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OPTIMIZATION OF DIAGNOSTIC PROCESSES USING DECISION TREES IN ECG DATA ANALYSIS – LETS WEB SYSTEM ANALYSIS ENGINE

OPTYMALIZACJA PROCESÓW DIAGNOSTYCZNYCH Z WYKORZYSTANIEM DRZEW DECYZYJNYCH W ANALIZIE DANYCH EKG – SILNIK ANALIZY SYSTEMÓW INTERNETOWYCH LETS

ABSTRACT

The article presents the capabilities of the LETS Web system, which uses Internet of Things (IoT) technology to analyze medical data to optimize diagnostic processes. The article focuses on implementing decision tree algorithms that analyze electrocardiogram (ECG) data to identify cardiac conditions. The study used three variants of decision trees that differed in structure and ECG parameters. Each variant was tested for its ability to accurately classify cardiac health conditions ranging from simple arrhythmias to complex arrhythmic changes. The study showed that modifications to the structure of the decision trees significantly affected their effectiveness. The most advanced variant of the tree, using multivariate data analysis, showed the highest efficiency in diagnosing complex conditions. The effectiveness of the different variants of decision trees varied, confirming the importance of selecting the suitable diagnostic model for the specifics of the data and clinical goals.

STRESZCZENIE

W artykule przedstawiono możliwości systemu LETS Web, który wykorzystuje technologię Internetu Rzeczy (IoT) do analizy danych medycznych w celu optymalizacji procesów diagnostycznych. W artykule skupiono się na implementacji algorytmów drzewa decyzyjnego, które analizują dane elektrokardiograficzne (EKG) w celu identyfikacji różnych schorzeń kardiologicznych. W badaniu wykorzystano trzy warianty drzew decyzyjnych różniące się strukturą i zastosowanymi parametrami EKG. Każdy wariant przetestowano pod kątem możliwości dokładnego klasyfikowania schorzeń serca, od prostych arytmii po złożone zmiany arytmii. Badania wykazały, że modyfikacje struktury drzew decyzyjnych w istotny sposób wpływają na ich efektywność. Najbardziej zaawansowany wariant drzewa, wykorzystujący wielowymiarową analizę danych, wykazał największą skuteczność w diagnozowaniu złożonych stanów. Skuteczność różnych wariantów drzew decyzyjnych była zróżnicowana, co potwierdza znaczenie wyboru odpowiedniego modelu diagnostycznego dla specyfiki danych i celów klinicznych.

KEYWORDS: *Internet of Things (IoT), Categorization Decision Trees, ECG Diagnostics, Medical Data Analysis, Diagnosis Automation*

SŁOWA KLUCZOWE: *Internet rzeczy (IoT), drzewa decyzyjne kategoryzacji, diagnostyka EKG, analiza danych medycznych, automatyzacja diagnostyki*

INTRODUCTION

Healthcare has long been regarded as one of the most promising application areas for Internet of Things (IoT) technology (Choudhuri et al., 2019). The potential of this technology is wide-ranging and can be used in various medical fields, such as remote patient monitoring, fitness programs, care for people with chronic illnesses, and support for seniors. As wireless technologies advance, offering more comprehensive coverage and faster data transfer, it will become possible to instantly transmit medical information and diagnose vast amounts of medical data. Such advances will contribute to greatly accelerating diagnostic processes, which could revolutionize how healthcare is delivered.

Medical decision support systems are becoming crucial in rapidly evolving technologies. Systems based on self-detection and self-analysis play an increasingly important role in helping doctors analyze medical data and identify potential pathologies (Ali et al., 2020; Shanthi et al., 2018). Using massive databases, these advanced tools use machine learning and artificial intelligence algorithms to identify and aggregate critical information and detect anomalies, automating diagnosis.

It is worth noting that decision support systems in medicine speed up the diagnosis process and support selecting an appropriate treatment method. Thanks to advanced data analysis and predictive models, doctors can personalize therapies for individual patients, which is especially important for chronic diseases and complex health conditions. The diagnosis and treatment process thus becomes more individualized, aligning with the latest trends in personalized medicine. Implementing such systems into clinical practice can revolutionize healthcare management, making it more efficient and patient-centered.

The automation of diagnosis requires a specific scheme of action that must be meticulously planned, and it is worth quoting Wulff's classification (Wulff et al., 2000). It distinguishes three main types of diagnosis. The first, probabilistic or Bayesian diagnosis, is based on statistical probabilities. For example, if a patient is found to have lung tumors with a high likelihood of developing cancer, the system may automatically recommend referring the patient to a surgical department. Another type, pattern diagnosis, follows the analysis of data from various hospital systems, which together describe

the specific symptoms of a disease. The third form, causal diagnosis, involves deducing and establishing a chain of causes leading to a particular pathology.

Many advanced techniques are available in clinical decision support. Among the most promising are decision trees, neural networks, systems based on rough set theory, systems based on conditional probabilities, etc.

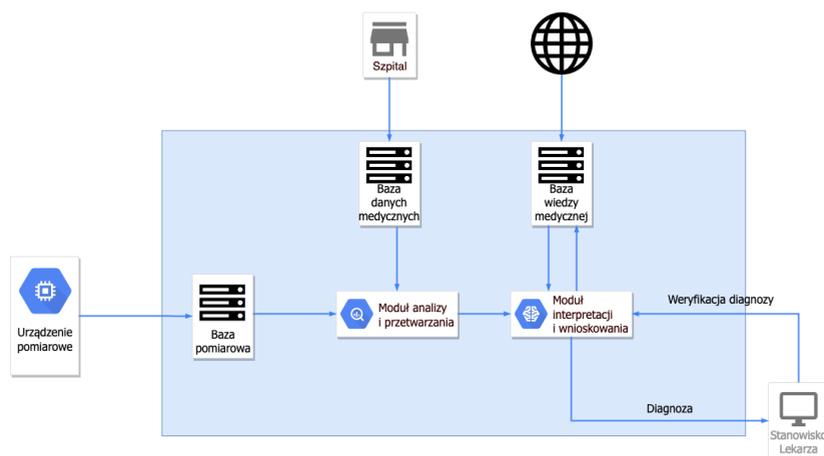
Artificial neural networks are particularly relevant in this context, designed to mimic the functioning of the human nervous system. Several key features characterize these systems:

- The ability to learn and develop knowledge,
- The ability to process information in parallel,
- The ability to work with incomplete data,
- Generation of approximate results,
- Self-analysis and statistical information transfer to the system.

Neural networks are built by connecting elements called neurons. Although a single neuron cannot create an intelligent device, neural networks – especially multi-layer ones with hidden layers – can effectively learn and analyze data. Hidden layers, located between the input and output layers, transform input signals, making it easier for the output layer to recognize patterns accurately. These networks find applications in various areas of medicine, such as:

Self-diagnosis of a patient's condition based on symptoms, advanced analysis of medical images to identify pathologies, filtering signals from medical devices, and searching for regularities in medical databases are examples of the implementation of neural networks in medicine. An example of implementing neural networks in medicine is the Watson Health Care system (Ahmed et al., 2017), developed by IBM. It is used to analyze medical cases where it is difficult to determine the diagnosis. Other examples of applications of artificial neural networks can be found in studies (Hireš et al., 2022; Wójcik et al., 2021).

Figure 1. Scheme of the platform used for measurement data archiving, processing, analysis, and interpretation



The article presents the application of decision tree algorithms in the analysis engine of the LETS Web platform, which is based on Internet of Things technology (IoT). This advanced platform uses various algorithms to analyze and process medical data to optimize the diagnostic process. The platform's structure is designed to support the continuous data flow between three primary databases: the measurement database, the medical database, and the medical knowledge database. The processing, analysis, interpretation, and inference modules are integral parts of the platform and critical elements that enable rapid and efficient diagnosis.

The diagram shown in Figure 1 illustrates a simplified architecture of a distributed platform for archiving, processing, analyzing, and interpreting measurement data. This platform provides the foundation for a complex medical decision-support system in an IoT environment.

The LETS Web analytics engine, a vital platform component, integrates data acquired from multiple sources – from hospital systems to specialized devices like monitoring vests (Przysucha et al., 2022) to databases containing disease information. The processing of this data is based on the use of selected deterministic, stochastic, and computational intelligence algorithms, which contribute to the speed and accuracy of diagnoses.

In the first stage, the data is cleaned using de-noising algorithms; then, it is segmented and analyzed using advanced computational techniques. The analysis engine also uses expert knowledge, including descriptions of known disease entities, which enables more precise inference and interpretation of results.

Decision tree algorithms implemented in the LETS Web platform play a vital role in diagnosing disease entities. They allow systematic and logical data analysis, leading to the development of practical diagnostic conclusions. The process culminates at the doctor's desk, which, using an intuitive user interface, verifies the diagnostic results and modifies them if necessary before they are stored in the knowledge base.

The collected data from the measuring device will go through early analysis such as:

- a. Segmentation of medical images: Using the collected medical images from imaging techniques such as CT, MRI, and PET, the algorithm will identify areas in the images that the doctor should pay special attention to in the diagnostic process. In addition, it will be used to determine the size, width, and volume of the pathological changes visible in the series of images.
- b. ECG signal analysis: ECG signals' transmission and early analysis will be designed to detect pathological changes in the myocardium separately.
- c. EIT analysis: With the help of impedance tomography, the analysis engine will be able to learn the correct lung function after pre-processing the data. Combined with other techniques, the analysis engine will be able to respond appropriately when changes occur in the lung region.
- d. Accelerometer and gyroscope readings: The analysis engine will be able to correlate data of the patient's position and movements with heart activity and lung capacity.

The main task of the LETS system analysis engine will be to interpret medical data correctly.

In this article, we present an essential part of the analytical engine of the LETS Web system, which is responsible for identifying cardiac disorders and disease entities. We show that techniques based on decision trees have been developed to effectively identify various disease states from the analysis of ECG data.

METHODS

ECG signal analysis is crucial in detecting pathological changes in the myocardium. Algorithms used in this process are used not only to process the signal but also to identify changes associated with individual heart refractions. The extracted parameters, such as the duration of the P, Q, R, S, and T refractions and the RR, PP, PR, RT, TP, QS, and QT intervals, form the basis for the doctor's diagnosis. Specialized algorithms make it possible to detect subtle changes in the electrocardiogram that may not be visible to the human eye, and their use requires immunity to noise and other ECG signal anomalies.

Ivaylo (Christov et al., 2004) developed an algorithm that detects QRS waveforms in real-time using an adaptive threshold that combines three parameters: slew rate, frequency rise in the signal, and low amplitude filtering. This algorithm, along with additional analysis of the RR interval, allows dynamic adjustment and adaptation to changing signal conditions, which makes it possible to detect anomalies effectively in any number of ECG channels.

Another approach, used by Qiuzhen Xue and Yu Hen Hu (Xue et al., 1992), uses a neural network to model the lower frequencies of the signal, which is nonlinear and nonstationary. The residual signal, which mainly contains the higher frequencies of the QRS waveform, is passed through a linear filter to localize the QRS complex. The residual signal, which includes primarily the higher frequencies of the QRS waveform, is then passed through a linear filter designed to detect the location of the QRS complex. They have also developed an algorithm that adaptively updates the matched filter template of the detected QRS complex in the ECG signal to adjust the template to the individual patient.

ECG signal analysis often encounters various types of artifacts, both technical and physiological. Technical artifacts can result from:

- poorly selected frequency response causing distortion, peak clipping, etc.
- influence of electrodes – e.g., metal electrodes would be scratched, then distortion and signal disruption may occur
- polarization phenomenon during the test. An extra layer of gel, incredibly inaccurately applied, may distort the reading – this causes the isoelectric line to float, among other things;

- interference from the network, in which case the isoelectric line will be jagged. Artifacts are prevented by using a so-called ECG with left-leg control. This uses an inverting amplifier onto which a 50Hz pass filter is clipped. The inverted signal is then applied to the primary amplifier. Superimposition of the primary and inverted signals takes place – removal of interference;
- camera noise – it gets rid of it by averaging the signal – smoothing;
- Common Mode Rejection Ratio CMMR – the solution is the proper selection of amplifier parameters;
- Signal loss caused by cables that are too long is removed by shortening the wires to minimize signal loss. Another group is physiological artifacts (originating from the body but not from the organ under study);
- originating from the muscles that support breathing (biopotentials) are especially prominent in respiratory arrhythmias. They are easily recognizable because they appear jagged lines in the ECG signal. The patient should be told to hold his breath to keep them out of the ECG signal. It is also helpful to use a 60,80 or 100Hz signal when examining the ECG;
- alternative methods should be used for involuntary muscle spasms, such as those caused by Parkinson's disease.

Classification trees, or decision trees, are a family of statistical methods that use diagrams, called undirected acyclic coherent graphs, to partition the data space into classes with similar properties sequentially. The development of decision trees began with the publication of a book by Breiman and co-authors (Breiman et al., 1984), which introduced the Classification and Regression Tree (CART) model. Another significant contribution to the development of these methods was the work of Quinlan (Quinlan et al., 1993) on the C4.5 algorithm, a modification of Breiman's proposal.

A decision tree consists of a root, where the recursive splitting process begins, and branches leading to subsequent nodes. The node from which the branches emerge is called the parent of the target nodes, descendants. A node with no children is called a leaf, containing information about the data belonging in the subspace to a particular class. A specific condition is checked

at each node, determining the choice of a further branch leading to the next node. A classification tree creates a model to classify future observations that are not yet assigned to a specific class.

The construction of a decision tree is based on a divide-and-conquer strategy, which is effective when there are few relevant variables but may be less effective in the presence of complex interactions. A decision tree usually presents a solution that is a local optimum rather than a global one. It is also possible that the process of variable selection by some decision tree models may be biased, leading to more frequent selection of quality or quantitative variables with more values.

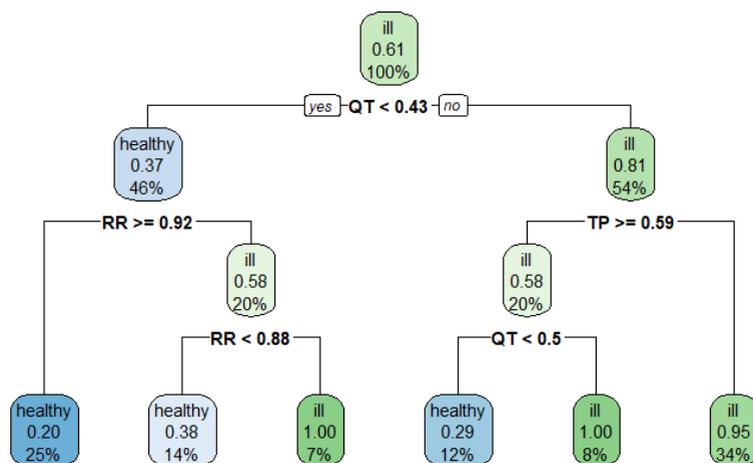
Decision trees are widely used in medicine. For example, CART-type trees were used to predict spontaneous intracerebral hemorrhage with a classification accuracy of 86% in a group of 347 patients (Gregório et al., 2018). Similarly, Selcer compared CART decision trees with logistic regression in diagnosing acute coronary syndrome in 3453 patients, achieving a classification accuracy of 76% with a sensitivity of 63% and specificity of 81% (Selker et al., 1995). Other studies have shown the use of CART trees in predicting major cardiovascular events in acute coronary syndrome (Chopannejad et al., 2022) or predicting death after acute myocardial infarction (Khera et al., 2021).

RESULTS

Three variants of the decision tree were constructed. In the first variant, the learning set consisted of 59 ECG readings, 23 of which were from healthy subjects and 46 from subjects with cardiac arrhythmias such as atrial fibrillation (AFIB), atrial premature beat (APB), Bigemina, and ventricular contractions (PVC). In the following two variants, the collection comprised 102 cases in which the proportions of healthy to diseased subjects were analogous. The disorder groups were Arrhythmia (Arrhythmia), Healthy (Healthy), Malignant Ventricular Arrhythmia (Malignant Ventricular Arrhythmia), ST-T Change (ST-T Change), Ventricular Tachyarrhythmia (Ventricular Tachyarrhythmia). The P, Q, R, S, and T waveforms were accurately determined for each ECG reading, and average times between waveforms, such as RR, PP, PR, RT, TP, QS, and QT intervals, were calculated.

These data were used to create a learning set, where the categorizing variable determined the patient's condition (healthy or sick), and the quantitative variables represented the above-mentioned mean times between refractions. The first experiment tested the possibility of constructing a decision tree for sick/healthy states. The constructed decision tree could recognize the given states with 100% efficiency. Figure 2 shows the diagram of the decision tree.

Figure 2. Diagram of the decision tree in the first experiment



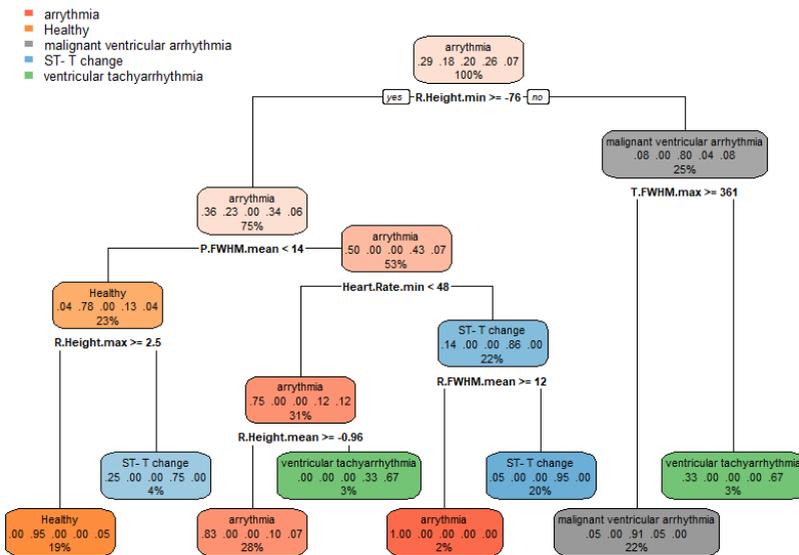
The classification tree shown in Figure 2 starts with an analysis of the QT interval, which divides the data into two main groups. The first group ($QT < 0.428$) includes 27 cases, of which 62.96% are healthy and 37.04% are sick. This group is further divided based on RR interval. Those with $RR \geq 0.9245$, accounting for 15 cases, have a higher chance of being healthy (80% healthy), while for $RR < 0.9245$, the chances of being sick increase, as illustrated by 12 cases with the majority sick (58.33%).

The second leading group of data, where $QT \geq 0.428$, includes 32 cases with most patients (81.25%). Further segmentation is based on TP time. If $TP \geq 0.588$ (12 cases), a further segmentation based on QT is observed, where those with $QT < 0.502$ are primarily healthy (71.43% healthy),

and those with $QT \geq 0.502$ are entirely ill (100% ill). In contrast, those with $TP < 0.588$ have a very high probability of disease (95% sick in 20 cases). All these segmentations lead to leaves that ultimately classify a patient as healthy or ill based on calculated parameters and established thresholds, demonstrating the use of classification trees in medical diagnosis and data analysis.

In the study's next step, the classification possibilities of various disease states were analyzed using a decision tree. As predictors, different combinations of ECG parameters, such as minimum R-wave height (R.Height.min), mean width at half height of P-wave (P.FWHM.mean), minimum heart rate (Heart.Rate.min), mean R-wave height (R.Height.mean) and maximum width at half height of T-wave (T.FWHM.max), allowed the identification of specific arrhythmia states and other abnormalities (Figure 3).

Figure 3. Specific arrhythmia states and other abnormalities



Arrhythmia was identified in two scenarios with different probabilities. The first scenario ([.83 .00 .00 .00 .10 .07]) for patients with a minimum R-wave height greater than or equal to -76 , a mean P-wave width of at least 14,

a minimum heart frequency less than 48, and a mean R-wave height greater than or equal to -0.96 . The second scenario ([1.00 .00 .00 .00 .00 .00 .00]) involved patients who additionally had a heart frequency of 48 or more and a mean R-wave width of at least 12. The healthy condition was classified with high probability (95%) for patients with a minimum R-wave height greater than or equal to -76 , a mean P-wave width less than 14, and a maximum R-wave height of at least 2.5. Malignant ventricular arrhythmia was found in cases where the minimum R-wave height was less than -76 , and the maximum T-wave width was at least 361. ST-T changes were identified in two conditions. The first ([.25 .00 .00 .75 .00]) is for patients with a minimum R-wave height greater than or equal to -76 , a mean P-wave width of less than 14, and a maximum R-wave width of less than 2.5. The second ([.05 .00 .00 .95 .00]) for patients with a minimum R-wave height greater than or equal to -76 , a mean P-wave width of at least 14, a heart rate of 48 or more, and a mean R-wave width of less than 12. Ventricular tachyarrhythmia was predicted in two cases. The first ([.00 .00 .00 .00 .33 .67]), where the minimum R-wave height was more significant than or equal to -76 , the mean P-wave width was at least 14, the minimum heart frequency was less than 48, and the mean R-wave height was less than -0.96 . The second ([.33 .00 .00 .00 .00 .67]) involved patients with a minimum R-wave height of less than -76 and a maximum T-wave width of less than 361.

The confusion matrix for tree no two is presented in Table 1. shown.

Table 1. Confusion matrix for the tree (variant 2) for predicting disease entities

| | Arrhythmia | Healthy | Malignant ventricular arrhythmia | ST – T change | Ventricular tachyarrhythmia |
|----------------------------------|------------|---------|----------------------------------|---------------|-----------------------------|
| arrhythmia | 26 | 0 | 0 | 3 | 2 |
| Healthy | 0 | 18 | 0 | 0 | 1 |
| Malignant ventricular arrhythmia | 1 | 0 | 20 | 1 | 0 |
| ST – T change | 2 | 0 | 0 | 22 | 0 |
| Ventricular tachyarrhythmia | 1 | 0 | 0 | 1 | 4 |

The learning set contained 102 records. Correctly identified based on the tree were 90. The construction of another variant of the tree focused on developing and verifying the effectiveness of the classification tree model in identifying and predicting arrhythmias, ST-T changes, and ventricular tachyarrhythmias. In this tree, decisions are based on more complex combinations and a more comprehensive range of ECG parameters, including R-wave height, P-wave width, heart rate, and additional parameters such as mean and maximum T-wave width. The tree applies more complex and precise predictions, considering subtle parameter differences, which allows for diagnosing specific arrhythmias and other cardiac conditions. Due to the large size of the tree diagram, only the verbal description of the classification is reported.

The study identified several cases of arrhythmia based on complex combinations of parameters:

Arrhythmia with high certainty (0.96) was diagnosed when the minimum R-wave height (R.Height.min) was at least -76 , the mean width at mid-height of the P-wave (P.FWHM.mean) was more significant than or equal to 14, the minimum heart rate (Heart.Rate.min) was less than 48, the mean R-wave height ranged from -0.96 to 3.21, and the mean width of the T-wave (T.FWHM.mean) was less than 212.

Arrhythmia with absolute certainty (1.00) was classified in several situations depending on several reciprocal parameters.

A healthy condition was classified (1.00) for those with $R.Height.min \geq -76$, $P.FWHM.mean < 14$, $Heart.Rate.mean < 128$, and $R.Height.max \geq 2.5$.

Malignant ventricular arrhythmia and ST-T changes were identified with absolute certainty (1.00) based on specific parameter values, as indicated in arrhythmia cases.

Ventricular tachyarrhythmia was diagnosed with a combination of parameters, such as $R.Height.min \geq -76$, and various combinations of P.FWHM.mean, Heart.Rate.Mean, and T.FWHM.mean, depending on R.Height and Heart.Rate.

The confusion matrix shows that the algorithm misclassified only one case.

Table 2. Prediction confusion matrix for experiment number 3

| | Arrhythmia | Healthy | Malignant ventricular arrhythmia | ST – T change | Ventricular tachyarrhythmia |
|---------------------------------|------------|---------|----------------------------------|---------------|-----------------------------|
| Arrhythmia | 30 | 0 | 0 | 0 | 1 |
| Healthy | 0 | 18 | 0 | 0 | 0 |
| Malignant vntricular arrhythmia | 0 | 0 | 20 | 0 | 0 |
| ST – T change | 0 | 0 | 0 | 27 | 0 |
| Ventricular tachyarrhythmia | 0 | 0 | 0 | 0 | 6 |

DISCUSSION AND CONCLUSION

The article discusses the advanced LETS Web system based on Internet of Things (IoT) technology and uses various algorithms for medical data analysis to optimize diagnostic processes. This system integrates data from multiple sources such as hospitals, specialized monitoring devices, and disease knowledge bases, enabling effective processing and analysis of medical information. A vital component of this system is the analytical engine, which uses advanced deterministic, stochastic, and computational intelligence algorithms to accelerate and improve diagnostic processes. Specifically, the article details the implementation and operation of a decision tree algorithm within the analytical engine, which is used to classify disease entities based on EKG analysis. The decision tree allows for systematic and logical analysis of EKG data, identifying various cardiac conditions. This algorithm utilizes complex decision criteria based on detailed electrocardiogram parameters, enabling precise diagnosis of even subtle changes in heart activity.

The study tested three variants of the decision tree to assess their classification capabilities in different configurations. Each tree variant was adjusted to specific diagnostic requirements, and various combinations of EKG parameters were used. This allowed for understanding how modifications in the tree structure affect the efficiency of identifying individual disease states.

The first variant of the tree focused on basic parameters such as QT and RR intervals, which allowed for the effective classification of the most common heart rhythm disorders. The second variant, more complex, included additional metrics such as P.FWHM (average width at half height of the P wave) and various statistics related to the R wave, enhancing its ability to identify more subtle and rare arrhythmias. The third variant was the most advanced, integrating multidimensional data analysis, including complex time patterns and frequency variability, enabling the recognition of complex patterns associated with advanced cardiac conditions, such as malignant ventricular arrhythmia and advanced ST-T changes.

The classification capabilities of each tree variant differed depending on the model used. Despite its simplicity, the first variant effectively identified typical rhythm disorders, making it useful in standard medical applications. Due to its greater detail, the second variant was more effective in diagnosing complex cases that simpler models might overlook. The third variant, using the broadest spectrum of data, offered the highest accuracy and was particularly valuable in clinical situations requiring deep analysis and precise recognition of rare or critical heart conditions. The study confirmed that the complexity and accuracy of the decision tree model directly affect its ability to precisely classify, emphasizing the importance of choosing the suitable model for the data specifics and diagnostic goals in medical practice.

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