Musik in bayern
ISSN: 0937-583x Volume 90, Issue 11 (Nov -2025)
https://musikinbayern.com **DOI https://doi.org/10.15463/gfbm-mib-2025-*538***

Disease Prediction and Medicine Recommendation system

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To Cite this Article
[1]Dr. Harikrishna Bommala, [2]Dr. Mani Deep Karumanchi, [3]Pattipati Naveen Kumar, [3]Sonali Vishnu Katke, [3]Kanna Praveen Kumar, [4]Dr. A. Naresh" **Disease Prediction and Medicine Recommendation system**" *Musik In Bayern, Vol. 90, Issue 11, Nov 2025, pp468-476*

Article Info
Received: 30-09-2025 Revised: 08-11-2025 Accepted: 18-11-2025 Published: 29-11-2025

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Abstract— **The proposed project aims to develop a disease prediction and medicine recommendation system using machine learning techniques. It will analyze patient data and provide actionable insights for healthcare providers. The system will predict diseases based on patient demographics, medical data and other relevant factors. It will also recommend medications and treatment plans based on diagnosed diseases. The project will involve data collection and preprocessing, model development, system implementation, evaluation, validation, deployment and integration. By harnessing the power of machine learning and data analytics, it has the potential to revolutionize healthcare delivery, improve patient outcomes, and drive advancements in medical research and practice.**

Keywords— **Disease prediction, Medicine recommendation, Healthcare, Demographics data.**

I. INTRODUCTION

In today's healthcare landscape, the demand for data mining techniques has become increasingly apparent. The ability to extract valuable insights from large databases empowers medical practitioners to make informed decisions and improve the quality of healthcare services. Through classification methods, such as decision trees, random forests, and Naïve Bayes algorithms, healthcare professionals can effectively analyze patient data and assist in early diagnosis and treatment planning. Various diseases and health-related issues, including malaria, dengue, impetigo, diabetes, migraine, jaundice, and chickenpox, pose significant threats to individuals' health and well-being, potentially leading to fatal outcomes if left untreated. By harnessing the power of data mining, the healthcare industry can enhance decision-making processes by uncovering hidden patterns and relationships within vast databases of patient information.

The aim of this paper is to present an automated system developed to discover and extract valuable knowledge related to diseases from historical databases containing disease-symptom records. Utilizing established data mining algorithms such as decision trees, random forests, and Naïve Bayes, our system employs rule sets derived from these algorithms to analyze patient data and predict disease outcomes. Through this project, we seek to address the pressing need for efficient disease prediction and healthcare decision support systems. By leveraging data mining techniques, our system aims to improve the accuracy and timeliness of diagnoses, ultimately leading to better patient outcomes and enhanced healthcare delivery. Additionally, we aim to highlight the practical applications of decision trees, random forests, and Naïve Bayes algorithms in healthcare settings, demonstrating their potential to revolutionize medical decision-making processes.

II. LITERATURE SURVEY

An Approach for Developing Diabetes Prediction and Recommendation System was developed by Saima Sultana, Abdullah Al Momen, Mohoshi Haque, Mahmudul Hasan Khandaker, Nazmus Sakib. The severity and impact of diabetes on individuals and society, underscoring the importance of early diagnosis and prediction in managing the disease. The study employs Multiple Linear Regression (MLR) to predict diabetes based on basic medical information, achieving an accuracy of 83%. Additionally, the article proposes using Reinforcement Learning to provide suggestions for diabetic patients to better control the disease. The overarching message is that while diabetes cannot be cured once developed, it can be managed effectively, especially if diagnosed early. The proposed system aims to empower individuals by predicting their likelihood of developing diabetes, allowing them to make lifestyle changes or seek medical intervention accordingly. Ultimately, the goal is to reduce the prevalence of diabetes and associated mortality rates.

A Medical-History-Based Potential Disease Prediction Algorithm was developed by Wenxing Hong, Ziang Xiong, Nannan Zheng, and Yang Weng.The journal article explores the synergy between healthcare big data analysis and deep learning technology in predicting potential diseases based on patients' medical histories. Introducing a novel deep-learning-based recommendation algorithm, the "medical-history-based potential disease prediction algorithm," the paper aims to mitigate delays in treatment caused by unclear symptom descriptions or limited professional knowledge. Experimental results showcase the algorithm's efficacy in enhancing prediction accuracy.This underscores the algorithm's contributions, emphasizing its adeptness in handling both high-order relations among disease features and low-order combinations of diseases, thereby enhancing its comprehensiveness. Noteworthy features include the use of attention networks to reduce noise and the joint learning of deep and factorization machine parts to effectively merge relations. Moreover, the conclusion advocates for the significance of accurate potential disease prediction in aiding medical examinations and suggests future research directions.

Recommender systems in the healthcare domain: state-of-the-art and research issues was developed by Thi Ngoc Trang Tran Alexander Felfernig Christoph Trattner Andreas Holzinger. The article provides a systematic overview of existing research on healthcare recommender systems, delving into various recommendation scenarios and approaches, including food, drug, health status, healthcare service, and healthcare professional recommendations. Additionally, the article offers working examples to elucidate recommendation algorithms and discusses future challenges in the development of healthcare recommender systems. The authors highlight the emergence of health recommender systems as valuable tools for supporting patients and healthcare professionals in making informed decisions. They summarize the recommendation scenarios covered

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in the article and the diverse algorithms employed, including collaborative filtering, content-based, knowledge-based, hybrid, and context-based recommendations, as well as various machine learning techniques.

A Survey of Recommendation Systems: Recommendation Models, Techniques, and Application Fields was developed by Hyeyoung Ko, Suyeon Lee, Yoonseo Park and Anna Choi. The intersection between advanced technical aspects and business applications. By analyzing a significant number of articles and conferences, the study systematically categorizes recommendation models and technologies, shedding light on emerging trends over the past decade. It underscores the critical need for diverse recommendation systems to address the growing complexity of item information in today's web and application services landscape. Moreover, it emphasizes the transformative potential of real-time data in enhancing recommendation outcomes, particularly in healthcare contexts, where timely advice can significantly impact patient care. The study also delves into the evolution of recommendation system models, with a notable shift towards hybrid approaches that leverage the strengths of both content-based and collaborative filtering methods. Additionally, it explores the expanding role of neural network technology in recommendation systems, signaling a promising avenue for future research and development. Furthermore, the study provides valuable insights into the practical applications of recommendation systems in real-world business contexts, demonstrating their instrumental role in driving growth and innovation. Overall, it offers a comprehensive overview of the evolving landscape of recommendation systems, while paving the way for further exploration into tailored solutions for specific business needs.

An approach for prediction of diseases to suggest doctors and hospitals to patient based on recommendation system was developed by Shashidhar V, Pradyumna A Kubear, Manoj M, Jalapreetha J, Malashree.This journal emphasizing the critical role of patient satisfaction in assessing the efficacy of medical services. It stresses the importance of leveraging medical data analysis to enhance patient care and optimize resource allocation in hospitals. Furthermore, the project introduces an innovative approach to disease prediction, employing machine learning algorithms like KNN, random forest, and decision trees to empower users with proactive healthcare recommendations. Additionally, the system facilitates seamless communication between patients and healthcare providers, allowing for real-time updates of symptoms and continuous improvement of service quality. By encouraging user reviews, the platform fosters a collaborative environment aimed at delivering personalized and effective healthcare solutions. Additionally, its comprehensive approach to healthcare management extends beyond disease prediction to encompass holistic care coordination, ensuring that patients receive the support and resources they need throughout their healthcare journey. In essence, this project represents a paradigm shift in healthcare delivery, where data-driven insights and patient-centered care converge to drive positive outcomes and revolutionize the healthcare landscape.

Disease Prediction and Doctor Recommendation System using Machine Learning Approaches was developed by Anand Kumar, Ganesh Kumar Sharma, U.M. Prakash.This journal represents a significant advancement in healthcare technology, offering a streamlined approach to disease prediction and diagnosis. By leveraging classification algorithms and an interactive interface, the system provides a user-friendly platform for patients to input symptoms and receive accurate disease predictions. Furthermore, its ability to recommend appropriate medical specialists adds value by guiding patients towards optimal care pathways.The project's potential to alleviate strain on healthcare facilities by reducing wait times and optimizing resource allocation. Additionally, the integration of data storage capabilities lays the foundation for future improvements and research endeavors. The proposed implementation of deep learning algorithms and expansion to mobile applications demonstrates a forward-thinking approach to enhancing accessibility and effectiveness.Overall, the project embodies the convergence of data science and healthcare, promising to revolutionize traditional diagnostic practices and improve patient outcomes. As advancements continue and technology evolves, the potential for such systems to reshape the healthcare landscape remains vast, offering hope for more efficient and personalized medical care for all.

III. DATASET AND PRE-PROCESSING

HIPPA provides protection for healthcare information. It is against the law to disclose a patient's medical records without that patient's consent. Government health records and databases required a number of licenses to access. As a result, we are employing datasets for our research that were easily accessible online and ready for download.

A. Data Gathering

For input, a sample of 4922 patient records with 41 diseases and 133 columns as symptoms amidst which the user can give the symptoms his processing as the input.

B. Data preprocessing

The data mining technique that transforms the raw data or encodes the data to a form which can be easily interpreted by the algorithm is called data preprocessing. The preprocessing techniques used in the presented work are:

Data Cleaning: Data is cleansed through processes such as filling in missing value, thus resolving the inconsistencies in the data.

Data Reduction: The analysis becomes hard when dealing with huge database. Hence, we eliminate those independent variables(symptoms) which might have less or no impact on the target variable(disease). In the present work, 95 of 132 symptoms closely related to the diseases are selected**.**

IV. METHODOLOGY

Models Selected

The system is trained to predict the diseases using three algorithms

- Disease Tree Classifier
- Random forest Classifier
- Naïve Bayes Classifier

Initially, each classifier was trained separately to create the prediction model. Subsequently, the results were analyzed, given the critical importance of accurately predicting diseases for proper patient treatment. Different prediction levels were assigned based on the consensus of multiple classifiers. However, upon examination, it was observed that in numerous cases, all three classifiers predicted the same diseases based on symptoms. Additionally, there were instances where two classifiers agreed on a specific disease while the third classifier predicted a different one. we established different prediction levels based on the collective outputs of multiple classifiers. If all classifiers predict the same disease, it's categorized as a High Level prediction. Conversely, if a disease is predicted by two classifiers but not the third, it's considered an Average Level prediction. In cases where all classifiers predict different diseases, the final prediction is determined by the Random Forest classifier due to its higher accuracy and absence of overfitting issues. Table 1 provides descriptions of prediction levels for various diseases.

Table 1 Final Prediction and Level of Prediction of Diseases

ML Algorithm	**Disease (If all models predict the same disease)**	**Disease (If two models predict the same disease)**	**Disease (If all models predict different disease)**
Decision Tree	Hepatitis C	Allergy	Hepatitis B
Random Forest	Hepatitis C	Allergy	Chicken Pox
Naive Bayes	Hepatitis C	Drug Reaction	Drug Reaction
Final Prediction	Hepatitis C	Allergy	Chicken Pox
Prediction Level	Strong	Average	weak

The block diagram of the proposed architecture is depicted in Figure 2. The description and working of the algorithms are given below.

Musik in bayern
ISSN: 0937-583x Volume 90, Issue 11 (Nov -2025)
https://musikinbayern.com DOI https://doi.org/10.15463/gfbm-mib-2025-*538*

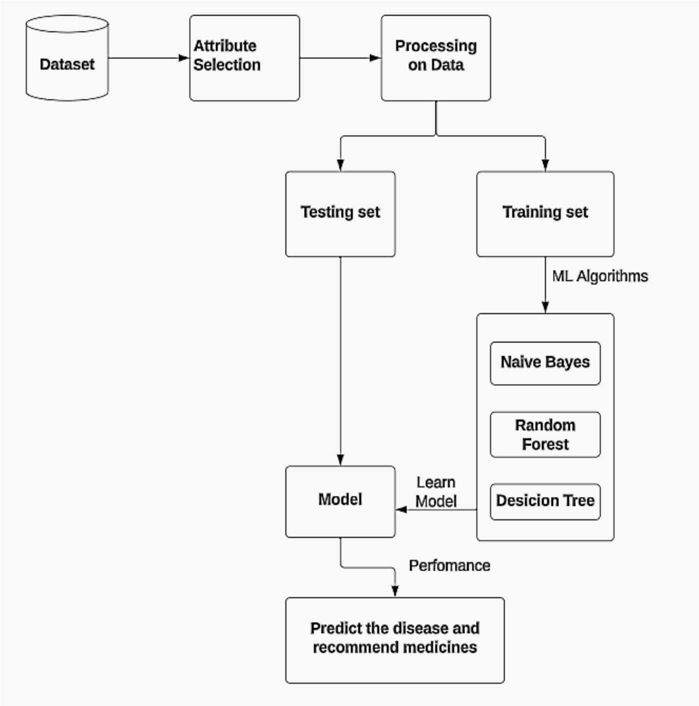

Fig. 1 Block Diagram of the Model

A. Decision Tree Classifier

The classification models built by decision tree resemble the structure of tree. By learning the series of explicit if-then rules on feature values (symptoms in our case), it breaks down the dataset into smaller and smaller subsets that results in predicting a target value(disease). A decision tree consists of the decision nodes and leaf nodes.

- Decision node: Has two or more branches. In our work presented, all the symptoms are considered as decision nodes.
- Leaf node: Represents the classification that is, the Decision of any branch. Here the Diseases correspond to the leaf nodes

Decision trees are a popular machine learning algorithm used for both classification and regression tasks. The algorithm partitions the feature space into regions, each associated with a specific class label or regression value. Here are the basic formulas and concepts associated with decision trees

Entropy:

Entropy measures the impurity or disorder of a set of examples.

The formula for entropy is:

$$H(S) = -\sum_{i=1}^{c} p_i \log_2 (p_i)$$

where S is the set of examples, c is the number of classes, and p_i is the probability of class i in set S.

Information Gain:

Information gain measures the effectiveness of an attribute in classifying examples.

The formula for information gain is:

$$IG(D, A) = H(D) - \sum_{v \in Values(A)} \left|\frac{D_v}{D}\right| H(D_v)$$

where D is the dataset, A is an attribute, D_v is the subset of (D) for which attribute A has value v, and H(D) is the entropy of dataset D.

Gini Impurity:

Gini impurity measures the probability of misclassifying an example if it were randomly labeled.

The formula for Gini impurity is

$$Gini(D) = 1 - \sum_{i=1}^{c} p_i^2$$

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where D is the dataset, c is the number of classes, and p_i is the probability of class i in dataset D.

Decision Tree Splitting:
The decision tree algorithm recursively splits the dataset based on the attribute that maximizes information gain or minimizes impurity until a stopping criterion is met (e.g., maximum tree depth, minimum number of samples per leaf). The splitting process continues until all leaves are pure (contain instances of only one class) or until a stopping criterion is met.

B. Random Forest

Gini Impurity:

$$Gini(X_m) = 1 - \sum_{i=1}^{c} p(i|X_m)^2$$

where:
- $Gini(X_m)$ is the Gini impurity for node (X_m)
- $p(i|X_m)^2$ is the proportion of instances of class i among the training instances in node X_m.
- c is the number of classes.

Information Gain :
$IG(X,f) = H(X) - H(X|f)$
where:
- IG(X,f) is the information gain achieved by splitting dataset (X) on feature (f).
- H(X) is the entropy of dataset (X).
- H(X|f) is the conditional entropy of dataset X given feature f.

Out-of-Bag (OOB) Error Estimation:
The out-of-bag error can be calculated as the error rate of the model on the training instances that were not used during the construction of a particular tree within the Random Forest.
Random Forest Prediction:
In classification tasks, the Random Forest predicts the class with the most votes among the individual decision trees. In regression tasks, it predicts the average of the outputs from all trees. These formulas capture the essence of how Random Forest operates, from constructing decision trees to making predictions and estimating error rates.

C. Navie Bayes

Naive Bayes is a probabilistic classification algorithm based on Bayes' theorem with the "naive" assumption of independence between features. Here are the key formulas and concepts associated with Naive Bayes:
Bayes' theorem calculates the probability of a hypothesis (class label) given the evidence (features).
The formula for Bayes' theorem is:

$$P(C_k|X) = \frac{P(X|C_k) \times P(C_k)}{P(X)}$$

where:
$P(C_k|X)$ is the probability of class C_k given the evidence X,
$P(X|C_k)$ is the likelihood of evidence given class C_k,
$P(C_k)$ is the prior probability of class C_k
P(X) is the probability of evidence (often treated as a constant).

Naive Assumption:
Naive Bayes assumes that the features are conditionally independent given the class label.
This simplifies the calculation of $P(X|C_k)$ to the product of the individual probabilities of each feature given the class:
$P(X|C_k) = P(x_1|C_K) \text{ X } P(x_2|C_K) \text{ x } \ldots\ldots\ldots\text{x } P(x_n|C_k)$
Where x_i represents the individual features of the input X.

Maximum A Posteriori (MAP) Estimation:
In practice, Naive Bayes classifies instances by choosing the class with the highest posterior probability.
The formula for MAP estimation simplifies to:

$$\hat{y} = \arg max_k P(C_k) \times \prod_{i=1}^{n} P(x_i|C_k)$$

where is $\hat{y}$ the predicted class label, and $P(C_k)$ and $P(x_i|C_k)$ are estimated from the training data.

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https://musikinbayern.com DOI https://doi.org/10.15463/gfbm-mib-2025-*538*

Different Variants:

There are different variants of Naive Bayes, such as Gaussian Naive Bayes, Multinomial Naive Bayes, and Bernoulli Naive Bayes, which handle continuous, discrete, and binary features, respectively. The probability distributions $P(x_i|C_k)$ differ depending on the type of features.

V. RESULTS AND ANALYSIS

The user enters five symptoms into the graphical user interface. When the "None" option is chosen, the user is presented with a list of symptoms to choose from. The user can list up to five symptoms he/she is experiencing. After the symptoms have been provided, the algorithm is chosen. The symptoms are processed and the disease as output for the algorithm chosen. Along with the predicted disease, it recommends the medication, description of that disease, diet to follow and also precautions to take.

GUI Result

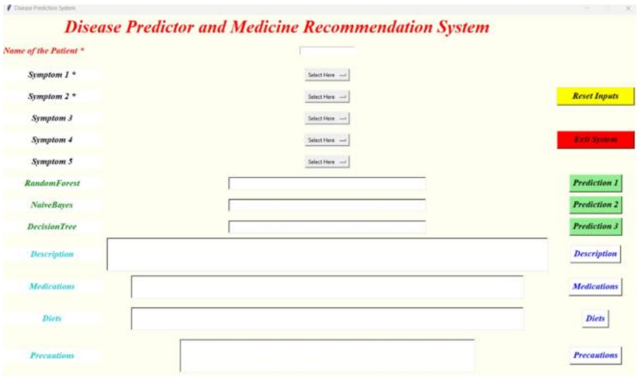

Fig.2 A disease prediction GUI with no data.

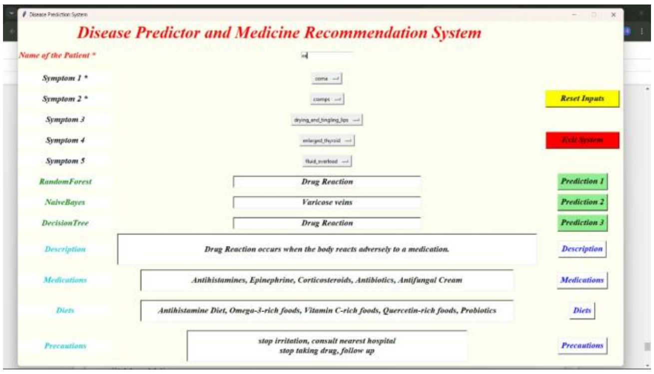

Fig.3 Predicted result

Once the symptoms are given, the algorithms are to be selected. As the algorithms are selected, the symptoms are processed, and the disease is searched based on the rule set that has been defined in the Methodology section.

The Random Forest Algorithm demonstrated robust performance in disease prediction tasks, leveraging its ensemble learning approach to handle complex datasets and achieve high accuracy rates. Its ability to mitigate overfitting and handle both numerical and categorical data proved advantageous in identifying patterns and predictive markers for various diseases .Emerged as a promising approach for drug recommendation, leveraging its ability to analyze patient data and identify associations between patient profiles and treatment outcomes. By considering factors such as genetic predisposition, comorbidities, and treatment response data, Random Forest-based drug recommendation systems can tailor treatment regimens to suit the unique needs of each patient, thereby maximizing therapeutic efficacy and minimizing adverse effects.

Both Decision Tree and Naive Bayes algorithms exhibited limitations in disease prediction and drug recommendation tasks. Decision Tree showed moderate performance, yet its susceptibility to overfitting limited effectiveness in nuanced predictions. Similarly, Naive Bayes, while computationally efficient, struggled with complex scenarios due to its assumption of feature independence. In drug recommendation tasks, both algorithms lacked the ability to capture intricate patient-treatment relationships. While Decision Trees offered insights into simple decision boundaries and Naive Bayes provided efficiency, their effectiveness in nuanced treatment recommendations was compromised. These findings underscore the necessity of employing more sophisticated algorithms, like Random Forest, for comprehensive disease prediction and personalized drug recommendation in healthcare.

After training, the system was tested on 41 new patients records considering 132 symptoms. The accuracy score is given as by

Table2 Accuracy's for each algorithm

Algorithm	Accuracy
Decision Tree	0.9354838709677419
Random Forest	0.9512195121951219
Navie Bayes	0.9431818181818182

VI. CONCLUSION

The study highlights the immense potential of Random Forest algorithms in transforming disease prediction and medicine recommendation tasks with health guidance. Their capability to effectively manage complex datasets and prevent overfitting addresses critical challenges in accurately diagnosing diseases and recommending optimal treatment strategies. Moreover, Random Forest's adeptness in capturing intricate relationships between features enhances its utility in deciphering the multifaceted nature of medical data. However, there remains a pressing need for further exploration into the integration of diverse ML algorithms and advanced techniques. Additionally, the incorporation of supplementary features and data sources holds promise for augmenting the precision and efficacy of disease prediction and drug recommendation systems. By delving deeper into these avenues, future research endeavors can unlock new insights and propel the evolution of personalized healthcare to unprecedented heights, ultimately benefiting patients and healthcare providers alike.

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