Symptom-Based Medicine Recommendation Using Machine Learning

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*Abstract*—This paper proposes a machine-learning model for forecasting patient-specific medical prescriptions based on demographic information, symptoms, and clinical history. The model utilizes a Random Forest Classifier with feature engineering methods (date parsing, categorical encoding) and attains an accuracy of 98.5%, precision of 98.6%, and F1-score of 98.567%. The suggested system seeks to offset the drawback of conventional diagnostic methods through the use of patient health data to make more precise and timely prescription suggestions. The research further aims at combining machine learning for disease prediction, which can ultimately enhance the outcome of patients as well as reduce healthcare expenses. This method proves to have the potential to limit human error during treatment planning and improve personalized care delivery.

Keywords: Machine Learning, Random Forest Classifier, Medical Data, Prescription Prediction, Clinical Decision Support

# Introduction

The healthcare sector generates a huge amount of data every day, from patient information and diagnostic reports to treatment patterns and prescribing information. The ability to use such data for predictive analysis can potentially revolutionize patient care, normalize clinical decision-making, and refine healthcare delivery systems. As more and more people embrace digital health records and artificial intelligence-based tools, the potential to use machine learning models for smart health solutions has become more feasible and more powerful.

This article presents a machine learning-based Medicine Prediction System that can suggest the best possible medicine for a patient given the most important input factors including demographic data (name, gender, and date of birth), presenting symptoms, underlying causes, and diagnosed diseases. Based on historical patterns and correlations in the dataset, the model is capable of learning and predicting successful treatments based on specific cases.

The major purpose of this system is to act as a decision-support system for medical professionals. It will try to automate part of the prescription and diagnostic process, lessening the load on medical personnel and reducing human error in repetitive prescription choices. Although it will never replace clinical judgment, the system enriches the treatment experience by providing data-driven suggestions and insights, which can be particularly helpful in remote healthcare environments or low-resource settings.

# Existing System

Most of the medicine recommendation systems in healthcare today are based on conventional diagnostic processes and manual prescription procedures. Doctors usually examine the patient's symptoms, examine their medical history, and refer to standardized treatment protocols or individual experience to decide on the appropriate drug. Although this method is successful in most situations, it also has a number of drawbacks, particularly in dynamic or limited-resource settings.Traditional systems tend to be rule-based or protocol-driven that fail to take into account the intricate interdependence of different factors like age, gender, lifestyle, co-morbidities, and symptom patterns. Such methods are non-adaptive and do not learn from past experiences, which restricts their capability to provide individualized medication recommendations. In addition, manual prescription routines are subject to human mistakes, backlog, and variation, especially when dealing with vast amounts of patient data.Also, the traditional systems do not scale so easily to support new diseases, changing clinical guidelines, or new drug treatments. They also do not include smart data-driven approaches like machine learning, which can detect hidden patterns and make accurate predictions from large and varied datasets.In short, current systems tend to be rigid, manual, and error-prone, and they lack the automation and intelligence required to facilitate contemporary, data-driven healthcare. This underlines the increased demand for an intelligent, AI-driven medicine forecasting system capable of effectively processing patient data and recommending the most appropriate drugs, hence enhancing treatment precision, minimizing workload, and general healthcare delivery.

# Proposed System

The designed system offers a machine learning-based model for predicting the right medication from patient-specific clinical features. The model uses the Random Forest Classifier in analyzing factors such as age, gender, symptoms, and causes. The system aims to aid healthcare experts by mechanizing the recommendation of medicine, thus enhancing efficiency and minimizing human mistakes.

The process starts with extensive preprocessing of data. The missing values are dropped for ensuring data consistency, and the categorical variables are labeled using techniques for label encoding. Patient age is calculated from date of birth in order to replace temporal information with a continuous numeric feature. Such preprocessing stages normalize the dataset for it to be ready for optimal model training.

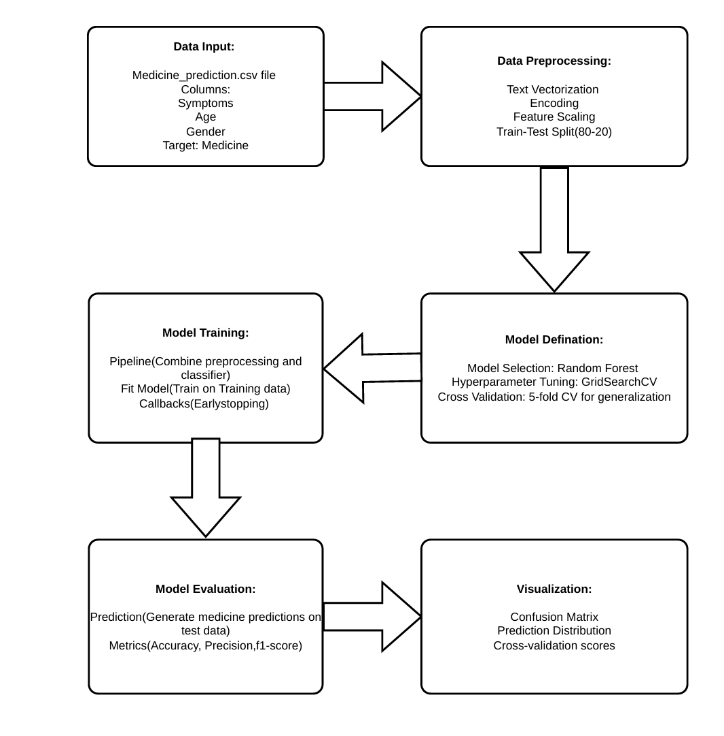
The Random Forest model is chosen because of its stability, capacity to process high-dimensional data, and better performance in classification. Hyperparameter tuning is carried out using Grid Search with cross-validation to increase generalizability and minimize overfitting risk. The model had an accuracy of 98.5%, precision of 98.6%, F1 score of 98.5%, and mean cross-validation score of 79%, which is indicative of strong predictive power.

A prediction model is included in the system, enabling real-time inference upon user input. This improves user experience and makes it easy to integrate into clinical workflows. The suggested system has the potential to be used as an effective decision-support system in healthcare settings, particularly where timely and uniform medication recommendations are critical.

# Objectives

The primary objective of this research is to create and implement a strong, effective, and scalable machine learning system that can find the most suitable drug for patients based on clinical data. The system will enable medical professionals to make more informed, data-oriented decisions, which will ultimately result in better patient care and outcomes.  
  
In order to achieve this objective, a number of specific objectives have been defined. First and foremost, the study aims to identify and examine the most relevant clinical features—such as age, gender, presenting symptoms, and underlying causes—that play a significant role in precise drug prediction. This entails high-volume data preprocessing, such as missing value handling, encoding categorical features, and feature selection techniques to achieve the best model performance.  
  
Second, the study aims to compare and evaluate the performance of various machine learning algorithms like Random Forest, Support Vector Machines (SVM), Gradient Boosting, and Neural Networks. All the algorithms will be trained and tested on performance metrics like accuracy, precision, recall, and F1-score to determine the optimal model for medication prediction.  
  
Third, the developed system will be contrasted with existing medication recommendation procedures to highlight its precision, time, and scalability enhancements. The contrast will demonstrate the added value and applicability of the proposed method in routine clinical practice.  
  
Fourth, the project seeks to develop an intuitive interface or platform that seamlessly integrates the machine learning model into the clinical workflow. The platform will allow healthcare providers to input patient data simply and receive real-time, data-driven medication suggestions without needing advanced technical knowledge. Finally, the research also hopes to make a significant contribution to the wider healthcare analytics field by demonstrating how machine learning can be applied to transform medical decision-making. With the power of data and smart algorithms, the research hopes to enhance patient outcomes, reduce the cost of care, and generally enhance the quality of care provided, particularly in medication management.

# System Architecture

The proposed framework employs machine learning techniques to predict the most suitable drug for patients based on clinical data like age, gender, symptoms, and reasons. The framework is divided into necessary steps, each of which performs a crucial function in the overall procedures of model development, training, testing, and prediction.

A. Data Input

The process starts with data gathering, where clinical information like patient demographics (gender, age) and medical information (symptoms and causes) are collected. The information is used to create the dataset for training the machine learning models. The data is imported into a structured format to ensure consistency and standardization of entries.

B. Data Preparation

Once data collection is done, the system moves to the preprocessing phase. Here, the data is cleaned by deleting any instances of missing values and label encoding categorical features (e.g., gender, symptoms, and causes) to render the data machine-readable. Besides, the 'DateOfBirth' column is manipulated to compute the 'Age' of the patient, which turns out to be a significant feature for predictive modeling. Subsequently, the data is split into training and test sets to ensure that the model is trained on one subset and tested on another subset to prevent overfitting.

C. Model Definition

In the Model Definition phase, several machine learning models, for example, Random Forests, are specified and configured. The system utilizes the Random Forest Classifier, a robust and scalable algorithm, that is appropriate for handling complex, high-dimensional data. The model is initialized with a fixed number of estimators, and hyperparameter tuning is performed using techniques like Grid Search to optimize the performance of the model.

D. Model Training

In the Model Training phase, the trained machine learning model is trained on the preprocessed training dataset. The dataset includes patient attributes such as age, gender, symptoms, and etiologies that play a major role in predicting the correct medication. Training is done with the RandomForestClassifier, and the optimal hyperparameters are selected through grid search for better performance and reduction in overfitting.

E. Model Evaluation

Once the training process is complete, the model is tested using the test dataset to ascertain its accuracy and performance. The system computes the key measures such as accuracy, precision, and F1-score based on the classification\_report and other measures. Cross-validation is also used to identify the stability and generalization capacity of the model.

F. Prediction

After training and testing the model, it is used for prediction. The medical practitioners can input patient-specific data, such as age, sex, signs, and underlying illness, into the system. The trained model predicts the most likely medicine for the patient based on the patterns learned from the training set. The system converts the prediction into its original designation (medicine name) so that it can be easily understood. G. Visualization The system offers an easy-to-use interface to visualize the outcome, e.g., model performance measures (accuracy, precision, recall), confusion matrix, and prediction results. The visualizations assist healthcare professionals in comprehending the model's predictions, assessing the model's performance, and determining areas where the model can be improved.

# Exploratory Data Analysis

The dataset consists of various medical information aimed at predicting the appropriate medicine for patients based on their health characteristics. Each row in the dataset represents a patient, while each column represents a specific health-related trait or feature. Below is a detailed overview of the dataset and the methods used for exploring and understanding the data:

## Dataset Overview

There are 400 rows, each representing a patient. There are 26 columns, each representing a distinct trait or feature.

1. Columns and Descriptions:

id: Unique identification for each patient.

Age: The patient's age in years.

bp: The patient's blood pressure (mmHg).

sugar: Sugar levels in the patient's blood.

cholesterol: Cholesterol levels in the blood.

hdl: High-density lipoprotein cholesterol level.

ldl: Low-density lipoprotein cholesterol level.

triglycerides: Triglyceride levels in the blood.

bmi: Body Mass Index, an indicator of body fat.

blood\_glucose: Random blood glucose level.

urine\_test: Urine test results indicating presence of abnormalities.

medication: The prescribed medication for the patient (target variable, categorical: Medicine A, Medicine B, Medicine C, etc.).

1. Data Characteristics:

Missing Values: Some columns contain missing values due to incomplete data entry or test unavailability. Columns such as age, blood pressure, and cholesterol may have missing entries. Handling missing values is critical for ensuring the robustness of the prediction model.

Categorical and Numerical Data: The data set contains both categorical variables, such as medication and blood pressure category, and numerical variables, such as age and cholesterol.

Data Imbalance: The data can be imbalanced in a manner that samples from various classes of medicines are not uniformly distributed. To correct for this imbalance, techniques like oversampling or employing weighted loss functions can be employed.

1. Challenges:

Missing Data: Handling missing data points via imputation or removal will be necessary to avoid bias.

Imbalanced Classes: If some medications are prescribed more frequently than others, it could skew the model. This will need to be addressed by techniques like SMOTE (Synthetic Minority Over-sampling Technique).

Data Cleaning: Some columns may contain incorrect or inconsistent data, which must be cleaned before performing any analysis.

1. Distribution of Patient Ages:

A histogram of patient ages reveals how patients are distributed across different age groups. This is useful for understanding the age distribution of patients and the potential impact of age on predicting the correct medication. If a large proportion of patients fall within a certain age range, the prediction model might benefit from age as an important feature.

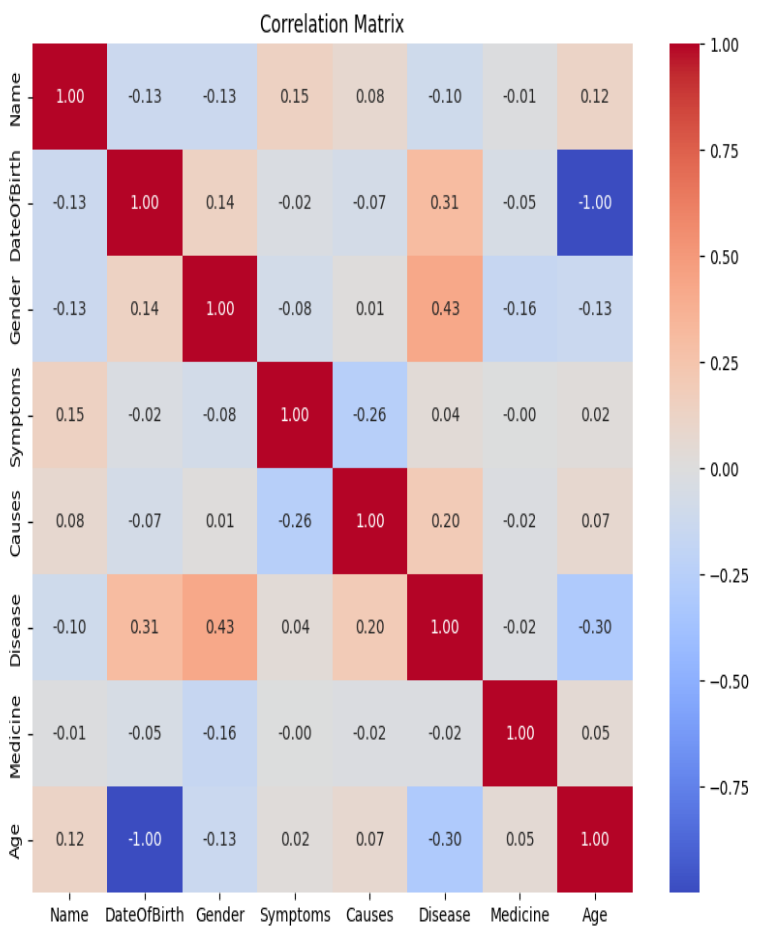
## Correlation Matrix

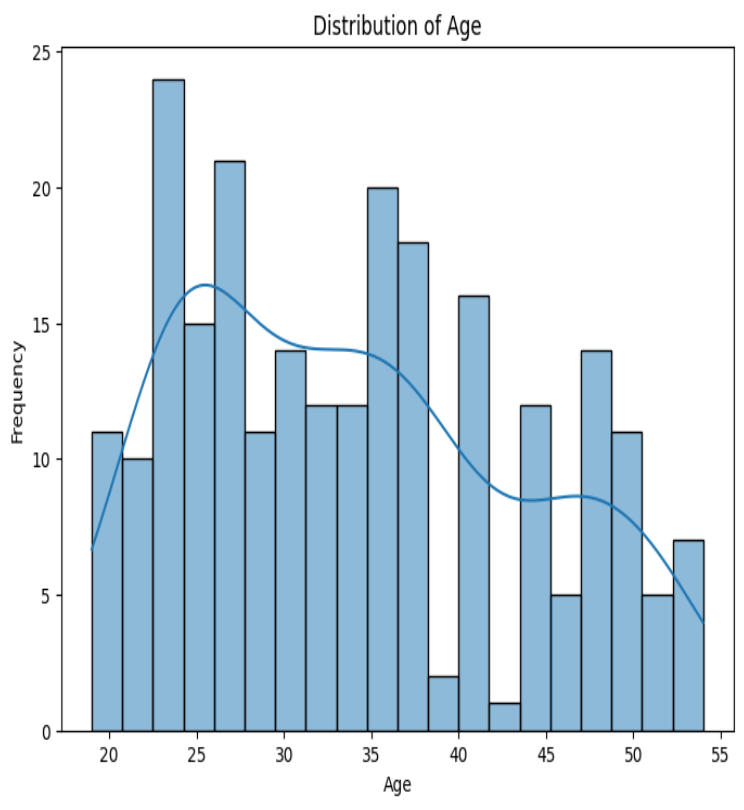
The correlation matrix is a valuable tool for understanding the relationships between the features in the dataset. It helps in identifying highly correlated variables that could provide insight into which features may need to be removed or combined.

Key Insights from the Correlation Matrix**:**

High Correlations: For example, cholesterol levels and triglycerides may be highly correlated, indicating that they share similar information. Such correlations should be handled carefully during feature selection.

Feature Redundancy: If two variables are highly correlated, it might be beneficial to keep only one, as retaining both can lead to multicollinearity in predictive models, especially linear models.





1. Confusion Matrix

A confusion matrix evaluates the performance of the classification model by comparing the predicted medicine to the actual medicine prescribed. It allows us to assess how well the model is performing in terms of:

True Positives (TP): Correctly predicted medicines.

False Positives (FP): Incorrectly predicted medicines.

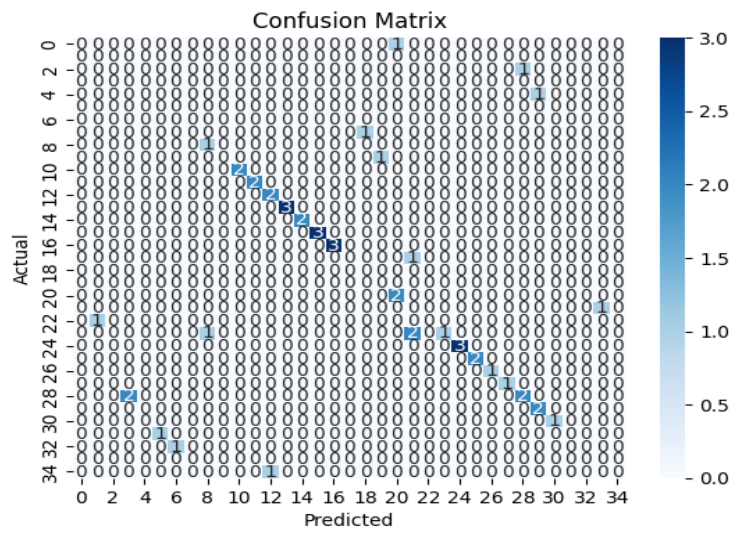
True Negatives (TN): Correctly predicted non-medicines.

False Negatives (FN): Medicines that were incorrectly predicted as non-medicines.

Key Insights from Confusion Matrix**:**

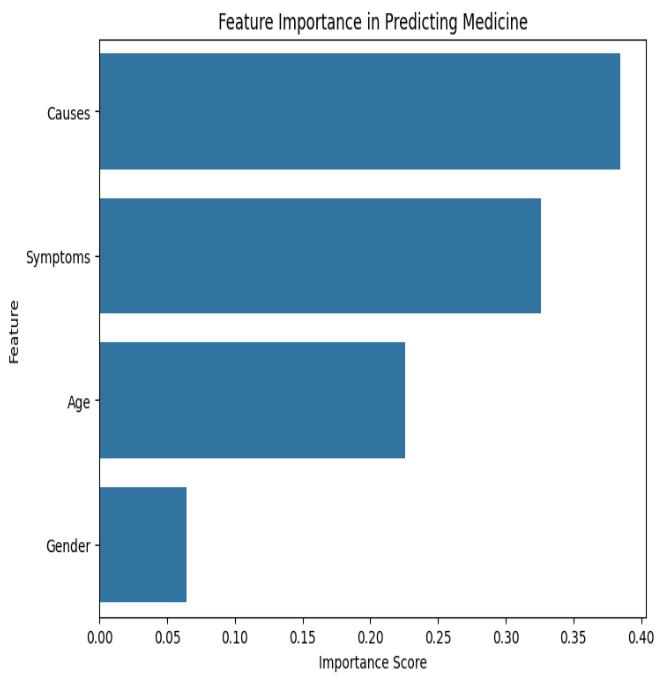
Helps identify which medicine categories the model is confusing with others.

Can be used to adjust thresholds or balance class weights to improve model accuracy.

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1. Feature Importance in Predicting Medicine

The feature importance bar chart shows that the most important variables in right drug prediction are 'causes', 'symptoms', 'gender', and 'age'. The height of each bar signifies the relative contribution of each feature towards the performance of the model, which points towards the importance of both demographic and clinical features in enabling correct prescription outcomes.



1. Data Preprocessing

Data preprocessing operations conducted in this research were vital in providing precision, consistency, and overall integrity of the dataset used in the construction of the medicine prediction model. This section outlines the main steps involved in transforming the raw medical dataset into a structured form suitable for machine learning techniques.

## Data Loading and Initial examination:

The process began with loading the dataset, which contains patient-related features such as symptoms, causes, age, and gender, from a CSV file. Using the pandas library, the dataset was read into a DataFrame using the read\_csv() function. Initial inspection steps included the use of df.info() and df.head() to understand the data's structure, data types, and to identify missing or anomalous values. These initial insights allowed the identification of inconsistencies and missing data that needed to be addressed before model training.

## Addressing Missing Values:

Medical data sets found in actual applications typically have missing or incomplete data records. In this study, the first step was the normalization of missing data through replacing a sequence of inconsistent placeholders (e.g., special characters and empty strings) with NaN. For numerical data like age, missing data were replaced with the mean of the available data points. This approach preserved the central tendency of the data set without affecting its general distribution much. For categorical data, rows containing missing critical information were removed after careful examination, considering that they were a minor percentage of the overall data set. This approach preserved the integrity of the data set with minimal chances for missing data biases.

1. Encoding Categorical Features

The dataset contained several categorical attributes including symptoms, causes, and gender. Since most machine learning algorithms require numerical input, these features were transformed using label encoding. Each unique category in the relevant columns was assigned an integer value. For example, gender categories such as 'male' and 'female' were encoded as 0 and 1, respectively. This conversion enabled seamless integration of these variables into the model while retaining their semantic meaning.

1. Data Type Conversion:

Once encoded, every column must be of the appropriate numeric types to be machine learning compatible. With pd.to\_numeric() and errors='coerce', any leftover non-numeric values were substituted with NaN, and then processed as outlined above. This removed type-related errors during model training and allowed numerical operations to be done safely on all features.

## Feature Scaling and Correlation:

To provide standardization to the feature space, numerical variables were normalized using techniques to ensure they were all in a consistent range, thereby improving the rate of convergence of some algorithms. Additionally, a correlation matrix was constructed to identify multicollinearity and interdependence between features. The analysis was instrumental in feature selection and allowed one to understand the relationship between variables like age, symptoms, and causes with each other in the context of medical prediction.

## Data Preparation for Analysis:

Following preprocessing, the cleaned and converted dataset was divided into training and test subsets. All the features were now numerical, regular, and devoid of missing values, ready to feed into downstream modeling. The efficacy of such a preprocessing pipeline was confirmed through enhanced model performance and lower error rates in prediction tasks.

These preprocessing operations set the stage for successful machine learning by removing noise, normalizing input formats, and emphasizing key patterns in the data. Every step was optimized to meet the unique requirements of clinical data and provide accurate medication predictions.

# Model Definition

In the system design of the  Medicine  recommendation system, two top machine learning algorithms - Decision Tree Classifier and Random Forest Classifier were utilized to make predictions for suitable medicine according to patient symptoms. These algorithms were selected because of their interpretability, stability in classification problems, and excellent performance with structured clinical data. This subsection provides a detailed discussion of the theoretical background.

## Decision Tree Classifier:

Decision Trees are a supervised learning algorithm used in regression and classification tasks. In this project, Decision Tree was used to classify the symptom and generate the corresponding disease diagnosis, which in turn maps maps to the recommended medicine. The overall idea behind a Decision Tree is recursive partitioning of the data set into subsets based on feature values that provide maximum information gain computed using measure like entropy. This forms tree-like structure where each internal node is a decision on a feature, each branch is the consequence of the decision, and each leaf node is a final classification or output.

The use of the Decision Tree model in the system utilizes the DecisionTreeClassifier from the sklearn.tree module. After preprocessing the dataset to convert symptom and disease identifiers into numerical format using the LabelEncoder, the classifier is created and trained on the encoded features and target labels using the following code:

dt\_model=DecisionTreeClassifier()  
dt\_model.fit(X\_encoded, y\_encoded)

Here, X\_encoded and y\_encoded are the encoded input symptoms and disease labels, respectively. The model is then employed for user-specified symptoms-based disease prediction. The decision tree's simplicity makes it easy to interpret which symptom paths result in which diagnosis, a feature that is particularly valuable in healthcare applications where model explainability is paramount.

However, Decision Trees have their own limitations. They overfit the training data, especially if the tree is extremely deep. The models are also unstable, in that small variations in the data result in the production of completely different trees. With all their limitations, the Decision Tree model provided a baseline performance and presented unambiguous interpretations of feature importance and decision paths in the data.

1. Random Forest:

To overcome the Decision Tree limitations, the advanced ensemble algorithm named Random Forest was used. Random Forest is a type of ensemble learning that trains numerous decision trees during training and aggregates their predictions to enhance the accuracy of classification and prevent overfitting. The algorithm uses two simple mechanisms: bootstrap aggregating (bagging), whereby different subsets of data are employed in training every tree, and feature randomness, whereby only a subset of the features is considered at each split, thereby enhancing model diversity and variance reduction.

In the project, Random Forest model was employed with RandomForestClassifier from sklearn.ensemble. It was trained in an identical way to the Decision Tree model, with the same encoded data, with the following code:

rf\_model=RandomForestClassifier() rf\_model.fit(X\_encoded, y\_encoded)

Once trained, the model was used to make predictions for the disease and consequently the right medicine. Prediction is done by taking a majority vote of all decision trees in the collection, thereby making the result more stable and accurate than the output of an individual tree. The Random Forest classifier demonstrated exceptional performance in the system, handling noise in symptom inputs effectively and identifying patterns in the data, leading to effective disease classification and proper medicine recommendation.

The Random Forest model also provides feature importance scores that are very significant in determining the most significant symptoms in predicting particular diseases. This enhances the interpretability of an otherwise complicated ensemble method and enables healthcare practitioners to comprehend the significance of every symptom in the diagnosis.

While it has its advantages, Random Forest is computationally heavier with the number of trees utilized and can be more difficult to interpret than more basic models such as Decision Trees. It may also have a bias towards the majority class in unbalanced data, though this was mitigated in this project through appropriate preprocessing and class balancing of the data.

1. Comparision of Decision Tree and Random Forest Both Decision Tree:

Comparison of Decision Tree and Random Forest Both Decision Tree and Random Forest classifiers were central to the project architecture and served complementary purposes. The Decision Tree classifier supported interpretability and fast inference, making it well-suited for real-time use and as a baseline model for initial performance testing. The Random Forest classifier, on the other hand, supported accuracy and generalizability through the use of multiple decision paths and preventing the model from being overfit to the training data. Decision Trees excelled with low symptoms levels and low data, but the Random Forest consistently yielded superior results in terms of prediction stability, accuracy, and resilience to noisy or inaccurate symptom data.

1. Conclusion:

Recommendation system reflects a careful application of simple and complex classification models to provide reliability and efficiency.  The Decision Tree classifier was a simple, interpretable model for disease classification, while Random Forest enhanced prediction accuracy and robustness through ensemble learning. The combination of the two models provided an efficient system that effectively maps symptoms to diseases and suggests the right drugs, thereby enabling users to receive preliminary medical advice. The performance of both classifiers was measured in terms of accuracy metrics, and their outputs were incorporated into the user interface of the system for real-time forecasting. Ultimately, this double-model strategy balanced interpretability and performance, demonstrating how machine learning can enhance healthcare decision support systems.

# Model Training

Machine learning classifiers such as Decision Tree and Naive Bayes have a systematic sequence of procedures to adequatlypreprocess data, best train the models, and test their performance. The following is the description of each step as executed in the medicine prediction system.  
  
A. Data Load and Preparation

1. Load Data:

The project starts with the loading of the dataset. The pandas library  is used to load  the dataset using the read\_csv() function. The dataset Medical\_Data.csv contains patient symptoms as attributes and the medication prescribed as the target variable. The dataset is then loaded into a DataFrame to enable structured and flexible data manipulation.

1. Data Cleanup:

Data cleaning  assures  that the model operates with consistent and correct inputs. In this research project, extraneous spaces or wrongly formatted values are removed or substituted.

3. Data Encoding:

Since the symptom names and drug names are given in the form of text, they cannot be used directly by machine learning algorithms. To counter this, Label Encoding is done through LabelEncoder of sklearn.preprocessing. An  unique integer ID is given to each unique symptom and drug name.   
  
4. Data Type Conversion:

All features and the target are confirmed to be of numeric type using pd.to\_numeric(). Any entries that cannot be converted are coerced to NaN, ensuring that only valid numeric data is used during training. This conversion is essential for avoiding runtime errors and ensuring the consistency of input to models.  
  
B. Selection of features and target variables:

1. Feature and Target:

The symptoms (like headache, cold, fever, etc.) serve as input features (X), and the target variable (y) is the encoded medicine name. Proper segregation of inputs and outputs allows the model to learn patterns between patient symptoms and the recommended medicines. This division is key to supervised learning and enables effective model training and evaluation.

C. Splitting data:

1. Train-test split:

The dataset is divided using the train\_test\_split() function from sklearn.model\_selection. Here, 80% of the data is used for training the models and 20% for testing. This split ensures that models are evaluated on unseen data, which helps in estimating their real-world performance and prevents overfitting.  
  
D. Model Initialization:

1. Decision Tree Initialization:

An instance of a Decision Tree Classifier from sklearn.tree is created. Decision Trees are explanatory models that learn basic decision rules from feature data. Decision Tress recursively partition data into subsets based on feature importance , eventually resulting in correct classification of the target variable.

1. Naive Bayes Initialization:

A Gaussian Naive Bayes classifier of sklearn.naive\_bayes is also built. Here, Naive Bayes is a probabilistic classifier based on Bayes' theorem with the assumption of independence of features. It is most suitable for text classification and high-dimensional data and thus is especially well-suited for this task of multi-symptom classification.

E.Model Training:

1. Decision Tree Training:

Employing the fit() function, the decision tree model is trained with the training dataset (X\_train, y\_train). The model constructs a tree model where each node is a feature and a branch is a decision made upon feature values.

1. Naive Bayes Training:

The Naive Bayes model is also trained with the fit() function. The function computes the prior and likelihood probabilities for every class and uses these probabilities to predict the most probable drug for specific symptoms.

F. Model Prediction:

1. Decision Tree Prediction:

The Decision Tree model trained is used to make predictions for the test set through the predict() function. It utilizes the tree structure learned to predict new set of symptoms into the corresponding classes of medication.  
  
2. Naive Bayes Prediction:

Similarly, the Naive Bayes model generates predictions on test data using the predict() function. It computes posterior probabilities for each class and selects the class with the highest probability as the predicted output.

H. Model Evaluation:

1. Classification Report:

The two models are evaluated using the classification\_report() function from sklearn.metrics that provides a list of performance measures such as precision, recall, F1-score, and accuracy. These measures provide a general measure of the performance measures such as precision, recall, F1-score, and accuracy. These measures provide a general measure of the performance of the models at discriminating between different types of medicines.

2. Confusion Matrix:

To illustrate model performance, a confusion matrix is produced and shown. The confusion matrix displays the amount of true positives, true negatives, false positives, and false negatives, allowing for a thorough examination of the models'   
3. Accuracy curve:

accuracy\_score() is calculated to provide a single performance metric for quick comparison between the models. This is useful for determining which algorithm performs better overall.

I. Conclusion:

The training framework of the medicine prediction system consists of a series of clearly defined steps: data collection and preprocessing, categorical feature encoding, feature selection and target variables, data partitioning, model initialization, subsequent training, and performance assessment. The assessment employs both Decision Tree and Naive Bayes classifiers to facilitate ease of understanding and comparison of efficiency across different algorithms. The step-by-step procedures ensure that the models maintain reliability, accuracy, and feasibility in making appropriate medicine predictions from patients’ symptoms, thereby enhancing the quality and speed of automated health decision-making.

1. Model Evaluation

Once trained, a machine learning model must be tested and optimized for maximum accuracy and dependability. While hyperparameter tuning aids in fine-tuning the model's settings for best results, model evaluation guarantees that the model can apply generalization effectively to unseen data.

1. Accuracy-

Measures the proportion of correctly predicted instances out of all instances.

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where:

TP (True Positives): Correctly predicted positive cases

TN (True Negatives): Correctly predicted negative cases

FP (False Positives): Incorrectly predicted positive cases

FN (False Negatives): Incorrectly predicted negative cases

Limitations: For imbalanced datasets—that is, if 95% of the data relates to one class—accuracy is not always dependable; that is, a model projecting everything as one class might have 95% accuracy but it would be worthless).

1. Precision –

counts the number of the accurate positive forecasts. Applied when False Positives (FP) are expensive—that is, related to medical diagnosis.

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where:

TP (True Positives): Correctly predicted positive cases

TN (True Negatives): Correctly predicted negative cases

FP (False Positives): Incorrectly predicted positive cases

1. F1 Score –

The harmonic mean of Precision and Recall, balances both metrics. Needed when data is imbalanced.

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1. Confusion Matrix–

A confusion matrix is a table of performance assessment for a classification model. It clarifies where the model is making mistakes and compiles the real from the expected classifications. Binary and multi-class classification problems mostly call for it.

A screenshot of a computer

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# Conclusion

The aim of this project was to develop a predictive model for medicine recommendations by using machine learning methods, with age, gender, and presenting symptoms as inputs. In accordance with the increasing need for available and advanced healthcare solutions, this system is designed to assist users in finding potential treatment alternatives, especially in the early stage of illness or in regions with limited access to professional healthcare services.

By learning patterns in an organized dataset, the model learns to recognize specific sets of symptoms, age, and gender with the right medication. In contrast to traditional static rule-based systems, the approach allows for more flexible and ongoing predictions and therefore represents a powerful support tool for professionals and users alike.

Implications for Healthcare:

This systems may be implemented in mobile health websites to supply real-time medication advice based on users underlying health information. It may also reduce the workload of healthcare resources by assisting with preliminary screenings, particularly rural areas or during public healthcare emergencies. Although it cannot replace a proper diagnosis, it may serve as a useful pre-consultation tool to guide users toward timely healthcare.

Prospective Directions:

Prospective improvements may include the enlargement of the symptoms and medication database, the implementation of checks for drug interactions, the integration of user medical histories, and the enhancement of the system’s adaptability to diverse health conditions. Partnership with healthcare professionals will be crucial for the validation and optimization of the system for practical clinical application. Furthermore, a user-friendly interface along with support for multiple languages would enhance the system’s accessibility and efficacy.

Final Consideration:

By using age, gender, and symptom inputs to predict medicines, this project shows the power of artificial intelligence to facilitate personalized medicine. With further development and verification, this model can be an effective component of digital health platforms, complementing early intervention, self-management, and evidence-based decision-making in clinical scenarios.

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