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БАҒДАРЛАМАЛЫҚ ҚАМТАМАНЫ ӘЗІРЛЕУ ЖӘНЕ БІЛІМ ИНЖЕНЕРИЯСЫ

АҚПАРАТТЫҚ ЖӘНЕ КОММУНИКАЦИЯЛЫҚ ЖЕЛІЛЕР ЖӘНЕ КИБЕРҚАУІПСІЗДІК

ИНТЕЛЛЕКТУАЛДЫ ЖҮЙЕЛЕР

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SYMPTOMATIC ASSESSMENT OF DISEASES USING DECISION TREES AND ANALYSIS OF ELECTRONIC MEDICAL RECORDS

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Abstract. Supervised machine learning algorithms have emerged as the primary data mining tool. The use of health data to diagnose disease has lately revealed the potential use of these technologies. The purpose of this research is to find various forms of regulated machine learning algorithms as well as major trends in measuring performance and illness risk. In this article, we will attempt to anticipate patient illnesses based on their symptoms. We employ the decision tree algorithm to reach this aim, which will aid in the diagnosis of patients' health. The data set includes physiological measures for 42 different illnesses (diseases) and 129 different features (symptoms). We created a categorized decision tree model that uses standardization techniques known as format reduction to generalize data and delivers training to a dataset in a short amount of time. Developed trained models are then utilized to forecast illnesses, including their causes and preventative strategies, after they have been normalized.

Keywords: Decision tree, physiological measurements, EMR (Electronic Medical Records), machine learning, accuracy

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ШЕШІМ АҒАШТАРЫН ЖӘНЕ ЭЛЕКТРОНДЫҚ МЕДИЦИНАЛЫҚ ЖАЗБАЛАРДЫ ТАЛДАУДЫ ҚОЛДАНА ОТЫРЫП, АУРУЛАРДЫ СИМПТОМАТИКАЛЫҚ БАҒАЛАУ

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Аннотация. Машиналарды оқытудың бақыланатын алгоритмдері деректерді шығарудың негізгі құралына айналды. Жақында ауруларды диагностикалау үшін медициналық деректерді қолдану осы технологиялардың ықтимал қолданылуын анықтады. Бұл зерттеудің мақсаты-машинаны оқытудың реттелетін алгоритмдерінің әртүрлі формаларын, сонымен қатар өнімділік пен ауру қаупін өлшеудегі негізгі тенденцияларды табу. Бұл мақалада біз пациенттердің ауруларын олардың белгілері негізінде болжауға тырысамыз. Алға қойылған мақсатқа жету үшін біз пациенттердің денсаулығын диагностикалауға көмектесетін шешімдер алгоритмін қолданамыз. Деректер жиынтығына 42 түрлі аурудың және 129 түрлі белгілердің физиологиялық көрсеткіштері кіреді. Біз деректерді жалпылау үшін форматты қысқарту деп аталатын стандарттау әдістерін қолданатын және қысқа мерзімде мәліметтер жиынтығын оқытуды қамтамасыз ететін шешім ағашының санатталған моделін жасадық. Содан кейін біздің оқытылған модельдеріміз қалыпқа келтірілгеннен кейін ауруларды, оның ішінде олардың себептері мен алдын-алу стратегияларын болжау үшін қолданылады.

Түйін сөздер: Шешім ағашы, физиологиялық өлшеулер, Электронды Медициналық Жазбалар (ЭМЖ), машиналық оқыту, дәлдік

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СИМПТОМАТИЧЕСКАЯ ОЦЕНКА ЗАБОЛЕВАНИЙ С ИСПОЛЬЗОВАНИЕМ ДЕРЕВЬЕВ РЕШЕНИЙ И АНАЛИЗА ЭЛЕКТРОННЫХ МЕДИЦИНСКИХ ЗАПИСЕЙ

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Аннотация. Контролируемые алгоритмы машинного обучения стали основным инструментом для извлечения данных. Использование медицинских данных для диагностики заболеваний недавно выявило возможное применение этих технологий. Цель данного исследования состоит в том, чтобы найти различные формы регулируемых алгоритмов машинного обучения, а также основные тенденции в измерении производительности и риска заболеваний. В этой статье мы попытаемся предсказать заболевания пациентов на основе их симптомов. Для достижения поставленной цели мы используем алгоритм решений, который помогает диагностировать здоровье пациентов. Набор данных включает физиологические показатели 42 различных заболеваний и 129 различных симптомов. Мы разработали классифицированную модель дерева решений, которая использует методы стандартизации, называемые сокращением форматов, для обобщения данных и обеспечивает обучение набору данных в короткие сроки. Затем наши обученные модели используются для прогнозирования заболеваний, включая их причины и стратегии профилактики, после нормализации.

Ключевые слова: Дерево решений, физиологические измерения, Электронные Медицинские Записи (ЭМК), машинное обучение, точность

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Introduction

The process of identifying which disease is responsible for a patient's symptoms is known as medical diagnostics. Because certain symptoms and indicators are non-specific, the diagnosis is the most difficult challenge to solve. The most important step in the therapy of any disease is to identify it. Machine learning is a field that can aid in the prediction of illness diagnosis based on previously trained data (Shaik et al., 2017;

Diyar Qader et al., 2019). Machine learning has sparked a lot of interest and is now employed in a variety of nations. When applied to handle serious problems like cancer, heart disease, and dengue fever, machine learning has proved to be beneficial. Many researchers employ decision-making algorithms as one of their projection approaches (Nahar et al., 2018). Various machine learning approaches have been developed by many researchers to accurately identify various illnesses (Iswanto Iswanto et al., 2019).

In medicine, machine learning approaches are becoming increasingly significant, particularly for illness identification in medical data.

Machine learning enables machines to learn without the need for specific programming. Using machine learning techniques to create a model, you can forecast the first diagnosis and suggest remedies (Reem et al., 2018). Early detection and treatment are the most effective ways to minimize the number of fatalities caused by any disease (Gopi Battineni et al., 2020). As a result, several medical researchers are creating novel prediction models for illness detection based on machine learning algorithms (Diyar Qader Zeebare et al., 2019).

Text summarization and decision tree techniques are used in this article. The data was provided from the website kaggle.com (*https://www.kaggle.com/kaushil268/disease-prediction-using-machine-learning*, 2020). We have specified the dataset as research-based testing and training data.

Methods and Algorithms

Data mining is a method of identifying patterns in data using intelligent methods. Extracting patterns and perceptions from large amounts of data is a complex process. The value of these methods has been demonstrated in the field of medicine through experiments with various algorithms. One of such algorithms is data classification. This is the process of defining models that can explain different classifications of data. For classifying large datasets, decision trees are frequently utilized (Deepika et al., 2020). The decision tree divides information between root and end nodes (Arumugam et al., 2021).

A decision tree (DT) is a controlled machine learning technique that divides data repeatedly depending on specified factors to solve regression and classification issues. The data is separated into nodes, and the ultimate solution is represented by three hosts. The purpose of the decision tree is to use data from the discipline to study the basic rules of decision-making and implement a model that can predict mop variables (Yash Jayesh Chauhan, 2018). At the training stage, the tree is created using training data. Class names are stored in domain nodes while solution nodes are not in domain nodes. At the training stage, the tree is created using training data. Class names are stored in domain nodes while solution nodes are not in domain nodes (Adel Sabry Eesa et al., 2015; Adel Sabry Eesa, 2015). Decision trees are used to organize clear and numerical information. The linear relationship between the parameters does not affect the authenticity of the tree (Xiaolu Tian, 2019). Does not require pre-processing of data. Reconstruction of trees increases the likelihood of excessive assembly (Deva Kumar, et al., 2020). The child node and the three-leaf node in Figure 1 show the basic decision tree and the field of medicine is the application of the application tree. The circles represent each variable

(C1 C2 and C3) and the squares represent the selection results (Class A and Class B). Each branch is classified as true or false depending on the value of the results of the previous node test in order to successfully classify the sample into classes.

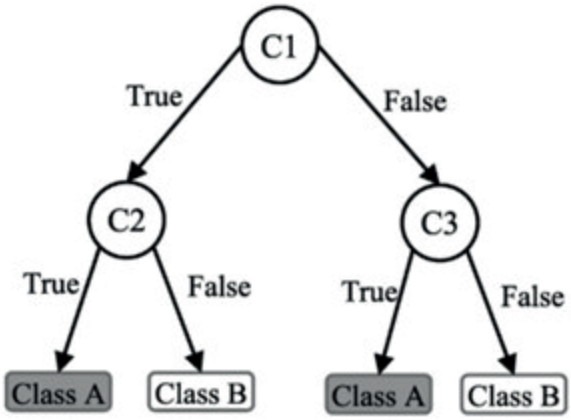

Figure 1 – « A decision tree is illustrated»

The decision tree approach is a popular data extraction method for creating predictive models based on various explanatory functions. This path divides the population into groups based on the number of branches on trees that produce inverted trees with internal root and leaf nodules. A decision tree is a nonparametric approach for working with big, complicated data sets without the need of several parametric structures. The study data can be separated into training and test datasets if the sample size is high enough. A training dataset is used to model the three, and a validation dataset is utilized to achieve the best final model for choosing the suitable tree size (Rakhmetulayeva et al., 2018: 231–238).

The decision tree predicts the disease based on the main symptoms. First, we collect the first five user tokens and store them in an array with a number assigned to each element. These inputs are entered into a prognostic model of the disease. This quality corresponds to the collection of data on diseases ending with the highest level of trust on the part of public peripheral nodes.

We repeat the process described above by increasing the size of the tree in a repeating section to create a tree. We set the current node to the last node if there is no doubt that the output for this symbol has been edited (Rakhmetulayeva et al., 2021: 1730–1739). We use electronic medical records to add additional symptoms to the database in order to better predict the disease based on symptoms.

Building a Decision Tree: General Rules:

1. Choose the best features/attribute which is the ability to subdivide or subgroup data in the most efficient way
2. Check if all elements have the same attributes and there are no additional attributes or instances
3. End the iterative process.

Results and discussion

In this section we will see the results of using the decision tree. Accuracy indicator Accuracy (P) recall (R) and F-indicator are metrics used to evaluate the performance of the algorithm. The measure of accuracy (given in equation (1)) provides an accurate measure of positive analysis. The correct set of positive results [as defined in equation (2)] is determined taking into account. The measurement F [given in equation (3)] evaluates accuracy (Apurb Rajdhan et al., 2020).

$$P = (TP) / (TP + FP) \quad (1)$$

$$R = (TP) / (TP + FN) \quad (2)$$

$$PR = (TP) / (TP + FN)\ F\text{-}\ Score = (2 * P * R) / (P + R) \quad (3)$$

• TP True positive: the patient is infected with the illness, and the test results are positive.

• FP False positive: despite the fact that the patient does not have the condition, the test results are positive.

• TN True negative: the patient is not afflicted with the disease, and the test results are negative.

• FN False negative: although the patient has the disease, the test results are negative.

The data set includes physiological measures for 42 different illnesses (diseases) and 129 different features (symptoms). The data set which was used from the website kaggle.com. Figure 2 shows part of the data.

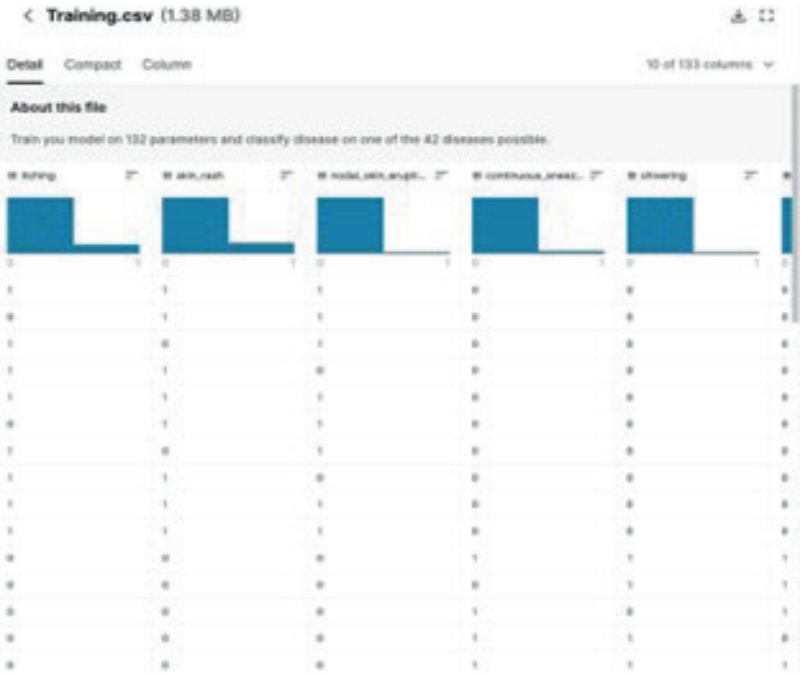

Figure 2 – «42 types of diseases»

The above methods are tested using pre-generated datasets during training and implementation. The confusion matrix is used to calculate the performance metric shown above. The performance of the model is summed up in a confusion matrix. Figure 3 shows various variants of the optical illusion matrix of the proposed model.

```
[[1 0 0 ... 0 0 0]
[0 1 0 ... 0 0 0]
[0 0 1 ... 0 0 0]
...
[0 0 0 ... 1 0 0]
[0 0 0 ... 0 1 0]
[0 0 0 ... 0 0 1]]
-----------------
```

Figure 3 – «Decision Tree Confusion matrix»

The accuracy estimates for the categorization of the decision tree (*http://acadpubl.eu/ap*, 2020) are shown in Figure 4. As we can see the accuracy of the decision tree is 97.6 % which represents good result for the study. It means that in the future when we do comparative work on other machine learning algorithms we will choose the best algorithm.

```
from sklearn.tree import DecisionTreeClassifier
dt = DecisionTreeClassifier(random_state = 42)
dt.fit(x_train, y_train)
dt.predict(x_test)
dt.score(x_test, y_test)
```

```
0.9761904761904762
```

Figure 4 – «Decision Tree classification accuracy»

Conclusion

In the field of medicine, machine learning has emerged to give tools to evaluate disease-related data (Priyanka Sonar et al., 2019). As a result, machine learning technologies play an essential role in early illness diagnostics. This article gives an overview of the machine learning approaches and standard datasets that are used to forecast illnesses such as fungal infection, gastroenteritis, hypertension, hyperthyroidism and many more.

According to the findings of this study, the decision tree algorithm is the most effective algorithm for illness prediction, with an accuracy score of 97.6 %. The study may be improved in the future by establishing a web application based on the decision tree algorithm and employing a larger dataset than the one used in this analysis, which will assist to deliver better findings and aid health professionals in successful and efficient forecasting of illnesses.

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