International Journal of
INTELLIGENT SYSTEMS AND APPLICATIONS IN ENGINEERING
ISSN:2147-6799 www.ijisae.org Original Research Paper

A Method for Predicting and Classifying Fetus Health Using Machine Learning

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Submitted: 11/11/2022 **Revised:** 20/01/2023 **Accepted:** 09/02/2023

Abstract: Each year on average 3 million pregnant women and newborns die every 15 seconds mostly from preventable causes, according to the estimates released by UNICEF, WHO, the UN population division, and the World Bank group. Birth is a joyful occasion everywhere. In the United States, complications during pregnancy or delivery result in the deaths of approximately 700 women annually. Due to covid, traffic in metropolitan areas, and long office hours, it is currently extremely difficult to leave the house even for a medical checkup. Next, imagine that a pregnant woman needs to go to the doctor for her regular checkup. As part of her examination, she will travel to hospitals, laboratories, and other locations. As a result, she will have to spend a lot of money and work a lot, which will make her exhausted, which is bad for both her and her unborn child. A fetus is a child that is still in the embryonic stage when it is born. During this time, the fetus grows and develops, requiring regular examinations. We are all aware that a pregnancy lasts for nine months, during which time a variety of factors can cause the newborn to be disabled or die, which is a very serious situation that must be avoided. One of the most important tools for analyzing the health of the fetus in the womb is performing a CTG (continuous cardiotocography), which is commonly used to evaluate the heartbeat and the health of the fetus during pregnancy.

Keywords: *Gini index, Machine Learning, Prediction analysis, Random Forest Classification.*

1. Introduction

The health of the unborn child is known as fetal health. The fetal mortality rate in the United States in 2019 was approximately 5.6, or approximately 6 babies per 1000 babies, according to the sources. By knowing about fetal health and taking the necessary precautions for fetal health, the rate of fetal mortality can be decreased. There are additional constant features that can be used to determine the health of the fetus, such as acceleration, baseline value, histogram mean, kicks, etc., but the methods used to determine the health of the fetus from these values differ. Therefore, to predict fetal health with an emphasis on accuracy, our strategy involves utilizing and applying machine learning principles to the dataset we have.

The term dataset refers to a collection of records. These records contain the values that provide some meaning and are crucial in determining the baby's health. We are utilizing Kaggle's dataset for this prediction. Although there are approximately 21 features and 21 records in the dataset, our prediction only considers only 5 features. Pre-processing is the name of this procedure. The Random-Forest-Classifier algorithm will produce the output as Normal, pathologic, and suspect if we provide these five features as its input[1].

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The process of selecting the data and rejecting all other features is referred to as pre-processing or data pre-processing. Pre-processing refers to selecting features based on the percentage of their role in predicting health. To obtain accurate and unambiguous data, we also clean our datasets during this procedure by removing data with null feature values[1].

One machine learning method for classification and prediction is the Random Forest Classifier. To enhance the dataset's predictive accuracy, random forest classifiers make use of many decision trees that are constructed from various subsets of the dataset and take into account the average. There are two major distinctions between the Random Forest Classifier and the Decision Tree Classifier. The first is about the data from the training set. While the Random-Forest-Classifier requires multiple training datasets, the Decision Tree Classifier[2], [3] only requires one training set. The number of trees needed for prediction is another difference.

Based on the number of training datasets, Random Forest Classifiers require more than one tree for prediction, whereas Decision Tree Classifiers only require one tree. We only get one output from the Decision Tree Classifier because it only has one tree. However, because there are more trees in the Random-forest-Classifier[4][1], there are more outputs, and most of these outputs will be used to produce the final result. We can predict the outcome with greater accuracy and less overfitting when we apply the majority. In data science, the term overfitting refers to the condition in which a constructed model matches its training data exactly.

The database we used for implementation is MongoDB. For prediction, we are storing the user's information, login credentials, and report values in the database. The user will be able to view or download the previous result because the prediction data will be stored and accessible to them. PDFKIT is a Python module for converting an a.html file to a pdf file. With the help of web kit wkhtmltopdf, we will convert the.html file into a series of characters and create the pdf file from these characters. The user will receive the PDF via email if necessary, and it will be kept in the local folder. The pdf report file is sent to the user's email address via SMTP or Simple Mail Transfer Protocol. We chose SMTP for implementation because it takes less time to send a message to the end user than other libraries do. Additionally, since we are sending an email rather than downloading it at the user's end, we can guarantee that the user’s data is safe with us.

The main backend program uses Flask. Flask is a micro framework that gives us features and helpful tools for making a web app. We choose Flask over other frameworks because it is easy to use, has good documentation, is simple to write code, and has a large developer community that makes errors easy to debug.

Before the fetus is delivered from the woman's womb, it is difficult to fetch information about the fetus during pregnancy. Therefore, the information is not readily available, obstetricians rely on indirect information to assess the fetal condition. One of the most important pieces of information is the fetal heart rate, but electronic fetal heart monitoring has limitations that make it difficult to keep accurate records of communication and time management. Cardiotocography, which consists of distinct signals and is primarily utilized for recordings of the fetal heart rate the primary method by which obstetricians rely on the information is an additional component. However, doctors are increasingly noticing that FHR patterns exhibit significant intra and inter-observer variability. However, there is a possibility that an incorrect diagnosis of fetal pain will necessitate unnecessary interventions[1]. As a result, the primary goal of the study is to use machine learning algorithms to classify the methods. While a doctor may make mistakes, a prediction algorithm might do a great job in this situation and help monitor the results and provide a more accurate analysis than a doctor or someone else could. Premature birth (PTB) is a serious problem for public health that affects families and society in negative ways. This is one of a kind. Both neonatal mortality and morbidity are the leading causes of infant death and illness worldwide and the second leading cause of infant loss in developing nations. PTB, a child who is now five years old, has made significant progress over the past two decades. Healthcare is the subject of a significant body of research. Medical care became available during pregnancy and delivery. Researchers and professionals investigate a variety of successful strategies for reducing the number of preterm births and complications in pregnant women. These efforts include healthcare services. Given to all pregnant women to keep them safe from PTB and other health issues, interventions are designed to raise women's awareness of early warning signs of problems during pregnancy. An essential component of the examination is a pregnant woman's maternal history, neonatal research aims to provide specific treatments to newborns[1].

The healthcare industry has a significant impact on people's lives all over the world. Despite recent medical advancements that have improved quality of life and decreased the number of deaths from cancer, heart disease, and other diseases, there is still a large population that does not have access to the best medical treatment. The effectiveness of routine examinations and prompt treatment in preventing fatalities or serious illnesses is increasingly being documented. However, these aspects of health care are neglected, particularly in many low-income nations, where inadequate medical services frequently result in multiple deaths. In recent decades, artificial intelligence has made rapid progress and has been successfully utilized in several significant fields, including finance, governance, and others. The methods of machine learning have a lot of potential applications in the field of health care, particularly for detecting and preventing deaths that could have been avoided. This research paper examines the use of ultrasound images of the fetus to identify abnormalities in the fetus during the first trimester of pregnancy.

Machine learning-based classification approaches for early diagnosis and prediction of fetus abnormalities are proposed in this study as a means of identifying the abnormalities. With advancements in imaging classification techniques and machine learning approaches, abnormality detection during the first trimester of pregnancy has greatly improved. Manuscript.

2. Related Work

[5]Classification of the CTG For anticipation Fetal risk using Machine Learning techniques. AUTHORS: Hakan Sahin, Abdulhamit Subasi

Based on CTG data, the purpose of this study was to evaluate the classification performance of eight distinct machine-learning approaches. The obstetricians refer to the CTG as a continuous electronic record of the baby's heart taken from the mother's abdomen, implying that the record will be comparable to an ECG. Additionally, the CTG is a technique for measuring fetal well-being. Using the data from the various fetal health determining attributes, this machine learning technique aims to classify the final output as pathological or normal. They used datasets consisting of 1831 instances and 21 attributes. In their paper, they showed that random forest had the highest accuracy of 99.2%, support vector machines had the highest accuracy of 98.42%, and KNN had the highest accuracy of 98.96%. Other methods also predicted with up to the same accuracy. They demonstrated that there is no significant difference in the classifier's accuracy.

[6]Variable-length Accelerometer Features and Electromyography to Improve Accuracy of Fetal Kicks Detection During Pregnancy Using a Single Wearable Device. AUTHORS: Marco Altini ,Elisa Rossetti , Michael J Rooijakkers , Julien Penders , Dorien Lanssens , Lars Grieten , Wilfried Gyselaers.

In their exploration, they proposed utilizing a solitary wearable gadget in the mid-region to work on the fetal kick during pregnancy. AI was utilized to contrast their result and the anticipated result from the known datasets, which were equipment related. Fully intent on diminishing misleading up-sides and expanding positive prescient worth (PPV) when a reference accelerometer beyond the stomach region is inaccessible, they offer two systems for further developing fetal kick location exactness with a solitary wearable gadget. Variable-length accelerometer highlights were one of the two systems they proposed. One more choice was to join electromyography and accelerometer information because the two strategies planned to give more relevant data about maternal development utilizing a solitary wearable gadget. They contrasted their strategy with a framework with six accelerometer sensors and 22 accounts and reference maternal comments, featuring how variable-length highlights and EMG elements can further develop kick discovery PPV by up to 11% and 10%, individually.

[7]A Hybrid Filter-Wrapper Attribute Reduction Approach For Fetal Risk Anticipation. AUTHOR: Subha V., Murugan D., Boopathi A. Manivanna

In their paper, they analyze the Cardiotogram (CTG) data and use one of the machine learning concepts are known as Support Vector Machine to predict fetal risk. Additionally, they developed a hybrid approach that combines the information gain attributes with the opposition-based firefly algorithm, or OBFA. They suggested these approaches to extract the most relevant features, which will enhance the SVM's classification performance. Additionally, they demonstrated that the proposed hybrid approach outperforms the alternatives.

Table 1: Output of various SVM accuracies

	Data set	***Accuracy***
Without FS	Full feature set	88.75
With FS	IG	89.47
	FA	91.92
	OBFA	92.85
	Hybrid IG-OBFA	96.24

The results of various SVM accuracies are presented in Table 1. Feature selection is represented by the FS. According to the table above, their Hybrid-OFGA method accuracy is 96.24 percent.

[8]Genetic Algorithm Based Feature Subset Selection for Fetal State Classification AUTHOR: Subha V, Murugan D, Boopathi A. Manivanna.

A method for classifying cardiogram data using a multiclass support vector machine (MSVM) and an optimized Genetic Algorithm (GA) featured subset was presented in their paper. Additionally, various performance metrics have been evaluated, and the experimental results show that an optimized set performs better than a full feature set. GAs are stochastic search algorithms based on natural selection and the process of evolution. The first step is to select a population of potential solutions. Traditionally, this population encodes everyone as a binary bit string. Genotypes or chromosomes are the names given to these bit strings.

Table 2: Comparison of average accuracy of MSVM

Data set	***Accuracy (average)***
Set of Full feature	88.75
Set of the Training set	94.85
Set of Testing set	91.35

The average accuracy of MSVM with and without feature selection is compared in Table 2. With the full feature set and the optimal feature set, the average accuracy is 91.35 percent.

[9]Determination of Fetal State from Cardiotocogram Using LS-SVM with Particle Swarm Optimization and Binary Decision Tree. AUTHOR: ErsenYJlmaz ÇaLlarKJlJkçJer

To ascertain the fetal state, we classify the cardiotocography with the help of a binary decision tree and a least squares support vector machine (LS-SVM). Particle swarm optimization is used to optimize the parameters of LS-SVM[4], [10]. The method's robustness is evaluated through 10-fold cross-validation. The overall accuracy of the classification is used to assess the method's performance. Cobweb representation and receiver operating characteristic analysis are also presented to evaluate and illustrate the method's effectiveness. The proposed method has a remarkable classification accuracy rate of 91.62%, as shown by the results of the experiments. Suykens and Vandewalle first proposed LS-SVM as an improvement to the SVM regression formulation. The modification's goal is to solve a set of linear programming problems rather than a quadratic programming problem[1]–[26].

3. Proposed Work

Generating a report and analyzing the results of tests on pregnant women to identify and determine the health of the fetus. A website built with a random forest classifier prediction algorithm based on datasets and the results of numerous previous tests will provide a solution. by utilizing the results of tests performed on pregnant women as input and predicting whether the fetus will be healthy, abnormal, or pathological. The same information will be included in the report and sent to the user via MAIL as a PDF.

- Obtaining the dataset and creating a clean dataset.
- Training the dataset to achieve maximum accuracy.
- To design an interface that is easy to use.
- To use the provided input to generate the PDF of the result from a package.
- To send the PDF to the email of the user.

The flowchart of the learning model is shown in Figure 1 and the proposed model and system architecture are shown in Figures 2 and 3. The random forest classifier generates a set of decision trees by using the arbitrary portion of the training dataset. It combines the votes from various decision trees to select the final class for the test objects. Breiman's 2001 random forest classifier was categorized into three classes. Let ‘A’ is the dataset comprising of ‘C’ data points and ‘f’ features containing ‘N’ classes, B_i, i=1,2,..., N. A distinct subset is drawn from the dataset ϕ_K chosen at random from the dataset ‘A’ in such a way that $\phi_K \subseteq A$ (bootstrap sample), containing the set of features S, $S \subseteq f$. A tree is trained with it $h(x, \phi_K)$ as a weak classifier for the training set, where the input value is x.

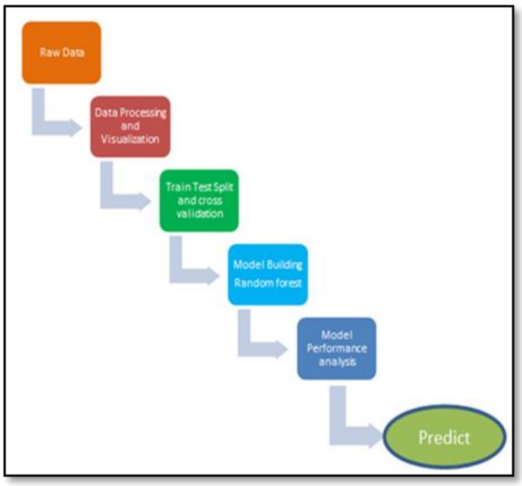

Fig 1. Learning model flow

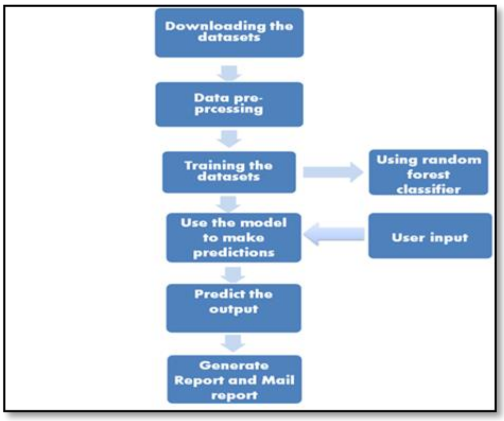

Fig 2. Proposed learning model flow

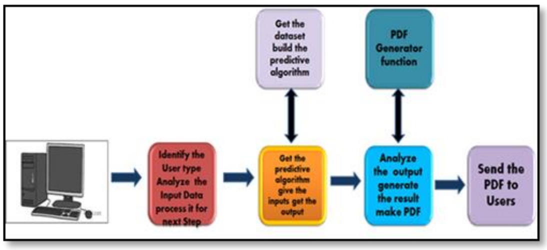

Fig 3. Proposed system structure

Table 3: Class distribution of CTGs

State of fetus	*Abbreviations*	*FHR recordings*
Normal	N	1655
Suspect	S	295
Pathologic	P	176
Total		2126

Tibshirani and Wolpert et al. (Tibshirani 1996) out-of-bag estimates were proposed by Wolpert and Macready in 1999 to estimate the generalization error. According to Breiman (2001), these estimates are as accurate as test data of the same size as the training set. By putting aside a small amount of, the out-of-bag error can be calculated ϕ_K as out-of-bag. All k trees are affected. In the end, the class of the vector in the out-of-bag that received the most votes from the trees is predicted to be that class. In the estimation of the out-of-bag error estimate, this class is compared to the true class.

Classification results are presented using precision, recall, and the F-measure. The proportion of instances that belong to a class, also known as precision or positive predictive value (PPV), is the definition of precision. From all instances, including TP(True Positive) and FP (False Positive), which the classifier identified as belonging to this particular class.

$$Precision = \frac{TP}{TP+FP} \qquad (1)$$

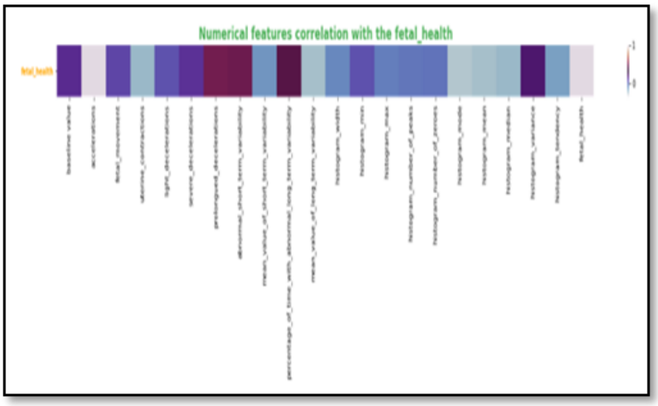

Fig 4. Explanation of features

The proportion of instances classified in one class out of the total instances belonging to that class is what is referred to as recall or sensitivity. TP(True positive) and FN (False Negative) are included in the total number of instances of a class.

$$Recall = \frac{TP}{TP+FN} \qquad (2)$$

Precision and recall combined to form F-measure and defined in equation 3.

$$F - measur = (2 * Precision * recall) \Big/ (Precision + Recall)$$

(3)

The Supervised ml algorithm RF is used in Classification and Regression problems. Using various samples, it creates decision trees and uses the majority vote for classification and the average for regression. Simply put, an ensemble is the combination of multiple models. As a result, predictions are made based on a collection of models as opposed to a single model.

Ensemble employs two approaches:

1. **Bagging:** It replaces sample training data to create a different training subset and uses majority voting as the final output[21].
2. **Boosting:** It creates sequential models so that the final model has the highest accuracy, transforming weak learners into strong learners.

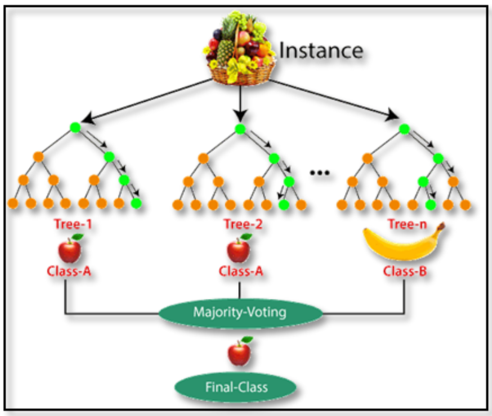

Fig 5. Random Forest classifier example

The Steps followed by Random Forest Algorithm[1]:

- From the k records of the data set, n random records are selected for Random Forest.
- For all the samples, individual decision trees are created.
- Output is generated by each decision tree.
- Collective Voting or averaging is considered the final output for regression and classification, respectively.

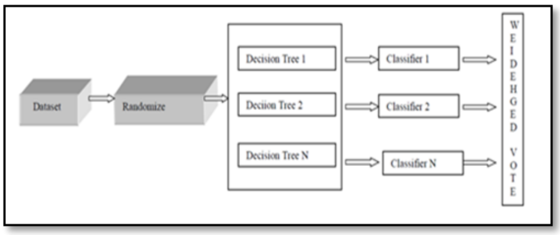

Fig 6. Random Forest classifier working

Random forest diversity, immunity to the curse of dimensionality, parallelization, train-test split, and stability are the important characteristics of a random forest classifier. The predictive power is increased by the hyperparameters which are n_estimators, max_features, and mini_sample_leaf.

Sorting based on Random Forest: Because the prediction in a medical database is unbalanced, the traditional Random Forest classification method is used. The algorithm is improved to provide high prediction accuracy and the highest possible tolerance level for abnormal datasets. The Random Forest algorithm consists of these two phases. The bootstrap method is used to first extract the number of subsamples from the original samples, after which decision trees are created for each sample. Second, a voting procedure and the classification of the decision trees are carried out by the algorithm. For the prediction's outcome, the classification with the most votes are chosen.

Step 1: The dataset is broken up into the test, validation, and training sets. From the original dataset, the data are randomly extracted into an X+1 dataset. Each set of data is used to construct the bootstrap method. X sets from the X+1 dataset serves as the training set and the remaining sets as the validation set. The test dataset is taken from the uncollected sample.

Step 2: Build the classifier based on the Random Forest. A random forest model is constructed from the inputs of N training sets. The decision tree is built in its final form. Let T represent the set of data points.

$$T=\{(x_1,y_1)(x_2,y_2)\dots(x_n,y_n)\}$$

Training Samples (N) are given as,

$$N=\begin{bmatrix} xA1 & \cdots & xz1 \\ \vdots & \ddots & \vdots \\ xAn & \cdots & xZn \end{bmatrix}$$

Step 3: Evaluate the precision of each sub-classifier to determine the weighted value. The validation set is then used as the model's input after the dataset is classified.

Step 4: The test set is now used as input, and the model's performance is evaluated.

Step 5: Additionally, each sub-classifier K's classification result is evaluated, it is the classification weight result.

Proposed Algorithm

Input: Features T($M_n Z_n$)

Output: Normal, Pathological, or Suspect

Random Forest:

1. Highlights check

For each component T($M_n Z_n$)

Track down the best separation

2. best separation

For each column in the dataset

M= all columns <= current M

Z = all segments > current Z

compute the score

On the off chance that the score is ideal, update it

3. Characterize the Gini File (M_split, Z_split, N)

P(M)=M_i/N_i

P(Z)=Z_i/N_i

For each (i=1…n)

P = Likelihood of ΣM_i+=P^2

P = Likelihood of ΣZ_i+=P^2

Gini File = $1-\Sigma M_i$, $1-\Sigma Z_i$

4. Prediction

4. Results and Discussion

For the proposed model we are using the machine learning repository Kaggle which provides the CTG dataset to predict the outcome. It was one of the open-source standard datasets. The CTG dataset [4], [10]–[13] contains 21 features created by combining the results of uterine contraction pressure, fetal heart rate signal, and other measurements. The target variable in this data is the fetal health status, which can be classified as Normal (N), Suspect (S), or Pathological (P). There are 2126 observations in the dataset, of which 1655 samples belong to the N-class, 295 to the S- class, and 176 to the P-class. The dataset is imbalanced because a significant number of instances belong to a single class, for instance, 77.85% of all samples belong to the Normal-class. For ease of comprehension, Figures 6 and 7 also provide a visual representation of the CTG data distribution.

4.1.1. Selection of Features and Scaling

In machine learning, a technique called feature selection is used to select the features in a dataset that are most important. The target variable has a strong correlation with the selected features. In addition, the feature selection method aids in avoiding the dread of dimensionality and makes training models simpler [4], [12].

The CTG dataset has the shape (sample, feature) of there are 21 features [6], [8], [10]–[12], [16], [24]in the dataset, but not all of them are equally essential for making predictions. To extract the K(=05) best features from the CTG data, the study used the Chi-square feature selection method and reduced the data's shape to (2126, 05). The final classifier model's complexity and degree of computation will be reduced because of the reduced feature size. Figure 8 depicts the feature importance score and the most important features at the bottom. The correlation between the target class and the features is indicated by the Chi-square score. Frequency distributions are kept in the contingency tables using this approach. In i^{th} position of the contingency table, the observed frequency of a feature is O_i and the frequency expected is E_i. The Chi-square value of the feature is calculated as,

$$X^2=\sum_i^n \frac{(O_i-E_i)^2}{E_I} \quad (4)$$

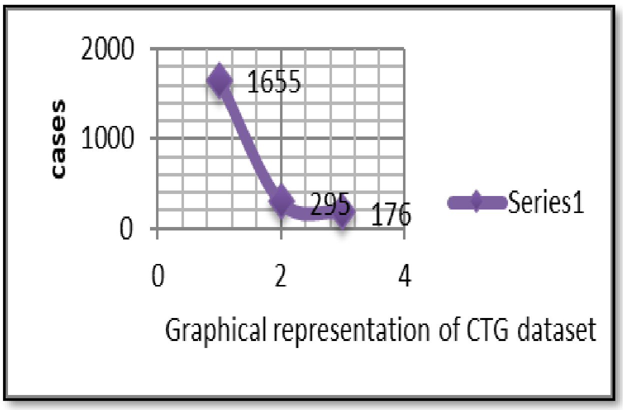

Fig 7. Graphical representation of the CTG dataset

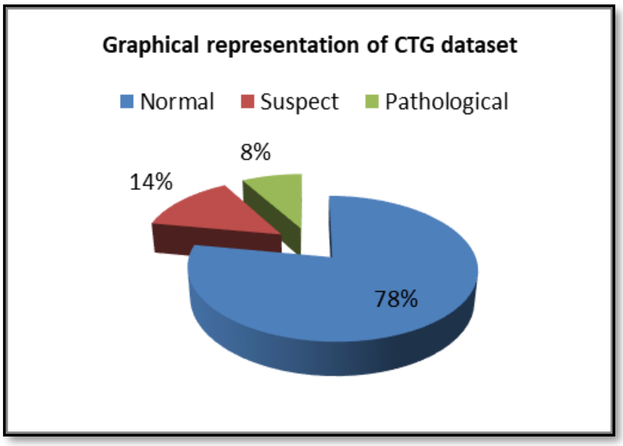

Fig 8. Graphical representation of the CTG dataset

The feature observation values frequently fluctuate in an unstable range in real-world data. Additionally, features with a high weight have the potential to bias the results of experiments and have a greater impact on the objective function. A crucial data processing technique in studies of machine learning is feature scaling, in which a dataset's independent features (variables) are normalized on a fixed scale. It makes it possible for each feature to contribute equally to optimizing the objective function.

After splitting the dataset, using the Min-Max feature scaling method the training and testing data are normalized in the range of [0,1]. Scaling is needed to make bias-free and accurate predictions from the CTG data, where the CTG has both continuous and discrete values. In the feature space 'P' is a random feature its actual value is P_{val} and the normalized value is P_{scaled} respectively. Where P_{min} and P_{max} are the minimum and maximum values of the feature in the list. To calculate the normalized value of feature 'P' using the Min-Max feature scaling is defined in eqn. (5).

$$P_{scaled} = \frac{P_{val}-P_{min}}{P_{max}-P_{min}} \qquad (5)$$

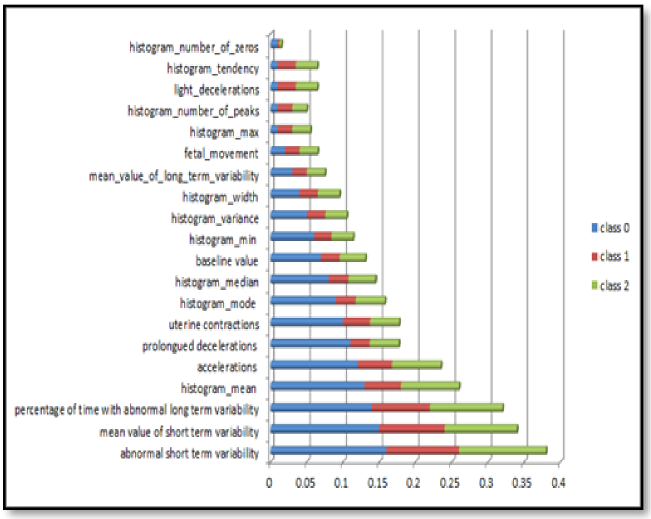

Fig 9. A picture of proof of how we selected 5 parameters

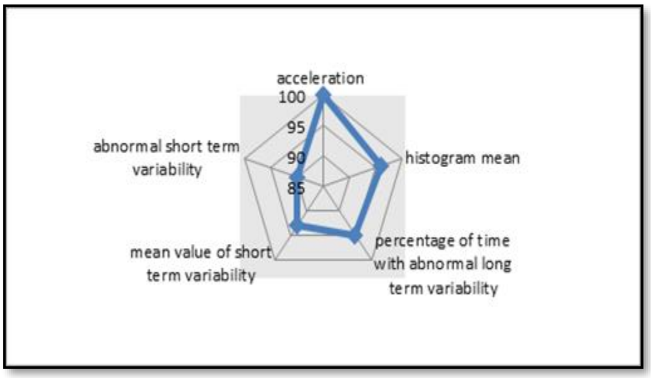

Fig 10. A picture of proof of 5 parameters' importance in the prediction

1.Short-Term Abnormal Variability: The term short-term variability refers to a range of 3-5 beats per minute (BPM) that the fetal heart experiences from one moment to the next.

2. Short-term variability mean value: In the ECG, it is the average of the absolute differences between adjacent intervals.

3. Period with abnormal long-term variation: A fetal heart "acceleration" is a significant long-term variation. These are usually triggered by fetal movement, last 10 to 20 seconds or more, and are at least 15 beats per minute higher than the baseline.

4. Mean of the histogram: Mean of the fetus's heart rate over various periods.

5. Accelerations: Acceleration is a sudden rise in FHR above baseline with a start-to-peak time of fewer than 30 seconds and a duration of fewer than 2 minutes. The duration of the acceleration is the time between the initial shift in heart rate from the baseline and the time of return to the FHR to the baseline.

4.1.2. Tools and Technologies Used

1. IDE versus code: Visual Studio Code is a simple code editor that supports debugging, task running, and version control for development.

2. Notebook Google Colab: It lets anyone write and run any Python code through a browser, Colab is ideal for machine learning, data analysis, and education.

3. Dataset Kaggle is an online community for enthusiasts of machine learning and data science.

4. CSS and front-end HTML: The fundamental scripting language that web browsers use to display web pages is Hyper Text Markup Language (HTML). Cascading Style Sheets (CSS) language is used to style HTML documents.

5. Python backend: We built our website using the Flask module and other Python modules for prediction, classification, and other tasks.

6. The MongoDB database: Open-source NoSQL database management software is MongoDB. As an alternative to conventional relational databases, NoSQL is utilized.

7. API, PDFKIT, and SMTP: PDFKIT is a Python module that makes use of the web kit wkhtmltopdf to generate a PDF from an HTML page. The user received the email using the Simple Mail Transfer Protocol.

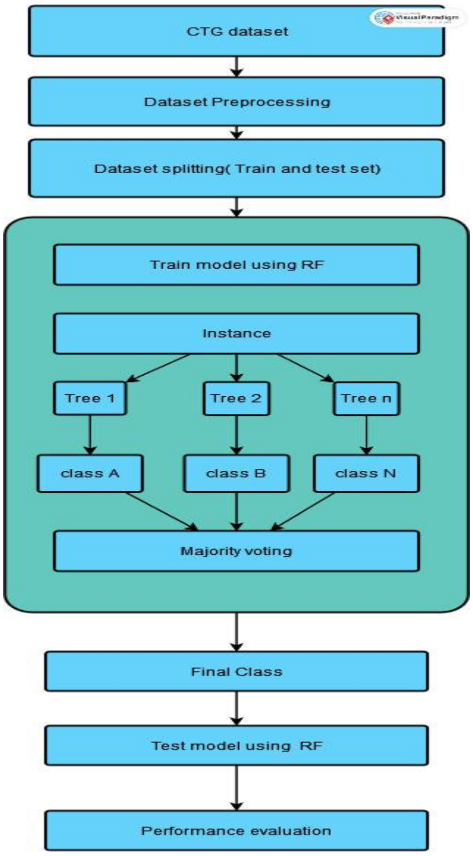

Fig 11. working principles of Random Forest Classification

4.1.3. Implementation of random forest classifier

Code snippet

```
fetal_data = pd.read_csv('fetal_health.csv')
fetal_data = fetal_data.iloc[1:]
abnormal_short_term_variabiliity,mean_value_of_short_term_variability all other features.
fetal_data_x = fetal_data.drop(['fetal_health', 'baseline value', 'fetal_movement',
'uterine_contractions', 'light_decelerations', 'severe_decelerations',
'mean_value_of_long_term_variability',
                        'histogram_width', 'prolongued_decelerations',
                        'histogram_min', 'histogram_max', 'histogram_number_of_peaks',
                        'histogram_number_of_zeroes', 'histogram_mode', 'histogram_median',
'histogram_variance', 'histogram_tendency'], axis=1)
fetal_data_y = fetal_data['fetal_health'] split method
fetal_data_x_train, fetal_data_x_test, fetal_data_y_train, fetal_data_y_test = train_test_split(
   fetal_data_x, fetal_data_y, train_size=0.7, random_state=40)
, max dept as 5
fetal_health_classifier = RandomForestClassifier(
   random_state=40, n_jobs=-1, max_depth=5, n_estimators=100, oob_score=True)
fetal_health_classifier.fit(fetal_data_x_train, fetal_data_y_train)
```

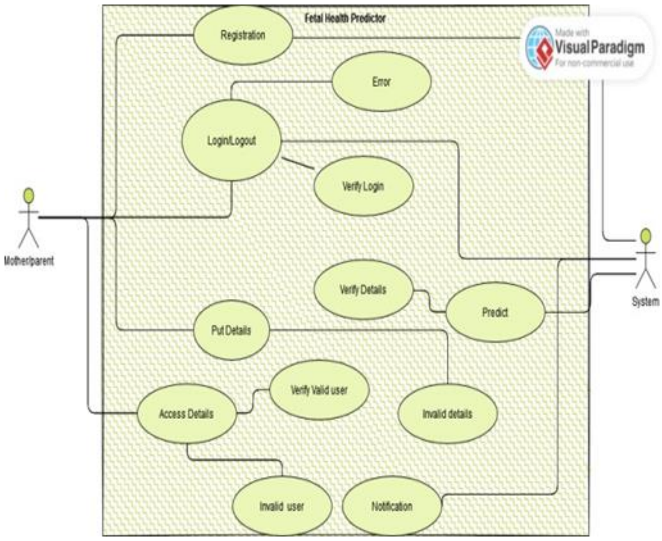

Fig 12. Use case diagram.

4.1.4. Implementation code for sending reports to a user

Code snippet

```
import smtplib
from email.message import EmailMessage


def sendEmailTouser(mailid):


   msgContent = EmailMessage()
   msgContent['Subject'] = 'FETAL HEALTH  PREDICTION REPORT'
   msgContent['From'] = 'MR PREDICTOR'
   msgContent['To'] = mailid
   with open("res.pdf", "rb") as f:
      fileContent = f.read()
      file_name = f.name
      msgContent.add_attachment(
         fileContent, maintype="application", subtype="pdf", filename=file_name)
   with smtplib.SMTP_SSL('smtp.gmail.com', 465) as server:
      server.login("dkgurucharan@gmail.com", "ciyanmakgicvdvpb")
      server.send_message(msgContent)
```

Fig 13. Graphical representation of the CTG dataset

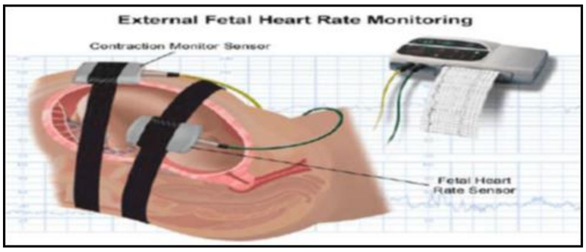

Fig 14. Placement of the machine

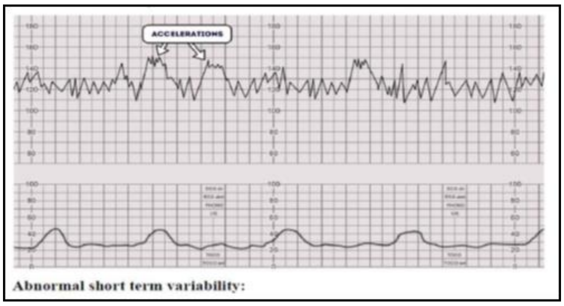

Fig 15. Acceleration value

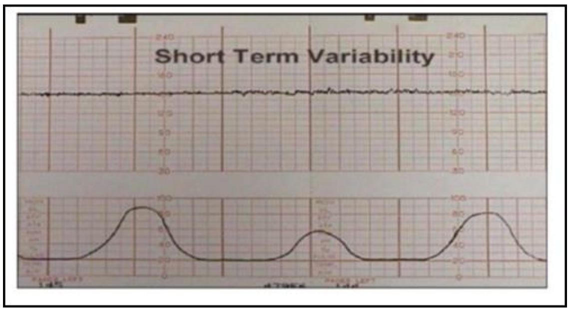

Fig 16. Short-term variability

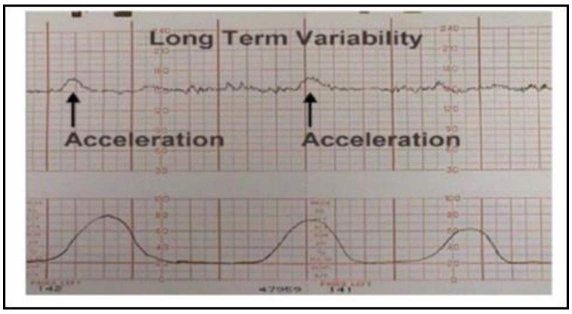

Fig 17. Long-term variability

4.2. Snapshots

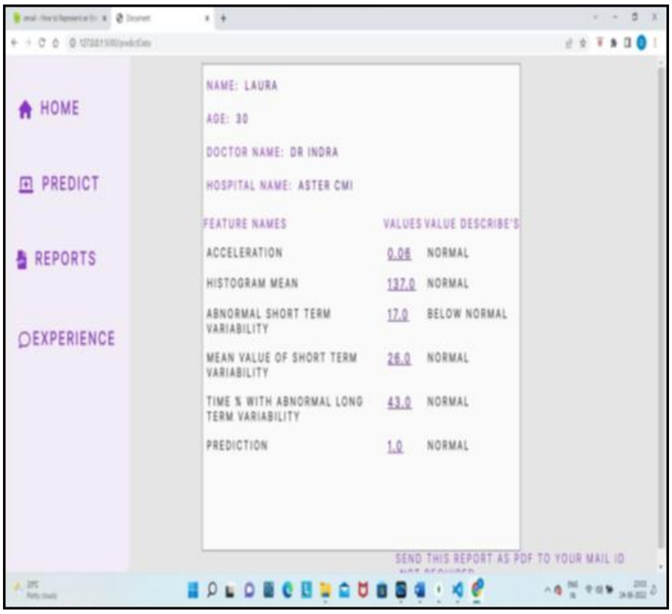

Fig 18. Patient details

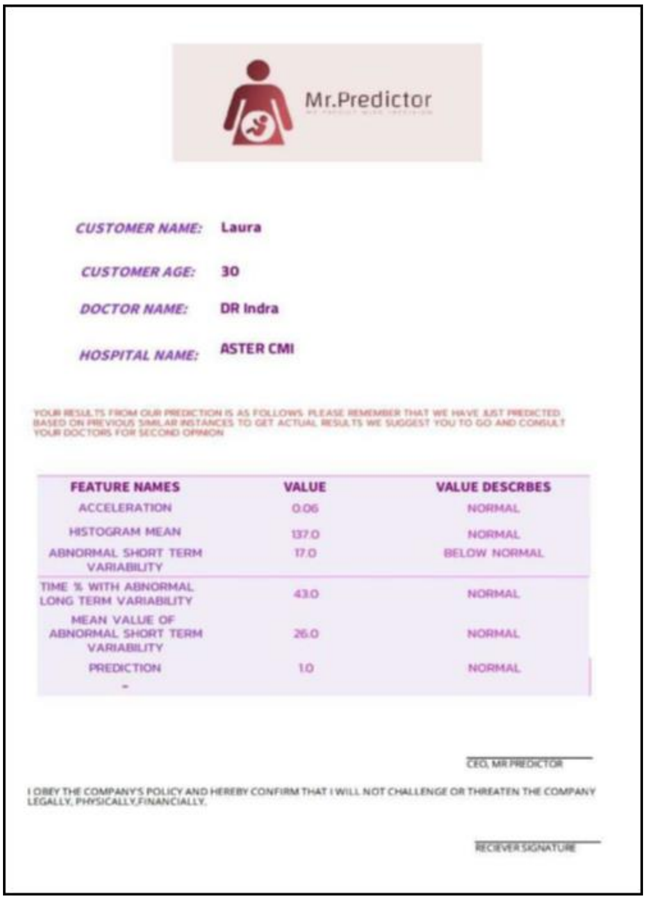

Fig 19. Prediction Page

5. Conclusion

We will be able to predict the fetus's health more accurately at the end of this paper. The parents will save money, time, and stress thanks to our efforts. Because it is a web application, anyone, at any time, can use it. We can prevent child mortality by monitoring and predicting fetal health. This web application can be used for a variety of purposes by multiple domain-specific users in addition to the mother or parents. Among our intended customers are.

- Doctors.
- Government officials who are involved in health-related programs.
- Pharmaceutical companies.
- Non-Governmental Organizations that Protect Mothers and Children.

Pregnancy is a natural process, but sometimes things don't go as planned. In today's world, fetal abnormalities like hypoxia, acidosis, or a congenital heart defect are becoming a global issue. However, early detection can assist in mitigating future dangers. It is impossible to accurately diagnose the health of the fetus without the CTG data. However, obstetricians manually examine this essential data, which occasionally may be misleading and may result in life-threatening conditions. This article, therefore, proposes a random forest classifier that incorporates the gini index algorithm as a means of automatically predicting fetal abnormalities in the CTG dataset. In the study, a decision tree construction method was used to construct the classifier model. The learning model was then constructed and utilized to predict the CTG samples. A good accuracy of about 96.62 percent was achieved by the model. Most of the features in the CTG dataset that were available were used in the models developed in previous studies. Mohammad Saber Iraji made use of a variety of different models for neural networks. The DSSAEs (deep stacked sparse auto-encoders) model used all 21 features and had an accuracy of 96.77 percent. In contrast, the CTG dataset's defined features made up less than 70% (five features) of this study's performance. The five most significant features from the CTG data were selected using a Random Forest Classifier and the feature selection technique like Chi-square. However, despite maintaining the common feature selection method and the number of features, the respective study has increased prediction accuracy.

Acknowledgments

I would like to express my heartfelt gratitude to our supervisor, Dr. Poornima A.S., for her unwavering support and guidance throughout the research process. Her expertise, insights, and encouragement were invaluable in helping us to complete this work. Finally, I would like to thank my family and friends for their love and support throughout the research process. Without their encouragement and support, I would not have been able to complete this research.

Author contributions

Shruthi K: Conceptualization, Methodology, Software, Field study **Shruthi K:** Data curation, Writing-Original draft preparation, Software, Validation., Field study **Poornima A.S:** Visualization, Investigation, Writing-Reviewing, and Editing.

Conflicts of interest

No potential conflict or competing of interest was reported by the authors.

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