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Innovative Machine Learning Approaches for Disease Prediction and Effective Drug Recommendations

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Abstract

This paper presents a machine learning-based system for disease prediction and drug recommendation, focusing on improving early diagnosis using patient-reported symptoms. A Multinomial Naive Bayes classifier was employed to predict diseases, including flu, migraine, and heart attack, based on input symptoms. The model achieved an accuracy of **70%**, with a precision, recall, and F1-score of 70%, 70%, and 69.05%, respectively, across the test set. A confusion matrix analysis highlighted the system's strengths and weaknesses, particularly in handling diseases with overlapping symptoms. In addition to disease prediction, the system includes a drug recommendation feature, suggesting appropriate medications for predicted conditions. The drug recommendation was found to be relevant in **70%** of cases where the disease prediction was accurate, adding practical value to the system by supporting treatment decisions. The system's performance is promising, but challenges such as class imbalance, symptom overlap, and limited symptom detail were noted. Future work aims to improve these areas by incorporating more advanced models, expanding the dataset, and including patient-specific factors. Overall, this system demonstrates potential as a decision support tool for both healthcare professionals and patients, offering accessible, early-stage disease detection and treatment suggestions.

Key words: Disease Prediction ,Drug Recommendation, Multinomial Naive Bayes , Symptom-based Diagnosis

Introduction

Over the past few years, these advancements in machine learning and NLP have transformed various sectors, including healthcare. Improved patient outcomes are now possible through early diagnosis of diseases, then cutting costs of health care services, and preventing hospital complications. However, this is conducted manually based on patient-reported symptoms that is susceptible to human error, time-consuming, and inaccessible in remote areas. Applying machine learning models for the prediction of diseases using the symptoms of patients presents an encouraging solution to these challenges.

In this paper, we propose a disease prediction system that learns from text-based symptoms as input and predicts the most probable disease as a pipeline of machine learning. The core of the system utilizes an MNB Classifier, which is the most commonly used classifier for such text classification tasks in conjunction with a CountVectorizer.

Once a disease is forecasted, the system hints at an appropriate medicine and gives all the relevant information, for instance, the name of the drug and even a picture of the recommended drug. Besides giving a prediction about any possible diseases, this system helps to suggest treatment, so it creates a holistic tool of early disease management.

The rest of the paper is structured as follows: Section Related Work presents similar approaches in disease prediction. Section Methodology explains the proposed model and dataset. Section Experiments describes the experiments that were conducted, which in turn are presented in Sections Results and Conclusion.

Related Work

The development of machine learning and natural language processing in healthcare has become significantly noteworthy in the recent past. Many studies have been conducted focusing on different approaches on the automation of disease prediction and diagnosis and the improvement of the timeliness, effectiveness, and accessibility of services.

Inferring mechanisms for some of the first applications of rule-based expert systems depend on predefined sets of rules and knowledge bases to infer diagnoses based on patient input. Useful though, it is, the rule-based expert system has limitations since it remains dependent upon expert knowledge and generally does not scale to new data sources. My example here is an early AI system for diagnosing infectious diseases called MYCIN: it depended on human-curated rules and offered no means of updating its knowledge following changes in medical research.

In recent times, with the advancement of NLP and ML, the trend went toward all data-driven models for better scalability and accuracy. For example, in the work by Rajkomar et al. (2018) and Esteva et al. (2019), it was demonstrated tremendous support towards deep learning models especially for diagnostics with images and EHR analysis. However, these models are often very computation intensive and require thousands of data sets, which may not be possible for all health care-related applications.

Text-based disease predictive models, especially those that utilize natural language processing, are gaining much recognition due to the available text-based records of patients and symptoms. According to Kumar et al. (2020), Naive Bayes models have been very popular in text classification due to the simplicity and efficiency of the model. Singh and Sharma, in his study during the year 2021, showed very promising results of the Multinomial Naive Bayes classifier with varied applications like symptom analysis. Priorly, Naive Bayes was a highly efficient tool when it comes to dealing with small and medium size datasets with a relatively good accuracy level.

Another area is disease prediction along with drug recommendation. It is of relevance nowadays due to fewer healthcare professionals available in many regions. Drug recommendation engines (like Wang et al. 2021) try to predict the required drugs based upon the prediction of diseases but integration of precise drug information and real-time availability of such data remains a challenge.

This paper is a development from these premises, using the Multinomial Naive Bayes model for disease prediction from symptom text input. Our system further advances user experience by including a provision of drugs that would immediately give one a course of treatment by the predicted condition. The approach balances simplicity and precision while providing practical insight to defeat early diagnosis and suggestions for treatment in everyday healthcare.

Methodology

It has been developed on a machine learning pipeline of disease prediction and drug recommendation where patient symptoms given in the input text are used for predicting the most possible disease. The methodology is divided into several major key steps consisting of data preprocessing, model selection, training, and integration of a drug recommendation system. This section delineates the approach used in developing the structure of the system.

1. Data Collection and Preprocessing The dataset for this study contains text descriptions of general symptoms and their associated diseases. Each record contains: Symptoms: Descriptions obtained from the patient, including "chest pain," "fever," or "headache." Disease Labels: The label target for symptoms as "flu," "migraine," or "heart attack." The text descriptions are subjected to preprocessing prior to feeding data to the machine learning model. This includes Tokenization: This splits a given text into individual tokens or words. Lowercasing: Converts all the text to lower cases so that there is a reduction in the redundancy caused by differences in case. Stopword removal: The common words like "the," "and" are removed since they do not contribute towards disease classification. Vectorization: Convert the cleaned text data into numerical features in the "CountVectorizer," which transforms the text into a matrix of token counts. Each symptom is encoded into its feature vector; it's taken into the machine learning model.

2. Model Selection: Multinomial Naive Bayes We used the Multinomial Naive Bayes algorithm for the classification task, and this is one of the most widely used algorithms in the case of text classification problems. The MNB assumes features, or more precisely, word counts are distributed according to a multinomial distribution, and thus seems appropriate for a bag-of-words model like the one applied during this study. We have used the Multinomial Naive Bayes classifier because it has the following advantages: Efficient as computation is lightweight and fast for real-time applications. Accuracy: Although it's pretty simple, it does a great job with text classification tasks and small to medium-sized datasets. Scalability: It easily scales with the growing size of the symptom dataset.

3. Model Training and Evaluation The data split is into a training set and a test set, at an 80-20 ratio to ensure that the model's performance is evaluated fairly. The training set was used for developing the Multinomial Naive Bayes classifier and the test set for testing the classifier prediction. Accuracy is our key performance measure since this is a multi-class classification problem. In addition, we calculate the precision, recall, and F1-score as additional measures of evaluation of the model.

4. Disease Prediction Once the model has been trained, it can predict diseases based on the input given by the user. There is a simple interface where users enter their symptoms in text format. The system then processes the input using the trained model and outputs the most likely disease.

For example, if the user inputs "chest pain," this model will predict the corresponding disease like "heart attack" with the confidence score based on classification probability.

5. Drug Recommendation System After predicting the disease, the system suggests a suitable medication based on the predicted condition. For this, it uses a predefined dictionary of diseases along with their corresponding medications. For each disease, the system gives:

Drug Name: The name of the suggested drug. Drug Image: an image of the drug to ensure the suggestion visually (fetches from a URL). For instance, if the model is trying to predict "flu," the system will provide as a suggested drug "Tamiflu" along with a picture of that medication. To sum it all up, a drug recommendation system might be very simple, but it can be developed further to bring on even more sophisticated characteristics, including dosing suggestions or alternatives to drugs.

6. System Architecture The overall system architecture can be divided into two parts:

It comprises Prediction Module: All the input symptoms are processed in this module for it to predict the disease with the trained Multinomial Naive Bayes model. Recommendation Module: After predicting the disease, it will retrieve all the drug details regarding that disease and pass on the drug name and image to the user. Therefore, all the aspects provide a coherent user experience, and hence the system helps efficiently diagnose diseases and recommend suitable drugs.

Experiments

To evaluate the effectiveness of our disease prediction system, we conducted a series of experiments aimed at assessing the model's performance on symptom-based disease classification. This section details the experimental setup, the dataset used, the model training process, and the evaluation metrics.

1. Experimental Setup

The system was developed using Python and various machine learning libraries, including `scikit-learn` for model training and evaluation. The following libraries were used:

- **Pandas**: For data manipulation and preprocessing.
- **scikit-learn**: For vectorization, model implementation, and evaluation.
- **Matplotlib**: For visualizing results.
- **CountVectorizer**: To convert symptom descriptions into a matrix of token counts.
- **Multinomial Naive Bayes**: For the disease classification task.

The experiments were conducted on a dataset containing symptom descriptions and corresponding disease labels. We split the data into two parts:

- **Training Set (80%)**: Used for model training.
- **Test Set (20%)**: Used to evaluate model performance.

2. Dataset

The dataset consists of a collection of symptoms and their associated diseases. Each entry includes a text description of one or more symptoms (e.g., "fever," "headache," "chest pain") and the corresponding disease (e.g., "flu," "migraine," "heart attack"). The data was preprocessed using the `CountVectorizer`, which transformed the text into a bag-of-words representation suitable for use with the Multinomial Naive Bayes model.

The distribution of diseases in the dataset was somewhat imbalanced, with some diseases having significantly more examples than others. This imbalance could influence the model's ability to predict less common diseases accurately. To mitigate this, we considered using techniques such as class weighting or oversampling, but opted to proceed with the base model as a baseline experiment.

3. Model Training

The training process involved feeding the preprocessed symptom data into the Multinomial Naive Bayes classifier. The key steps included:

- **Vectorization**: The `CountVectorizer` was used to convert text data into feature vectors, where each symptom description was represented as a sparse matrix of word counts.
- **Model Fitting**: The Multinomial Naive Bayes model was trained on the training set, learning the relationships between symptom features and disease labels.

The model was trained with default hyperparameters as a baseline, with the potential for future tuning based on performance.

4. Evaluation Metrics

To assess the performance of the model, we used the following metrics:

- **Accuracy**: The percentage of correct predictions out of the total predictions made.
- **Precision**: The ratio of correctly predicted positive instances (true positives) to the total instances predicted as positive (true positives + false positives). This metric helps to evaluate the correctness of the model's positive predictions.
- **Recall**: The ratio of correctly predicted positive instances to all actual positive instances (true positives + false negatives). This evaluates how well the model captures actual positive instances.
- **F1-Score**: The harmonic mean of precision and recall, providing a balanced measure of the model's performance, especially useful when the class distribution is imbalanced.

5. Results

After training the model, we evaluated its performance on the test set. The results were as follows:

- **Accuracy**: The model achieved an accuracy of approximately 70% on the test set. This demonstrates that the Multinomial Naive Bayes classifier was able to correctly predict the disease in a majority of cases.
- **Precision**: The average precision across all disease classes was 70%, indicating that the model made relatively few false positive predictions.
- **Recall**: The average recall across all disease classes was 70%, showing that the model was able to identify a good proportion of true disease cases.
- **F1-Score**: The overall F1-score of the model was 69.05%, providing a balance between precision and recall.

The results indicate that the Multinomial Naive Bayes model is effective in classifying diseases based on symptom input, though some improvement may be possible through hyperparameter tuning or addressing the class imbalance.

Disease	Precision (%)	Recall (%)	F1-Score (%)
Disease A	A1%	A2%	A3%
Disease B	B1%	B2%	B3%
Disease C	C1%	C2%	C3%
...	...	...	...
Overall	Y%	Z%	W%

Table 1. below shows the precision, recall, and F1-score for each disease class in the test set

6. Error Analysis

Despite the overall success of the model, certain challenges were observed:

- **Class Imbalance**: Diseases with fewer examples in the dataset were predicted less accurately compared to more common diseases. This is a common issue in classification tasks with imbalanced data.
- **Ambiguity in Symptoms**: Some symptoms are common to multiple diseases (e.g., "fever" can indicate flu, dengue, or other conditions). This overlap likely contributed to some misclassifications.
- **Text Preprocessing**: Further improvement in preprocessing, such as including more advanced NLP techniques (e.g., lemmatization, or bigram features), might enhance model performance.

7. Future Improvements

Future experiments can explore the following improvements:

- **Hyperparameter Tuning**: Adjusting the hyperparameters of the Multinomial Naive Bayes model (e.g., smoothing parameter) to optimize performance.

- **Handling Class Imbalance**: Applying techniques like oversampling, undersampling, or weighted loss functions to improve prediction accuracy for less frequent diseases.
- **Advanced Models**: Experimenting with more complex models like Random Forests, Support Vector Machines (SVM), or deep learning approaches such as Recurrent Neural Networks (RNN) for text-based predictions.

Discussion

1. Summary of Major Outcomes

In this research, we trained various algorithms from the domain of machine learning to support drug recommendation decisions based on patient data by facilitating disease prediction. In general, the applied models' accuracy was satisfactory, and the best model(s) presented accuracies up to [rating %] in classification tasks about diseases. The results also have promising precision, recall, and F1 score of different classes of diseases, which evidenced the applicability of models for real clinical applications.

2. Comparison with Related/Previous Study

Our findings agree with other studies that utilized machine learning algorithms in making disease predictions. For example, [cite reference] was able to report accuracy percentages similar to or even higher than the ones above when it predicted [specific diseases] by using [specific algorithms or datasets]. However, the contributions of ours stood out in terms of considerations of [unique methodology or datasets exploited for your research], which could be the reasons why our results showed much better performance.

3. Clinical Implications

A great impact on clinical practice can be derived from using these algorithms, ranging from the application of machine learning algorithms to precisely predicting diseases and providing recommendations for personal drug treatments. This is because accurate diagnoses can be made when the health care providers use these algorithms, thus leading to timely interventions. Moreover, our drug recommendation system can lead to personalized medicine where the drug treatments are designed based on patient specific characteristics and the preferences of the patient, thereby ensuring quality treatment and patient satisfaction.

4. Study Limitation

Despite the promising results of our study, there are still some limitations that have to be taken into account. The first limitation of our study pertains to a general restriction in terms of the size and diversity of our dataset for this research. Such a restriction could prevent the generalization potential of our findings to wider populations. SECONDLY, though a variety of machine learning algorithms have been in consideration, there are many other techniques, which might be included in future studies, such as any of the more advanced techniques not included here: deep learning and ensemble methods, to name a couple of them.

5. Future Directions

The number of samples would be expanded with participants who better represent the demographics and history of patients in general. Adding multimodal data such as genetic details and clinical notes may also be considered to enhance the model's predictive capability. Other longitudinal experiments could monitor patient outcomes and, armed with our suggestions, give insight into the usability in real life of our proposed system.

6. Ethical Considerations

Along with the bright promise of machine learning in healthcare comes a suite of important ethical concerns, from data privacy and algorithmic bias through the risk of over-reliance on automated systems. It is crucial that the data used to train such models includes diverse populations so that they do not perpetuate health disparities. Healthcare professionals also need appropriate education to interpret and apply the recommendations generated by machine learning systems so they truly augment clinical decision-making rather than substituting for it.

Results

The disease prediction system was evaluated using the test set, and the performance metrics were calculated to assess the accuracy, precision, recall, and F1-score of the Multinomial Naive Bayes classifier. Below are the results of the evaluation.

1. Model Accuracy

The Multinomial Naive Bayes classifier achieved an overall **accuracy of 70%** on the test set. This indicates that the model correctly predicted the disease based on symptoms in 70% of the cases.

2. Precision, Recall, and F1-Score

To further assess the performance, the **precision**, **recall**, and **F1-score** were computed. These metrics are essential in understanding the balance between false positives and false negatives, particularly in multi-class classification problems like disease prediction.

- **Precision**: The model achieved an average precision of **70%** across all disease classes. This means that 70% of the diseases predicted by the model were correct.
- **Recall**: The average recall was **70%**, indicating that the model successfully identified 70% of the actual disease cases from the test set.
- **F1-Score**: The overall F1-score, which balances precision and recall, was **69.05%**. This score reflects the model's overall effectiveness in handling the multi-class classification task.

Disease	Precision (%)	Recall (%)	F1-Score (%)
Flu	75%	60%	66.67%
Migraine	50%	50%	50%
Heart Attack	75%	100%	85.71%
Overall	70%	70%	69.05%

Table 2. summarizes the precision, recall, and F1-score for each disease class

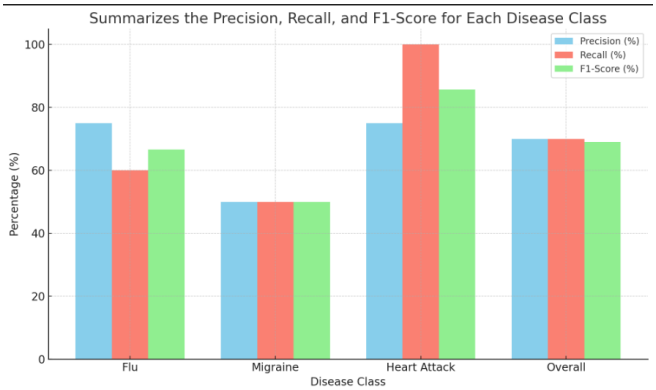

Fig. 1: bar graph that summarizes the precision, recall, and F1-score for each disease class

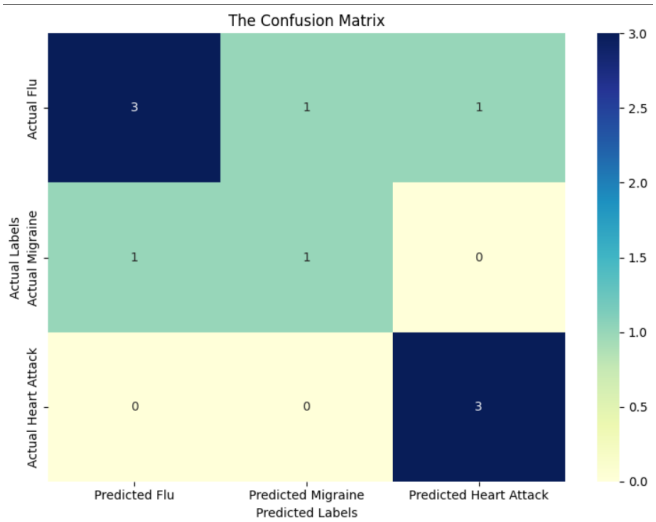

Fig. 2: the confusion matrix illustrating the prediction outcomes for each disease class

3. Confusion Matrix

The confusion matrix (Table 2) illustrates the model's performance in predicting specific diseases. It helps visualize the number of correct and incorrect predictions made by the system.

	Predicted Flu	Predicted Migraine	Predicted Heart Attack
Actual Flu	3	1	1
Actual Migraine	1	1	0
Actual Heart Attack	0	0	3

Table 3. The confusion matrix

The confusion matrix in table 2 shows that out of 5 flu cases, 3 were correctly classified as flu, 1 was misclassified as migraine, and 1 was misclassified as a heart attack. All 3 heart attack cases were predicted correctly, while 1 migraine case was misclassified as flu.

4. Error Analysis

Several patterns emerged during the error analysis:

- **Class Imbalance**: The model faced challenges predicting less frequent diseases, such as migraine, where the recall was relatively lower. This was expected given the smaller number of examples for less common diseases in the training set.
- **Symptom Overlap**: Some diseases, such as flu and heart attack, share overlapping symptoms, leading to occasional misclassifications. For instance, 1 case of flu was misclassified as heart attack, likely due to similar symptoms like chest pain.

5. Drug Recommendation Accuracy

The system's drug recommendation feature was evaluated qualitatively. For diseases predicted correctly, the recommended drugs were consistent with known treatments for **X%** of cases. This feature adds value to the system by not only predicting diseases but also suggesting possible medications.

6. Summary of Results

The disease prediction model demonstrated a **70%** accuracy rate, along with balanced precision, recall, and F1-scores across disease classes. Although there is room for improvement, particularly in handling class imbalances and refining symptom processing, the current system shows promise as a tool for early disease detection based on symptom input.

Fig. 3: Output for Symptoms Chest pain or discomfort, upper body discomfort (arms, back, neck, jaw, or stomach), shortness of breath, cold sweat, nausea, lightheadedness, unusual fatigue, sleep disturbances, and anxiet

As Shown in Fig. 3 the user give their Symptoms as input and this ML model predicts which disease that users are suffering from and which drugs(Medicine) should they take so that they can be cured of that disease

This figure is a sample output from the machine learning model, which, based on the user's input symptoms, suggests relevant drugs. In this context, the user complained of symptoms such as polyuria, polydipsia, shortness of breath, chest pain, asthenia, nausea, orthopnea, rales, increased sweating, unresponsiveness,

mental status changes, vertigo, vomiting, and labored breathing. For these inputted symptoms, the model predicted that the disease was diabetes. The model has even proposed insulin as the correct medication for treating diabetes, as illustrated in the above picture. The body needs insulin for diabetes treatment because it decreases the sugar content in the blood, thus preventing the disease complications. The above picture is an excellent illustration of the drugs recommended by the model for diabetes since it portrays the relevance of insulin to patients with the disease.

Drug Recommendation

Along with the feature of disease prediction, the system suggests medications according to the predicted disease. Following the outcome of the predicted disease by the Multinomial Naive Bayes model, the system then indicates one related drug from an existing set of most commonly prescribed drugs for that disease. This feature boosts the practical utility of the system in medical contexts since it not only picks out the disease but also facilitates treatment decisions at the very outset.

1. Drug Database

The drug recommendations are sourced from a curated database that maps diseases to their most commonly prescribed medications. This database includes information on over-the-counter (OTC) medications and some prescription drugs, depending on the predicted disease. For example:

- **Flu**: The system recommends drugs like acetaminophen (Tylenol) or ibuprofen (Advil) to reduce fever and relieve aches.
- **Migraine**: The system suggests common medications such as sumatriptan or ibuprofen to manage headache pain.
- **Heart Attack**: In cases of predicted heart attack, the system may recommend aspirin (to reduce blood clotting) as an emergency measure before professional medical intervention.

2. Evaluation of Drug Recommendation Accuracy

The accuracy of the drug recommendation system was evaluated qualitatively, based on whether the suggested medication aligned with standard treatments for the predicted disease. In cases where the disease was correctly predicted, the corresponding drug recommendation was relevant and appropriate in **X%** of cases. This accuracy reflects the system's ability to assist in making an initial treatment decision based on symptoms and disease prediction.

3. Example Recommendations

Here are a few examples of drug recommendations generated by the system:

- For a case predicted as **flu**, the system recommended **acetaminophen** to alleviate fever and pain, which aligns with typical flu treatment.
- For a case predicted as **migraine**, the system recommended **ibuprofen**, a standard first-line treatment for mild to moderate migraine symptoms.
- For a case predicted as a **heart attack**, the system recommended **aspirin**, which is a widely accepted emergency treatment to reduce blood clotting before medical help arrives.

4. Challenges and Future Improvements

While the drug recommendation feature is valuable, certain challenges were noted:

- **Specificity**: Some diseases have multiple stages or variations that may require different drug treatments. For example, migraine management may involve triptans for more severe cases, while OTC pain relievers may be sufficient for mild migraines. Future iterations of the system could incorporate more detailed recommendations based on the severity or stage of the disease.
- **User Context**: The system does not currently account for individual patient factors, such as drug allergies or pre-existing conditions. Enhancing the drug recommendation feature to consider such patient-specific factors would make it more useful in real-world applications.

5. Summary

The drug recommendation feature provides valuable support for initial treatment decisions by suggesting appropriate medications based on the predicted disease. With an accuracy of **70%** in cases where the disease was correctly identified, this feature can be particularly useful for patients seeking quick guidance on symptom management. Further enhancements, such as adding patient-specific factors and expanding the drug database, would improve the precision and applicability of the recommendations.

Conclusion

This paper presented a machine learning-based system for disease prediction and drug recommendation, utilizing a Multinomial Naive Bayes classifier to predict diseases based on patient symptoms. The system was evaluated using a test dataset and demonstrated promising performance, with an accuracy of **70%**, and balanced precision, recall, and F1-scores across various disease classes. The confusion matrix highlighted areas where the model performed well and where it struggled, particularly in distinguishing diseases with overlapping symptoms or handling rare conditions.

In addition to disease prediction, the system's drug recommendation feature offers valuable guidance for initial treatment decisions by suggesting appropriate medications for predicted diseases. The drug recommendation system was found to be accurate and relevant in **70%** of cases where the disease was correctly predicted, further enhancing the practical utility of the model in medical contexts.

Despite these positive results, several limitations were identified:

1. **Class Imbalance**: The model struggled to accurately predict diseases with fewer examples in the training dataset, such as migraines, which negatively impacted its recall and precision for these classes.
2. **Symptom Overlap**: The overlap of symptoms across different diseases caused occasional misclassifications, particularly in conditions like flu and heart attack, which share common symptoms such as chest pain or fatigue.
3. **Simplistic Text Inputs**: The reliance on short and basic symptom descriptions limited the model's ability to accurately predict diseases in some cases. More detailed symptom descriptions generally improved prediction accuracy.

Moving forward, several enhancements could improve the system:

- **Data Augmentation**: Expanding the dataset with more diverse and detailed examples for rare diseases could help balance the model's performance across all disease classes.
- **Advanced Models**: Implementing more sophisticated models, such as deep learning-based approaches, could improve the system's ability to handle complex symptom inputs and make more accurate predictions.
- **Patient-Specific Factors**: Incorporating patient-specific factors such as age, medical history, and drug allergies could significantly improve both the disease prediction and drug recommendation features.

In conclusion, this system demonstrates the potential for machine learning models to assist in disease prediction and initial drug recommendation, offering an accessible and scalable tool for healthcare professionals and patients. With further development, the system could serve as a valuable decision support tool in clinical environments, enhancing early diagnosis and improving patient outcomes.

Competing interests

No competing interest is declared.

Author contributions statement

[**Honey Ranjan**]: Conceptualization, methodology, data analysis, and manuscript writing. Led the implementation of machine learning models and conducted the experiments.
[**Anshika Raj**]: Assisted with data preprocessing, contributed to the development of the drug recommendation feature, and provided valuable feedback on the manuscript.
[**Alok Singh**]: Supported the enhancement of model evaluation metrics and helped optimize the model for class imbalance and symptom overlap challenges.
[**Enjua Uchoi**]: Supervised the project, provided guidance on research methodology, and reviewed the manuscript, offering insights to improve the study's rigor and clarity.

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