A symptom-driven medical diagnosis support model based on machine learning techniques

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ABSTRACT

Medicine is a human science that is constantly evolving, and this evolution generates a large mass of data that needs to be exploited with the multitude of IT resources available to guarantee and maintain this scientific progress. Some diseases share most symptoms, whereas others could have a low probability of being identified in an early stage. Thus, when facing a such situation, an inexperienced doctor may have difficulty making the right diagnosis or may test different cases, which will be a big waste of time. In this paper, we are going to make this embarrassing situation less complex by giving practitioners every probable disease, and even the least probable ones according to the given symptoms. Indeed, this work will push the diagnosis deeper to reveal hidden symptoms and pathogenesis, to help practitioners make the right decisions. To develop such a solution, the data is organized by matching each disease with its known symptoms, then we used naive Bayes as a classification model, and different metrics to evaluate the performance of this experiment. This work proves that machine learning has become very effective in the medical sector, especially when we notice that the accuracy exceeds 90% in the detection of diseases.

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1. INTRODUCTION

The massive technological advancement has greatly accelerated disease diagnosis and treatment plans. Various hospitals have adopted the technological approach due to cost reduction, time saving and accurate results [1], [2]. Moreover, health information technologies could reduce drug events and produce a better relationship between doctor and patient [3]. We also notice that the dynamic community of bioinformatics researchers, who have elevated data science to a foundational competency, have consistently created highly reproducible approaches that work in different settings and with different patients. This group of researchers employed computers as their laboratories in one of the basic sciences, and which has been one of the early domains where big data was sequestered as medical science [4].

Furthermore, big data and machine learning have the power to guide practitioners toward the most effective medical decision and treatments, as they could improve care quality without having any need to test unnecessary diagnostic and therapies [5]. The collection of massive data has formed large-scale datasets from different medical sectors such as biological science, radiological, bioinformatics, and even medical prescriptions written in human natural language. Therefore, this big quantity of data needs an intelligent treatment to produce relevant results in the aim of helping clinical decisions [6]. To produce these results, different technics are applied while converging to the same objective; we notice machine learning, deep learning, reinforcement learning, and also natural language processing. These artificial intelligence technologies, combined with human intelligence, have the power to accomplish difficult tasks with ease. They can help with accurate diagnosis, making efficient treatment and follow-up plans, risk prediction, productivity improvement, and even reducing medical errors [7], [8].

Using these machine learning techniques, we could work on situations with different levels of complexity, such as the analysis of radiological images while revealing relevant results that could lead to interpreting some of the images in priority. Another case could be the situation of patients, some of them may need to be redirected to a specialist where others will simply receive psychological support. These data science techniques will not be able to replace human intervention, but will be used as a complement and help practitioners to better manage their interventions and to devote themselves much more to the most complex situations. It is a practical way to create collaboration between medicine and artificial intelligence.

In this paper, we study the power of machine learning classifiers to identify diseases according to some given symptoms. This work won't be just a simple classification that have to determine concerned disease, but also to be able to predict even low probability diseases. In some cases, an unexperienced doctor or even an experienced one could be confused when a patient has symptoms for a common disease, but at the same time these symptoms can reveal a serious disease in an early stage. Therefore, the doctor must experiment with different clinical plans for a more accurate diagnosis to define the different possible cases. However, by following this method, we may waste too much time that could be important in the healing phase, a time where a disease in an early stage may become in an advanced one. So, this work provides a solution to overcome this situation and give to practitioners enough time and possibilities to deeply analyses every case encountered. This study represents the results obtained by applying naive Bayes as a model learning on a dataset formed from data collected on the web portal of the U.S. National Library of Medicine (NLM) [9]. The main objective is to give the possibility to determine a hidden disease behind the symptoms of other ones.

This work is described as follows. Section 2 describes a literature review on machine learning for healthcare, medical research, and some preliminary comparisons of different models. Section 3 presents the research methodology which explains the overall structure of our study as well as the techniques and methods we used in this work. Then in section 4, we will present and discuss the results of this experiment. Finally, in conclusion, we evaluate the model in terms of achieving the objectives and we will talk about some future work.

2. RELATED WORKS

Taking advantage of the great technological advances in hardware and software, as well as the power of various ma- chine learning algorithms, many studies have deeply exploited big data in order to prove the benefits of artificial intelligence in the medical sector. Laabidi and Aissaoui [10] comparing the performance of different machine learning algorithms in order to determine the best performing model for predicting diabetes and prostate cancer. This study proved that algorithms can be very accurate when it comes to predicting diseases. In the same context, Shah *et al.* [11] conducted a study with the objective of determining whether or not a patient could develop heart disease. They worked on four different models while comparing their performance. The main objective was to work with lesser attributes and tests [11]. This study also demonstrated that classification models are very effective when it comes to producing medical outcomes with good accuracy. Kosarkar *et al.* [12] implemented a system using three algorithms, decision tree, random forest, and naive Bayes. Their work consists in comparing the performances of the three classifiers using K fold cross validation, which showed that these algorithms gave very good accuracy with a small advantage of naive Bayes. However, looking at the result of the example given by the author, we find that naive Bayes and decision tree classifiers give the same result, while random forest gives a different result. At this level and in general we will choose the favorite result of the most of the classifiers, but with a precision as close as the one on the example this could put the practitioner in doubt if he has to decide which disease is the most probable. Therefore, a complementary diagnosis will be necessary.

Chen *et al.* [13] developed a heart disease predict system by using a combination of 14 attributes to determine the presence of heart disease. The attributes were a mixture of personal information's and others about the presence of symptoms. The use of artificial neural network (ANN) as an algorithm generated good results, including an accuracy of over 80%. This experiment leads to talk about the efficiency of machine learning technics even in some of the most advanced and critical medical fields such as cardiology. With this development of big data analysis, disease prediction and its analysis methods are receiving more attention in scientific research. Indeed, different researches have been conducted to improve the classification of diseases and even the risk to develop future diseases [14]. Chen *et al.* [15] worked on structured and unstructured data from real life hospital datasets in order to be able to give predictions with an effective accuracy. Their work aims in another sense to find a solution to the problem of missing data that could impact the quality of the results, they finally proposed a new convolutional neural network based multimodal disease risk prediction (CNN-MDRP) that gave an accuracy of 94.8% [15]. In the same context, many studies conducted on computer-aided diagnosis (CADx) demonstrated the great utility of medical diagnostic tools in improving clinical decisions and reducing unnecessary interventions [16], [17].

Still in the same context but this time with a prediction of diseases using symptoms expressed by the user himself, gadekar *et al.* [18] worked on a prediction system based on a set of symptoms provided by the patient. Such a system can be useful to inform the patient on the possible disease he may have, but remains insufficient or even risky if the patient is not precise in his diagnosis or if he takes the initiative to consume drugs without medical opinion. Indeed, the majority of models that aim at predicting diseases are based on a symptom/disease approach, such an approach can reach a good accuracy but remains unable to reveal if there is a disease hidden behind the symptoms of another or if a disease is present at an early stage.

3. METHOD

3.1. Proposed experimental process

Our disease prediction model is based on an iterative approach, in which the model is fed with the necessary parameters through several iterations until the optimum result is obtained, as shown in the diagram in Figure 1. Indeed, when a patient visits a doctor, their primary objective is to accurately convey their symptoms to receive appropriate treatment. For the doctor, the main goal is to elicit clear and precise information about the patient's health to make an accurate diagnosis. Our experiment, illustrated in Figure 1, follows a structured process consisting of the following steps:

– Step 1: the doctor inquiries about the patient's health status, guiding the patient to describe their symptoms and feelings. The doctor's task at this stage is to verify the patient's statements and generate an initial set of symptoms and signs.
– Step 2: the initial set of symptoms and signs identified by the doctor is input into the machine learning model for the first iteration. The model outputs predictions of likely diseases, ranked in descending order according to their probability scores. Additionally, the model suggests further symptoms and signs to check for each listed disease, aiding the practitioner in refining the diagnosis.
– Step 3: upon receiving the model's predictions, the doctor interprets the results in the context of the patient's condition. If the assessment is sufficient to make a decision, the diagnosis is considered optimal. The practitioner may request additional tests, if necessary, to confirm the diagnosis. If further investigation is required, the doctor verifies the additional symptoms suggested by the model with the patient. This process can be repeated iteratively until the doctor is confident in the diagnosis. The number of iterations is unlimited and depends on the results obtained and the practitioner's judgment. This iterative approach helps eliminate doubtful cases and identify dangerous conditions accurately.
– Step 4: once the doctor finalizes the diagnosis and determines the patient's illness, a treatment protocol can be planned and implemented for the patient's care and follow-up.

In conclusion, Figure 1 summarizes the process adopted in our study. It is a medical diagnosis support process designed to help the doctor, whether beginner or experienced, to better master the diagnosis phase in terms of «Time management» and «Case management».

3.2. Data

The data used in this study come from the NLM, located on the campus of the National Institutes of Health in Bethesda, Maryland, a center of information innovation since its founding in 1836 [19]. This library is considered the largest biomedical library in the world, with data collected through a network of over 8000 collaborators providing access to information across the United States. The NLM has developed a repository called Unified Medical Language System (UMLS) which is a set of files and software that brings together many health and biomedical vocabularies and standards to enable interoperability between IT systems [20]. It integrates more than 2 million names for approximately 900,000 concepts from more than 60 families of biomedical vocabularies. It also integrates 12 million relationships between these concepts [21]. Vocabularies integrated into the UMLS metathesaurus include the NCBI taxonomy, gene ontology, medical subject headings (MeSH), online mendelian inheritance in man (OMIM), and the digital anatomist symbolic knowledge base as illustrated in Figure 2 [20], [21].

For our study, the main objective is to extract data from UMLS database in order to associate diseases with their symptoms. Each disease is identified by a code "CUI" made up of an alphabetical character, which in our case is the letter "C", followed by a number of seven digits, giving a code in the following format "Cxxxxxxx". for example, if we take "Hepatitis C" as the disease, we'll find the following code "C0019196" associated with it. For symptoms, we use the same code format, i.e. the letter "C" followed by seven digits, e.g. for "Headache" we have the following code "C0018681", but the particularity of symptoms is that there are several ones for the same disease. For more clarity, let’s stay with the case of “Hepatitis C”, this disease has several symptoms, which can be listed in Table 1. In order to get the right dataset for our study, the data collected from the NLM needed some transformations to obtain relevant data and reliable results.

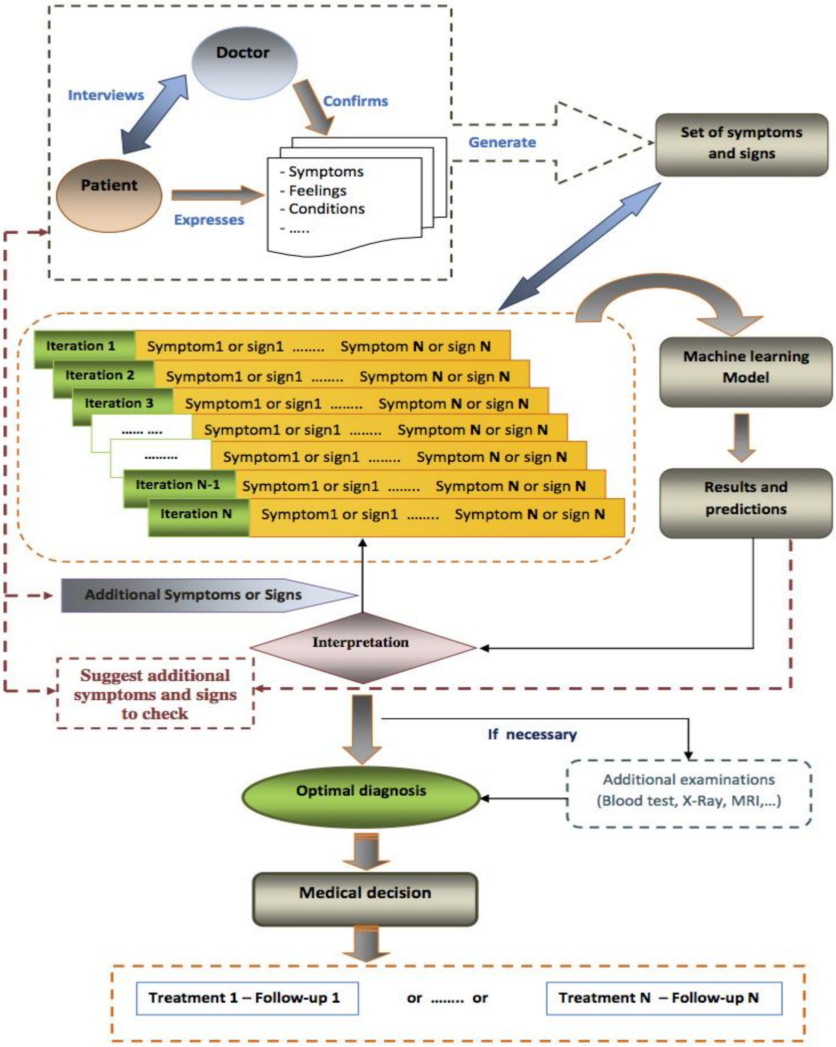

Doctor
Interviews
Confirms
Patient
Expresses
- Symptoms
- Feelings
- Conditions
- .....
Generate
Set of symptoms and signs
Machine learning Model
Results and predictions
Iteration 1 Symptom1 or sign1 .... Symptom N or sign N
Iteration 2 Symptom1 or sign1 .... Symptom N or sign N
Iteration 3 Symptom1 or sign1 .... Symptom N or sign N
.... Symptom1 or sign1 .... Symptom N or sign N
.... Symptom1 or sign1 .... Symptom N or sign N
Iteration N-1 Symptom1 or sign1 .... Symptom N or sign N
Iteration N Symptom1 or sign1 .... Symptom N or sign N
Additional Symptoms or Signs
Interpretation
Suggest additional symptoms and signs to check
If necessary
Additional examinations (Blood test, X-Ray, MRI,...)
Optimal diagnosis
Medical decision
Treatment 1 – Follow-up 1
or .... or
Treatment N – Follow-up N

Figure 1. Global scheme of the experiment

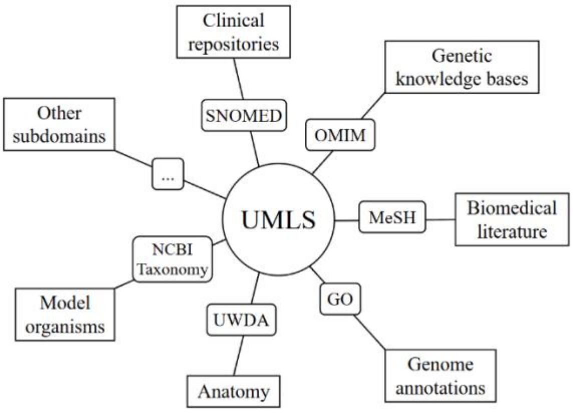


Figure 2. The various subdomains integrated in the UMLS from the NIH sources

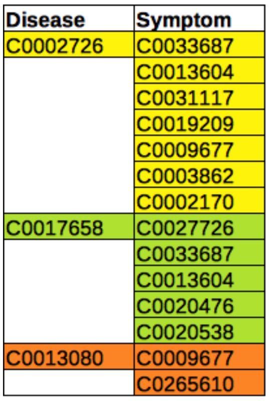
Table 1. Hepatitis C symptoms description

CUI	Symptoms	CUI	Description of symptom
C0019196	Ascites	C0003962	Accumulation or retention of free fluid within the peritoneal cavity
	Abdomen distended	C0000731	Distention of the abdomen.
	Feeling suicidal	C0424000	A risk factor for suicide attempts and completions
	Coughing	C0010200	A sudden, audible expulsion of air from the lungs through a partially closed glottis, preceded by inhalation
	Ache	C0234238	A dull persistent (usually moderately intense) pain
	Macerated skin	C0558143	A softening and breaking down of skin resulting from prolonged exposure to moisture
	Heavy feeling	C0581912	NAN
	Hallucinations, Auditory	C0233762	The false perception of sound
	Chills	C0085593	The sudden sensation of being cold. It may be accompanied by SHIVERING
	Asterixis	C0232766	A clinical sign indicating a lapse of posture

3.3. Data preprocessing

As previously mentioned, the data collected needed some pre- processing to extract what was needed for this work. Despite having access to a vast quantity of data, not all of it was essential for our purposes. Our primary challenge was to extract a dataset that accurately linked each disease with its known symptoms. Of course, to achieve accurate and relevant results, the data needed to be thoroughly cleaned and verified. The first step in our preprocessing was to list the disease codes and symptom codes, allowing us to check their formats and identify any missing values. We then mapped the symptoms associated with each disease to establish an initial model that could list all known symptoms for a given disease. The resulting model is illustrated in Figure 3.

At this stage, we had an initial understanding of the structure of our dataset; however, the current format was not suitable for input into the machine learning model. Additionally, the existing format contained significant duplications, which were unnecessary and could potentially hinder the analysis. To address this issue, we transformed the dataset to adopt a binary logic, indicating the presence or absence of symptoms for each given disease. This transformation allowed us to create a dataset that could be effectively utilized by machine learning algorithms while eliminating duplications that might affect result accuracy. The new dataset is organized in a tabular format, with rows representing diseases and columns representing symptoms. To better explain how the dataset works, let's take the case of hepatitis C again, for known symptoms of this disease we'll put ones '1', otherwise we'll put zeros '0'. As a result, our dataset will appear in the form presented in the Figure 4. Finally, our dataset contains 398 rows as diseases and 1016 columns as symptoms with no duplicate attributes. It should be noted that these values are subject to change, as data is periodically updated at source.



Disease	Symptom
C0002726	C0033687
	C0013604
	C0031117
	C0019209
	C0009677
	C0003862
	C0002170
C0017658	C0027726
	C0033687
	C0013604
	C0020476
	C0020538
C0013080	C0009677
	C0265610

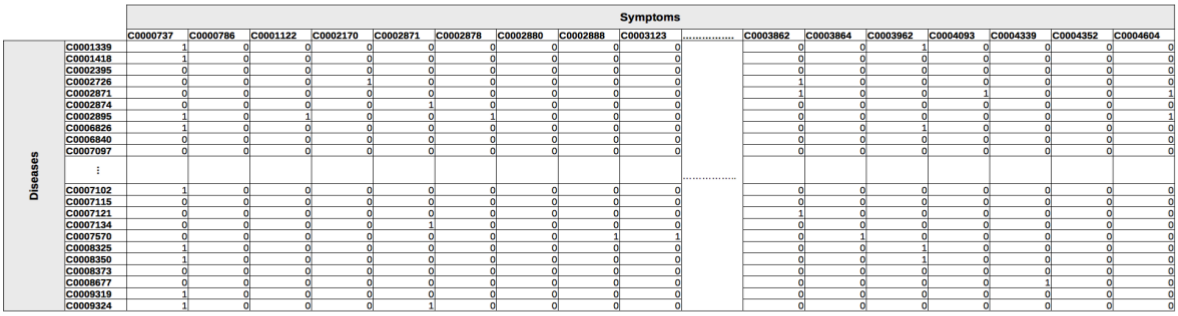
Figure 3. First result of listing some diseases and their symptoms

3.4. Naive Bayes

Naive Bayes is a simple supervised algorithm based on Bayes' theorem, a mathematical concept for obtaining probabilities. It assumes strong (naive) independence between attributes and attempts to maximize the posterior probability in determining the class. Predictors are unrelated and have no correlation to one another, but all attributes contribute independently to maximize the probability [11]. We can use the naive Bayes model without using any Bayesian methods. However, naive Bayes still one of the best classifiers for dealing with medical real-world datasets and even complex ones [22].

$$P(X/Y) = \frac{P(Y/X)\times P(X)}{P(Y)} \quad (1)$$

Where P(X/Y) is the posterior probability, P(X) is the class prior probability, P(Y) is the predictor prior probability, and P(Y/X) is the likelihood probability of predictor. Naive Bayes remains a simple, easy-to-implement and efficient algorithm that can handle non-linear and complicated data. However, according to some studies, there is a loss of accuracy due to the fact that this algorithm is based on the assumption and class conditional independence [11].



		Symptoms																
		C0000737	C0000786	C0001122	C0002170	C0002871	C0002878	C0002880	C0002888	C0003123	……………	C0003862	C0003864	C0003962	C0004093	C0004339	C0004352	C0004604
Diseases	C0001339	1	0	0	0	0	0	0	0	0		0	0	1	0	0	0	0
	C0001418	1	0	0	0	0	0	0	0	0		0	0	0	0	0	0	0
	C0002395	0	0	0	0	0	0	0	0	0		0	0	0	0	0	0	0
	C0002726	0	0	0	1	0	0	0	0	0		1	0	0	0	0	0	0
	C0002871	0	0	0	0	0	0	0	0	0		1	0	0	1	0	0	1
	C0002874	0	0	0	0	1	0	0	0	0		0	0	0	0	0	0	0
	C0002895	1	0	1	0	0	1	0	0	0		0	0	0	0	0	0	1
	C0006826	1	0	0	0	0	0	0	0	0		0	0	1	0	0	0	0
	C0006840	0	0	0	0	0	0	0	0	0		0	0	0	0	0	0	0
	C0007097	0	0	0	0	0	0	0	0	0		0	0	0	0	0	0	0
	⋮										……………							
	C0007102	1	0	0	0	0	0	0	0	0		0	0	0	0	0	0	0
	C0007115	0	0	0	0	0	0	0	0	0		0	0	0	0	0	0	0
	C0007121	0	0	0	0	0	0	0	0	0		1	0	0	0	0	0	0
	C0007134	0	0	0	0	1	0	0	0	0		0	0	0	0	0	0	0
	C0007570	0	0	0	0	0	0	0	1	1		0	1	0	0	0	0	0
	C0008325	1	0	0	0	0	0	0	0	0		0	0	1	0	0	0	0
	C0008350	1	0	0	0	0	0	0	0	0		0	0	1	0	0	0	0
	C0008373	0	0	0	0	0	0	0	0	0		0	0	0	0	0	0	0
	C0008677	0	0	0	0	0	0	0	0	0		0	0	0	0	1	0	0
	C0009319	1	0	0	0	0	0	0	0	0		0	0	0	0	0	0	0
	C0009324	1	0	0	0	1	0	0	0	0		0	0	0	0	0	0	0

Figure 4. Disease/symptoms dataset final form

3.5. Methodology

The following section presents the main objectives, data structure, and application of our disease detection model within the context of enhanced diagnosis.

- Main objective: Our primary objective is not only to detect diseases associated with observed symptoms but also to identify diseases that may be present at an early stage or those that are serious but share symptoms with benign conditions. To achieve this, we employed an input/output model where symptoms are used as input to generate an output representing the detected diseases. Our approach is unique in that we do not solely identify the most probable disease; instead, we produce an output that includes various potential diseases ranked in descending order of their probability scores.
- Data and strategy: To implement this work, our dataset is structured in a diseases/symptoms format, with rows representing diseases and columns representing symptoms. Each disease is associated with its known symptoms using binary logic: '1' indicates the presence of a symptom, while '0' indicates its absence, as shown in Table 2. The dataset is then divided into training and testing subsets, with approximately 70% of the data allocated for training and 30% for testing (test-size =0.3). This strategy ensures that our model can be effectively trained and validated for accurate disease detection and diagnosis.
- Application and diagnostic enhancement: Consider a patient presenting with various symptoms of differing severity. We first catalog these symptoms and convert them into coded form for input into our model. The model then generates an output list of potential diseases, each accompanied by its probability of being present in the patient. An essential aspect of our approach is that for each detected disease, the model suggests additional symptoms for the practitioner to verify. This provides the practitioner with comprehensive information, facilitating a more thorough and accurate diagnosis and enabling the most appropriate clinical decision-making.

3.6. Performance evaluation criteria

To evaluate the performance of a classifier, it is necessary to introduce two important parameters: sensitivity and specificity. When sensitivity represents the classifier's effectiveness in identifying positive samples to the total actual positive instances, specificity defines the ratio of incorrectly predicted positive instances to the total actual negative instances. On the other hand, the accuracy measures the overall correctness of the model's predictions. It considers both true positive and true negative instances. It can therefore be calculated as follows:

$$\text{Sensitivity} = \frac{TP}{TP+FN} \times 100 \quad (2)$$

$$\text{Specificity } = \frac{TN}{TN+FP} \times 100 \quad (3)$$

$$Accuracy = \frac{TP+TN}{TP+TN+FP+FN} \quad (4)$$

In addition, the F-score or F1 score is used to measure the performance of our model. It is a metric commonly used in machine learning and statistics to evaluate the performance of a classification model, and looks for potential imbalance problems. It combines and provides a balance between precision and recall, and is particularly useful when there is an uneven class distribution. F1 score is obtained as follows:

$$\text{Precision } = \frac{TP}{TP+FP} \quad (5)$$

$$\text{Recall} = \frac{TP}{TP+FN} \quad (6)$$

F-score is the harmonic mean of precision and recall.

$$\text{F} - \text{score} = 2 \times \frac{precision \times recall}{precision+recall} \quad (7)$$

Table 2. Predicted diseases sorted by descending probability score (Iteration 1)

Symptoms	Predicted diseases	Probability score	Additional signs or symptoms to check
- Fever	Acute bronchitise	3.165	'Rhinitis', 'Laryngitis', 'Pharyngitis', 'Myalgia'
- Cough	Myocarditis	1.588	'Diarrhea', 'Exanthema', 'Chest Pain', 'Palpitations'
- Headache - Fatigue	Pontiac Fever	1.576	'Common cold', 'Sore throat', 'Confusion', 'Diziness', 'Photophobia', 'Myalgia'
	Scarlet Fever	1.552	'Deglutition disorders', 'Vomiting', 'Pharyngitis', 'Peritonsillar abscess', 'Mucous membrane eruption', 'Strawberry tongue', 'Exanthema', 'Pallor', 'Nausea', 'Tonsillitis'
	Legionnaires' Disease	1.546	'Pleurisy', 'Rhinitis', 'Laryngitis', 'Confusion', 'Lethargy', 'Diarrhea', 'Dry cough', 'Chills', 'Myalgia', 'Chest pain', 'Pneumonia'
	Bronchopneu-monia	1.493	'Chest pain', 'Chills', 'Muscle aches', 'Myalgia', 'Dyspnea', 'Sweating', 'Tachypnea'
	Chikenpox	0.803	'Exanthema', 'Pruritus'
	Sarcoidosis	0.803	'Arthritis', 'Erythema nodosum'
	Antrax disease	0.800	'Bronchopneumonia', 'Chills', 'Hypoxia'

4. RESULTS AND DISCUSSION

Our study was designed to facilitate iterative deep diagnosis for practitioners. Initially, we utilized only four symptoms for our classification, as depicted in Table 3, and subsequently used our model to predict the diseases. As illustrated in Table 3, the output is a list of diseases ranked in descending order based on their probability scores, starting with the disease having the highest probability score, followed by the next highest.

At this initial stage, each predicted disease is not evaluated for its severity but rather for its probability of being present. The practitioner can then choose to deepen the diagnosis by examining the probability scores and analyzing each disease from a severity perspective. Table 3 indicates that the first iteration revealed diseases of varying severity, and the model suggests additional signs and symptoms to verify, thereby guiding the practitioner towards a more comprehensive diagnosis.

First, let's have a look to the results generated by our machine learning model in terms of probability of occurrence and severity. In our first iteration, the most probable disease is 'Acute bronchitis' with a probability of 3.165%. Acute bronchitis is not in itself a dangerous disease, but rather a self-limiting condition that will disappear after a few days or week [23]. But this does not prevent the disease from having complications in certain cases [23], and it is why the practitioner must ensure that it is indeed the disease in question in order to anticipate complications. In second place, we find myocarditis with a probability of 1.588%, but the score is nowhere near that of acute bronchitis, since there is a difference of more than half, which is enormous, especially when it concerns the medical field. In fact, the probability of developing myocarditis is small, but still alarming, given that the disease is dangerous, especially if you know that it remains asymptomatic in most cases, or unnoticeable since the symptoms are eclipsed by those of the inflammation that triggered the disease [24]. The presence of such a disease in an advanced stage (Rank 2 in our case) will certainly lead the doctor to diagnose it more thoroughly, in order to prevent complications such as heart failure and, in rare cases, cardiogenic shock [24]. For the next three ranks, the probability of disease is relatively close to that of myocarditis, except that the severity of the three diseases varies widely. Pontiac fever is ranked third with a score of 1.576%, this disease is considered benign and also self-limiting and can be mistaken for simple flu [25]. In forth position scarlet fever is present with a score of 1.552%, it is a childhood illness currently considered as mild disease if correctly treated [26]. Like myocarditis, Legionnaires’ disease (Legionella pneumonia) is present with a probability of 1.546%. This is not a very high score, but it’s important for the doctor not to overlook this result, as the disease is very dangerous, and as the prognosis of patients depends above all on two factors: “when the disease was diagnosed” and “when treatment was instituted” [27]. It should be mentioned that the mortality rate among senior citizens varies between 10 and 50% [28], which is very alarming, hence the need for early diagnosis. The rest of our list includes bronchopneumonia with a score of 1.493%, a disease that is very common in children and requires special attention to prevent complications. It’s a potentially fatal disease, as statistics show that more than 920,000 children under the age of 5 died of pneumonia, mainly bronchopneumonia, in 2015 [29]. Then we have Chickenpox (varicella) and sarcoidosis with 0.803%, the two diseases have the same probability but not severity. Chickenpox is usually considered as a childhood mild disease [30], whereas sarcoidosis is a chronic disease that is often asymptomatic at a certain level but requires follow-up and treatment by drug therapy if symptoms appear [31]. For patients in an advanced stage of the disease who are untreated, themortality rate is about 5% [31]. The last case in our ranking is anthrax with 0.8%, it is a notifiable infectious disease because it is very dangerous and requires a specific protocol [32]. Statistics report a mortality rate of 50% even with treatment [32].

The initial results from our model indicate that while the symptoms observed in the patient are familiar and common across all age groups, it is crucial to remain vigilant for serious pathologies that may be concealed behind these seemingly benign symptoms. For the purposes of our analysis, we focused on the first eight predicted results, which provided sufficient data to evaluate the model's performance. However, practitioners have the option to review all results in descending order to gain a comprehensive understanding of the case. Our findings reveal that among the eight predicted results, approximately four were fatal and dangerous diseases, underscoring the importance of early diagnosis and urgent treatment. This demonstrates that our model is an effective tool for practitioners to enhance their diagnostic process and identify potential hidden pathologies promptly, thereby saving valuable time. For instance, early detection of anthrax can save many lives, including the patients. Similarly, timely identification of Legionnaire’s disease can significantly improve patient outcomes.

Table 3. Predicted diseases sorted by descending probability score (Iteration 2)

Symptoms	Predicted diseases	Probability score	Additional signs or symptoms to check
- Fever - Cough - Headache - Fatigue - Rhinitis	Acute bronchitis	6.064	'Laryngitis', 'Pharyngitis', 'Myalgia'
	Legionnaires’ Disease	2.940	'Pleurisy', 'Laryngitis', 'Confusion', 'Lethargy', 'Diarrhea', 'Dry cough', 'Chills', 'Myalgia', 'Chest pain', 'Pneumonia'
	Myocarditis	1.523	'Diarrhea', 'Exanthema', 'Chest pain', 'Palpitations'
	Pontiac Fever	1.508	'Common cold', 'Sore throat', 'Confusion', 'Diziness', 'Photophobia', 'Myalgia',
	Scarlet Fever	1.479	'Deglutition disorders', 'Vomiting', 'Pharyngitis', 'Peritonsillar abscess', 'Mucous membrane eruption', 'Strawberry tongue', 'Exanthema', 'Pallor', 'Nausea', 'Tonsillitis'
	Bronchopneu-monia	0.780	‘Chest pain’, ‘chills’, ‘Muscle aches’, ‘Myalgia’, ‘Dyspnea’, ‘Sweating’, ‘Tachypnea’
	Chikenpox	0.772	'Exanthema', 'Pruritus'
	Sarcoidosis	0.772	'Arthritis', 'Erythema nodosum',
	Antrax disease	0.769	'Bronchopneumonia', 'Chills', 'hypoxia'

During our experiment, we conducted multiple iterations of our model to observe its behavior under varying parameters. The model demonstrated high sensitivity to modifications in symptoms, as evidenced by the results of the second iteration presented in Table 4. It is important to note that the symptoms selected for this iteration were chosen based on the disease with the highest initial probability, aiming to refine its diagnosis further. For practitioners, parameter selection will be more precise, informed by patient observation and case-specific interviews. Practitioners can iteratively adjust parameters and continue the diagnostic process until the most optimal result is achieved. This iterative approach can be supplemented with additional diagnostic methods, such as blood tests or medical imaging. In the second iteration, we observed that the probability of acute bronchitis increased significantly to 6.064%, which is expected given that the additional symptom selected is a key indicator for this condition. The most notable result was for Legionnaire's disease, which showed a probability increase to 2.94% from 1.546% in the first iteration, nearly doubling and highlighting the severity of this condition. For the remaining results, the ranking of predicted diseases and their probability scores showed minimal change, as depicted in Table 4. This consistency suggests the model's stability and reliability in identifying and ranking diseases based on their probability, even with parameter adjustments.

Table 4. Measurement results

Metric	Score (%)	Macro avg (%)	Weighted avg (%)
Accuracy	97.72		
Precision		96	97
Recall		96	98
F-score		96	97

In this study, our model demonstrated exceptional performance in processing medical data, as evidenced by the results in Table 4. The model achieved an accuracy of approximately 97.72%, indicating a high proportion of correct predictions across all classes. However, it is important to note that accuracy alone does not differentiate between false positives and false negatives, which is a critical consideration in medical diagnosis due to the varying costs associated with these errors. To address this limitation and provide a more comprehensive evaluation of the model's performance, we utilized the F1 score. The F1 score metric, which balances precision and recall, exceeded 96%. This high score confirms that the model not only maintains a high level of precision in positive predictions but also effectively captures all relevant positive instances. Such a balance is crucial in medical diagnostics, ensuring that the model reliably identifies true positives while minimizing false negatives. Overall, the F1 score results underscore the model's robustness and reliability, making it a valuable tool for medical practitioners who require accurate and comprehensive diagnostic support. As a conclusion to this section of our paper, we can see that our model was very useful in achieving the main objective expressed in the previous section. It was able to predict possible diseases based on the given symptoms while achieving very good performance.

5. CONCLUSION

This study enhances medical diagnostics by implementing a machine learning model to predict diseases based on observed symptoms, using a dataset linking diseases to symptoms and employing the naive Bayes classification algorithm. The iterative approach involves feeding the model with new or additional symptoms until an optimal diagnosis is achieved. The model has proven effective, establishing trust between practitioners and machine learning technology by providing predictions that encompass all potential diseases, including rare and unexpected ones. Notably, serious diseases such as myocarditis, Legionnaire's disease, and anthrax can present with symptoms similar to benign conditions like acute bronchitis. The study demonstrates the model's efficacy in saving time and resources, with performance metrics exceeding 95%, including a 96% F1 score and 97.72% precision. Despite its effectiveness, practitioners must still perform additional examinations for suspected dangerous diseases, as the model cannot replace the diagnostic insights gained from observing a patient's physical and psychological states. The developed model aids practitioners in making informed diagnostic and treatment decisions. Future work will integrate natural language processing to allow patients to express symptoms directly, and software development using microservices will facilitate user communication through dedicated applications and interfaces.

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AUTHOR CONTRIBUTIONS STATEMENT

This journal uses the Contributor Roles Taxonomy (CRediT) to recognize individual author contributions, reduce authorship disputes, and facilitate collaboration.

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C	:	**C**onceptualization	I	:	**I**nvestigation	Vi	:	**Vi**sualization
M	:	**M**ethodology	R	:	**R**esources	Su	:	**Su**pervision
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CONFLICT OF INTEREST STATEMENT

Authors state no conflict of interest.

DATA AVAILABILITY

The data supporting the results of this study are available from the U.S. National Library of Medicine. Their access is subject to restrictions as they were used under license for this study. Data can be obtained from the authors with permission from the National Institutes of Health (NIH) or directly from the NIH after obtaining a license.

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