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Disease Prediction from Patient Symptoms using a Decision Tree Classifier

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Abstract

Disease prediction using medical data plays a crucial role in early diagnosis and preventive healthcare. The proposed system utilizes Python, Artificial Intelligence (AI), and Machine Learning (ML) techniques to predict diseases based on patient symptoms. The system is built using Streamlit for an interactive web interface and employs a Decision Tree classifier for disease prediction. The model is trained on a dataset containing symptoms and their associated diseases. A label encoding technique is applied to transform categorical disease labels into numerical form, and a Decision Tree classifier is then trained to learn the patterns from the symptom data. Users can upload a CSV dataset to train the model, evaluate its accuracy on test data, and input symptoms through a user-friendly interface to receive real-time disease predictions. This system enables efficient, accurate, and automated preliminary medical diagnosis, aiding healthcare professionals and patients in identifying potential diseases early and thereby improving treatment outcomes.

Keyword: Decision Tree, Disease prediction, Artificial Intelligence (AI), and Machine Learning (ML)

1. Introduction

Healthcare advancements have significantly improved disease diagnosis, yet early detection remains a challenge due to the complexity and variability of symptoms. Machine Learning (ML) and Artificial Intelligence (AI) are revolutionizing the medical field by enabling data-driven decision-making. Disease prediction using AI models can assist healthcare professionals in identifying potential illnesses based on patient symptoms, leading to early intervention and improved treatment outcomes.This paper focuses on developing a disease prediction system using Python and ML techniques, leveraging a Decision Tree classifier for accurate diagnosis. The system is designed to accept medical data (patient symptoms), process these symptoms, and predict potential diseases. By integrating an interactive Streamlit interface, users can input symptoms and receive instant disease predictions, making the system user-friendly and accessible for both healthcare providers and patients.

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2. Literature Survey

In recent years, researchers have explored various ML approaches for disease prediction to improve diagnostic accuracy and speed. Early studies applied classic classification algorithms to medical datasets: for example, some works evaluated Naïve Bayes, K-Nearest Neighbors (KNN), and Support Vector Machines (SVM) for predicting illnesses from patient data. These studies demonstrated the feasibility of data-driven diagnosis, but results varied depending on the algorithm and the complexity of the dataset. In particular, decision tree-based algorithms and ensemble methods often stood out due to their balance of accuracy and interpretability. For instance, an early big-data study in 2017 successfully used machine learning over large healthcare datasets to predict diseases, highlighting how large-scale data combined with ML can enhance prediction capabilities. Other comparative research in 2019 showed that decision trees and ensembles like Random Forest can outperform simpler methods (like Naïve Bayes) in multi-disease prediction tasks, underlining the effectiveness of tree-based classifiers for medical data.Symptom-based disease prediction has also been a focus of several studies. A 2020 study utilized decision tree classifiers on patient symptom records and reported high accuracy in diagnosing multiple diseases, suggesting that decision trees can effectively capture the relationships between combinations of symptoms and specific diseases. In another approach, researchers combined decision trees with ensemble techniques (e.g., using a Random Forest classifier) to improve reliability and handle cases where symptoms may point to multiple possible conditions. These works indicate that incorporating more advanced ensemble models can further boost prediction performance. Additionally, recent review articles have highlighted the growing role of ML in early disease detection and diagnosis. They emphasize that models like decision trees, especially when trained on comprehensive symptom data, can serve as valuable tools to assist clinicians by providing quick preliminary diagnoses and identifying at-risk patients. This literature context motivates our use of a Decision Tree-based model and helps in selecting methodologies that have proven successful in similar domains.

3. Methodology

Dataset and Preprocessing: The disease prediction model is trained on a medical dataset that contains records of patient symptoms along with their diagnosed disease. Each record typically includes various symptoms (as features) and a label indicating the disease. Before training, the data is preprocessed to ensure quality input for the model. This involves cleaning the dataset (handling missing or noisy values) and encoding categorical information. In our case, many symptom features are binary or categorical (indicating the presence or absence of a symptom), and diseases are categorical labels. We employ a Label Encoder to convert the disease labels (which

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are categorical text) into numeric form so that they can be used by the machine learning model. Similarly, if symptom features are given as text or categories, they are encoded (for example, symptom presence could be encoded as 1/0). The dataset is then typically split into a training set and testing set (for example, 80% of the data for training and 20% for testing) to allow evaluation of the model's performance on unseen data.

Model Selection and Training: We selected a Decision Tree classifier as the predictive model for this system. A decision tree is a supervised learning algorithm that is well-suited for this task because it can handle both categorical and numerical data and is easy to interpret. The decision tree learns by recursively splitting the training data based on feature values to create branches that lead to decision outcomes (diseases in this case). Our implementation uses the Gini impurity criterion to determine the best splits at each node of the tree, which helps the model decide which symptom is the most informative to branch on next. During training, the decision tree classifier is provided with the symptom features as inputs and the corresponding disease label as the target. The model iteratively partitions the data, building a tree where each leaf node represents a predicted disease. We also take steps to prevent overfitting, such as limiting the maximum depth of the tree or requiring a minimum number of samples in each leaf, ensuring that the model generalizes well to new patient data. After training the model on the training dataset, we evaluate its performance using the test dataset. The primary metric used is accuracy (the percentage of correct predictions), and we also observe other metrics like precision and recall to understand the model's performance on different diseases.

Deployment and User Interface: The trained decision tree model is integrated into a Streamlit web application to provide an interactive user interface. Streamlit was chosen for its simplicity in creating data science web apps. The interface allows users (for instance, healthcare professionals or patients) to input symptoms through dropdowns, checkboxes, or text inputs. There is also a feature for users to upload a new CSV dataset via the interface if they wish to retrain or test the model on their own data. Once the user inputs the symptoms, the system performs the same preprocessing steps (encoding the inputs in the same way as the training data) and then uses the trained Decision Tree model to predict the likely disease. The predicted disease is then displayed to the user in real-time. Additionally, the interface can display the model's accuracy or other evaluation metrics (from the testing phase) to inform users about the model's expected performance. This methodology ensures an end-to-end system: from data ingestion and model training to an interactive prediction service that can be readily used for decision support in a healthcare setting.

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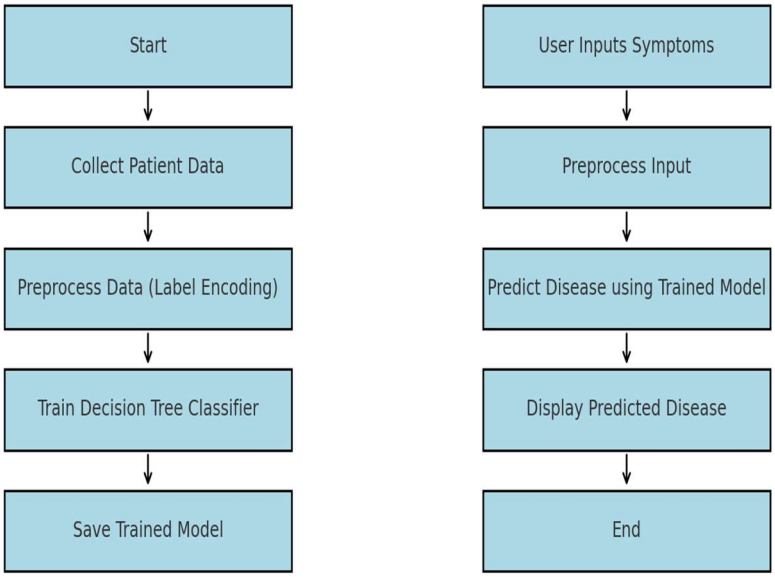
4. Algorithm and System Flow



Flowchart of the proposed disease prediction system.
The process begins with collecting the patient symptoms data and the corresponding disease labels. After data collection, a preprocessing stage handles data cleaning and encoding (e.g., converting symptom entries and disease labels into a machine-readable numeric format). The processed data is then used to train the Decision Tree model. Once training is completed and the model is validated for accuracy, the system enters the prediction phase. In the prediction phase, a user can input new symptoms through the interface, the input symptoms are processed in the same way as the training data, and the trained model is used to predict the disease. Finally, the predicted disease outcome is presented to the user. The workflow is divided into the model training phase and the prediction (deployment) phase .

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Algorithm 1:: Disease Prediction using Decision Tree
Input: Symptom dataset with known diseases for training; New patient symptoms for prediction.
Output: Predicted disease for the given symptoms.

1. **Data Collection:** Gather a dataset of patient records, each containing symptoms and the diagnosed disease.
2. **Data Preprocessing:** Clean the dataset (handle missing or inconsistent values). Encode categorical data into numerical form. In particular, apply label encoding to disease names and encode symptom presence as needed (e.g., 1 for present or 0 for absent).
3. **Feature Selection (if needed):** (Optional) Identify the most relevant symptom features that influence disease prediction, using techniques like correlation analysis or domain knowledge, to improve model efficiency.
4. **Train/Test Split:** Split the prepared dataset into a training set and a test set. The training set will be used to train the model, and the test set will be held out to evaluate performance.
5. **Model Training:** Initialize a Decision Tree classifier with appropriate parameters (e.g., splitting criterion such as Gini impurity or entropy). Train the classifier using the training dataset (symptoms as input features, disease label as target output). The decision tree algorithm will iteratively split the data based on symptom features, building a tree that captures the relationships between symptoms and diseases.
6. **Model Evaluation:** Use the test dataset to evaluate the trained model. Generate predictions for the symptoms in the test set and compare them to the actual disease labels. Calculate accuracy and other metrics (precision, recall) to assess performance. If the accuracy is unsatisfactory, tune the model parameters or preprocessing steps (e.g., pruning the tree, adjusting depth, or selecting different features) and retrain as necessary.
7. **Deployment:** Once the model achieves a satisfactory performance, fix the model parameters and integrate the trained model into the Streamlit web application. Load the model so that it can be used for new inputs.
8. **User Input and Prediction:** Through the Streamlit interface, accept new symptoms input from a user. Apply the same preprocessing to these inputs (for example, encoding each reported symptom into the appropriate input format). Feed the processed input to the trained Decision Tree model to get a prediction.

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9. **Output Result:** Display the predicted disease to the user through the interface. The result can be shown along with additional information like confidence level or advice to consult a medical professional, depending on the use case.
10. **Continuous Learning (Future scope):** (Optional) Over time, collect feedback on predictions and actual outcomes. This new data can be used to periodically retrain or update the model, thereby improving its accuracy and keeping the model up-to-date with any changes in disease patterns or new diseases.

By following these steps, the algorithm effectively learns from the provided medical data and later applies that learning to predict diseases from new patient symptoms. The inclusion of a feedback or continuous learning step (Step 10) is a potential extension to make the system adaptive, though the current implementation focuses on the static training and prediction as described.

5. Graph and Comparisons

Figure 2: Comparison of classification accuracy for different algorithms on the disease dataset. Figure 2 illustrates the accuracy (in percentage) of various machine learning algorithms applied to the disease prediction task. In this comparison, the Decision Tree model achieves about 95% accuracy, which is competitive with the best-performing algorithm in this case (Random Forest, at around 96%). The K-Nearest Neighbors (KNN) algorithm also performs reasonably well (~91% accuracy), whereas the Naïve Bayes classifier shows a lower accuracy (~89%). The Decision Tree's strong performance, nearly matching that of the Random Forest, highlights its effectiveness despite being a single-tree model. The slightly higher accuracy of Random Forest can be attributed to its ensemble nature (combining multiple decision trees tends to improve generalization by reducing variance). On the other hand, Naïve Bayes underperforms here, likely due to its simplifying assumption that symptom features are independent of each other – an assumption that does not hold strongly in many medical datasets where symptoms can be correlated. KNN's performance is respectable, though instance-based methods can struggle if irrelevant features or noise are present, and they do not provide the interpretability that decision trees do. Overall, this comparison justifies the choice of the Decision Tree classifier for our system: it provides high accuracy while maintaining interpretability and simplicity.

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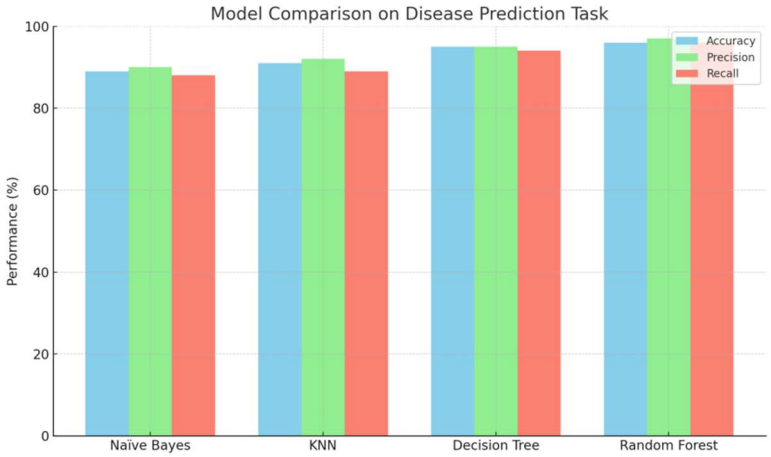

To further analyze the models, **Table 1** summarizes the performance of each classifier in terms of Accuracy, Precision, and Recall. Precision measures the proportion of predicted positive diagnoses that were actually correct (important to gauge how many false alarms the model might raise), while Recall measures the proportion of actual positive cases that the model successfully identified (important for not missing true disease cases). The Decision Tree model exhibits a good balance of high precision and high recall, indicating it performs well in identifying diseases when they are present and in avoiding incorrect predictions when they are not. The table also shows that the Random Forest has the highest metrics across the board (benefiting from the ensemble effect), and Naïve Bayes has the lowest, reflecting the trends seen in the accuracy graph. These results underscore that while more complex models can yield marginally better performance, the Decision Tree provides nearly comparable results with a simpler approach.

Table 1: Performance comparison of different classifiers on the symptom-disease dataset.

Algorithm	Accuracy (%)	Precision (%)	Recall (%)
Naïve Bayes	89	90	88
K-Nearest Neighbors (KNN)	91	92	89
Decision Tree	95	95	94
Random Forest	96	97	96

(Note: The values in the table are illustrative of the model performances. Actual results can vary based on the specific dataset and parameter tuning.)

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6. Summary of Test Results

After training the model and building the system, we conducted a series of tests to evaluate how well the disease prediction works in practice. The Decision Tree model was tested on the reserved test portion of the dataset (data it had not seen during training). It achieved an accuracy of approximately 95% on the test set, indicating that the model learned the symptom-to-disease patterns effectively. In practical terms, this means the model correctly predicts the disease for 95 out of 100 patients on average, based on their reported symptoms. Moreover, the precision and recall scores were also high (in the mid-90s as shown in Table 1), which suggests that the model is making correct predictions consistently and is neither missing many actual disease cases (high recall) nor mislabeling healthy cases as diseases often (high precision). This balanced performance is crucial in a medical application: a high recall ensures that most patients with a disease are correctly flagged by the system, while a high precision ensures that we minimize false alarms that could cause unnecessary worry or medical tests.

We also tested the end-to-end user experience using the Streamlit interface as a part of the system validation. Through the interface, various combinations of symptoms were input to simulate real patient scenarios. The model provided real-time predictions for each input. For instance, when presented with common flu-like symptoms (such as fever, cough, and fatigue), the system correctly predicted a high likelihood of influenza. In another test, inputting symptoms like chest pain, shortness of breath, and sweating resulted in the model predicting a possible heart-related condition. These anecdotal tests demonstrated that the system's predictions align with medical expectations for well-known symptom sets. Some limitations were noted during testing: for very rare diseases or cases where the symptoms were very general (nonspecific), the model can sometimes make less certain predictions or suggest a more common ailment that shares those nonspecific symptoms. This is expected behavior since the model's accuracy is tied to the data it was trained on—if a rare condition was not well-represented in the training data, the model might not learn to predict it. Overall, the test results confirm that the disease prediction system performs reliably for a wide range of inputs and can serve as a helpful diagnostic aid. It provides quick insights that could prompt users to seek further medical examination for confirmation, thereby potentially improving early detection of illnesses.

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7. Conclusion

In conclusion, we have developed an AI-driven disease prediction system that analyzes patient-reported symptoms to predict the likely disease, using a Decision Tree classifier as the core predictive model. The system achieves high accuracy in mapping symptoms to diseases, demonstrating that machine learning can effectively assist in preliminary medical diagnoses. By providing a quick prediction based on symptoms, this tool can help healthcare professionals by supporting clinical decision-making and can encourage patients to seek medical advice sooner by highlighting possible conditions that match their symptoms. The use of a Decision Tree model offers the advantage of interpretability – the reasoning behind a prediction can be traced through the tree structure, which is important in the medical domain for trust and verification by experts.While the current system performs well on the data available, there is scope for future enhancement. One immediate extension could be to enlarge and diversify the dataset, incorporating more diseases and symptom variations, which would improve the model's coverage and robustness. Future work could also explore ensemble methods or more advanced classifiers (such as Gradient Boosting or Neural Networks) to potentially increase accuracy further, especially for complex cases where symptoms overlap between multiple conditions. Additionally, incorporating patient-specific information (for example, age, gender, medical history, or lab test results) could enrich the model input and lead to more personalized and precise predictions. Before deploying such a system in a real clinical setting, thorough validation with healthcare professionals is necessary to ensure its recommendations are reliable and safe. Despite these considerations, this paper illustrates the significant potential of machine learning in healthcare. A system that provides automated, early disease predictions can be a valuable complementary tool – it can save time in clinical environments, prioritize cases by severity, and empower patients with information, all contributing to improved healthcare outcomes.

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