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Adaptive Gradient Driven Momentum Optimized Transfer Learning for Pregnancy Patient Risk Level Prediction

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Abstract
Maternal health is vital aspect of public health that affects health of mothers and unborn child. Conventional methods introduced but accurate prediction with minimal error rate remains challenges. Adaptive Gradient Driven Momentum Optimized Transfer Learning (AGMODTL) model is introduced for pregnancy patient risk level prediction. The AGMODTL model consists of different processes namely data acquisition, preprocessing, feature selection, classification and fine tuning. Initially, the number of maternal data samples is considered as an input layer for transfer learning. Then, the collected input maternal data points are collected from the dataset. Fine-tuning the layers of pre-trained model is a vital step using the elitist elephant herd metaheuristic algorithm thereby reducing errors and increasing the accuracy of the pregnancy patient risk level prediction. Experimental evaluation is carried out on the factor such as forecasting accuracy, precision, recall, F1 score, RMSE, specificity, confusion matrix with respect to the number of data samples.

Keywords: Pregnancy patient risk level prediction, Transfer Learning, SACCC.

1. Introduction

Pregnancy is vital phase in woman's life that needs uninterrupted medical concentration to ensure their well-being of mother and developing fetus. Ensemble XGBoost and DQN were developed in [1]. CatB ML model was introduced in [2].Different ML algorithms were developed in [3] .DT was introduced in [4]. ML model was developed in [5]. BBN model was developed in [6]. Binary logistic regression model and categorical DT were developed in [7].Stacking ensemble ML model was introduced in [8].LR model was introduce in [9].ANN ML model was developed in [10].Multivariable LR and modified Poisson regression models were developed in [11].Multivariable-adjusted LR was developed in [12] .Preeclampsia prediction model was developed in [13]. Long-term cardiovascular risk prediction model was introduced in [14].Ensemble Bagged Trees method was developed in [15].

1.1 Proposal key contribution

- To design AGMODTL for accurate pregnancy risk prediction.
- To minimize classification time, data preprocessing and feature selection are employed in AGMODTL

model.

- To enhance accuracy of risk level classification, Zijdenbos similarity index is employed to analyze different features and analyzes data samples and provides accurate prediction outcomes.

2. Related works

Quad-Ensemble ML framework was introduced in [16] .ML algorithms were introduced in [17] for improving maternal health risk prediction. Ensemble ML with various feature optimization methods were developed in [18]. RF and SVM classifier were introduced in [19]. PCA enhanced XGBoost model was developed in [20].Advanced ML and DL supervised models were developed in [21].RF and Gradient Boosting Classifiers were introduced in [22].High-risk pregnancy was identified in [23].RF classifier model was introduced in [24].ML models were developed in [25].Univariate analysis and multivariate binary LR analysis were developed in [26]. WRF algorithm was designed in [27]. ML and AI model were developed in [28]. RF was introduce in [29]. RF and SVM were developed in [30].

3. Proposal Methodology

AGMODTL integrates advanced DTL with optimized fine tuning to efficiently monitor and predict maternal health risk occurrences.

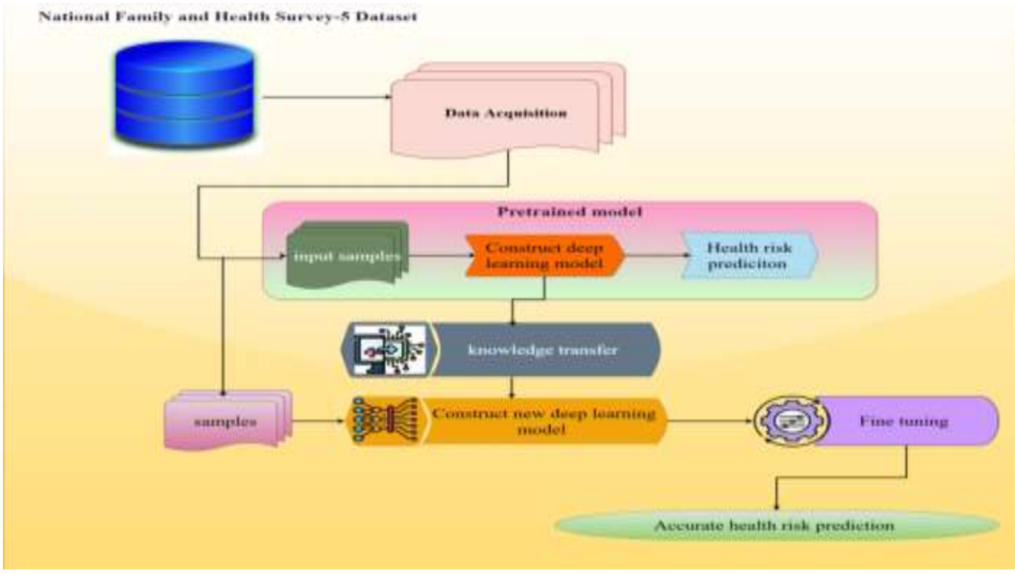

Figure 1 architecture diagram of proposed AGMODTL model

3.1 Dataset Acquisition

AGMODTL uses NFHS-5 dataset https://www.kaggle.com/datasets/ravisinghiitbhu/nfhs5.

3.2 Deep transfer learning model

AGMODTL model employs DTL to enhance accuracy of health risks prediction.

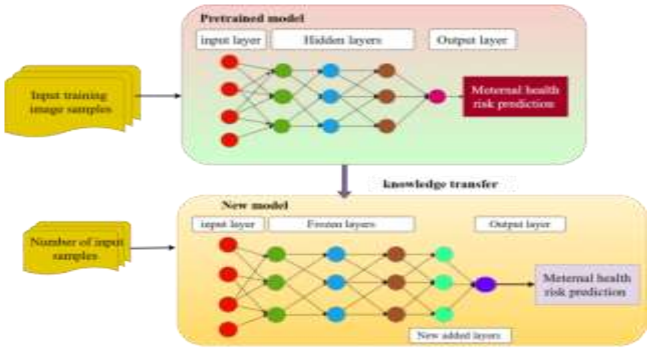

Figure 2 Schematic construction of DTL

3.2.1 Construction of Pre-trained classification for maternal health risk prediction

In structure of transfer learning model, pre-trained constructs Multilayer Perceptron classifier for training large volume of input data samples. Multilayer Perceptron classifier includes many layers.

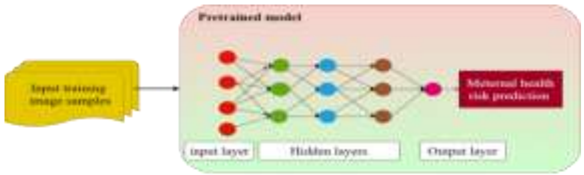

Figure 3 construction of pre-trained

Figure 3 ,Let us consider the dataset 'DS' and data samples 'S' , features $\{F_1, F_2, \ldots, F_m\}$are arranged in input matrix.

$$X = \begin{bmatrix} F_1 & F_2 & \ldots & F_m \\ S_{11} & S_{12} & \ldots & S_{1n} \\ S_{21} & S_{22} & \ldots & S_{2n} \\ \vdots & \vdots & \ldots & \vdots \\ S_{m1} & S_{m2} & \ldots & S_{mn} \end{bmatrix} \text{ Where, } n = rows, m = columns \quad (1)$$

Neurons then compute a weighted sum of these inputs, is expressed

$$Q = \sum\left(X * \omega_{i_h}\right) + b \ (2)$$

3.2.1.1 Preprocessing

New synthetic data samples 'S_{new}' generation process is expressed as

$$S_{new} = S_i + (S_n - S_i).\rho \ (3)$$

Distance between majority and minority samples in dataset is calculated as

$$d = \sqrt{\left(S_{maj} - S_{min}\right)^2} \quad (4)$$

Majority samples with less distance are selected and removed the others.

$$W = \arg\min d\ (S_{maj}) \quad (5)$$

Weighted average of the neighboring data i.e. proximal data is computed as

$$S_{miss} = \frac{\sum_{i=1}^{n} \beta_i S_i}{\sum_{i=1}^{n} \beta_i} \quad (6)$$

Let us consider '$S = \{S_1, S_2, \ldots, S_n\}$' , log-normally distributed as,

$$W = ln(S_n)(7)$$

For each transformed data samples, mean 'μ' and deviation 'σ' is computed as

$$\mu = \frac{1}{n}\sum_{i=1}^{n} W_i \qquad (8)$$

$$\sigma = \sqrt{\frac{1}{n}\sum_{i=1}^{n}(W_i - \mu)^2} \qquad (9)$$

Therefore, the outlier data is identified as

$$P(W;\mu,\sigma) = \frac{1}{\sigma\sqrt{2\pi}}\exp\left(-0.5\frac{(W_i-\mu)^2}{\sigma^2}\right) \qquad (10)$$

Where, $P(W;\mu,\sigma)$ denotes probability density function returns output from 0 to 1.

$$Z = \begin{cases} P(W;\mu,\sigma) > T \ ; \ normal \\ Otherwise \ ; \ outlier \end{cases} \qquad (11)$$

3.2.1.2 Feature selection

FS to enhance prediction accuracy by minimizing dimensionality.Initialize feature vector in distributed dataset.

$$F = \{F_1, F_2, \ldots, F_m\} \quad (12)$$

Association coefficient between features set and target is computed as

$$CC = 2 * \left[\frac{COV_{jk}}{\vartheta_j{}^2 + \vartheta_k{}^2 + D_{jk}}\right] \quad (13)$$

$$D_{jk} = \frac{1}{m}\sum_{j=1}^{m}\sum_{k=1}^{c}\left|F_j - \tau_k\right| \quad (14)$$

3.2.1.3 Classification

Classification is carried out to analyze selected features. Similarity is estimated as

$$R = ZS\ (S_{Train}, S_{Test}) \quad (15)$$

$$ZS\ (S_{Train}, S_{Test}) = 2 * \frac{|S_{Train} \cap S_{Test}|}{|S_{Train}| + |S_{Test}|} \quad (16)$$

Classified binary class output is generated at output layer with sigmoid activation function.

$$Y = f_{sigmoid}(h(t)) \quad (17)$$

$$f_{sigmoid} = \begin{cases} 1 \ ; high\ risk \\ 0 \ ; low\ risk \end{cases} \qquad (18)$$

// Algorithm 1: Pre-trained classification model
Input:Dataset 'DS', Samples '$S = \{S_1, S_2, \ldots . S_m\}$', Features '$F = \{F_1, F_2, \ldots \ldots, F_n\}$' **Output:** maternal health risk prediction
Begin **Step 1:Collect n**umber of number of Samples '$S = \{S_1, S_2, \ldots . S_m\}$', Features '$F = \{F_1, F_2, \ldots \ldots, F_n\}$' from input dataset 'DS' **Step 2: input** of Samples given to input layer of Multilayer Perceptron deep learning classifier **Step 3:** Transfer the input samples to hidden layer 1 **Step 4:**For each samples S_i --- **Hidden layer 1** **Step 5:** Measure the weighted sum using (2) **Step 6: For each** samples in an **image** **Step 7:** Perform the oversampling using (3) **Step 8:** Perform the undersampling using (4) and (5) **Step 9**: Handle missing data using (6) **Step 10**Compute probability density function '$P(W;\mu,\sigma)$' using (10) **Step 11**: **If** ($P(W;\mu,\sigma) > T$) **then**

Step 12: Samples is identified as normal
Step 13:**else**
Step 14 Samples is identified as outlier
Step 15: End if
Step 16: End for
Step 17: For each pre-processed dataset **--- Hidden layer 2**
Step 18: Measure the a correlation coefficient using (13)
Step 19: If $(\max CC)$ **then**
Step 20:features are said to be a relevant
Step 21: **else**
Step 22: features are said to be a irrelevant
Step 23: End if
Step 24:For each extracted features and training samples**----- Hidden layer 3**
Step 25: Measure Zijdenbos similarity coefficient using (15) (16)
Step 26: Obtain classification **results at output layer** with sigmoid activation using (17)
Step 27: if $(f_{sigmoid} = 1)$ then
Step 28: Sample is classified into high risk or high complication
Step 29: else
Step 30:Sample is classified into low risk or low complication
Step 31: End if
Step 36: End for
Step 37: Return final classification output
End

3.3 new model based maternal health risk prediction

In Figure 2, numerous layers referred to frozen layers are preserved from original model, their parameters unchanged during this process. PE is calculated as

$$PE = \left[\frac{Number\ of\ misclassified\ data\ samples}{n}\right] \quad (19)$$

Weight adjustment is done through Nesterov gradient momentum scheme.

$$\omega_{t+1} = \omega_t - \eta\ M_t \quad (20)$$

$$M_t = \alpha\, M_{t-1} + (1-\alpha)\left[\frac{\partial PE}{\partial \omega_t}\right] \quad (21)$$

At first, populations of elephant i.e. weights are initialized in search space.

$$\omega_b = \omega_1, \omega_2, \omega_3 \ldots . \omega_b \quad (22)$$

Once population is initialized, fitness of each elephant is estimated as

$$F(\omega) = \arg\min PE \quad (23)$$

Elitist approach is combined and identifies the best weight among others as

$$A = \begin{cases} \omega_b > \omega_b & select\ curent\ best\ weight \\ Otherwise\ ; & Remove\ the\ others \end{cases} \quad (24)$$

- **Clan-Updating Operator**

New position of each elephant is updated through matriarch.

$H_{i+1} = H_i + u * 0.5|H_{best} - H_i| * r$ (25)

Best elephant is identified for each clan is identified as follows,

$H_{best} = B * H_{center}$ (26)

Where, B symbolizes influenced factor $\beta \in [0,1]$, 'H_{center}' represent center individual of clan. It is given by,

$H_{center} = \frac{1}{K} * \sum_{r=1}^{K} H_r$ (27)

- **Separating Operator**

It imitates male elephants leaving from herd and implemented by replacing elephant worst fitness in each generation.

$H_{worst} = H_{min} + (H_{max} - H_{min} + 1) * rand$ (28)

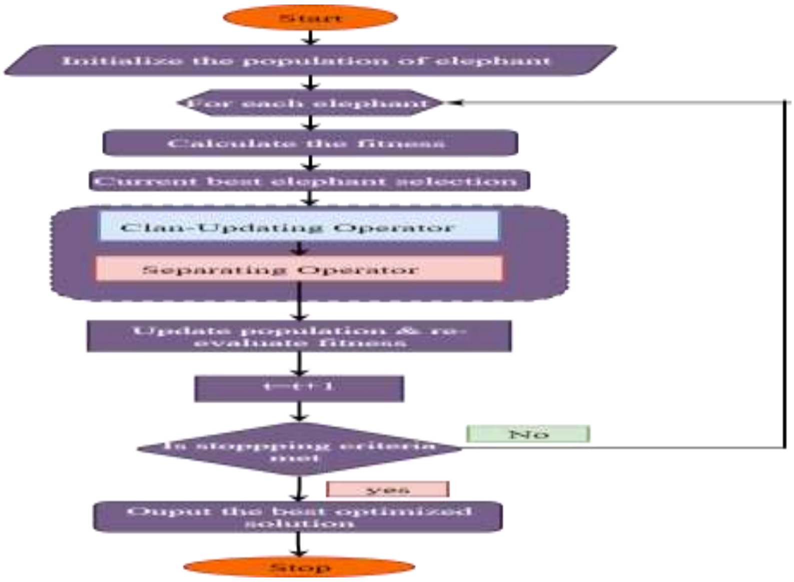

Figure 4 Flow diagram of elitist elephant herd metaheuristic algorithm

Figure 4 shows elitist elephant herd metaheuristic algorithm to select optimal weight for minimizing error during prediction. Newly accurate classification results are obtained at output layer.

$Y_{new} = f_{sigmoid}(h(t))$ (29)

// Algorithm 2: New classifier model based maternal health risk prediction
Input: Dataset 'DS', Samples '$S = \{S_1, S_2, \ldots . S_m\}$', Features '$F = \{F_1, F_2, \ldots\ldots, F_n\}$' **Output:** Accurate maternal health risk prediction
Begin **Step 1: Collect n**umber of number of Samples '$S = \{S_1, S_2, \ldots . S_m\}$', Features '$F = \{F_1, F_2, \ldots\ldots, F_n\}$' --- **input layer** **Step 2: For each** Samples S_i--- **Hidden layer 1** **Step 3:**Compute the weighted sum using (2) **Step 4:** Perform the oversampling and undersampling using (3) (4) **Step 5:** Handle missing data using (6) **Step 6**: Remove outlier using (10) **Step 7**: **End for** **Step 8**: **For each pre**-processed dataset **--- Hidden layer 2** **Step 9:**Measure the a correlation coefficient select relevant features using (13)

Step 10: End for
Step 11:For each training samples----- **Hidden layer 3**
Step 12: Measure the Zijdenbos similarity coefficient using (15) (16)
Step 13: Obtain classification **results**
Step 14: End for
Step 15: For each classification result **-----[Hidden layer 4]**
Step 16 Measure the classification error ‘ RE using (19)
Step 17 Update the weights using (20) (21)
Step 18: End for
Step 19: Initialize the population of the weights using (22)
Step 20: for each weight ‘ ω_b’
Step 21: Compute the fitness ‘$F(\omega)$’ using (23)
Step 22: End for
Step 23: Select current best using (24)
Step 24: While (t < Max_t) **do**
Step 25: for each current best
Step 26: Execute the clan updating operator using (25)
Step 27: Execute the Separating Operator using (28)
Step 28: Verify the fitness of updated position
Step 29: t=t+1
Step 30: Go to step 24
Step 31: End for
Step 32: End while
Step 33: Return (optimal solution)
Step 34: Process the entire structures
Step 35: Obtain final disease classification results at output layer **using (29)**
End

4. Experimental Setup

Analysis is to estimate efficiency of AGMODTL with [1],[2] by Python. .

4.1 Implementation results

136,136 maternal records data sample are collected from dataset in figure 5

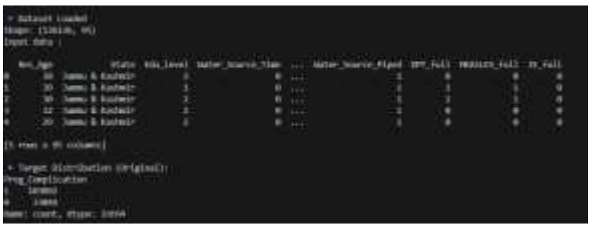

Figure 5 sample data collection **from the dataset**

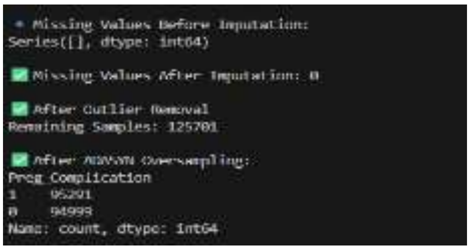

Figure 6 data preprocessing

Figure 6 shows dataset contained no missing values before imputation, this remained unchanged after imputation.

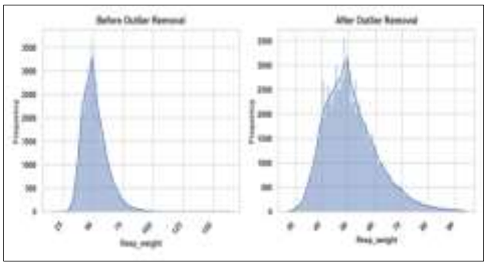

Figure 7 results of before and after outlier removal

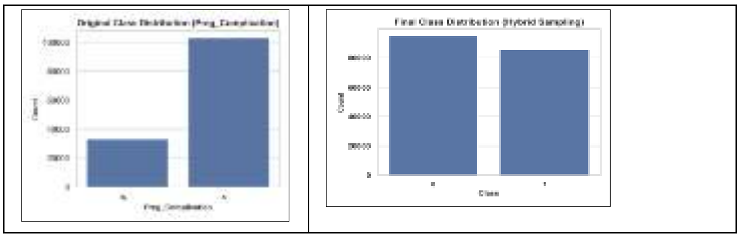

Figure 8 results of before and after class balancing

To achieve this, 32 key features with similarity score near to '1' from 95 features.

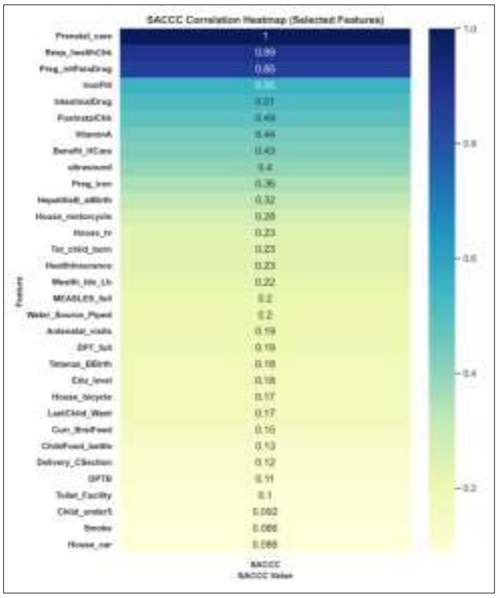

Figure 9 heatmap for selected features

Selected Features:

	Feature	SACCC
76	Prenatal_care	1.000000
69	Resp_healthChk	0.893796
48	Preg_IntParaDrug	0.847093
52	IronPill	0.551012
53	IntestinalDrug	0.514858
68	PostnatalChk	0.489111
51	VitaminA	0.443372
72	Benefit_HCare	0.420091
67	ultrasound	0.401348
36	Preg_Iron	0.355359
49	HepatitisB_atBirth	0.321696
9	House_motorcycle	0.277139
7	House_tv	0.234782
15	Tot_child_born	0.230236
27	HealthInsurance	0.229229
14	Wealth_Idx_Lb	0.215257
92	MEASLES_full	0.202048
90	Water_Source_Piped	0.195922
31	Antenatal_visits	0.193433
91	DPT_full	0.189678
30	Tetanus_BBirth	0.177570
2	Edu_level	0.176119
8	House_bicycle	0.171664
19	LastChild_Want	0.168553
20	Curr_BrstFeed	0.149718
21	ChildFood_bottle	0.127824
32	Delivery_CSection	0.119576
70	DPT8	0.113912
4	Toilet_Facility	0.100355
12	Child_under5	0.091638
73	Smoke	0.086303
10	House_car	0.086296

Figure 10 selected 32 features

classification is carried out by Zijdenbos similarity index implemented in TL.

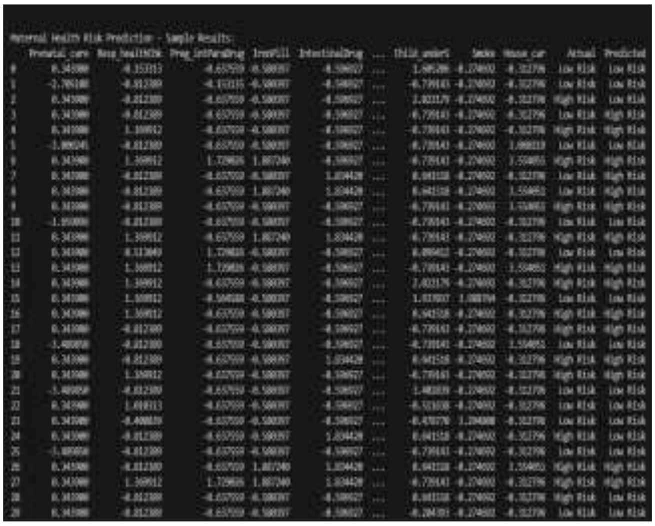

Figure 11 classified results

5. Performance Analysis

AGMODTL is comparing [1] and [2]with various metrics.

5.1 Evaluation metrics

Accuracy: It estimates ratio of correct classification of low and high risk samples by method,It is calculated as follows,

$$Acc = \frac{TP+TN}{TP+FP+TN+FN} \quad (29)$$

Precision: it refers to accuracy of positive predictions made by model.

$$Pre = \frac{TP}{TP+FP} \quad (30)$$

Recall: It is ratio of TP predictions to total number of actual positive instances.

$$Rec = \frac{TP}{TP+FN} \quad (31)$$

F1-score: It combines Pre as well as Rec to one value, providing balanced assessment of model accuracy.

$$F1\ score = 2 * \left(\frac{Pre*Rec}{Pre+Rec}\right) \quad (32)$$

Specificity: It evaluates model ability to correctly differentiate between different classes of complication prediction.

$$Spe = \frac{TN}{TN+FP} \quad (33)$$

Classification time: It is amount of time consumed for differentiates classes of complication prediction.

$CT = \sum_{i=1}^{m} S_i * Time\ (Classification)$(34)

5.1 Performance assessment of Accuracy

Table 1 shows Accuracy of AGMODTL improved by 3% and 6% than the [1] , [2].

Table 1 Comparison of accuracy

Number of data samples	Accuracy (%)		
	Proposed AGMODTL	Ensemble XGBoost-DQN [1]	CatB [2]
10000	0.98	0.95	0.94
20000	0.97	0.94	0.92
30000	0.96	0.93	0.91
40000	0.95	0.92	0.9
50000	0.94	0.91	0.89
60000	0.95	0.92	0.9
70000	0.94	0.91	0.88
80000	0.95	0.92	0.89
90000	0.96	0.93	0.9
100000	0.96	0.92	0.90

5.2 Performance assessment of precision

In Figure 12 ,AGMODTL increases Pre by 3% and 5% than the [1], [2].

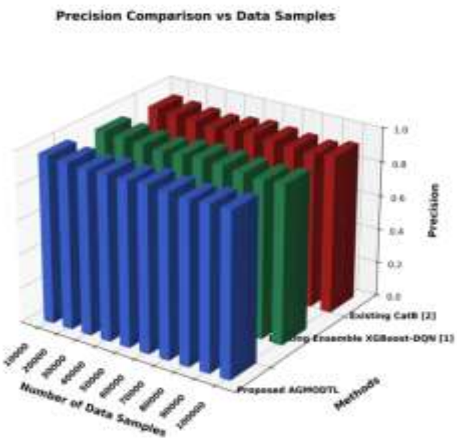

Figure 12 graphical analysis of Pre

5.3 Performance assessment of recall

In table 2 recall of AGMODTL is improved by 3% and 5% than the [1] and [2]

Table 2 Comparison of Recall

Number of data samples	Recall		
	Proposed AGMODTL	**Ensemble XGBoost-DQN [1]**	**CatB [2]**
10000	0.99	0.97	0.97
20000	0.98	0.95	0.94
30000	0.97	0.94	0.92
40000	0.96	0.95	0.93
50000	0.97	0.94	0.92
60000	0.96	0.93	0.91
70000	0.97	0.95	0.93
80000	0.98	0.95	0.92
90000	0.97	0.94	0.93
100000	0.98	0.95	0.94

5.4 Performance assessment of F1 score

In Figure 13 shows AGMODTL achieves F1-score 3% , 5% than the [1], [2].

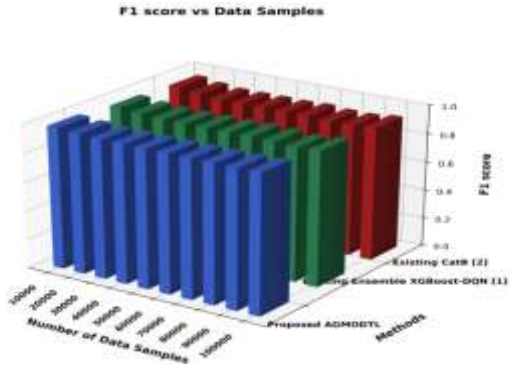

Figure 13 graphical analyses of F1

5.5 Performance assessment of specificity

In Table 3 illustrates AGMODTL improved specificity by 7% and 11% than the [1] , [2].

Table 3 Comparison of specificity

Number of data samples	specificity		
	Proposed AGMODTL	**Ensemble XGBoost-DQN [1]**	**CatB [2]**
10000	0.95	0.88	0.84
20000	0.94	0.87	0.83
30000	0.93	0.88	0.84
40000	0.92	0.89	0.85
50000	0.93	0.88	0.86
60000	0.94	0.87	0.84
70000	0.93	0.88	0.85
80000	0.92	0.87	0.84
90000	0.93	0.85	0.82
100000	0.91	0.83	0.80

5.6 Classification time

In Figure 14 AGMODTL achieved 9% in CT and 16% than the [1],[2]

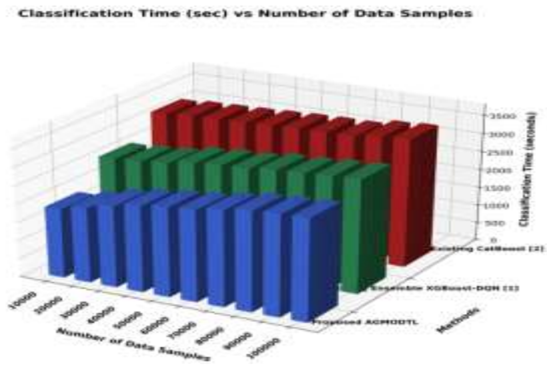

Figure 14 graphical analyses of CT

5.7 Performance analysis of ROC , AUC

ROC, AUC are used for evaluating performance of binary classification models.

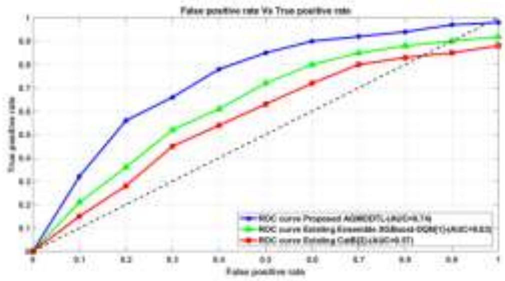

Figure 15 ROC-AUC curves

5.8 Confusion matrix analysis

In figure 16, confusion matrix of AGMODTL is presented.

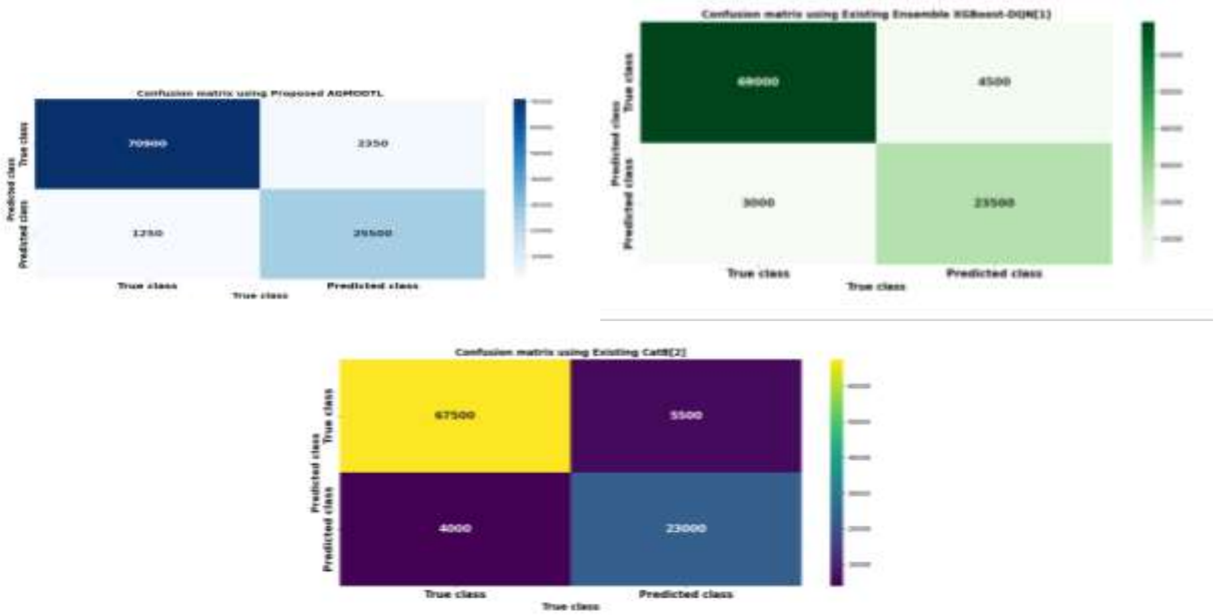

Figure 16 confusion matrix using AGMODTL model, [1] and [2]

6. Conclusion

AGMODTL introduced to provide highly pregnancy risk classification .Experimental expose AGMODTL outperforms conventional approaches.

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