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Scientific research article

GDMSafe: Enhancing gestational diabetes prediction through visceral adipose tissue and ensemble learning models

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SUMMARY

Introduction: Globally, diabetes is common chronic disease, which occurs when the pancreas in the body cannot generate enough insulin or body cannot utilize the generated insulin. Particularly, Gestational Diabetes Mellitus is the frequent condition, associated with the high maternal and fetal and morbidity. It is significant to detect the disease earlier to evade consequences in the future. Traditionally, detection of gestational diabetes comprises of the GCT (Glucose Challenge Test), OGTT (Glucose Tolerant Test). Conversely, it is the time consuming, inconvenience and subjectivity process. **Purpose:** To address the issue, conventional researches used AI (Artificial Intelligence) technology to automate the detection procedure. Nevertheless, it is limited by accuracy, speed, handling of larger datasets and high error rate. To overcome the problem, proposed model aimed at developing a predictive model to ascertain GDM based on the Visceral Fat deposit by leveraging the benefits of Ensemble learning methods. Contradicting the principles of Occam's razor, ensemble models introduce complexity but still reduces the generalization error. **Methodology:** A group of 133 pregnant women upto 20 weeks of gestation from Physionet is utilized for this study and it has been already proven that there exists a strong correlation between VAT and GDM. **Results:** Convincing ROC and Accuracy is achieved and a comparison with PIMA Indian dataset demonstrate the robustness of the model for predicting Gestational Diabetes to move the knowledge in this field a little further along.

Keywords: Gestational Diabetes Mellitus; Visceral Adipose Tissue; Random Forest; Ensemble Methods

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RESUMEN

GDMSafe: Mejora de la predicción de la diabetes gestacional mediante tejido adiposo visceral y modelos de aprendizaje conjunto

Introducción: A nivel mundial, la diabetes es una enfermedad crónica común, que ocurre cuando el páncreas del cuerpo no puede generar suficiente insulina o el cuerpo no puede utilizar la insulina generada. En particular, la Diabetes Mellitus Gestacional es una condición frecuente, asociada a alta morbilidad materna y fetal. Es importante detectar la enfermedad a tiempo para evitar consecuencias en el futuro. Tradicionalmente, la detección de la diabetes gestacional se compone de la prueba de provocación con glucosa (TCG) y la prueba de tolerancia a la glucosa (PTGO). Por el contrario, es un proceso que consume tiempo, es inconveniente y subjetivo. **Propósito:** Para abordar el problema, las investigaciones convencionales utilizaron tecnología de IA (Inteligencia Artificial) para automatizar el procedimiento de detección. Sin embargo, está limitado por la precisión, la velocidad, el manejo de conjuntos de datos más grandes y una alta tasa de error. Para superar el problema, el modelo propuesto tuvo como objetivo desarrollar un modelo predictivo para garantizar la GDM basada en el depósito de grasa visceral aprovechando los beneficios de los métodos de aprendizaje de conjunto. Contradiciendo los principios de la navaja de Occam, los modelos de conjunto introducen complejidad pero aun así reducen el error de generalización. **Metodología:** Para este estudio se utiliza un grupo de 133 mujeres embarazadas de hasta 20 semanas de gestación de Physionet y ya se ha demostrado que existe una fuerte correlación entre VAT y DMG. **Resultados:** Se logra una ROC y una precisión convincentes y una comparación con el conjunto de datos indios PIMA demuestra la solidez del modelo para predecir la diabetes gestacional y hacer avanzar un poco más el conocimiento en este campo.

Palabras clave: Diabetes Mellitus Gestacional; Tejido adiposo visceral; Bosque aleatorio; Métodos de conjunto

RESUMO

GDMSafe: Melhorando a previsão do diabetes gestacional por meio do tecido adiposo visceral e modelos de aprendizagem de conjunto

Introdução: Globalmente, o diabetes é uma doença crônica comum que ocorre quando o pâncreas não consegue gerar insulina suficiente ou o corpo não consegue utilizar a insulina gerada. Particularmente, o Diabetes Mellitus Gestacional é uma condição frequente, associada a alta morbidade materna e fetal. É importante detectar a doença precocemente para evitar consequências no futuro. Tradicionalmente, a detecção do diabetes gestacional compreende o TCG (Teste de Provocação de Glicose) e o TTGO (Teste de Tolerância à Glicose). Por outro lado, é um processo demorado, inconveniente e subjetivo. **Objetivo:** Para abordar o problema, a pesquisa convencional usa tecnologia de IA (Inteligência Artificial) para automatizar o procedimento de detecção. Entretanto, é limitado pela precisão, velocidade, manuseio de conjuntos de dados maiores e alta taxa de erro. Para superar o problema, o modelo proposto teve como objetivo desenvolver um modelo preditivo para determinar o GDM com base no depósito de gordura visceral, aproveitando os benefícios dos métodos de aprendizagem do Ensemble. Contrariando os princípios da navalha de Occam, os modelos de conjunto introduzem complexidade, mas ainda reduzem o erro de generalização. **Metodologia:** Utilizou-se neste estudo um grupo de 133 gestantes com até 20 semanas de gestação da Physionet e já foi comprovado que existe uma forte correlação entre VAT e GDM. **Resultados:** ROC e precisão convincentes são alcançados e uma comparação com o conjunto de dados indiano PIMA demonstra a robustez do modelo para prever diabetes gestacional para levar o conhecimento neste campo um pouco mais adiante.

Palavras-chave: Diabetes Mellitus Gestacional; Tecido adiposo visceral; Floresta aleatória; Métodos de conjunto.

1. INTRODUCTION

Gestational Diabetes Mellitus (GDM) usually happens in the second half of the pregnancy [1, 2]. The excess blood glucose travels through the placenta, giving the fetal high blood glucose levels [3, 4]. This causes the baby's pancreas to make extra insulin to get rid of the blood glucose. During the prenatal visit, the risk assessment is made by the presence of fasting hyperglycemia and various other risk factors associated with GDM such as Overweight, Ethnic race, Blood Sugar levels, Age factor, Family history, Hypertension, etc. [5]. To reduce the risk factor of the disease, it is necessary to detect the disease earlier. Classically, GDM is functioned with the GCT (Glucose Challenge Test), OGTT (Glucose Tolerant Test). It is the time invasive and in need in need of qualified doctors to process the results. Besides, it can be prone to human error. Congruently, technology based GDM detection is needed to overcome the problem. One such technology is AI (Artificial Intelligence), which uses ML (Machine Learning) and DL (Deep Learning) for the automatic detection of GDM [6].

Correspondingly, several conventional models attempted to attain better detection of diabetes mellitus with ML and DL techniques [7, 8]. For instance, in the existing model, CNN based architecture has been used for the detection of diabetes. It has processed with the data of diabetic retinopathy. The function involved in the classical model are data acquisition, preprocessing and classification. Accordingly, outcome of the classification signifies the better efficacy of the diabetic detection [9]. Similarly, diabetes detection has been designed with the SVM (Support Vector Machine) and hierarchical clustering. Besides, CNN has been used for the detection and examination of every part in the classification. The outcome of the detection signifies the better efficiency of the traditional model [10]. Likewise, enormous pioneering methods tried to achieve efficient detection of diabetes [11]. However, lacks in accuracy and speed. Moreover, researches on GDM is limited in the existing models [12]. Several Existing models is focused on the detection of diabetes mellitus but inadequate in the GDM based detection [13-16]. Accuracy is the essential factor, which determines the overall performance of the model where numerous classical mechanism lacks in accuracy [17].

In essence, the contributions of the works are:

- To utilize feature selection mechanism using recursive features elimination to select significant features in the data.
- To use data augmentation with the SMOTE based technique to alleviate class imbalance problem.
- To employ bagging and boosting model for the prediction of Gestational Diabetes Mellitus. Besides, it analyzes the best hyper parameters for enhancing the predictive accuracy.

In the conventional method, ML based model has been used for the classification of GDM. It has been processed with the sequential data which has been taken from the cell free DNA from the maternal plasma. Besides, classification has been processed using the CNN based architecture. The experimental results signifies that the classical model attained better performance with the accuracy of 88.14% [17]. Similarly, ML and data mining based model has been deployed for the detection of GDM. The input data has been collected from the pregnant women data through the data mining process. Further, it has functioned with normalization and dimension reduction method. The classification has been functioned with the CNN based architecture where the results of the classification signifies better performance with the better accuracy [18]. Congruently, convolutional LSTM based detection of diabetes. The database used for the project has been taken from the Pima Indians diabetes database. The experimental results signifies batter efficacy of the traditional models with the better accuracy [19]. In the same way, DL based GDM detection model has been conventional mechanism. To achieve this, three set of layers has been used such as cloud layer, fog layer and IoT layer. Besides, EPM (Explainable Prediction Algorithm) and data finding methodology. The outcome of the experiment represents the better performance of the GDM prediction [20].

Correspondingly, CNN and bidirectional LSTM based method has been used for the GDM detection [21]. It has been functioned with the PIMA dataset. It has been processed with the PIMA dataset. The efficiency of the classical model signifies the better performance with better accuracy [22]. Similarly, Deep LSTM model has been used for the prediction of diabetes mellitus. For that, diabetes dataset has been used in the classical method. The better efficacy of the classification has been used in the traditional mechanism with better accuracy [23]. In the existing approach, SMOTE based oversampling method has been used in the conventional method. To attain this, Pima Indian diabetes dataset for the classification of diabetes mellitus. The better efficiency of the prediction has signified through the results [24]. Consistently, LSTM based diabetes mellitus prediction method has been designed in the traditional system. For that, PIDD dataset has been utilized in the conventional method. The experimental outcome signifies the better performance of the exiting model with better accuracy [25, 26].

Compatibly, weighted entropy based deep features has been used for the classification of diabetes mellitus [13, 14]. Besides, hybrid RNN with LSTM aided mechanism has been utilized to examine the blood glucose level and prediction of diabetes [15, 16]. Moreover, CNN has been used for the feature extraction [27]. The classification outcome indicates that the classical method attained better performance in the diabetes prediction [28]. Similarly, deep CNN and LSTM based mechanism has been utilized for the detection of diabetic retinopathy. To accomplish this, shark sell jaya optimization has been utilized to improve the performance of the prediction. The experimental outcome represents the better performance of the classification. In the exiting method, DL based diabetes mellitus on the terms of DNA sequences. To attain this, CNN and LSTM based mechanisms have been used in the classical method. The outcome of the classification represents better efficiency with better accuracy.

2. METHODOLOGY

The proposed model predicts the Gestational Diabetes Mellitus (GDM) using the Physionet Visceral Adipose Tissue dataset during pregnancy by employing a series of techniques to improve classification accuracy. It begins with data pre-processing, followed by feature selection using recursive feature elimination to identify key features. To enhance model efficiency, data augmentation is applied through the SMOTE technique. The classification process is then carried out using ensemble methods, specifically bagging and boosting. GDM, a serious health condition that can lead to complications such as kidney failure, blindness, and heart disease, requires early detection to minimize future risks. Although conventional models have struggled with accuracy and speed, the proposed system aims to address these issues by integrating these advanced procedures, as illustrated in Fig. 1.

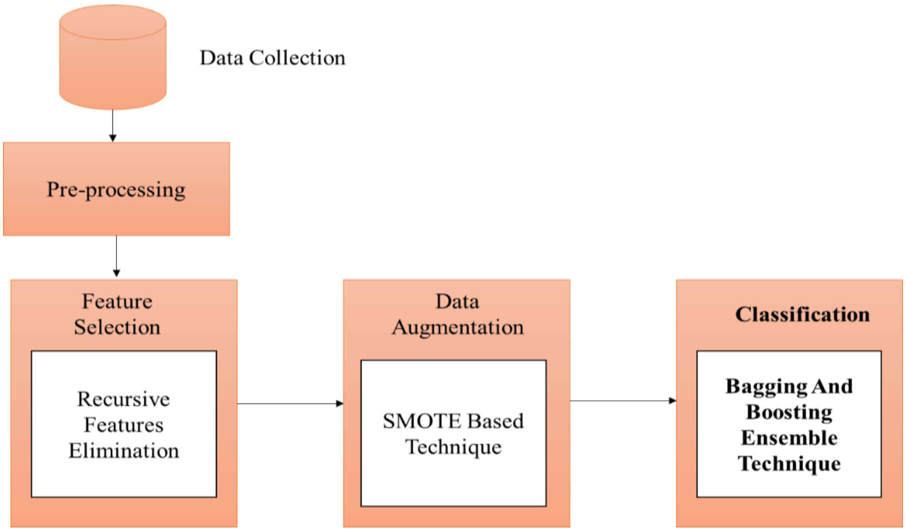


Figure 1. Methodological Flow of the Presented Model

Figure 1 depicts the design flow of the respective research. It is identified that the presented approach comprises of the following procedures.

- Data Collection
- Data Pre-processing
- Feature selection
- Data Augmentation
- Classification

Correspondingly, detailed description of the proposed model is signified in the following subsections.

2.1. Data collection

The proposed model is performed by adopting the machine learning methods using the Physionet Bank Visceral Adipose Tissue Measurement published on March 2020, Version 1.0 for ascertaining the presence of GDM among pregnant mothers. It is processed with the cohort analysis with the pregnant women for the period in gestation of 20 weeks. The analysis is followed with the 15 parameters until the delivery of the pregnant women. In the scan of consistent trimester, VAT evaluation is take placed where the biometric examination is carried out in terms of parental care data. The data for the analysis is processed with the medical records of the pregnancy women. The various attributes of the dataset are listed in Table 1.

Table 1. Attributes of the Dataset

Data in Early Gestational Period (20 Weeks)	
Number	Unique Id for the case
Age (years)	Age in years
Ethnicity	0 – White, 1-Not white
Diabetes Mellitus Previous	0 – No; 1- Yes
Mean Diastolic BP	Mean diastolic blood pressure in mmHg
Mean Systolic BP	Mean systolic blood pressure in mmHg
Central Armellini Fat	Maternal Visceral Adipose tissue measurement in mm
Current Gestational Age	Weeks and days of pregnancy
First fast glucose	First measured fasting glucose in mg/dl
BMI pregestational	Pregestational body mass index in kg//m
Data at the outcome of Delivery	
Gestational age	Age at birth (weeks and days)
Type of Delivery	0 – Vaginal Birth; 1 – Caesarean section
Gestational DM	0 – No; 1 -Yes

2.2. Preprocessing

Out of the 133 pregnancy patient records, there were 26 values missing values for the attribute First Fasting Glucose and 5 missing values for number of pregnancies. Missingvalues imputation is one of the biggest tasks in preprocessing and a suitable imputation will produce quality dataset for betteranalysis of clinical trials. To discover what works best for the dataset, each statistical techniques for examining the missing values in the dataset was tried and tested. Case deletion for the 5 missing values of 'Number of Pregnancies' attribute was made as this deletion will not have a greater impact in the precision, and the 26 missing values for the attribute fastglucose level is a good 'Line of Dignity' to observe and was imputed using multiple imputation methods. Predictive models can be computationally expensive, but repeated imputation would significantly increase this cost. Time and overhead. Yet it is crucial to have imputed values as close as possible to unobserved values. Given the stochastic nature of the algorithms, the algorithms were run for different parametric values. It is clearly evident that there is only a minor fluctuation in the mean performance. KNN is sensitive to outliers and involves expensive computations. The Expectation Maximization Imputation is better than Mean Imputation as they preserve the relationship with other variables (Algorithm 1).

```
Algorithm 1: MVIMPUTE(D,N)
Input: D - DataSet
Output : D′ - Preprocessed Dataset Procedure:
for each sample Ri in D do
for attributes A1,A2,A3..An Є Ri do
If Ai == NULL then Ci := Class(Ai)
        (a) Compute Mean(Ai)= $( \sum_{i=1}^{N} Ai )/N$
        (b) Compute Median(Ai)= A[(N+1)/2]
        (c) Compute Mode(Ai)=most frequent value
        (d) Compute ConceptMostMean(Ai)
$= (\sum_{i=1}^{N} Ai )/N$ , where Class(Ai)=Ci
(e ) for k=1..9 step 2 do
            (i) Computer k-Nearest Neighbour using
$\sqrt{\sum_{i=1}^{n}(qi - pi)(qi - pi)^2}$
         (f) Compute $\theta = argmaxlog(\sum z\ p(x, z|\theta))$
         (g)Impute the Missing Values with the computed values.
end
end
Fit the model and validate the performance of the classifier. D′=Perform imputation with the value that yields max{ Accuracy
Return D′
```

2.3. Feature Selection

Feature Engineering is a kind of Machine Learning itself that uses the process of domain knowledge to improve Machine Learning. A feature is a characteristic that is important to a predictive model and the best features selected greatly influence the results. Feature Selection considerably reduces the complexity of the model and faster training can be achieved. Figure 2 shows the feature selection methods.

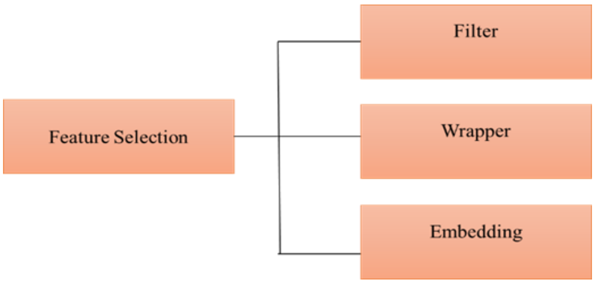


Figure 2. Feature Selection Models

Figure 2 depicts the mechanism in the feature selection. The model is built by considering the correlation among the independent variables and removing the irrelevant features to the model to improve the prediction performance of the predictors was performed. There are three categories for feature selection methods: filter, wrapper, and embedding. The Filter technique assigns a statistical weight to each prediction and quantifies each property. Wrapper techniques characterize feature selection as a gluttonous search for the best characteristics, in which a variety of combinations of subsets are gathered, assessed, and compared with one another. Embedded techniques assess the utility of the feature subset selected by the learning procedure. The model is built while the features that are most important to the model's accuracy are determined. In this study, a rapper method of feature selection that uses filters internally known as Recursive Feature Elimination was used to remove redundant attributes. Not all modes can be paired with RFE. The top nine features selected are VAT, Glucose, current gestation age, no. of pregnancies, BMI, diastolic and systolic BP, age, and ethnicity. The attributes gestational age, ethnicity and outcome attributes were not taken into consideration. Eventually, the zero-importance features were opted out for the prediction process. The features arranged according to their importance shows that VAT is the most influential attribute and also the cumulative feature importance plot shows the number of features selected that yields maximum accuracy. Algorithm 2 signifies the RFE(D′) mechanism.

Algorithm 2: RFE(D′)

```
Input: D′ - DataSet, N-number of features Output : D′′ - FS_Dataset
Procedure:
Initialize a pipeline of models, M={'LR','DT','RF','GB'} n_features=N        ' Subset size
For i in 1..n_features do
Identify the Collinear features using Equ (1)
$Rxy = \sum(xi - x)(yi - y / \sqrt{\sum(xi - x)^2 \sum(yi - y)^2}$
Compute the feature importance score for each
feature end
Remove features with zero-feature score For each model mi in M
Fit mi using CrossValidation Determine Acc = TP/TP+TN
End For
Return FS_Dataset
```

* LR-Logistic Regression DT- Decision Tree RF-Random Forest GB-Gradient Boost

Correspondingly, Fig. 3 shows the feature importance of the proposed model.

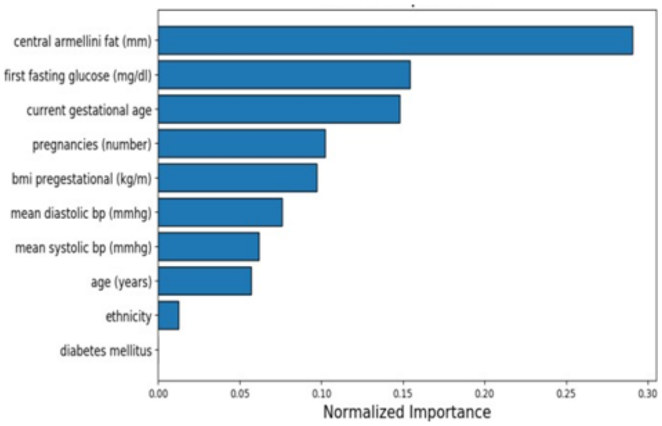


Figure 3. Feature Importance.

2.4. Data Augmentation

The understanding of the dataset, the class imbalance problem was dealt with suitably. Apparently, the success of the prediction model depends on the dataset; the problem of class imbalance greatly influences the performance of the classifier. The PhysioNet Bank dataset contains dichotomous records attributing to 1-Presence of GDM and 0-Absense of GDM. Out of the 133 records, 18 were only contributing to No GDM class and it is clearly a Class-imbalance problem to be addressed too. One of the approaches for this class imbalance challenge is to oversample the minority class. The SMOTE method concentrates on the feature space to create new instances with interpolation between the positive instances that are close together. It starts by selecting a minority class-instance and finding its k-nearest neighbors (typically k=5). A synthetic instance is created in the feature space between the two examples, one that is randomly selected from the k-nearest neighbor and the random sample itself. New plausible synthetic minority class samples were created, and the data set is augmented with GDM-1 {115 records} and GDM-0 {115 records} (Algorithm 3). SMOTE on the minority class is followed by an undersampling of the majority class. This pipeline performs better than just oversampling alone.

Algorithm 3: SMOTEVAT(FS_D)

Input: FS_D - Feature Selected DataSet Output : D′ - Synthesized Dataset Procedure:

```
A=Φ; B=Φ
for each sample Ri in D do if Ri.target=1
A=A U Ri
else
B=B U Ri
Initialize k=5; N=3 ′ k-no of neighbours, N- sampling_rate Choose X=random(A)
for each x in A && x <> X do
Calculate the Euclidean distance :
$d(p, q) = d(q, p) = \sqrt{}(q1 - p1)^2 + (q2 - p2)^2 + (q2 - p2)2+ \quad +(qn - pn)(qn - pn)^2$
n
$= \sqrt{\sum}(qi - pi)2$
i=1
End for
Sort the distance, determine the k nearest neighbours, say K for i in 1..N do
kx= pick random(ki), k Є K and for i=(1..5)
Generate new synthetic instance using $x' = x + rand(0,1) * | x - xk |$
end for
D′= D U x′
Return D′
```

2.5. Classification

The dataset experimented initially using a simple MultiLayer Perceptron (MLP) sequential model with plain stack of layers starting with an input layer of 9 inputs attributes, followed by two hidden layers with 64 nodes, closely stacked by two consecutive hidden layers with 8 nodes each and a final output layer used for classification. The detailed architecture of the 6-Layer stacked network is presented in Table 2.

Table 2. Network Architecture

Layer	**Output Shape**	**Parameters #**
Dense	(None,64)	640
Dense	(None,64)	4160
Dense	(None,8)	520
Dense	(None,8)	72
Dense	(None,1)	9

Model: "sequential" Total params: 5,401
Trainable params: 5,401
Non-trainable params: 0

Table 2 represents the architecture of the proposed network. A stochastic gradient descent optimizer with a learning rate of 0.01 and a ReLu activation function was used to create this MLP Five-Fold Model repeated stratified cross-validation was performed on the dataset with a preferred loss function of binary cross entropy and an accuracy of 75.8% was achieved. The accuracy achieved was not optimal and in order to produce a better predictive model a set of experiments with the bagging and boosting methods were performed.

2.5.1. Bagging Based Ensemble Learning

A Bagging classifier is an ensemble meta-estimator that randomly picks subsets of data from the original set and constructs a tree-based classifier. Such trees generated are then combined to form a final prediction by fitting the base classifiers each on random subsets of the original dataset and then aggregate their individual predictions. Figure 4 represents the generation of trees and majority voting in the classification mechanism.

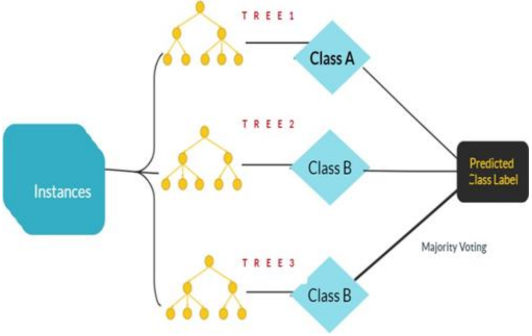


Figure 4. Generation of Trees and Majority Voting

2.5.2. Boosting Based Ensembles

To reduce bias and variance in a supervised learning, a family of machine learning algorithm is used to convert the weak learners to strong ones. The algorithm initiates by training a model with the full training set, and consequent models are constructed by fitting the residual error values of the initial model. In this way, Boosting method prepares itself to give higher weights to those instances that were wrongly estimated by the previous model. A final estimation is produced by combining the results of the weighting of the predictions made by the succession of developed models according to their accuracy scores by averaging to form a final prediction as given in Equation 1.

$$f(x) = \frac{1}{M} \sum_{m=1}^{M} f_m x \qquad (1)$$

The equation represents the average of M functions $f_m(x)$, giving a single function f(x) that combines their values.

The base estimator chosen was a CART decision tree with different seed values and a KFold of 3. The accuracy obtained was 90.57%. Also, using a random forest as a base estimator with different seed values were experimented with a KFold of s10. The accuracy achieved was 92.59%. Clearly, for this dataset on GDM, the random forest bagging ensemble obtained high degree of accuracy in comparison to the CART ensemble.

2.5.3. *Max_Features*

Max_features is the number of features that a single tree in Random Forest may include. It is widely accepted that the more features there are, the more accurate a prediction will be. This is not always true, though, as it lessens the variability of each individual tree, which is the USP of random forests. But, a closer inspection reveals that we increase the computational time of the algorithm by increasing the max_features (Algorithms 4 and 5). Hence, we need to maintain a good balance between computational time and number of features used in the system.

```
Algorithm 4: GDMSafePred(D)
Input : DataSet - D
Number of Instances - N Output : M-Prediction Model Procedure:
    (i) D′=MVIMPUTE(D, N)
    (ii)FS_D=RFE(D′)
    (iii)D″=SMOTEVAT(FS_D)
    (iv) M=RF(D″)
    (v)Save M for Prediction
 End;
```

```
Algorithm 5: RF(D″,i,n,k)
Input: DataSet - D″;   i - max_depth;   n-no_of_trees;
k-no of features Output: Model - M
Procedure:
  Do
  nt=1; count=0
    do
      count=count+1
      Randomly pick ‘k’ features from ‘m’ features, where k<m
      Calculate the best split using Entropy calculation
        $H(X) = -\sum_{x \in X} p(x) \log p(x)$
      Split node into child nodes
    while ( count <=i)
    nt=nt+1
  While (nt <= n)
  For q in 1..n do
    Evaluate the Predicted outcome Pq on Test data
  vote=mode(Pq)
  Return M
```

2.5.4. Key Parameters for Tuning

As parameters selection and optimization plays a vital role in a classifier, the best hyper parameter that was selected for this classifier implementation is discussed here.

2.5.4.1. Seed Values

Proper setting of Random Seed value in ML experiments are required. Non-determinism may impact your model's convergence rate, the stability of your results, and the final quality of a network.

2.5.4.2. Number of Trees

This feature determines the number of trees in the forest of a model. The number of trees parameter was set sufficiently large enough to stabilize the error rate. The rule of thumb is to have the number of trees to be 10 times the number of features. Trying with the different parameter values, it was set be 100 to have a good balance between ROC AUC and processing time.

3. RESULTS AND DISCUSSIONS

3.1. Exploratory Data Analysis

As the dataset contains more numerical data, to understand the different attributes of the dataset, exploratory data analysis (EDA) was made to have a thorough understanding of the underlying dataset. This exposes the trends, patterns, associations and correlations among the data, which are not readily apparent. This will consequently help in performing advanced analytics of the data. Figure 1 provides a visual data exploration of the tabular data, and a univariate analysis is made to get deeper understanding of the data. The measures of central tendency and the measures of dispersion are understood to identify the spread. Bivariate Analysis determines the empirical relationship between the variables and determines the association among them. Scatter plot that maps each variable to a point in 2D space is presented in Fig. 2. Few insights obtained on the dataset are: (a) The highest age range among the mothers is 25 years. (b) 57% are of white ethnicity and 43% are of black race. (c) All cases in the dataset show no presence of previous diabetes. (d) The maximum value of BMI is 55 kg and the average stands at 27 kg. (e) The VAT measurements averages to 44 mm and it has been proved that a 45 mm threshold was determined to be the best demarcation value to predict GDM with an accuracy of 66%. It clearly states that for less values of the Visceral Adipose Tissue Measurement, the risk of GDM is less and as the VAT measurement increases, there is a probability of GDM to occur. Finally, an attempt to elucidate the interrelationship between the variables was made through a correlogram by finding the correlation coefficients. In Fig. 5, the blue dots represent positive correlation and red represents negative correlation.

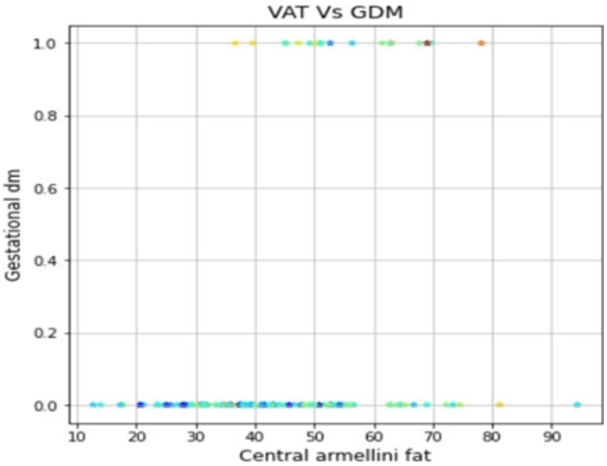


Figure 5. VAT Measurement Vs Gestational Diabetes

Figure 5 represents the VAT vs GDM analyzed in the respective model. Accordingly, Fig. 6 and Fig. 7 portray the correlation matrix of the projected system.

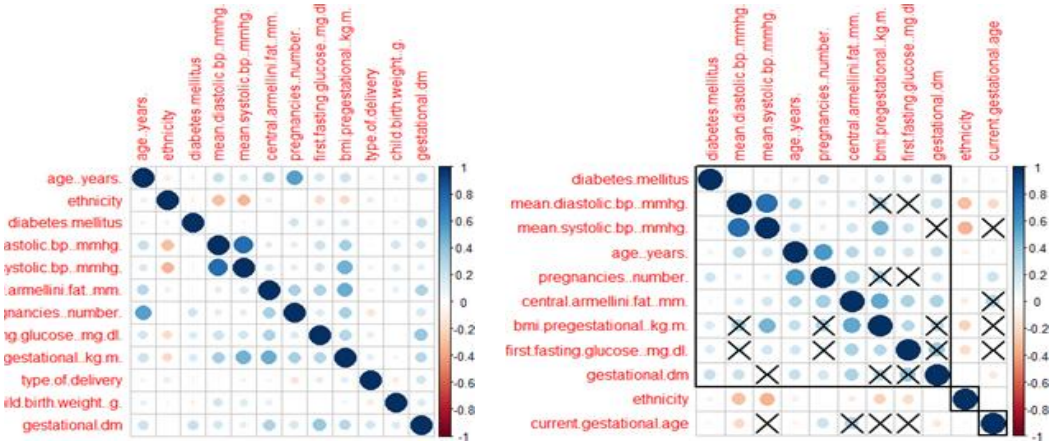


Figure 6. Correlogram-Correlation Matrix Plot.

Figure 6 represents the correlation matrix of the presented approach. Here, Blue indicates a positive correlation and red indicates negative. Figure 7 depicts the attributes distribution in the projected system.

Age

Ethnicity

Previous Diabetes

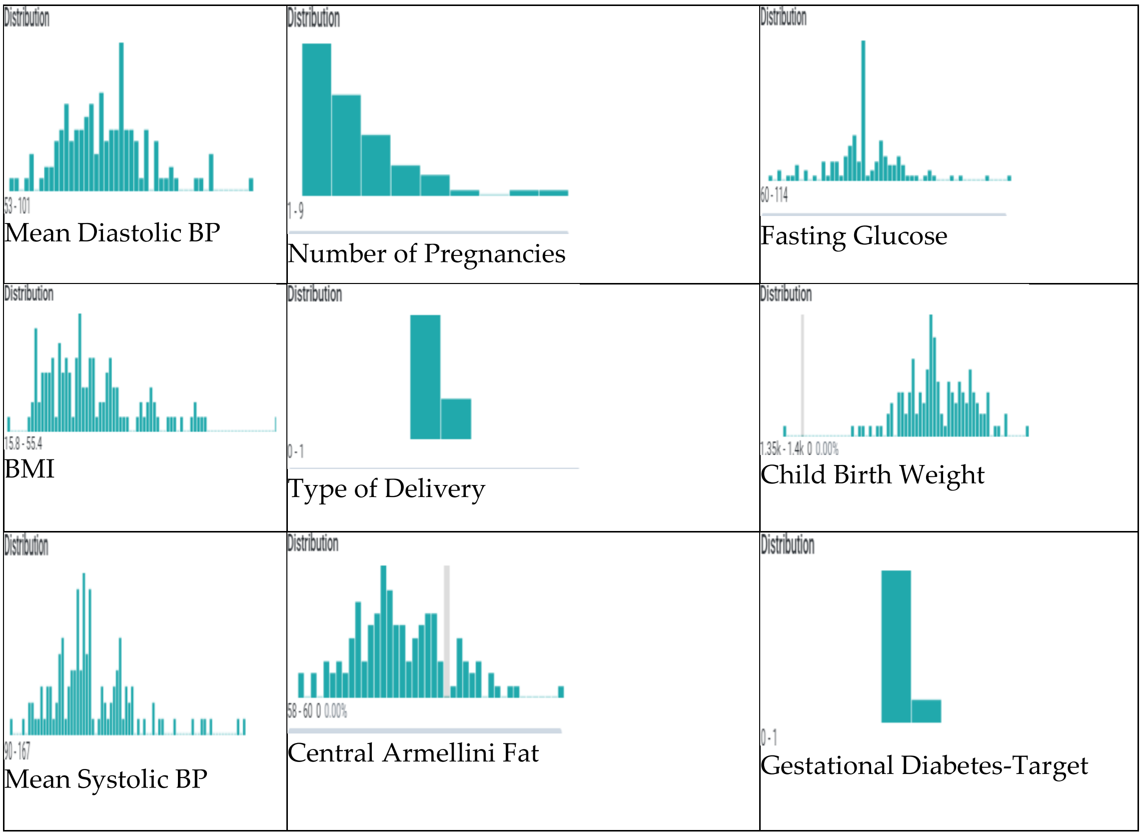


Figure 7. Distribution of Attributes - Univariate Analysis

Correspondingly, Fig. 8 depicts the Bivariate Analysis-Scatter Plot in the presented model.

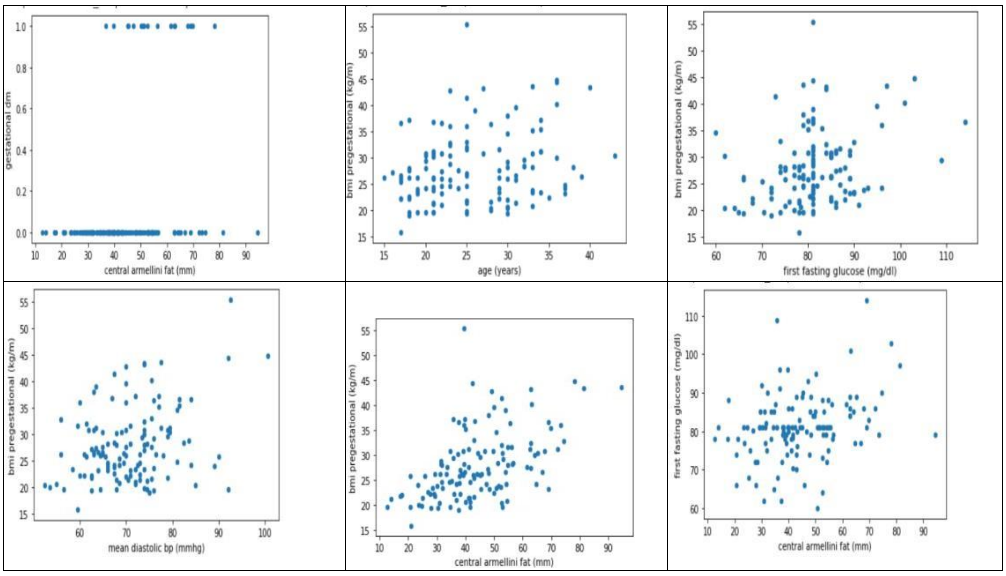


Figure 8. Bivariate Analysis-Scatter Plot

Otherwise, Fig. 9 represents the baseline model of the feature selection.

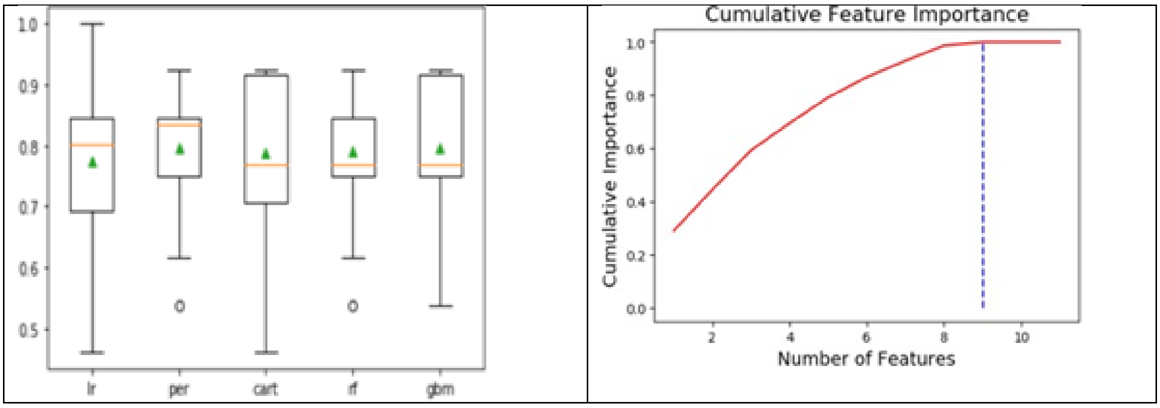


Figure 9. Baseline Models-BoxPlot

3.2. Performance Metrics

The factors utilized to measure the efficacy of the presented approach is represented in this section.

3.2.1. Accuracy

The accuracy is the essential metrics utilized to analyze prediction amount, which are accurately correct in the proposed model. The formula for accuracy is depicted in subsequent equation.

$$\text{Accuracy} = \frac{\text{TP+TN}}{\text{TP+FP+TN+FN}}$$

Where TP, TN, FP, FN are True Positive, True Negative, False Positive and False Negative.

4.2.2. AUC Curve

The AUC is utilized to compute the two-dimensional area that is under the ROC curve.

3.3. Global Results

The section represents the outcome attained by the proposed model. The different boosting algorithms like XGBoost, AdaBoost and GradientBoost were fit and tested on the dataset and the evaluation metrics are signified in Table 3. Thus, Table 3 illustrates the performance of the boost classifier; it is identified that the AdaBoost attained higher accuracy. Table 4 and Fig. 10 signifies the performance of the proposed model.

Table 3. Performance of Boosting Classifier

Classifiers	**Accuracy**	**CrossValidation**
XGBoost	89.19%	10 Fold CV
AdaBoost*	91.93%	10 Fold CV, no of trees=30
Gradient Boost	87.86%	10 Fold CV, no_trees=30

Table 4. Performance Chart

Classifier	**Accuracy**
RF- Gini	92.59
RF-Entropy	92.59
ExtraTrees Classifier-Gini	85.19
ExtraTrees Classifier Entropy	81.48

K-NN	85.19
NN Classifier	88.89
Weighted Ensemble	92.05

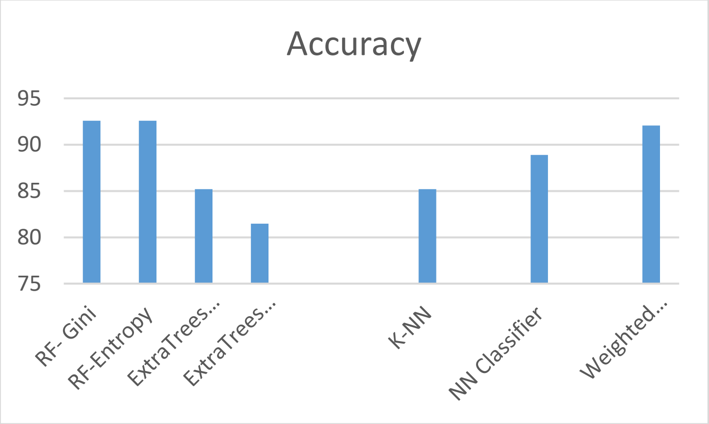


Figure 10. Outcome of the Presented Method

Figure 10 and Table 4 represent the outcome accomplished by the presented system. Here, multiple machine learning algorithms were wrapped up as voting ensembles by averaging the predictions of the arbitrary models. To gauge the predictive performance of the different models experimented; accuracy was used as the evaluation metric. Table 5 represents the accuracy yielded with the different classifiers and it is obvious that the Random Forest algorithm gives the highest accuracy comparatively.

In Random Forest, each of the trees built in the ensemble is formed with a random sample taken with replacement. Despite this fact of the randomness involved, a random subset of features is also picked up. The forest's bias somewhat increases in this situation, but its variance decreases as a result of the averaging of fewer connected trees, leading to a better model overall. The predictive performance on the dataset is 92.59%. Bagging enhances the benefits of the single model while minimizing its drawbacks, which could result in a combined model with reduced errors. The highest accuracy achieved is 92.59% with Random Forest Bagging Classifier.

Accordingly, the mean accuracy of each of the strategy was evaluated using a Decision TreeClassifier and is presented in Table 5.

Table 5. Statistical Strategies of Missing Value Imputation for Fast Glucose Attributes

Imputation Method	**Methods &Parameters**	**Accuracy(%) -Decision Tree**
Most CommonImputation	Mean: 81 Median: 80 Mode : 79	74.35 74.35 79.48
Concept MostCommon Imputation	Class: 1 Mean: 81 Class: 0 Mean: 81	74.35 74.35
K Nearest Neighbour imputation	k=1 to 9	87.40
Expectation Maximization Imputation	Loops=10	87.70

Table 5 represents the statistical Strategies of Missing Value Imputation for Fast Glucose Attributes. Similarly, RFE method was experimented with by hyper tuning the parameters such as Baseline model and Number of Features presented in Table 6.

Table 6. RFE - Hyper parameter Tuning

Baseline Model		**Mean Accuracy**			
Max_Features					
	5	6	7	8	9
Logistic Regression	0.776	0.78	0.76	0.77	0.79
Perceptron	0.797	0.79	0.80	0.80	0.80
CART	0.78	0.79	0.79	0.79	0.79
RF	0.79	0.796	0.80	0.78	0.79
GBM	0.79	0.807	0.79	0.80	0.80

Table 6 represents the RFE hyper parameter tuning. Accordingly, Tables 7, 8 and 9 signifies tuning seed values, tuning no of trees and tuning maximum number of features.

Table 7. Tuning Seed Values

Classifier	seed	num_trees	max_features	kFold	Mean Accuracy
RF	10	100	4	10	91.44
RF	15	100	4	10	91.46
RF	20	100	4	10	91.02
RF	25	100	4	10	91.48
RF*	**30**	**100**	**4**	**10**	**92.59**
RF	35	100	4	10	92.46

Table 8. Tuning No of Trees

Classifier	seed	num_trees	max_features	kFold	Mean Accuracy
RF	30	10	4	10	89.20
RF	30	25	4	10	89.68
RF	30	50	4	10	90.15
RF	30	75	4	10	91.91
RF*	**30**	**100**	**4**	**10**	**92.59**
RF	30	150	4	10	90.55

Table 9. Tuning Maximum No. of Features

Classifier	seed	num_trees	max_features	kFold	Mean Accuracy
RF	30	100	2	10	90.11
RF	30	100	3	10	90.57
RF*	**30**	**100**	**4**	**10**	**92.59**

Figures 7, 8 and 9 indicate the tuning seed values, tuning no of trees and tuning maximum number of features. It is identified that the RF attained higher accuracy than the other models. Correspondingly, the respective method is evaluated using a Decision Tree Classifier with Repeated Stratified KFold validation with the hyperparameters {nsplits=10, repeats=3, random=1} and obtained a mean ROC of 87.7%.

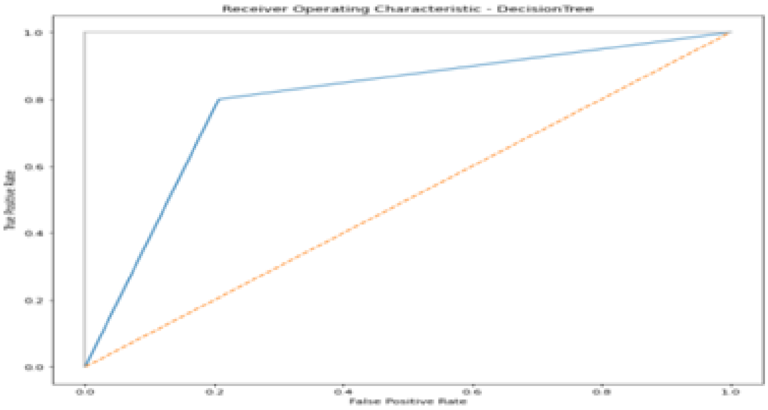


Figure 11. ROC curve

Figure 11 represents the ROC curve of the respective method. Building a decision support system is the core of machine learning and building a good model with optimal accuracy will be the solution to the prediction problem. This proposed work experiments with the different ensemble method, which is a potential technique to get a highly precise model. It is a computational knack of amalgamating different set of learners to improvise the predictive power of the model. Wide varieties of ensemble experiments were conducted and the results are recorded.

3.4. Comparative Analysis

The section represents the comparative analysis of the proposed model with the existing model.

3.4.1. Comparison with PIMA Indian Dataset

The proposed study on the prediction of Gestational Diabetes Mellitus was also performed using the benchmark PIMA Indian Diabetes dataset. The National Institute of Diabetes and Digestive and Kidney Diseases is the source of the PIMA Indian dataset. The primary goal for collecting this dataset was to predict diabetes from a cohort of 768 cases based on their diagnostic parameters. The attributes of PIMA datasets are No. of times Pregnant, Glucose, BP, Skin Thickness, Insulin, BMI, Pedigree, and Age. The PhysioNet Visceral Adipose Tissue Measurement Dataset with gestational outcome was used to execute the task of predicting GDM from maternal VAT at delivery time. The common attributes between PIMA and PhysioNet Visceral Adipose Tissue were taken into consideration to evaluate the prediction of diabetes. The results are tabulated with comparative analysis. With these six predominant and likely common attributes, the various ML bagging and boosting techniques were investigated and it was observed that high accuracy was achieved with RF classifier on PhysioNet VAT dataset and PIMA dataset as well for the prediction of Gestational Diabetes Mellitus. Evidently, in previous studies a 45 mm threshold of Visceral Adipose Tissue measurement was identified as the best cut-off value to predict GDM with an accuracy of 66%. The proposed model also ascertains that there exists a strong association between VAT depth and GDM. It is apparent that along with other important features, the presence of Adipose Tissue measurement aids in the prediction of GDM to a greater extent. Table 10 and Fig. 11 illustrates the common features in the PIMA and PhysioNet Dataset.

Table 10. Common Features - PIMA & Physionet

S. No	**Physionet- Visceral Adipose Measurements**	**PIMA Indian Diabetes**
1	Age	Age
2	Blood Pressure	Blood Pressure
3	Visceral Measurement	Skin Thickness
4	No. Of Pregnancies	No.of Pregnancies
5	Glucose Fast	Glucose Fast
6	BMI	BMI

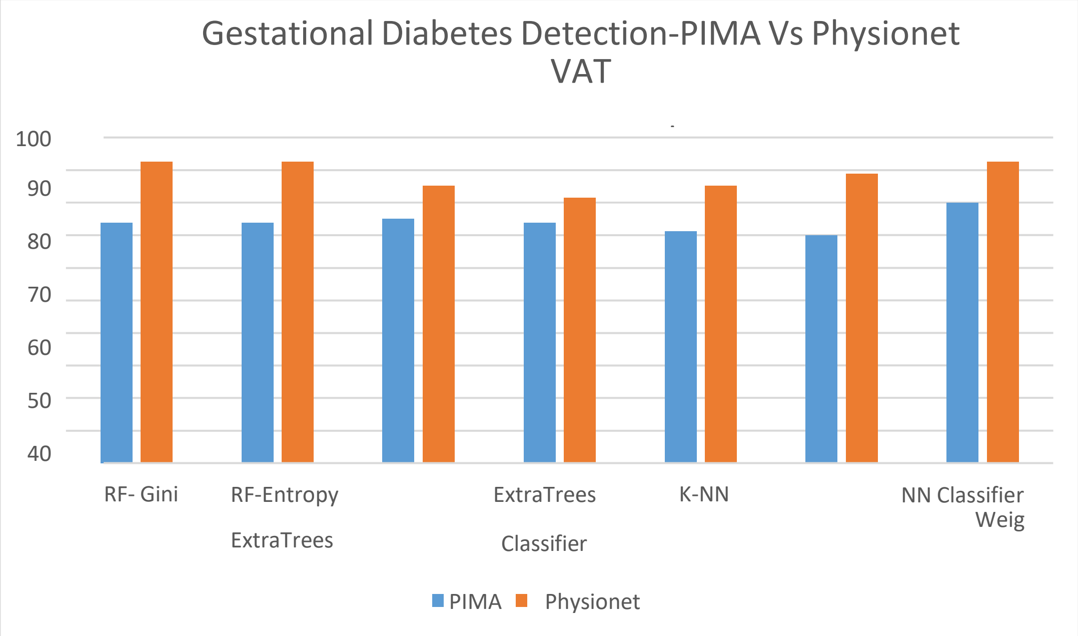


Figure 12. Comparison with PIMA Indian Dataset

Figure 12 illustrates the comparison of PIMA Indian dataset. Accordingly, Table 11 represents the efficiency comparison of the proposed model with the existing mechanism.

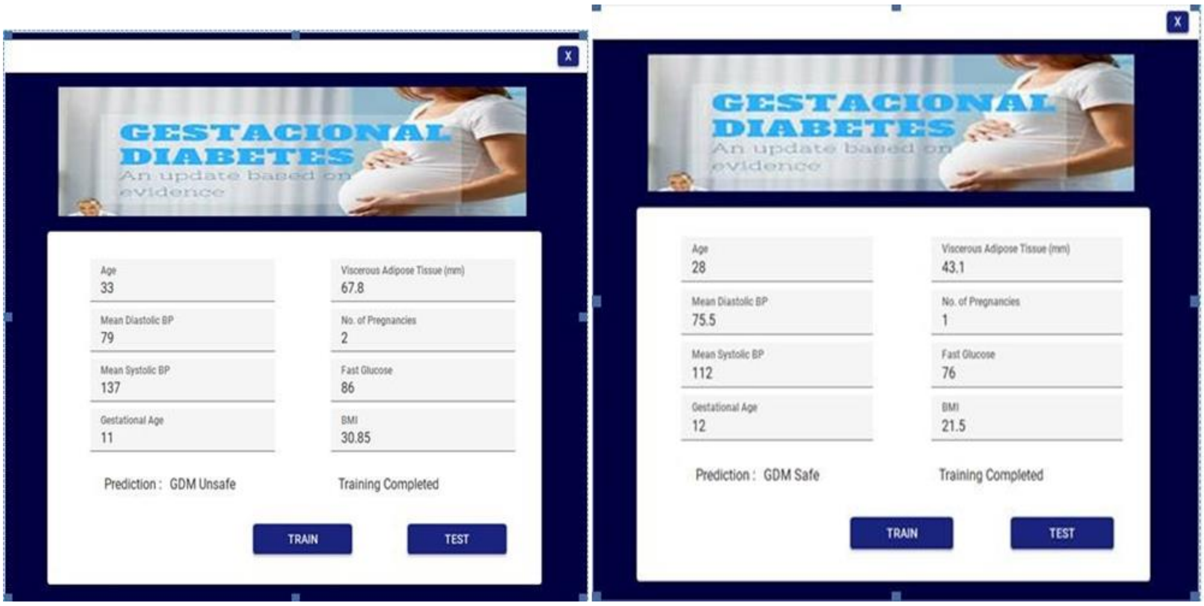
Table 11. Performance Comparison

Models	**PIMA**	**Physionet VAT**
RF- Gini	**73.75**	**92.59**
RF-Entropy	73.75	92.59
ExtraTrees Classifier-Gini	75	85.19
ExtraTrees Classifier Entropy	73.75	81.48
K-NN	71.25	85.19
NN Classifier	70	88.89
Weighted Ensemble	80	90.50

Table 11 shows the comparative analysis of the proposed model with the conventional model. It is identified that the presented method attained better efficiency than the classical methods.

3.5. Applications

Rapid diagnosis is necessary for Gestational Diabetes Mellitus (GDM), a public health issue that poses dangers to both the mother and the fetus. The work done is summarized in the development of a tool to be able to collect pregnant women data in the early weeks of gestation and also to infer the occurrence of GDM with high level of confidence. Further the interface can be extended by adding new symptomsand defining relationships between the new signs and the corresponding diseases. Figure 13 signifies the Prediction of Input Query Patient Using GDMSafe Tool.



Age
33

Mean Diastolic BP
79

Mean Systolic BP
137

Gestational Age
11

Viscerous Adipose Tissue (mm)
67.8

No. of Pregnancies
2

Fast Glucose
86

BMI
30.85

Prediction : GDM Unsafe

Training Completed

Age
28

Mean Diastolic BP
75.5

Mean Systolic BP
112

Gestational Age
12

Viscerous Adipose Tissue (mm)
43.1

No. of Pregnancies
1

Fast Glucose
76

BMI
21.5

Prediction : GDM Safe

Training Completed

Figure 13. Prediction of Input Query Patient Using GDMSafe Tool

4. CONCLUSION

The implemented work was able to obtain insight on the Visceral Adipose Tissue data. Predicting well in advance the occurrence of GDM may help the mothers to take adequate measures and precautions to combat GDM. With Random Forest, one of the most common ensemble approaches that uses a decision tree as a classifier, the best accuracy is attained. By varying the hyperparametes like random state, number of trees, maximum number of features and performing cross validation, it has been successfully demonstrated that RF provides more reliable and accurate predictions. The prediction tool provides useful knowledge to health care professionals and can also serve as a reference in their decision to predict GDM. However, most of the studies for GDM Prediction have made use of PIMA Indian Diabetes dataset. To the best of the knowledge, this is the first predictive model using the Visceral Adipose Dataset published recently in the public repository of PhysioNet Bank. In our view, the result emphasis the validity of the model. This study paves way for further progress in this direction as clinical studies suggests that VAD measured by ultrasound in early pregnancy may predict the onset of GDM, substantiating the previous findings in the literature.

DECLARATIONS

- **Conflict of Interest**: The author reports that there is no conflict of Interest.
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- **Ethics Approval**: Not Applicable

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