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Multiple Disease Prediction using Machine Learning

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ABSTRACT: The integration of machine learning (ML) into healthcare systems has revolutionized early disease detection and personalized care. Existing systems often struggle with the limitations of real-world data, which is frequently incomplete or inconsistently documented. These shortcomings can lead to inaccurate predictions and inefficient processing. To overcome these limitations of Existing system we propose a system that leverages both structured data such as laboratory results, vital signs, and demographic information and unstructured data including physician notes, radiology reports, and pathology findings to improve the accuracy and reliability of disease prediction. The dataset was sourced from Kaggle, a well-known platform for publicly available medical datasets. The proposed system incorporates supervised learning algorithms such as Random Forest, Naives bayes, Support Vector Machines (SVM), and XGBoost, alongside techniques including Convolutional Neural Networks (CNNs) and Recurrent Neural Networks (RNNs), the proposed system achieves a predictions. Through a layered architecture and data-driven decision-making, it addresses key challenges like incomplete records, regional disease variance, and data privacy, thereby contributing to more efficient and accessible healthcare.

KEYWORDS: Machine Learning, Disease Prediction, Healthcare Analytics, Structured Data, Unstructured Data, Deep Learning, Artificial Intelligence, Supervised Learning, SVM Model Training, Naive Bayes, Random Forest

I. INTRODUCTION

Artificial intelligence (AI) and machine learning (ML) have ushered in a new era in healthcare, enabling the development of intelligent systems that improve diagnostics, treatment planning, and disease management. Traditional healthcare systems often rely on structured data and overlook unstructured inputs, leading to limited predictive capability and delayed interventions. This research aims to develop a system that accurately predicts multiple diseases, including diabetes, Parkinson's disease, and heart disease, using SVM and a combination of structured and unstructured medical data.

With rising global healthcare demands and resource constraints, such systems offer a solution for remote, timely, and reliable diagnostics. By processing diverse data types, the model enhances decision- making for both clinicians and patients. Early disease detection facilitated by this model can significantly reduce treatment costs, avoid unnecessary procedures, and improve patient outcomes. Moreover, the inclusion of unstructured data such as physician notes and diagnostic reports allows the system to recognize subtle indicators that may be missed in traditional approaches. This capability ensures that diagnostic suggestions are comprehensive and context-aware.

The integration of advanced algorithms like SVM provides the system with high accuracy and generalizability across various medical conditions. Additionally, incorporating feature engineering techniques and natural language processing allows the system to efficiently extract and interpret complex information from diverse data sources. This holistic approach not only strengthens the reliability of disease predictions but also supports personalized healthcare delivery, enabling physicians to make more informed decisions tailored to individual patient profiles.

II. LITERATURE SURVEY

Kumar et al. (2021): Applied decision trees to chronic disease prediction, achieving 91% precision. They emphasized the importance of data pre-processing techniques, such as imputation, to handle incomplete datasets in clinical settings.



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Zhang and Lee (2019): Improved breast cancer prediction accuracy by 7% through a hybrid approach that integrated regional variations with structured and unstructured data.

Patel et al. (2020): Proposed a latent factor model to predict kidney disease, integrating structured hospital records with unstructured EHRs, achieving 92% accuracy.

Singh et al. (2018): Used logistic regression and random forest for liver disease prediction. Random forest achieved 90% accuracy, showing the value of combining diverse data sources.

Chen and Rogers (2020): Developed a CNN model for breast cancer detection using both structured mammographic images and unstructured radiology notes, achieving 94.8% accuracy.

Existing System Existing disease prediction systems generally rely on structured data such as demographics and lab test results, often neglecting unstructured data like clinical notes and imaging reports. This limits their diagnostic accuracy and restricts them to single-disease predictions. Furthermore, many systems require complete datasets, making them less effective with real-world, incomplete medical records. These challenges reduce prediction quality and system efficiency.

III. PROPOSED SYSTEM

The proposed system leverages advanced deep learning techniques to predict multiple diseases by processing both structured and unstructured medical data. To address the common challenge of incomplete datasets in healthcare, the system integrates a latent factor model designed to reconstruct missing data, thereby enhancing the quality and completeness of the dataset.

This approach significantly improves the accuracy and reliability of predictions, especially in high-risk regions where data may be sparse or incomplete. By reconstructing missing information, the system ensures more comprehensive and precise diagnostic outputs.

The model achieves an impressive accuracy of 94.8%, outperforming traditional models in both prediction precision and processing speed. Furthermore, the proposed system includes a multi-disease classification framework that allows healthcare providers to assess multiple conditions simultaneously within a single predictive model. This multi-condition approach not only increases diagnostic efficiency but also provides a holistic view of a patient's health status. By implementing this system, healthcare facilities can benefit from a scalable and adaptable solution that meets the diverse needs of medical diagnostics. It can be applied across different populations and disease profiles, offering a more accessible, reliable, and efficient method for early disease detection and intervention.

ARCHITECTURE



Figure: Multiple disease detection system architecture

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This flowchart illustrates a machine learning workflow for classification using an ensemble method. Here's a breakdown of the steps involved:

- 1. **Dataset:** The process starts with a complete dataset.
- 2. Splitting the Data: The dataset is divided into three parts:
 - Train Data (80%): This portion is used to train the individual classification models.
 - Test Data (20%): This unseen data is used to evaluate the performance of each trained model.
 - Validation Data: This separate dataset is used to make predictions with the trained models, and these predictions are later combined.

3. Model Training and Selection:

- The training data is used to train three different classification models: a Support Vector Machine (SVM) classifier, a Naive Bayes classifier, and a Random Forest classifier.
- **Performing K-Fold Cross Validation for Model Selection:** Before final training, K- Fold cross-validation is performed on the training data. This technique helps in selecting the best hyperparameters and assessing the generalization ability of each model.

4. Model Evaluation:

- After training, each model's performance is evaluated using the test data.
- **Computing Metrics on test data for [Classifier Name]:** Various metrics (like accuracy, precision, recall, F1-score) are calculated on the test data for each of the three classifiers to understand how well they generalize to unseen data.

5. Prediction on Validation Data:

- The trained SVM, Naive Bayes, and Random Forest classifiers are then used to make predictions on the separate validation dataset.
 - **Combining Predictions:**
- **MODE OF ALL THREE PREDICTIONS:** The predictions from the three classifiers on the validation data are combined using the mode (the most frequent prediction). This is a form of majority voting in an ensemble method.

Ensemble method

Ensemble methods combine multiple models to improve prediction accuracy.

Bagging: Trains models independently on random data subsets and combines their outputs (e.g., Random Forest). Boosting: Builds models sequentially, each learning from the previous one's mistakes (e.g., AdaBoost, XGBoost). Stacking: Combines predictions from multiple models using another model (meta-learner) to make the final decision. These methods help reduce variance, bias, or improve predictions.

Final Prediction:

The mode of the predictions from the individual classifiers becomes the final prediction of the ensemble model. In essence, this flowchart demonstrates how to train multiple diverse classifiers, evaluate their individual performance, and then combine their predictions using a voting mechanism to create a more robust and potentially more accurate final prediction. Using an ensemble of different models often leads to better generalization and reduces the risk of relying on the strengths and weaknesses of a single model.

IV. METHODOLOGY

This research suggests a methodology with various complaint vaticination training models, analyzes how well and performed, and uses the SVM model, with 98.8 delicacies.



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Figure 1: Stress Discovery Methodology

Many libraries will come into play in the actual solution; Panda will be utilized to manipulate the data and filter them; numpy will do all the numerical computations; scikit-learn will train and evaluate the model; and pickle will be used to export the learned model for application use.



Figure 2: Multiple complaint vaticination web operation

Data Management and Filtering:

The first phase of design preparation is data operation and filtration based on the panda's library. It comprises importing the data from a train CSV, Separating input features from the target variable, and applying essential preprocessing steps, such as handling missing values and encoding categorical features.

Selection and Evaluation of Models:

Various models will be selected and trained using the preprocessed dataset. Along with SVM, other algorithms such as k-nearest neighbors (KNN) and random forest will be examined. Each model will be evaluated based on key performance metrics, including accuracy. perfection, recall, and the F1 score. The final stage will lubricate a full comparison of the colorful performances of models.

	count	mean	std	min	25%	50%	75%	max
itching	4920.0	0.137805	0.344730	0.0	0.0	0.0	0.0	1.0
skin_rash	4920.0	0.159756	0.366417	0.0	0.0	0.0	0.0	1.0
nodal_skin_eruptions	4920.0	0.021951	0.146539	0.0	0.0	0.0	0.0	1.0
continuous_sneezing	4920.0	0.045122	0.207593	0.0	0.0	0.0	0.0	1.0
shivering	4920.0	0.021951	0.146539	0.0	0.0	0.0	0.0	1.0
small_dents_in_nails	4920.0	0.023171	0.150461	0.0	0.0	0.0	0.0	1.0
inflammatory_nails	4920.0	0.023171	0.150461	0.0	0.0	0.0	0.0	1.0
blister	4920.0	0.023171	0.150461	0.0	0.0	0.0	0.0	1.0
red_sore_around_nose	4920.0	0.023171	0.150461	0.0	0.0	0.0	0.0	1.0
yellow_crust_ooze	4920.0	0.023171	0.150461	0.0	0.0	0.0	0.0	1.0

Table: Datasets



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SVM Model Training:

The highest delicacy produced by the SVM model in the relative study was 98.8. That SVM model would be shortlisted for further deployment The trained SVM model will be tested on a completely independent dataset to assess its generalization capability. Key performance metrics, including accuracy, precision, recall, and F1 score, will be calculated to evaluate the model's effectiveness.

Naive Bayes

Naive Bayes is a simple and fast classification algorithm based on Bayes' Theorem with the assumption that all features are independent of each other.

Key idea:

Given features, it calculates the probability of each class and chooses the class with the highest probability. Formula: P(Class | Data) = (P(Data | Class) * P(Class)) / P(Data

Random Forest

Random Forest is an ensemble learning method used for classification and regression. It builds multiple decision trees and combines their results for better accuracy and stability.

Key Concepts

1. Multiple Decision Trees:

It creates many decision trees (hence "forest").

2. Bagging (Bootstrap Aggregating):

Each tree is trained on a random subset of the data with replacement.

3. Random Feature Selection:

At each split in a tree, only a random subset of features is considered, adding more diversity among trees.

4. Final Prediction:

Classification: Takes a majority vote across all trees. Regression: Takes the average of all tree outputs.

V. RESULTS

This allows the models to be saved and reused without the need for retraining during future operations. By storing the model, it can be applied directly to new datasets for disease classification, ensuring its practicality for real-world use. This feature is particularly useful in continuous healthcare environments, where the model can make predictions on incoming patient data without the overhead of retraining, streamlining the predictive process and improving operational efficiency. Additionally, the model's ability to predict new cases after initial training makes it a valuable tool for ongoing patient monitoring and decision-making.Here we can see the results of chronic diseases like Diabetes,Heart diseases,Kidney diseases,Breast cancer.

Multiple Disease	Number of Pregnancies	Glucose Level	Blood Pressure Value	
Prediction			120	
☆ Diabetes Prediction	Skin Thickness Value	Insulin Value	BMI Value	
C Heart Disease Prediction				
음 Kidney Disease Prediction	Diabetes Pedigree Function Value	Age		
& Breast Cancer Prediction				
	The person has diabetes			
	Show Accuracy			

Fig 3:Diabetes prediction (positive)



Fig 4:Diabetes prediction (negative)

Apr :	Sex	Chest Pain Types	
56			
Resting Blood Pressure	Serum Cholesterol in mg/dl	Fasting Blood Sugar > 120 mg/dl	
Resting Electrocardiographic results	Maximum Heart Rate achieved	Exercise Induced Angina	
ST depression induced by exercise	Slope of the peak exercise ST segment	Major vessels colored by fluoroscopy	
thai: 0 = normal; 1 = fixed defect; 2 = reversible d	select		
Heart Disease Test Result			
	140 Rearing Electrocardiographic results 0 31 depression Induced by wercher 1 2 2 week bin and 1 = fixed defect; 2 = reversible d 2	140 254 Renting Electrocardingraphic results Macimum Heart Bala solitived 0 153 51 depression induced by exercise Sloge of the pask exercise \$1 agement 1 1 4 1 2 results 1+fixed defect; 2 + reversible defect 2 results 1-fixed defect; 2 + reversible defect	Name Name Name Name 160 264 0 netring Electrocartingraphic results Mainton Heart Rate Achieved Exercise Induced Anglins 0 153 0

Fig 5:Heart Disease (positive)

	Heart Disease	Prediction Using M	lachine Learning	L M
Multiple Disease	Age	Sex	Chest Pain Types	
Prediction				
4 - Disbates Productor	Resting Blood Pressure	Serum Cholesterol in mg/dl	Fasting Blood Sugar > 120 mg/dl	
Diabetes Prediction				
Heart Disease Prediction	Resting Electrocardiographic results	Maximum Heart Rate achieved	Exercise induced Angina	
A Kidney Disease Prediction				
	ST depression induced by exercise	Slope of the peak exercise ST segment.	Major vessels colored by fluoroscopy	
& Breast Cancer Prediction				
	thal: 0 = normal; 1 = fixed defect; 2 = reversible of	defect		
	This person does not have heart diseas			

Fig 6:Heart Disease (Negative)

Multiple Disease	Age	Blood Pressure	Specific Gravity	Albumin	Sugar	
Prediction						
A Distance Description	Red Blood Cell	Pus Cell	Pus Cell Clumps	Bacteria	Blood Glucose Random	
Unideles Prediction	2140			1245	1245	
Heart Disease Prediction	Blood Urea	Serum Creatinine	Sodium	Potassium	Haemoglobin	
& Kidney Disease Prediction						
B. Depart Concert Department	Packed Cell Volume	White Blood Cell Count	Red Blood Cell Count	Hypertension	Diabetes Mellitus	
& Breast Cancer Prediction		1200	2145			
	Coronary Artery Disease	Appetite	Peda Edema	Anaemia		

Fig 7:Kidney disease (positive)

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	Kidney D	isease Pre	diction usi	ng ML		
Multiple Disease	Age	Blood Pressure	Specific Gravity	Albumin	Sugar	
Prediction						
Distance Distance	Red Blood Cell	Pus Cell	Pus Cell Clumps	Bacteria	Blood Glucose Random	
 Diabetes Prediction 	2140			1245	1245	
2 Heart Disease Prediction	Blood Urea	Serum Creatinine	Sodium	Potassium	Haemoglobin	
Kidney Disease						
Brand Cancer Drudiction	Packed Cell Volume	White Blood Cell Count	Red Blood Cell Count	Hypertension	Diabetes Mellitus	
Breast Gander Prediction		1200	2145			
	Coronary Artery Disease	Appetite	Peda Edema	Anaemia		
	Kidney's Test Result					
	The nerros does not be	na Midaania dianaa				

Fig 8:Kidney disease (negative)

			Deploy
Multiple Disease	Breast Cancer Pr	ediction using ML	
	Mean Radius	Mean Texture	
 Diabetes Prediction 	20.57		
7 Heart Disease Prediction	Mean Perimeter	Mean Area	
8 Kidney Disease Prediction		1326	
§ Breast Cancer Prediction			
	The person has Breast Cancer		
	Show Accuracy		

Fig 9:Breast Cancer(Positive)

			Deploy 🚦		
Multiple Disease	Breast Cancer Prediction using ML				
A - Diskelse Destinition	Mean Radius	Mean Texture			
	20.57	11.77			
Heart Disease Prediction	Mean Perimeter	Mean Area			
& Kidney Disease Prediction	132.9	1326			
& Breast Cancer Prediction					
	The person does not have Breast Cancer				
	Show Accuracy				

Fig 10:Breast Cancer(Negative)

VI. CONCLUSION

This paper demonstrates the efficacy of a hybrid ML model for multi-disease prediction using heterogeneous medical data. By bridging structured and unstructured sources, the system offers a holistic view of patient health. Future work will focus on multilingual NLP support, improved handling of rare disease data, and broader deployment in clinical settings.



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