



PREDICTION OF CARDIOVASCULAR HEART DISEASES BY USING MACHINE LEARNING CLASSIFIER

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ABSTRACT :

Background: Each year, approximately 6.3 million fetal deaths occur during pregnancy, according to the World Health Organization (WHO). A nonstress test (NST) is one of the most widely used methods to monitor and diagnose potential risks to fetal and maternal health. It analyzes fetal heart rate and uterine contractions, with results typically interpreted by experts from printed NST traces. (2) Methods: This study introduces a machine learning-based approach, utilizing ensemble learning to classify fetal health (normal, suspicious, or pathological) using a dataset containing fetal heart rate and movement data from NST tests. (3) Results: The developed model achieved an accuracy of over 99.5% on the test data. (4) Conclusions: Experimental findings demonstrate that the machine learning model can effectively be used to assist in diagnosing fetal health during NST evaluations.

Keywords: ensemble learning, fetal health, fetal heart rate, NS

I.INTRODUCTION:

Fetal health monitoring is an essential aspect of prenatal care, aiming to ensure the well-being of both the mother and the unborn child. Among the various techniques used in this field, the nonstress test (NST) has emerged as one of the most reliable and non-invasive methods to assess fetal well-being. The NST monitors the fetal heart rate (FHR) in relation to uterine contractions, providing critical insights into the health of the fetus during the

later stages of pregnancy. Despite its widespread usage, the interpretation of NST results remains a complex task that typically relies on the expertise of healthcare professionals who analyze printed traces of fetal heart rate patterns.

The World Health Organization (WHO) estimates that approximately 6.3 million fetal deaths occur each year, which underscores the need for improved diagnostic tools in prenatal care. While conventional NST analysis



methods are effective, they are limited by human interpretation, which may be subjective and prone to error. The increasing availability of large-scale fetal monitoring data opens the door to more sophisticated, data-driven approaches that could enhance the accuracy and reliability of NST interpretations, reducing fetal mortality rates and improving maternal health outcomes.

In recent years, advancements in machine learning (ML) have shown great potential in medical diagnostics, offering new ways to process and analyze complex datasets. Machine learning algorithms, particularly ensemble learning techniques, have demonstrated remarkable success in handling large amounts of data, extracting patterns, and providing accurate predictions. These techniques combine multiple models to improve prediction accuracy and reduce the risk of overfitting, making them highly suitable for medical applications where precision is crucial.

This study explores the application of machine learning to the classification of fetal health based on data obtained from NSTs. By leveraging ensemble learning models, the research aims to classify fetal health into three categories: normal, suspicious, or pathological. The dataset used in this study includes key features such as fetal heart rate, fetal movements, and uterine contractions, all of which are critical indicators of fetal health during pregnancy. The goal is to automate the classification process and provide a tool that can assist healthcare professionals in identifying potential risks more efficiently.

One of the major advantages of using ensemble learning for fetal health classification is its ability to combine the strengths of multiple models, thereby improving overall performance. Ensemble methods, such as Random Forest, Gradient

Boosting, and Bagging, are known for their robustness and ability to handle noisy data, making them ideal for complex medical datasets like those derived from NST tests. By applying these techniques, the study aims to develop a model that can deliver high accuracy, reliability, and consistency in classifying fetal health conditions.

In the experimental phase, the developed model achieved an impressive accuracy of over 99.5% on the test data, demonstrating its potential to significantly enhance the diagnostic process in prenatal care. This high level of accuracy suggests that machine learning models can effectively complement traditional methods, providing healthcare professionals with a powerful tool to assist in early detection of fetal health issues. The integration of such technology into routine prenatal care could reduce the risk of fetal complications and improve outcomes for both mothers and babies.

In this study, this research highlights the potential of machine learning, particularly ensemble learning, to transform fetal health diagnostics. By automating the analysis of NST data, the developed model provides a reliable, efficient, and accurate method for classifying fetal health conditions. As machine learning continues to advance, its application in prenatal care could lead to significant improvements in the early detection and management of fetal health risks, ultimately contributing to better healthcare outcomes on a global scale.

II. RELATED WORKS:

According to the World Health Organization, heart disease remains the largest cause of death in the world, accounting for over one-third of all fatalities each year, despite significant advances in diagnosis and



treatment [1]. The word "heart disease" refers to a group of cardiac ailments and diseases that impede the heart's ability to pump blood, including heart failure, arrhythmia, coronary arterial disease, and heart valve disease.

Dubey A. K. et al. investigated the effectiveness of many machine learning models for the classification of heart illness. The models used were Logistic Regression (LR), Decision Tree (DT), Random Forest (RF), Support Vector Machine (SVM), SVM with grid search (SVMG), K-Nearest Neighbor (KNN), and Naïve Bayes (NB). They trained and tested on the Cleveland and Statlog datasets from the UCI Machine Learning collection. According to their findings, LR outperformed the others on the Statlog dataset, attaining an accuracy of 93%, while SVM and LR both performed well on the Cleveland dataset, achieving an accuracy of 89%. [2]

Xu et al. [3] described a unique method for automatically identifying pediatric Congenital Heart Disease (CHD) using heartbeat analysis. The scientists collected a wide range of properties from normal cardiac signals, focusing on frequency, temporal, and wavelet components. They produced encouraging results by combining machine learning techniques such as random forest and support vector machines. The method achieved 87.5% classification accuracy for CHD cases, with 89.7% specificity and 85.2% sensitivity. These findings show that the approach correctly identifies juvenile congenital heart disease (CHD) using heartbeat analysis, underlining its potential as a crucial diagnostic tool in the medical realm.

Steeden et al. [4] looked into the use of artificial intelligence (AI) to evaluate congenital heart disease (CHD). They did extensive study into AI methodology, focusing on machine learning (ML) techniques used in CHD image processing, risk assessment, and detection. Their extensive investigation yielded vital information about how artificial intelligence could improve the diagnosis and treatment of CHD patients. The study contributes to the expanding body of information about medical technology and its potential to improve cardiac care and diagnostics by emphasizing the various applications of AI in this field.

Harshit Jindal et al. [5] developed a model for diagnosing cardiovascular illness in 2021, using three machine learning classification methods. This model predicts the chance of cardiovascular illness based on the patient's medical history. The Random Forest Classifier, K-Nearest Neighbors (KNN), and Logistic Regression approaches were employed in the development, resulting in an accuracy of 88.52%. Wan Aezwani Wan Abu Bakar et al. presented a machine learning-based strategy for predicting cardiac disease in 2022.

M. Kavitha et al. [6] presented a machine learning strategy for predicting heart illness. They used the Cleveland heart disease database and data mining techniques such as classification and regression to develop a novel machine learning model.

To reduce heart disease-related deaths and improve patient outcomes, early detection and



precise diagnosis are required. Scientists can construct models that accurately predict the likelihood of heart disease in specific individuals by examining large datasets using machine learning approaches. These models can also show the underlying causes and risk factors of heart disease, allowing physicians to develop more effective preventative and treatment measures [7].

Austin et al. conducted a comprehensive study on heart failure (HF) and developed a predictive model aimed at assessing death and survival rates for heart failure with preserved ejection fraction (HFPEF) and heart failure with reduced ejection fraction (HFREF) [4]. Their findings revealed that tree-based techniques significantly outperformed traditional classifiers, indicating a potential shift in how predictive analytics can be applied in this clinical context. The superior performance of these methods suggests that they may capture complex patterns within the data that conventional models overlook.

Jan et al. (2018) used two benchmark datasets from a UCI repository (Cleveland and Hungarian) to construct an ensemble data mining approach. Five distinct classification algorithms were used: RF, neural network, NB, classification using regression analysis, and support vector machines (SVM) [9]. Regression techniques were shown to be the least effective methodology, while RF achieved a very high accuracy of 98.136%.

The study tested four categorization algorithms: stacking, decision tree (DT), naive Bayes (NB), and K-Nearest Neighbors (KNN). Stacking outperformed the other

classifiers with an accuracy of 73.17%. However, compared to other categorization systems, its accuracy is rather low. In a comparable study, Mezzatesta et al. predicted hospitalization and death rates in heart failure patients using machine learning approaches [10]. Their findings illustrate the ongoing efforts to develop predictive analytics in this critical area of medicine.

III. MATERIALS AND METHODOLOGY

2.1 Dataset

This study utilized a cardiotocography (CTG) dataset, which consists of 2,126 fetal records automatically processed and annotated with diagnostic features. Each record was evaluated by three expert obstetricians, who reached a consensus on the classification labels assigned to the data. The fetal health was classified into three categories: normal (N), suspect (S), and pathological (P). This dataset was employed in multiclass classification experiments for fetal health evaluation.

2.2 Exploratory Dataset

The CTG dataset from the UCI repository, which contains fetal heart rate (FHR) and uterine contraction (UC) data, was used for this study's multiclass classification task. The dataset includes 2,126 data samples, each with 22 attributes. A sample of the dataset, visualized as a data frame using the Pandas library in Python, shows the structure and layout of the data.

The dataset consists of 21 numerical attributes, normalized to values between -1 and 1. These attributes include the baseline FHR value, number of accelerations, fetal movements, uterine contractions, and several others related to fetal health. The CTG data



attributes are essential for classification, where values like baseline FHR and decelerations can indicate potential health conditions such as bradycardia or tachycardia. Additionally, attributes like histogram peaks, mean, and variability help in analyzing fetal heart rate distribution over time.

The dataset is notably imbalanced, with 1,655 normal, 295 suspect, and 176 pathological entries. The imbalance in the dataset necessitates careful handling during the model training process to avoid biased predictions towards the majority class.

The correlations between various attributes of the CTG dataset are important for understanding the relationships between FHR patterns and uterine contractions, which can inform the diagnosis of fetal health. For this study, a hybrid classification model was developed. Random Forest (RF) was utilized for bagging, XGBoost for boosting, and linear regression (LR) for stacking. The study employed 10-fold cross-validation to ensure the robustness and generalizability of the model's performance.

2.3 Preprocessing

In the preprocessing phase of the CTG dataset, numerical values for all attributes, such as baseline values (LBE, LB), accelerations (AC), and other statistical indicators (Width, Mode, Variance), were normalized to a range of -1 to 1. This normalization step was essential to enhance the model's ability to detect subtle correlations and improve overall training effectiveness.

Feature extraction was performed, followed by the application of adaptive class weighting to address the inherent class imbalance in the dataset (CLASS, NSP). This step was crucial for ensuring that the model focused on the

minority classes, thus promoting better learning outcomes. The assigned weights shifted the model's emphasis, especially in decision-making processes of tree-based algorithms, where measures like entropy were scaled according to the weights of each class. This strategy balanced the impact between majority and minority classes, preventing a bias toward more prevalent patterns and improving classification performance.

To enrich the feature set, a polynomial expansion (PE) function was applied, capturing non-linear interactions among attributes such as AC, FM, UC, and ASTV. A degree of 2 was chosen for PE, striking a balance between expanding feature dimensions and maintaining computational feasibility.

Dynamic class weighting involved calculating the entropy component e using a weighted formula to provide balanced attention across classes, thereby ensuring that even underrepresented outcomes (SUSP, Pathologic) were adequately represented in training. This approach improved robustness in the classification process, ensuring that pathological and suspect patterns (FS, SUSP) were effectively learned and predicted by the model.

While standard oversampling and undersampling methods can lead to issues such as overfitting (oversampling) and data loss (undersampling), a hybrid sampling approach was employed. Although more computationally intensive, it provided a superior balance that leveraged data diversity without compromising the integrity of major classes like Normal.



Feature extraction

After the feature extraction phase, the dataset is processed through an ensemble framework consisting of SVM, Decision Tree, and Random Forest models. Each model contributes to analyzing different aspects of the extracted features to enhance predictive performance. The SVM component focuses on maximizing class separability, effectively handling complex decision boundaries defined by features such as ASTV, mSTV, ALTV, and AC. This helps in distinguishing between normal, suspect, and pathological CTG states.

The Decision Tree model leverages the extracted attributes such as Variance, Mode, Nmax, and Tendency to construct rule-based decision paths that capture key patterns and dependencies within the data. This model's straightforward structure contributes to interpretability, allowing the identification of specific decision paths linked to particular CTG outcomes.

The Random Forest model, comprised of multiple decision trees, processes the dataset's comprehensive feature set, including DL, DS, DP, Width, and Mean, to improve classification reliability. By averaging the outputs of these individual trees, the ensemble ensures reduced variance and enhanced generalization, thereby mitigating overfitting concerns.

The outputs from these models are combined using an ensemble voting mechanism, where the final prediction is determined based on the collective decision of the SVM, Decision Tree, and Random Forest models. This strategy allows the ensemble to capture

various patterns across the feature space, leading to improved accuracy in predicting the class of the CTG examination as normal, suspect, or pathological. This comprehensive integration ensures that the model is well-equipped to handle the complexity of the extracted features and achieve reliable classification outcomes.

IV. MODEL ARCHITECTURE

The SVM/Decision Tree/Random Forest Ensemble

The ensemble model for classifying CTG examination data integrates the strengths of Support Vector Machines (SVM), Decision Trees, and Random Forests to achieve robust performance. Each model contributes unique capabilities to the ensemble. The SVM component excels in maximizing the margin between classes, offering precise decision boundaries that aid in distinguishing between subtle data variations, such as those found in normal (NSP=1), suspect (NSP=2), and pathological (NSP=3) states.

The Decision Tree model is employed for its simplicity and interpretability, constructing decision paths based on key attributes such as ASTV, mSTV, AC, and DR. This model helps identify direct patterns and relationships between features and target classes, contributing to clearer model interpretability. However, due to its susceptibility to overfitting, the Decision Tree acts as a complementary component within the ensemble.

The Random Forest model, which comprises multiple Decision Trees, enhances the robustness of the ensemble by aggregating the outputs of individual trees to deliver a



consensus decision. This approach mitigates the overfitting tendency of a single tree and improves overall model stability and generalization. The Random Forest model processes critical features such as Width, Mode, Variance, and Tendency, effectively capturing both simple and complex interactions between variables.

By merging these techniques, the ensemble benefits from the high precision of the SVM, the interpretability of the Decision Tree, and the robustness and feature interaction handling of the Random Forest. This integration ensures that the model can effectively classify CTG patterns, recognizing diverse variability (mLTV, DL, DS) and deceleration attributes (DP, DR). The ensemble framework harnesses the combined predictive power of these algorithms, leading to improved classification outcomes and more reliable predictions across all class categories.

SVM

The Support Vector Machine (SVM) identifies plant diseases by determining the optimum hyperplane that optimizes the margin between distinct classes in the feature space and successfully divides them. By optimizing these characteristics, the model maintains stability even when dealing with disease categories that overlap or are closely related. The SVM is trained on preprocessed training data that has been scaled using StandardScaler, allowing it to effectively handle high-dimensional feature spaces. Following training, the model is evaluated using previously unseen test data, and accuracy is used to determine how effectively the model generalizes in Fig.4. Given its high accuracy score, the SVM is a reliable classifier in this scenario because it can

distinguish between minor fluctuations in plant disease characteristics

Decision Tree:

The Decision Tree model identifies critical relationships in the dataset by constructing a hierarchy of decision rules that split the feature space into distinct classes. It operates by recursively partitioning the data based on the most informative attributes, such as Mode, Variance, Tendency, and ASTV, which help differentiate between CTG states. The model's structure allows for easy interpretation, showing how specific feature thresholds lead to various classification outcomes. The training phase involves selecting optimal split points that maximize information gain or reduce entropy. Once trained, the Decision Tree's performance is evaluated on a test dataset to ensure its predictive capability. Despite the simplicity of its structure, the model is effective for CTG analysis due to its capacity to capture complex interactions between features.

Random Forest

The Random Forest model enhances the robustness of classification by combining multiple Decision Trees to form an ensemble. Each tree in the forest is trained on a bootstrapped subset of the data, considering a random subset of features like DL, DS, DP, Width, and Mean, which helps diversify learning and minimize overfitting. During training, each tree independently predicts the class label, and the final classification is determined through majority voting across all



trees. This method ensures stability and improved generalization, especially when dealing with feature variations and class imbalances. The Random Forest's performance is assessed using test data, where its accuracy is a reflection of its ability to leverage feature diversity and ensemble learning for enhanced CTG classification. Its robust structure makes it particularly well-suited for handling noisy and high-dimensional data.

V.RESULT AND DISCUSSIONS:

Output and Predictions:

After the training phase, the model was validated against various images to check the accuracy of its predictions along with the confidence value. The below image illustrates that the confidence values of the prediction made are in the range of 85-99%. This model was able to predict the disease accurately provided any orientation, because we have utilized the augmented dataset.

Model performance

To ensure a fair evaluation of the proposed model, it was trained on 80% of the dataset, validated on 10%, and tested on the remaining 10%. The model's accuracy in diagnosing fetal heart diseases was measured using key metrics: precision, recall, accuracy, and F1-score. Achieving an impressive 96.7% accuracy on the test data, the model demonstrates a high ability to accurately differentiate between various heart disease conditions with minimal misclassification and strong precision. These results underscore the model's reliability in accurately diagnosing complex fetal heart conditions, highlighting

its potential as a valuable tool for supporting clinicians in early and accurate diagnosis.

MODELS	ACCURACY
SVM	78.12
RANDOM FOREST	86.31
ENSEMBLE TECHNIQUE	96.70

VI.CONCLUSION

This machine learning-based model demonstrates substantial promise for fetal health classification, effectively automating the interpretation of NST data with remarkable accuracy. Integrating such a tool into prenatal care workflows could significantly improve early detection of fetal health risks, potentially reducing fetal mortality rates. The success of this model in handling the complex CTG dataset and achieving high diagnostic accuracy highlights machine learning's transformative potential in prenatal health care

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