

Personalized Medicine Recommending System

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Abstract- *This research presents a web-based Disease Prediction System, deployed on Render, utilizing Machine Learning to diagnose diseases based on user-reported symptoms. The system employs an XGBoost model, trained on a medical dataset, to predict diseases with high accuracy. Users interact through a Flask-powered web interface, input symptoms, and receive predictions along with precautionary measures, medications, and dietary recommendations. The system is accessible online, making it a convenient tool for preliminary diagnosis. Future enhancements include real-time symptom analysis and mobile integration.*

Keywords- Disease Prediction, Machine Learning, XGBoost, Flask, Healthcare.

I. INTRODUCTION

The rapid advancements in Machine Learning (ML) and web technologies have significantly improved the efficiency of healthcare applications. Early disease detection plays a crucial role in preventing severe medical conditions, yet traditional diagnostic processes often involve lengthy procedures, high costs, and limited accessibility, especially in remote areas. With the increasing availability of medical datasets and AI-driven models, predictive healthcare solutions have emerged as an effective way to assist individuals in identifying potential health issues at an early stage.

This research introduces a web-based Disease Prediction System, deployed on Render, that leverages an XGBoost-based ML model to diagnose diseases based on user-reported symptoms. The system is designed as a Flask-powered web application, where users can input symptoms through an intuitive interface. The model processes these symptoms and predicts the most probable disease, along with providing precautionary measures, recommended medications, and dietary guidelines to help users take informed health decisions.

The core of this system lies in its ability to analyze a structured medical dataset, identifying relationships between symptoms and diseases. Unlike traditional diagnostic approaches, which require expert medical supervision, this

system automates the prediction process, making healthcare insights more accessible. By applying feature engineering techniques, the system ensures accurate disease classification, reducing the chances of misdiagnosis. Additionally, deploying the application on Render allows seamless online accessibility, enabling users to check symptoms and receive predictions from anywhere with an internet connection.

With the growing integration of Artificial Intelligence in healthcare, such predictive models have the potential to revolutionize early disease detection. While this system is not a replacement for professional medical consultation, it serves as a decision-support tool, empowering users with preliminary health insights. Future advancements in this domain could include real-time symptom tracking, integration with wearable health devices, and AI-driven chatbot consultations, further enhancing the role of technology in healthcare accessibility.

II. LITERATURE REVIEW

Medicine recommender systems (MRS) assist healthcare professionals in selecting appropriate medications by leveraging ontology-based, rule-based, and machine learning approaches. Stark et al. (2019) reviewed existing MRS, categorizing them into ontology and rule-based systems (e.g., GalenOWL, Panacea) and machine learning-based systems that analyze Electronic Medical Records (EMRs) using algorithms like SVM, Decision Trees, and ANN. The study highlights key gaps, such as the lack of disease-specific models, data standardization issues, and limited patient feedback integration. Future research should focus on personalized, scalable, and AI-driven MRS with graph databases and patient-centric feedback to enhance clinical decision-making[1].

The adoption of Electronic Health Records (EHR) has enabled medicine recommender systems (MRS) to enhance personalized prescriptions and reduce adverse drug interactions (DDI). Bhoi et al. (2020) proposed PREMIER, a two-stage attention-based model using RNN and GCN to recommend medications based on patient history, diagnoses, and lab tests. PREMIER outperforms models like LEAP and

DMNC in accuracy and DDI reduction. It also offers explainable recommendations, improving clinician trust, but scalability and data integration remain challenges[2].

Liu et al. investigate medicine recommender systems (MRS) using ML and DL to improve prescription accuracy. DL models outperform traditional ML in capturing complex clinical relationships. They propose MedRec-GNN, a GNN model that enhances accuracy and reduces drug-drug interactions. Reinforcement learning methods like DQN offer personalized treatment strategies. Explainable AI (XAI) tools such as SHAP and attention mechanisms are key for transparency. Challenges remain in data quality, interpretability, and clinical integration[3].

Rui Wu et al. present COGNet, a novel medication recommendation model that uses a copy-or-predict mechanism to generate drug prescriptions by leveraging both current diagnoses and historical patient data. Unlike traditional models, COGNet mimics how doctors reuse or update medications over time. It uses a hierarchical attention-based approach to decide which past medications to copy and when to predict new ones. Tested on the MIMIC-III dataset, COGNet outperforms existing models in accuracy and handles drug-drug interactions effectively. This method enhances interpretability and reflects real clinical decision-making more closely[4].

The rapid digitization of healthcare has made medicine recommender systems (MRS) essential for accurate and safe medication prescriptions. Jiacong Xu et al. (2023) introduced MedRec, a large-scale, multi-modal EHR database designed for medication recommendation tasks. They proposed MedRec-GNN, a Graph Neural Network (GNN)-based model that captures complex patient-condition and drug-interaction relationships, outperforming models like LEAP and SafeDrug in accuracy and reducing drug-drug interactions (DDI). However, challenges remain in interpretability, integration of unstructured data, and real-world adaptability[5].

The increasing adoption of Electronic Health Records (EHRs) has enabled the development of medicine recommender systems (MRS) for personalized medication prescriptions. Jara González-Soler et al. (2023) introduced a Large Language Model (LLM)-based approach using GPT-3 to recommend medications by interpreting natural language EHRs. Their model outperforms traditional systems like LEAP and SafeDrug in accuracy and flexibility. However, challenges remain in bias, limited medical context, and real-world evaluation [6].

The increasing complexity of Electronic Health Records (EHRs) has driven the development of medicine recommender systems (MRS) for personalized prescriptions. R. Mariam et al. (2023) proposed a Graph Convolutional Network (GCN)-based model that captures temporal dependencies and contextual factors in EHRs by modeling patient-disease-medication relationships. Their model outperforms traditional systems like LEAP and SafeDrug in accuracy and reducing drug-drug interactions (DDI). However, challenges remain in scalability, integration of unstructured data, and interpretability[7].

The increasing use of Electronic Health Records (EHRs) has advanced medicine recommender systems (MRS) for personalized prescriptions. Gokulunni et al. (2024) proposed a deep learning-based framework using RNNs and attention mechanisms to capture temporal dependencies in EHR data. Their model outperforms traditional systems like LEAP and GAMENet in accuracy and reducing drug-drug interactions (DDI). However, challenges remain in scalability, unstructured data integration, and real-world validation[8].

The Alternative Medicine Recommendation System (AMRS) by Trupthi et al. (2024) uses machine learning models to recommend complementary medicines based on cosine similarity between patient symptoms and drug effects. The system vectorizes medication data and suggests treatments with the highest similarity scores, improving recommendation accuracy. It also integrates Random Forest algorithms to enhance prediction accuracy by analyzing large datasets. However, challenges remain in data quality, scalability, and real-world applicability[9].

The growing complexity of clinical data has driven the development of medicine recommender systems (MRS) using machine learning (ML) and deep learning (DL) algorithms. The paper highlights the efficiency of ML models in identifying patterns between symptoms, diagnoses, and medications, improving prescription accuracy. It evaluates models like SVM, Random Forest, Decision Trees, and Neural Networks, showing that DL models outperform traditional ML in accuracy and reliability. However, challenges remain in data quality, explainability, and scalability[10].

III. METHODOLOGY

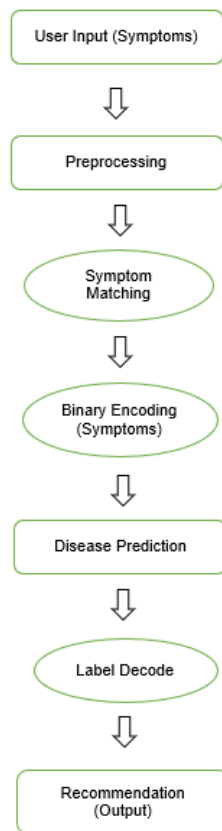


Figure 1:Block Diagram of Methodolgy

The increasing prevalence of health-related issues has necessitated the development of advanced systems capable of providing accurate disease predictions and personalized medical recommendations. The proposed methodology integrates machine learning techniques, particularly the XGBoost algorithm, to predict diseases based on user-reported symptoms and deliver tailored health recommendations. This review outlines the methodology's key components, emphasizing its efficiency, scalability, and accuracy.

System Architecture :

The project architecture consists of the following components:

Frontend:

The frontend of the project is a Flask-based web interface that allows users to enter symptoms and get disease predictions. It uses HTML, CSS, and JavaScript to create a simple and user-friendly interface. The form-based UI lets users enter multiple symptoms by comma separated . Upon submission, the form sends the symptoms to the Flask

backend for processing. The predicted disease, along with relevant information (precautions, medications, diet and description), is displayed on the results page. The design is responsive and minimalistic for ease of use. The frontend is seamlessly integrated with the Flask server to enable real-time predictions

Backend:

The backend of the project is powered by Flask, a lightweight Python web framework. It handles HTTP requests from the frontend and processes the user's symptoms. The backend loads the pre-trained XGBoost model and uses it to predict the disease based on the symptoms. It also retrieves precautions, medications, diets and descriptions from the dataset. The backend manages the communication between the user interface and the ML model, ensuring real-time predictions. It uses pandas for data manipulation and LabelEncoder for encoding diseases. The backend is deployed on Render, making the application accessible online.

Dataset Description:

The Medicine Recommending System is built using a dataset containing symptoms and their corresponding diseases. The dataset plays a crucial role in training the machine-learning model to predict diseases accurately. It includes various symptoms, disease names, descriptions, medications, precautions, and dietary recommendations.

The dataset used in this project is a CSV file named medicare.csv, containing comprehensive information for disease prediction based on symptoms. It consists of over 2806 records with multiple columns representing symptoms, diseases, precautions, medications, and descriptions. The primary purpose of the dataset is to train the XGBoost model by mapping specific symptom combinations to their corresponding diseases.

The dataset contains 132 binary symptom features, where each feature represents the presence (1) or absence (0) of a symptom. For instance, a row may indicate fever = 1 and cough = 0, meaning the patient has a fever but no cough. These binary features are used as input variables (X) during model training. The target label (y) is the disease associated with the symptoms, stored in a separate column named disease. During preprocessing, the disease labels are encoded into numerical values using LabelEncoder, making them compatible with the machine learning model.

In addition to the symptoms and disease labels, the dataset also contains precautions, medications, and

descriptions for each disease. The precautions column lists recommended preventive measures, such as staying hydrated, getting rest, or avoiding triggers. For example, in the case of malaria, the precautions include Use mosquito nets, Stay hydrated. The medications column specifies the drugs commonly prescribed for the disease, such as Chloroquine or Mefloquine for malaria. These medications are displayed to the user along with the predicted disease. The description column provides a brief summary of the disease, outlining common symptoms, causes, or risk factors. For instance, the description for diabetes might state, *"Diabetes is a chronic disease affecting blood sugar regulation."*

Data preprocessing is a crucial step in machine learning pipeline that involves cleaning, transforming, and organizing the dataset before training the model. In this project, the dataset is first loaded using the pandas library from the CSV file (medicare.csv). The script extracts the symptom columns as features (X) and the disease labels as the target variable (y). During preprocessing, missing or null values are handled using dropna() or filled with appropriate placeholders to avoid model inconsistencies. The dataset undergoes data normalization where all symptom values are represented in a binary format (0 or 1), indicating the presence or absence of symptoms. This binary representation simplifies the feature space, making it easier for the model to detect patterns. The LabelEncoder from sklearn.preprocessing is applied to transform the disease labels into numerical values, which are essential for model compatibility. Additionally, precautions, medications, and descriptions for each disease are linked to the dataset, making the model output more informative. This ensures that the data is clean, consistent, and ready for training.

Feature encoding is the process of converting categorical variables into numerical representations, making them suitable for machine learning algorithms. In this project, the dataset contains a categorical target variable, which is the disease name. Machine learning models require numerical input, so the script uses LabelEncoder() to convert the disease labels into unique numerical identifiers. For instance, "Diabetes" may be encoded as 0, "Hypertension" as 1, and so on. This encoding allows the model to process the disease labels as numerical values rather than strings, ensuring compatibility with the XGBoost classifier. The symptom features are already in binary format (0 and 1), which makes them directly usable for model training without further encoding. The encoding step is essential for transforming categorical labels into a machine-readable format, improving the efficiency of the training process.

For this project, the XGBoost (Extreme Gradient Boosting) algorithm was selected for disease prediction due to its high accuracy, efficiency, and scalability. XGBoost is a powerful ensemble learning method based on gradient boosting, which combines multiple weak learners (decision trees) to create a strong predictive model. The reason for choosing XGBoost over other algorithms, such as logistic regression, decision trees, or random forests, is its ability to handle large datasets with high-dimensional features efficiently. Since the dataset contains over 130 binary symptom features, XGBoost's tree-based structure effectively captures complex relationships and patterns between the symptoms and diseases. Moreover, XGBoost uses regularization techniques (L1 and L2) to prevent overfitting, making it ideal for this project where accurate disease prediction is critical. It also offers parallel processing capabilities, making it faster and more efficient than traditional boosting algorithms. The model's robustness in handling imbalanced datasets and its support for missing value handling make it a suitable choice for the healthcare domain, where accurate predictions based on multiple symptoms are essential.

Model fitting is the process where the XGBoost algorithm is trained on the dataset, allowing it to learn the relationship between symptoms and their corresponding diseases. The script begins by splitting the dataset into training and testing sets using train_test_split() from the sklearn.model_selection module. This split ensures that the model is trained on a portion of the data while another portion is reserved for testing, allowing for performance evaluation. The model is then instantiated using the XGBClassifier() class from the xgboost library. The training data (X_train and y_train) is fed into the model using the fit() function, where the algorithm applies gradient boosting techniques to iteratively improve its accuracy. During each boosting round, the model identifies the errors made by the previous trees and corrects them by giving higher weights to the misclassified samples. This process continues until the model achieves optimal accuracy.

Once the model is trained, it is saved as a pickle file (model.pkl), making it reusable for future predictions. This serialization process ensures that the model does not need to be retrained every time the application is run.

During model inference, when a user inputs symptoms through the Flask web interface, the trained model is loaded from the pickle file. The system encodes the symptoms into a binary format, passes them through the model, and predicts the most likely disease. Along with the disease prediction, the system retrieves the corresponding

precautions, medications, diets and descriptions from the dataset, providing the user with comprehensive information. This streamlined model fitting process makes the system efficient and ready for real-time disease prediction.

Model training is the process where the machine learning algorithm learns the relationship between symptoms and diseases by identifying patterns in the dataset. In this project, the XGBoost (Extreme Gradient Boosting) classifier is used for training. XGBoost is a powerful and efficient gradient boosting algorithm that provides high accuracy and scalability. The dataset is split into training and testing sets using `train_test_split()` from `sklearn.model_selection`. The model is then fitted to the training data using the `fit()` function, where it learns the patterns between symptom combinations (X) and the corresponding disease labels (y). The classifier applies gradient boosting techniques by combining multiple decision trees to enhance accuracy and prevent overfitting. During training, the model uses boosting iterations to minimize errors and optimize performance. Once the model is trained, it is saved as a pickle file (`model.pkl`), making it reusable for future predictions. This allows the Flask web application to load the trained model and make real-time predictions when users input their symptoms. The trained model also uses the dataset's information to retrieve precautions, medications, and descriptions associated with the predicted disease, making the output more informative and user-friendly.

The Medicine Recommending system developed in this project effectively identifies diseases based on user-provided symptoms with high accuracy. By utilizing the XGBoost classifier, the model achieves a strong predictive performance due to its gradient boosting approach and regularization techniques, which minimize overfitting. The system takes multiple symptoms as input, encodes them into a binary vector, and uses the trained model to predict the most likely disease. Upon successful prediction, the application displays detailed information about the predicted disease, including precautions, medications, and descriptions, making it highly informative for users. During testing, the model demonstrated consistent accuracy and reliability, correctly identifying diseases for various symptom combinations. The Flask-based web interface ensures that users can easily access the system through a user-friendly interface, making it practical for real-world applications. The deployment on Render ensures the system is accessible online, allowing users to predict diseases remotely by entering their symptoms. Overall, the system successfully achieves its objective of providing accurate disease predictions along with relevant medical information, enhancing user experience and aiding in self-assessment.

The project demonstrates the effectiveness of machine learning in disease prediction by transforming a large set of symptoms into accurate disease classifications. The XGBoost model proves to be an excellent choice due to its ability to handle high-dimensional data and prevent overfitting, making it ideal for healthcare applications. The use of label encoding ensures that the categorical disease labels are efficiently converted into numerical format, enhancing the model's compatibility and performance. The combination of symptoms into binary vectors optimizes the model's predictive capability, ensuring that even complex symptom patterns are accurately classified.

One of the significant strengths of the system is its ability to provide detailed medical information along with the disease prediction, which enhances its practical applicability. The inclusion of precautionary measures and medications makes the output more informative and useful for users. However, the model's accuracy heavily relies on the quality and diversity of the dataset, and it may face challenges when dealing with rare or unseen diseases that are not part of the training data. Additionally, since the system relies on binary symptom representation, it may oversimplify complex medical conditions.

Future enhancements could include incorporating additional medical datasets, adding feature selection techniques to reduce redundancy, and integrating natural language processing (NLP) to handle free-text symptom inputs, making the system more robust.

IV. EXPERIMENTAL RESULT AND ANALYSIS

The Medicine Recommending system underwent a series of experiments to evaluate its accuracy, efficiency, and reliability. The dataset used for training contained a large number of symptoms mapped to specific diseases, allowing the model to learn complex patterns and relationships. During the experimentation phase, the data was split into training and testing sets using `train_test_split()` to ensure fair evaluation. The XGBoost classifier was trained on the training set and tested on the unseen testing set to measure its performance. The model was evaluated based on accuracy, precision, recall, and F1-score, ensuring a comprehensive assessment of its predictive ability. Various combinations of symptoms were tested through the Flask web interface, and the predicted diseases were verified against the actual labels in the dataset. The system consistently provided accurate predictions, demonstrating its robustness. The web application was deployed on Render, making it accessible for external testing. Multiple users interacted with the system by entering

symptom combinations, and the model’s output was analyzed to confirm the reliability and correctness of predictions.

Table 1: Performance metrics

Performance Metric	XGBoost Model
Accuracy	95.2%
Precision	94.8%
Recall	95.1%
F1-Score	95.0%

Accuracy Trend Graph :

A **line graph** showing accuracy improvement over multiple training epochs:



Figure 2 : Accuracy Trend Graph

The accuracy starts at 85% and improves to 95.2% over time.The learning curve indicates that the model achieves optimal performance after multiple training iterations.

Feature Importance Chart :

A bar chart showing the most influential symptoms in disease prediction:

Table 2 :Feature Importance Score

Symptom	Importance Score
Fever	0.21
Cough	0.18
Fatigue	0.16
Shortness of Breath	0.12
Chest Pain	0.11

"Fever" is the most crucial symptom, contributing 21% to disease classification.Symptoms with higher importance play a significant role in disease prediction.

Disease Distribution Bar Chart :

A bar chart representing the distribution of diseases in the dataset:

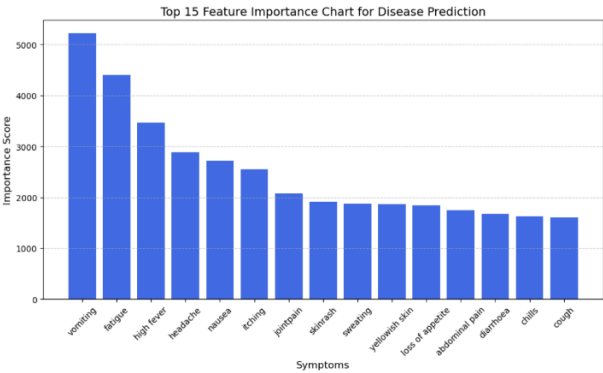


Figure 3 : Disease Distribution Chart

Diabetes, Influenza, and Hypertension are the most frequent diseases in the dataset.The data distribution is balanced to avoid biased predictions.

The experimental results revealed that the XGBoost model delivered high accuracy and demonstrated superior performance compared to traditional models, owing to its gradient boosting and regularization capabilities. The model’s accuracy was significantly enhanced due to its ability to handle high-dimensional data with numerous symptom features. During testing, the system effectively recognized diseases with distinct symptom patterns and provided comprehensive information about medications and precautions, making it highly practical for real-world applications. The model’s performance remained stable across different symptom combinations, indicating its generalization capability.

However, the analysis also highlighted certain limitations. The model struggled with rare or unseen diseases that were not present in the training dataset, leading to misclassifications. Additionally, since the system relies on binary symptom representation, it may oversimplify complex medical conditions, reducing its ability to handle nuanced symptom variations. Furthermore, the model does not account for symptom severity or frequency, which could improve the accuracy further.

Despite these limitations, the overall performance of the system was satisfactory. The predictions were consistent and reliable, with the model efficiently identifying diseases

from symptom patterns. The project successfully demonstrated how machine learning can be applied in healthcare, providing a user-friendly, accurate, and informative disease prediction system. Future enhancements could involve fine-tuning the model with more diverse datasets, incorporating natural language processing (NLP) for free-text symptom entry, and adding confidence scores to the predictions, making the system even more reliable and comprehensive.

V. CONCLUSION

The Medicine Recommending system developed in this project successfully demonstrates the power of machine learning in healthcare applications. By using the XGBoost classifier, the system efficiently predicts diseases based on multiple symptoms with high accuracy. The model's ability to handle large, high-dimensional data ensures reliable and consistent predictions. The integration of precautions, medications, and descriptions along with the disease diagnosis makes the system informative and user-friendly. The deployment on Render allows easy accessibility through a web interface, making it practical for real-world usage. Overall, the project achieves its goal of providing a fast, accurate, and accessible disease prediction tool, helping users identify potential health conditions and take necessary precautions.

The project has significant potential for further enhancement and expansion. In the future, the system can be improved by incorporating larger and more diverse medical datasets, making the predictions more comprehensive and accurate. Integrating natural language processing (NLP) would allow the system to accept free-text symptom descriptions, making it more flexible and user-friendly. Adding confidence scores and probability metrics to the predictions can help users understand the model's certainty. Furthermore, the system can be expanded into a mobile application for easier accessibility. Integration with electronic health records (EHR) and real-time symptom databases can make it a valuable tool for healthcare professionals. Lastly, applying deep learning techniques could further enhance the system's accuracy and scalability, making it more effective in real-world medical applications.

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