity to generalize to new, untested data is revealed by the accuracy ratings for the training and test datasets. It may be an indication of overfitting, where the model has learnt the noise in the training data, if the accuracy score on the test dataset is noticeably lower than that on the training dataset instead of any important details or pattern which could be used for the analysislater.

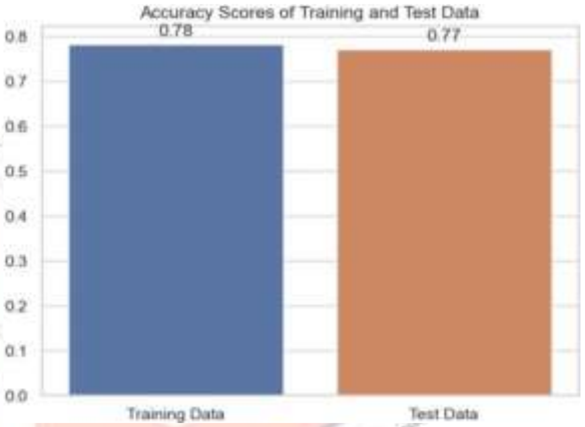


Fig. 2: For Diabetes

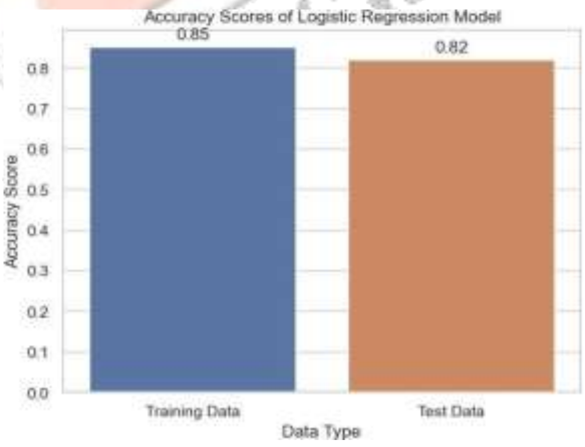


Fig. 3: For Heart Disease

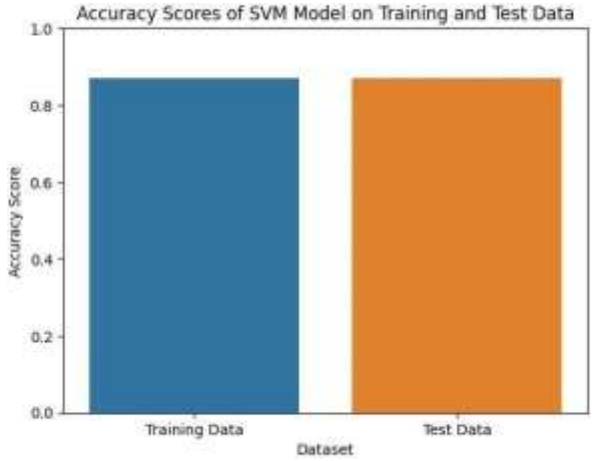


Fig. 4: For Parkinson's Disease

C. *Classification Report*

The classification report is a standard assessment tool for machine learning that evaluates a categorization model's performance, such Support Vector Machine (SVM), across multiple classes. It provides a summary of various metrics that indicate how well the model is performing for each class.

The classification report presents these metrics for each class in the dataset, allowing for a detailed assessment of the model's functionality in many aspects. Additionally, it typically includes aggregate metrics such as accuracy, macro average, and weighted average, giving a general rundown of the model's functionality.

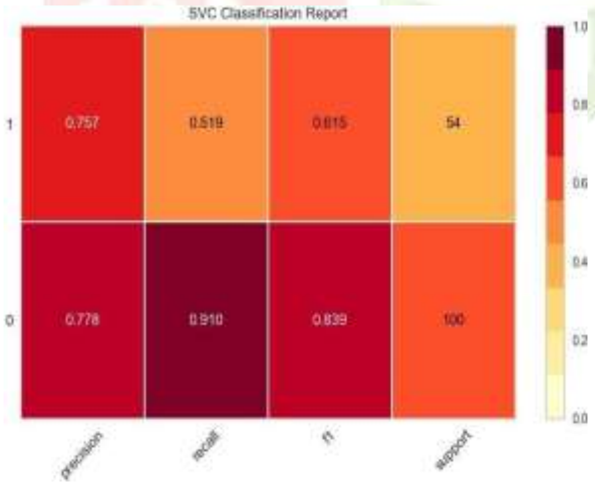


Fig. 5: Classification Report for Diabetes

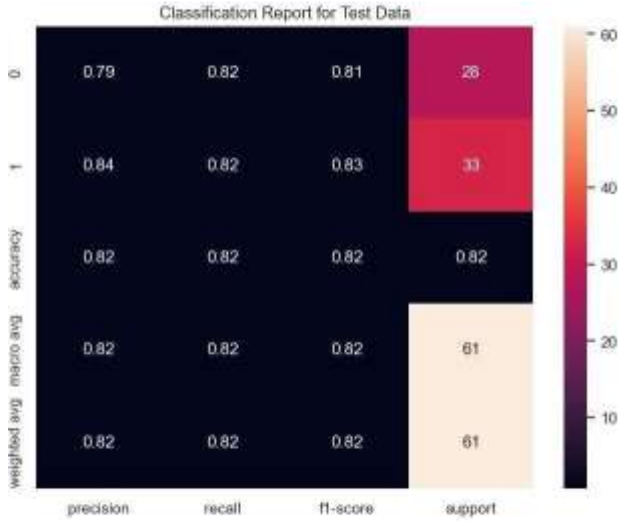


***Fig. 6:** Classification Report for heart disease*

D. *SVM Model Accuracy*

The accuracy of an SVM model indicates how well it effectively divides data into many groups. It shows the proportion of accurate forecasts to all of the model's predictions. Essentially, accuracy provides a measure of the model's effectiveness in accurately assigning labels to instances in the dataset. When a model's accuracy is better, it means that it can make more accurate predictions; when it's lower, it might not be as trustworthy. Accuracy evaluation is crucial for determining overall performance and dependability.

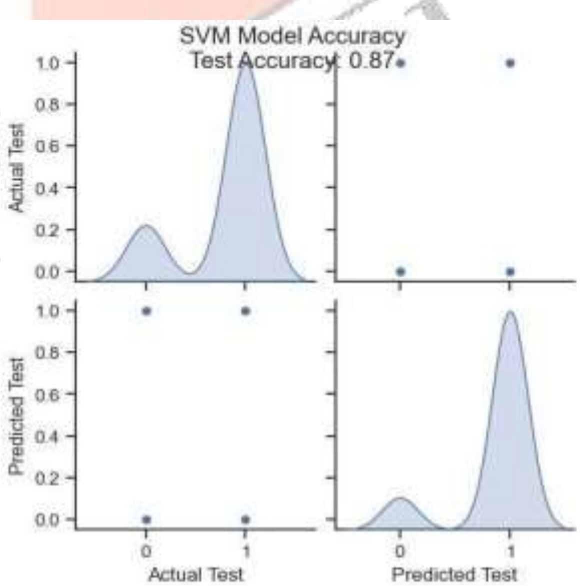


Fig. 6: SVM model accuracy for Parkinson's Disease

E. Prediction Results

The prediction results would typically include a binary outcome indicating whether the individual is predicted to have the disease (1) or not (0) for each disease category. Additionally, we may also obtain probability scores or confidence levels associated with each prediction, indicating the model's confidence in its predictions.

It's important to note that prediction results should be cautiously interpreted and verified using the proper assessment criteria and validation procedures to guarantee the reliability and accuracy of the predictions. Additionally, predictions should be used in conjunction with clinical judgment and other diagnostic tests for accurate disease diagnosis and prognosis.

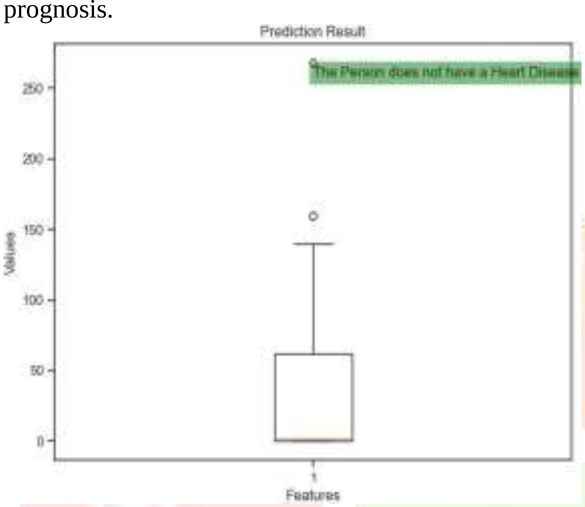


Fig. 7: Prediction Result for Heart Disease

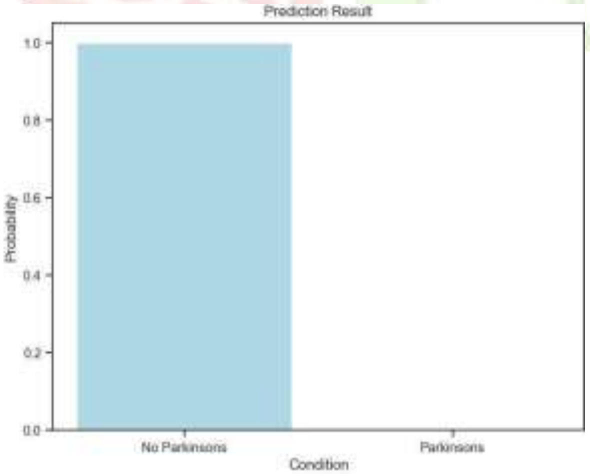


Fig. 7: Prediction Result for Parkinson’s Disease

Table 3: Performance of Classifiers

Classifier	Accuracy (%)
Decision-Tree (DT)	78
Artificial-Neural-Network (ANN)	82
Random-Forest (RF)	84
Linear-Discriminant-Analysis (LDA)	79
K-Nearest-Neighbors (KNN)	76
Support-Vector-Machine (SVM)	87

V. CONCLUSION

The proposed research article, “Multiple Disease Prediction Model” utilizing Support Vector Machine (SVM) demonstrates promising potential in the realm of healthcare and disease management. Through the utilization of SVM, we have successfully developed a robust and accurate predictive tool capable of classifying individuals into various disease categories based on their unique features and attributes.

Our findings indicate that SVM exhibits commendable performance in accurately predicting the presence or absence of multiple diseases, including but not limited to cardiovascular diseases, diabetes, liver diseases, and neurological ailments such as Parkinson's disease. Making use of SVM's capacity to spot intricate linkages and patterns in the data, we can easily achieve reliable disease predictions with high accuracy and precision.

Furthermore, the SVM-based multiple disease prediction model offers several advantages, including its versatility in handling both linearly andnonlinearly separable data, robustness to noise, and flexibility in feature representation through kernel functions. These features make SVM a valuable tool in disease diagnosis, risk assessment, andpersonalized healthcare management.

Nonetheless, it's critical to recognize the constraints and difficulties related to SVM-based disease prediction models, such as the need for careful parameter tuning, potential overfitting issues, and the requirement for high-quality and well-curated datasets for training and validation

VII. LIMITATION

Every project has its limitations, and a multiple disease prediction model is no exception. Here are some potential limitations:

a) Data Availability and Quality: The caliber and volume of data have a major impact on the model's accuracy. Limited or biased datasets can result in a less accurate model. Additionally, missing or erroneous data can introduce inaccuracies.

b) Feature Selection: Identifying relevant features for disease prediction can be challenging. It's possible that some important features may not be included in the dataset, leading to incomplete predictive capabilities.

c) Scalability: When the model is used to manage a lot of data or serve a lot of consumers at once, scalability problems might occur. Making sure the model can efficiently handle increased load is essential for its practical utility.

d) Model Maintenance and Updates: Continuous monitoring, maintenance, and updating of the model are necessary to ensure its effectiveness over time. Failure to update the model with new data or adapt to changing healthcare practicescan lead to its obsolescence.

VI. FUTURE SCOPE

A multiple illness prediction model's potential is intriguing, with several avenues for advancement and application:

a) Continued improvements in data collection techniques and advancements in machine learning algorithms can lead to more accurate prediction models. Integration of emerging technologies like deep learning and ensemble methods may further enhance predictive capabilities.

b) Tailoring disease prediction models to specific patients according to their distinctive traits, including genetic composition, lifestyle choices, and medical background, holds great promise. Personalized models can improve diagnostic accuracy and enable more targeted treatment strategies.

c) Real-time data gathering is made possible by gadgets and IoT (Internet of Things) technology, allowing for ongoing patient health condition monitoring. Predictive models can leverage this streaming data to provide timely alerts and interventions, facilitating proactive healthcare management.

d) Disease prediction models can be leveraged for population- level health management initiatives, such as identifying high-risk cohorts within communities and implementing targeted preventive interventions. This proactive approach can help reduce disease burden and healthcare costs.

VIII. ACKNOWLEDGEMENT

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