Integration of ResNet-50 with Adaptive Simulated Annealing for Enhanced Predictive Modeling of Gestational Diabetes

Xiong Jian[1, 2], Rajamohan Parthasarathy[2], Yinqing Tang[1], BinWen Huang[1*]
[1]Modern Educational Technology Center, Hainan Medical University, Haikou, Hainan, 571199, China
[2]Faculty of Engineering, Built Environment and Information Technology SEGi University, Kuala Lumpur, Malaysia

Keywords: Artificial Intelligence (AI), Recursive Feature Elimination (RFE), Adaptive Simulated Annealing (ASA), ResNet-50, chronic diseases

Received:

Chronic diseases such as cancer, diabetes, and cardiovascular disorders pose significant public health challenges due to their chronic duration and the costly nature of treatment. Gestational diabetes is a complex, costly, and long-term public health issue, particularly during pregnancy, necessitating early diagnosis and precise prognosis to improve both the mother's and the fetus's health. Early diagnosis and effective prediction of disease progression are essential for lowering healthcare costs and enhancing patient outcomes, but they often lack precision and adaptability. The research aims to develop an advanced Artificial Intelligence (AI)-based framework for the early diagnosis and predictive modelling of pregnancy complication datasets using gestational diabetes that includes clinical parameters, physiological biomarkers, and basic demographic information. The dataset is pre-processed by handling missing values and standardizing numerical features to ensure data quality and consistency. Recursive Feature Elimination (RFE) is applied for informative feature extraction. A modified ResNet-50 Deep Learning (DL) architecture is employed for both classification and early diagnosis tasks, while Adaptive Simulated Annealing (ASA) optimizes feature selection. The ResNet-50-ASA model achieved high accuracy (0.985), precision (0.969), sensitivity (0.889), specificity (0.865), F1-score (0.975) and Recall (0.983), enabling accurate early detection and prediction of gestational diabetes. The ResNet-50-ASA architecture outperformed conventional models, achieving high classification accuracy and robust generalization across validation datasets. The model demonstrated improved sensitivity in identifying early signs of chronic diseases like gestational diabetes. The proposed AI-driven pipeline effectively enhances early diagnostic capabilities and predictive modelling for chronic gestational diabetes. Incorporating advanced feature selection and DL techniques offers a promising direction for clinical decision support systems and proactive healthcare interventions.

Povzetek: Za zgodnje odkrivanja gestacijske sladkorne bolezni z običajnimi kliničnimi metodami je razvit AI-okvir ResNet-50 + ASA, ki po predobdelavi podatkov (KNN, Z-score, RFE) optimira izbor značilk in klasifikacijo.

1 Introduction

Chronic diseases such as diabetes, cancer, and cardiovascular diseases present major global health challenges. These conditions cause lasting disabilities, such as early deaths, and increased medical costs. The chronicity requires early detection to avoid complications and better patient outcomes. Despite advances in medicine, conventional diagnostic tests tend to miss faint early signs that interfere with early treatment [1]. When more than one chronic disease or comorbidity combines, treatment becomes more difficult and adds more health burdens. The combination of these diseases' forms complicated clinical syndromes requiring more specialized risk assessment techniques. With increasing worldwide comorbidity levels, scientists increasingly demonstrate interest in data-driven solutions that can identify concealed trends and facilitate predictive health care solutions [2].

Chronic diseases are difficult to manage in practice due to the progressive nature of the diseases, long treatment periods, and perpetual complications. Ongoing care means constant monitoring, medication, and lifestyle changes, which is a huge burden to patients and healthcare systems. The time lag in detection increases the chance of comorbidities, lowers survival, and adds to the growing economic and logistical load in global healthcare systems [3]. Gestational Diabetes Mellitus (GDM) is a condition of glucose intolerance first diagnosed during pregnancy, and it is a significant health hazard for both mother and child. GDM is rising globally, primarily because of the growing

trend in obesity and pre-gestational diabetes among women of childbearing age. GDM carries adverse outcomes, such as larger-for-gestational-age babies and preeclampsia, and therefore it is crucial to diagnose and treat GDM as early as possible to enhance maternal and fetal outcomes [4]. GDM screening is traditionally performed between 24 and 28 weeks of gestation, yet there is heterogeneity in recommendations for screening earlier in pregnancy among professional groups. The absence of agreement indicates the necessity of further research and the development of standardized guidelines and reflects the doubt about early diagnosis and treatment of GDM [5]. In the past, traditional methods of diagnosing diabetes, especially gestational diabetes, have not been consistent, flexible, or applicable in different settings. Routine techniques such as OGTT can miss the early or atypical cases since diagnostic tests give rise to possible delays in diagnosis. Non-personalized fixed thresholds mean that there must be a more data-driven, dynamic, and personalized approach to diagnosis [6].

GDM diagnosis is imprecise and not indicative of the individual risk factors associated with the subject in question, which may include family history, genetic predisposition, and BMI. This decline renders early-stage diagnosis a challenge for a method tailored to the person's risk factors for GDM, making personalized predictive models critical to understand patient diversity and capacity to intervene early [7]. Traditional diagnostic methods for GDM depend on standard glucose thresholds assessed between 24-28 weeks of gestation, often ignoring subtle early physiological and metabolic changes, and would fail to detect identifiable high-risk individuals before the development of complications and thus lose opportunities for early intervention [8]. Moreover, the current screening method does not best account for individual variability, including genetic predisposition and ethnicity, which limits personalized risk assessment and decreases diagnostic sensitivity in different population groups. There is a need for improved precision using integrative, individualized diagnostic approaches in GDM care [9]. Current diagnostic methodologies for GDM and its related conditions typically fail to combine systemic inflammatory markers, microbiome interactions, and individual risk factors. Many fail to detect early subclinical processes, and few appreciate the persistent biological relationships between these conditions, which affect diagnosis, precision, and efficacy for diverse, high-risk populations [10].

1.1 Research objective

The goal of the research is to develop an AI-based framework for early diagnosis and predictive modelling of chronic diseases, such as gestational diabetes, based on optimized DL techniques with feature selection. High classification accuracy and strong generalization across validation datasets were achieved by the ResNet-50-ASA architecture, outperforming traditional models. When it came to spotting early indicators of chronic conditions like gestational diabetes, the model showed increased sensitivity.

1.2 Key contributions

- An AI-enabled system develops with the potential to diagnose and predict chronic conditions, such as gestational diabetes, at an early stage, based on patient clinical manifestations, physiological manifestations, and demographics.
- To apply preprocessing techniques, including handling missing values and standardization, to ensure high-quality input data. RFE is used for feature extraction to allow for efficiency and relevance of the model.
- To develop a modified ResNet-50 with ASA tailored for disease classification and early detection tasks.
- To achieve superior diagnostic performance, demonstrating improved sensitivity and accuracy compared to traditional approaches.

1.3 Paper organization

The remainder of the sections are organized as follows: Research Background is discussed in Section 1. Previous AI-based techniques for early disease detection and chronic disease prediction models are covered in Section 2. Section 3 presents the proposed methodology, which involves data collection, data preprocessing, RSE for feature extraction, and design of the modified ResNet-50 with ASA framework. Section 4 contains experimental results. Finally, the investigation is summarized in Section 5 along with future research directions.

2 Related work

The intention of the research [11] was to use ML classification to estimate the number of patients who have chronic diseases. A Convolutional Neural Network (CNN) architecture was established for the extraction of features, in combination with K-Nearest Neighbour (KNN) similarity-based prediction. Limitations to the data involved dependence on symptom and lifestyle inputs. Higher accuracy than Logistic Regression (LR), Decision Tree (DT), and Naive Bayes (NB) models in chronic disease prognosis was demonstrated by the performance measures. The processing of data on chronic disease was utilized to improve patient lifestyle [12]. Four disease-specific datasets were processed using ML classifiers in Orange3. Restrictions include heterogeneous accuracy across algorithms and diseases. Outcomes emphasized that DT and Support Vector Machine (SVM) achieved perfect accuracy in identifying hypertension, Random Forest (RF) outperformed other models in determining kidney disease, and neural networks performed best in detecting diabetes.

Research aimed at enabling early prediction of cardiovascular disease utilizing hospital health databases [13].

A Categorical Boosting (CatBoost) model based on ML was created to allow for early diagnosis and automatic feature selection. Robust modelling over heterogeneous data was a challenge. An experiment used data mining tools to enhance heart disease prediction in people with diabetes [14]. A DT model was refined and compared to SVM and NB. Insufficient datasets delayed the generalizability of the model. However, the DT consistently performed better than the others and showed a higher level of accuracy in determining cardiovascular risk in people with diabetes. Table 1 illustrates the Comparative summary of recent GDM prediction studies and methodologies.

Table 1: Review of AI and biomarker-based approaches for gestational diabetes and cardiovascular risk

Reference	Method	Result	Advantage	Limitation
Dritsas and Trigka [15]	Postpartum observation research on GDM	High rates of dysglycaemia and metabolic syndrome 5 months postpartum	Identifies postpartum risk factors (e.g., BMI, breastfeeding)	Does not propose a predictive model; observational only
Huma and Basharat [16]	SMOTE for class imbalance + ML classifiers	Improved accuracy and AUC in cardiovascular prediction	Effective in handling class imbalance	High computational cost; imbalanced data scenarios were still complex
Gómez Fernández et al. [17]	Longitudinal postpartum analysis	Early GDM diagnosis linked to cardiometabolic issues	Highlights long-term risk to mother and child	Limited to a 5-month postpartum window
Venkatesh et al. [18]	Longitudinal cohort analysis	GDM linked to poor CV health in offspring aged 10–14	Uses long-term data for risk correlation	Causality cannot be firmly established
Qin et al. [19]	Longitudinal biomarker study	High ferritin and CRP in GDM participants	Identifies ferritin as an early biomarker for GDM	Limited generalizability; specific biomarker-focused

2.2 Research gaps

Even with advances in AI-based healthcare systems, there are still significant gaps in the early detection of GDM. Most models do not combine multimodal data such as clinical, demographic, and biomarker data, resulting in lower diagnostic accuracy [4]. Feature selection strategies are often inadequate, with insufficient use of complex techniques such as Adaptive Simulated Annealing to improve deep learning performance [11]. Furthermore, delayed diagnosis in contemporary clinical practice emphasizes the importance of AI techniques for early identification and intervention [5]. To fill these gaps, the research combines multimodal data, clinical, demographic, and physiological biomarkers into a single artificial intelligence framework. By employing ASA to optimize feature selection with a modified ResNet-50 architecture, the model improves clinical decision support and early diagnosis accuracy for gestational diabetes, providing fast, pregnancy-specific detection.

3 Methodology

The section begins by gathering a pregnancy complication dataset using a gestational diabetes dataset. After that, imputation of missing values and normalization improved the quality of the data. RSE is employed to extract important features. A ResNet-50 DL model integrated with ASA is subsequently used with modifications to improve diagnosis at an early stage and chronic disease prediction efficiency. The flow of the proposed model is illustrated in Figure 1.

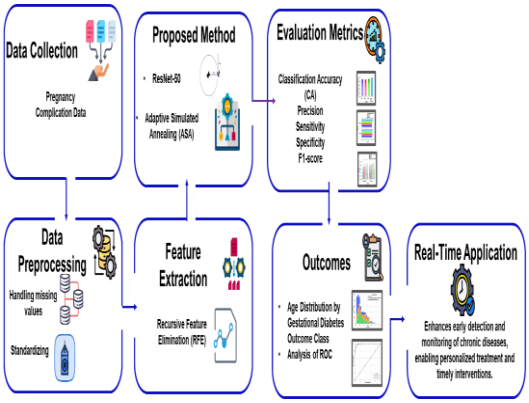

Figure 1: Methodology flow

3.1 Data collection

The dataset used in the research, Pregnancy Complication Dataset, was obtained from Kaggle (https://www.kaggle.com/datasets/harideepak/pregnancy-complication-dataset). It focuses on pregnancy complications in patients, emphasizing how lifestyle habits influence the onset and course of diabetes-related conditions during pregnancy. The dataset includes comprehensive medical and demographic features such as chronic disease history, glucose levels, genetic predisposition, along with Body Mass Index (BMI), offering a clinical view of patient health. The markers can demonstrate the impact of numerous other variables on pregnancy outcomes. Grouping markers can help the model identify stages of glucose-associated complications during pregnancy that would enable early detection and individualized approaches to treatment. The dataset was split into 80% for training and 20% for validation.

3.2 Data preprocessing

In this section, data preprocessing handled missing values by using KNN imputation, and z-score normalization is applied to reduce noise, enhancing data quality. Preprocessing was crucial for the clinical dataset centered on pregnancy-related problems, specifically gestational diabetes, to guarantee analytical robustness and model accuracy.

❋ **Handling missing values using KNN imputation**

The KNN method was adopted for estimating missing values in the clinical dataset. KNN uses Euclidean distance on available features to keep the data intact and allow for meaningful analysis. The Euclidean distance D_{xy} between two samples x and y can be calculated using (1).

$$D_{xy} = \sqrt{weight \times \sum(x_i - y_i)^2} \quad (1)$$

Where the ratio of the number of current (non-missing) features for that observation to the total feature dimensions n determines the weight (2).

$$weight = \frac{n}{n_{present}} \quad (2)$$

Where n is the total number of landscapes and $n_{present}$ is the number of non-missing features in a given record. The method guarantees that only information currently accessible is being considered in the proximity-based imputation while preserving important diagnostic attributes such as BMI and glucose levels. To identify patterns of gestational diabetes in its early stages, KNN imputation enabled a complete dataset to be accessed without modifying the initial data distribution.

❋ **Standardizing Clinical Features by Z-score Normalization**

To have consistent and good-quality data in the clinical dataset, Z-score normalization was applied to numerical features. This method reduces the interference caused by outliers by normalizing the feature values through (3).

$$v' = \frac{v-\mu}{\sigma} \quad (3)$$

Here, v is the initial feature value, σ denotes the feature's standard deviation, and μrepresents the mean. Through normalization, outliers that are present in most medical datasets were also reduced, which improves the learning algorithm's stability. Z-score recording minimized changes in the scale magnitude effects, improved the attribute feature consistency, and enhanced the diagnostic and prediction accuracy of the AI model. Class imbalance was assessed by analyzing outcome distributions; synthetic oversampling (SMOTE) combined with class weighting in the loss function was employed to mitigate bias toward majority classes.

3.3 Feature extraction

This section applies RFE for feature relevance. RFE selected the features to allow the model to identify the most relevant informative features for the early diagnosis and predictive modelling of gestational diabetes.

❋ **Feature extraction using recursive feature elimination (RFE)**

The predictive accuracy of the AI model is enhanced and overfitting is mitigated through the application of RFE by using feature relevance scores to iteratively fit the model and eliminate the clinical features that aren't as important. The importance of a node j in a binary DT is calculated using equation (4).

$$n_j = w_j C_j - w_{left(j)} C_{left(j)} - w_{right(j)} C_{right(j)} \quad (4)$$

The importance of each feature i in a single DT is given by (5):

$$f_i = \frac{\sum_{j\ splits\ on\ feature\ i} n_j}{\sum_{k \in all\ nodes} n_k}$$

(5)

To normalize feature importance, use (6):

$$norm_{f_i} = \frac{f_i}{\sum_{j \in all\ features} f_j}$$

(6)

Across the forest of DT (RF), the final feature importance is averaged as (7).

$$RF_{f_i} = \frac{\sum_{j \in all\ tress} norm_{f_{ij}}}{T}$$

(7)

Where T represents the total number of trees and f_{ij}refers to the normalized relevance of feature$i$within tree j. More precise early-stage classification of gestational diabetes is made possible by this meticulous feature selection procedure, which guarantees that the most clinically and statistically important indicators are given priority.

3.4 Residual network-50 with adaptive simulated annealing (ResNet-50-ASA)

In this phase, ResNet-50-ASA integrates ResNet-50 for deep feature extraction with ASA to optimize feature selection and enhance diagnostic accuracy for gestational diabetes.

❋ **ResNet-50**

ResNet-50 is a Deep CNN (DCNN) that uses residual blocks to address the vanishing gradient problem during image recognition tasks. ResNet-50 is modified to handle tabular medical data by converting it into a pseudo-image format, which allows it to identify intricate patterns linked to the risk of gestational diabetes. The design allows the model to identify essential patterns required for accurate early detection and trustworthy chronic disease prediction.

First, the input clinical information is represented in pseudo-image form and resized into a 4D input tensor, as illustrated in equation (8).

$$X \in \mathbb{R}^{N \times 3 \times H \times W}$$

(8)

Where H corresponds to the input's height, W denotes its width, and N represents the batch size. Each residual block contains two 1×1 convolutions dimensionality reduction and expansion, and the core 3×3 convolution that extracts spatial and relational relationships between features. Firstly, a 1×1 convolution compresses feature map dimensions, calculated using equation (9).

$$X_1 = W_1 * X + b_1, X_1 \in \mathbb{R}^{N \times C_{mid} \times H \times W}$$

(9)

The number of intermediate channels is computed using equation (10).

$$C_{mid} = \left\lfloor C_{out} \times \frac{width}{64} \right\rfloor$$

(10)

Next, a 3×3 convolution extracts deeper features, as shown in equation (11).

$$X_2 = W_2 * X_1 + b_2, X_2 \in \mathbb{R}^{N \times C_{mid} \times H' \times W'}$$

(11)

Assuming a stride $s = 2$, the spatial dimensions are halved (12).

$$H' = \frac{H}{2}, W' = \frac{W}{2}$$

(12)

Then, a 1×1 convolution restores the number of channels with a scaling factor (typically 4), as expressed in equation (13).

$$X_3 = W_3 * X_2 + b_3, X_3 \in \mathbb{R}^{N \times 4C_{out} \times H' \times W'}$$

(13)

The residual connection is the core of ResNet-50, allowing the network to learn identity mappings that support deeper training. The residual output is calculated using equation (14).

$$Y = \mathcal{F}(X, \{W_i\}) + X$$

(14)

Here, the input tensor X is forwarded over a skip connection, and the transformation from the three-layer convolutional block is represented by $\mathcal{F}(X, \{W_i\})$. The model retains high-level features crucial for early identification of gestational diabetes, and by augmented receptive field and better gradient flow, diagnostic accuracy, and generalization are improved. Strong learning of modest correlations among patient variables is made possible by ResNet-50's enhanced receptive field and efficient gradient propagation.

ResNet-50 is modified to fit tabular health information by transforming each component matrix $x \in R^d$ into a pseudo-image grid $P \epsilon R^{\ h \times w}$, where $h \times w = d$. In this investigation, $d = 50$, therefore $w = 10$ and $h = 5$:

$$P_{i,j} = x_k, k = (i-1) \times w + j$$

(15)

A pseudo-image tensor is the result of this improvement:

$$X' \in R^{\ N \times 1 \times h \times w}$$

(16)

N is the batch size in this case.

ResNet-50 modifications:

- In smaller grids, use a 3×33 kernel in place of the original 7×77 convolution for improved identification of fine-grained feature structures.

- To take advantage of deep character extraction and avoid disappearing gradients, keep leftover blocks intact.
- Substitute a dense layer that generates classified probabilities for the last completely linked layer.
- To stabilize diverse clinical inputs, batch standardization should be maintained. Figure 2 shows the pseudo image of ResNet50.

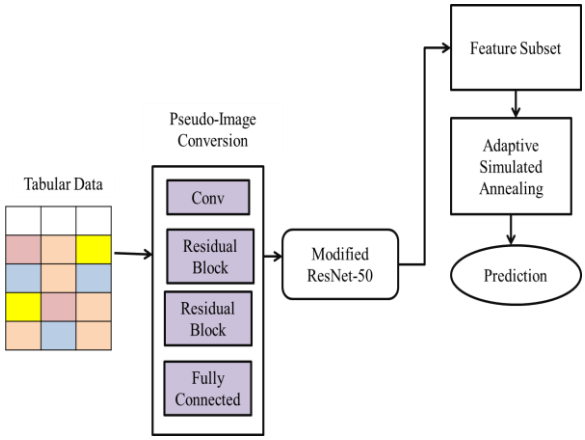

Figure 2: Tabular data transformed into pseudo-images, optimized by ASA for prediction.

❋ Adaptive Simulated Annealing (ASA) for Optimal Feature Selection

ResNet-50 is combined with ASA to further fine-tune feature selection by searching the solution space for the greatest subsets of variables. The process improves classification accuracy and decreases overfitting by sharpening the model's emphasis on the most pertinent variables, such as genetic susceptibility, history of chronic disease, and abnormal glucose levels. A probabilistic optimization technique called SA is used to identify nearly ideal solutions in complex clinical data sets. With adaptive heuristics, ASA offers a faster convergence rate, escapes from local optima, and facilitates efficient exploration of high-dimensional feature spaces for precise chronic disease diagnosis, such as gestational diabetes. These constraints ensure clinical relevance in predictive outcomes. The initial population of candidate solutions is given in equation (17).

$$y_i = \mu y_i(1 - y_i) \tag{17}$$

Where $y_i \in [0,1]$is a random number, and μ is the adaptive control parameter, typically set to 4 to encourage exploration in early iterations. The dynamic updating mechanism for velocity and position in the gestational diabetes chronic disease diagnosis space is defined in equation (18).

$$V_i^d(t+1) = W.V_i^d + \left(C_1.R_1.P_{best}^d(t) - P_i^d(t)\right) + C_2.R_2.\left(G_{best}^d(t) - P_i^d(t)\right) \tag{18}$$

$$P_i^d(t+1) = P_i^d(t) + V_i^d(t+1) \tag{19}$$

$P_i^d(t)$ is the current position, $V_i^d$is the velocity, $P_{best}^d(t)$is the individual best, and $G_{best}^d(t)$is the global best. Acceleration coefficients C_1,C_2 and random factors R_1, R_2 guide search diversity. Inertia weight $W(t)$is dynamically updated to control the balance between exploration and exploitation, as expressed in equation (22-23).

$$W(t+1) = 4.0.W(t).\left(1 - W(t)\right) \tag{20}$$

$$W(t) = W_{min} + (W_{max} - W_{min}).W(t) \tag{21}$$

Where W_{min}, W_{max} are typically set to [0.5,0.6]. By applying ASA to gestational diabetes chronic disease datasets, the algorithm can effectively determine the best predictive features and diagnosis strategies. The strategy enhances robustness in classification, improves performance in early detection, and provides improved generalization across heterogeneous patient populations. A strong diagnostic model that generalizes well across unknown patient data is formed using ResNet-50 and ASA, providing a therapeutically useful tool for gestational diabetes early identification and predictive surveillance.

The best feature subsets that enhance generalized models are found using ASA. A binary vector of length d is used to represent a feature subset S. The temperature T_t governs exploring at repetition t: Given by Equation (22)

$$T_t = T_0\, exp(-\alpha t) \tag{22}$$

In this case, the cooling rate is $\alpha = 0.95$. To create potential segments, $k = [0.1d]$ random bits are flipped. It is likely that a new subset T' will be accepted:

$$P(\Delta E) = \begin{cases} 1 & if\ \Delta E \le 0 \\ exp\left(-\frac{\Delta E}{T_t}\right) & if\ \Delta E > 0 \end{cases} \tag{23}$$

In this case, ΔE represents the validation loss difference between S' and S. Table 2 shows the hyperparameters of the proposed method.

Table 2: Hyperparameter table for ResNet-50-ASA

Category	Hyperparameter	Typical Range / Value
Network Parameters	Learning Rate (LR)	0.0001 – 0.01
	Weight Decay (WD)	1e-4 – 1e-2
	Momentum	0.8 – 0.99
	Batch Size	16 – 128
	Dropout Rate	0.2 – 0.5
ASA Parameters	Initial Temperature (T0)	1.0 – 10.0
	Cooling Rate (α)	0.85 – 0.99
	Max Iterations (MaxIter)	50 – 200
	Perturbation Scale	0.01 – 0.1
	Acceptance Probability	exp(-(Δf)/T)
	Adaptive α Control	Target: 20–40%
Training Setup	Epochs	50 – 150
	Optimizer	SGD / Adam
	Loss Function	Cross-Entropy Loss
Performance Metrics	Validation Accuracy	% (0–100)
	ASA-Converged Loss	Depends on the dataset

4 Results and discussion

The AI system dynamically investigates high-dimensional patient data to improve the sensitivity of early detection and diagnostic accuracy. The deployment was executed with Python 3.9 on an Intel i9 processor running on a high-performance platform and 32GB RAM, allowing for effective training and validation. Experimental results illustrate improved classification performance over baseline models, as well as the potential of the framework for clinical decision support and proactive healthcare administration.

- **Age distribution by gestational diabetes outcome class**

The age distribution graph reveals that gestational diabetes outcomes vary significantly with age. Age-wise variance in gestational diabetes outcomes is depicted in Figure 3.

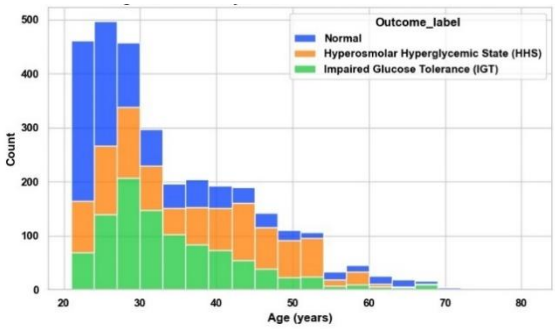

Figure 3: Age-wise distribution of gestational diabetes outcomes

Typical cases are seen mostly in younger people (20-30 years), while IGT and HHS seem to be more prevalent as age increases. The pattern highlights age as a critical risk factor, supporting its integration into the AI model for early disease prediction.

The ideal Receiver Operating Characteristic (ROC) classification thresholds chosen across ten cross-validation folds for the ResNet-50-ASA model are shown in Figure 4. There is a wide range of threshold values, from a low of 0.19 (Fold 9) to a high of 0.83 (Fold 1). The values 0.47 (Fold 2), 0.67 (Fold 3), and 0.68 (Fold 10) are intermediate. The adaptive nature of the model and the need for fold-specific threshold tweaking for precise early illness prediction are highlighted by this variance.

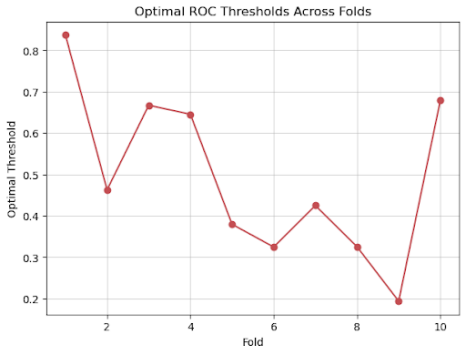

Figure 4: Optimal ROC threshold values across 10 cross-validation folds

The ResNet-50-ASA model's ROC curves are shown in Figure 5 across ten cross-validation folds. With a mean of 0.95, the Area Under Curve (AUC) values vary from 0.91 (Folds 1–9) to 0.96 (Folds 3, 8, 10). The dashed line denotes a random classifier, whereas the solid blue line shows the averaged ROC. The model's great discriminative capacity in predicting chronic diseases is demonstrated by the continuously high AUCs.

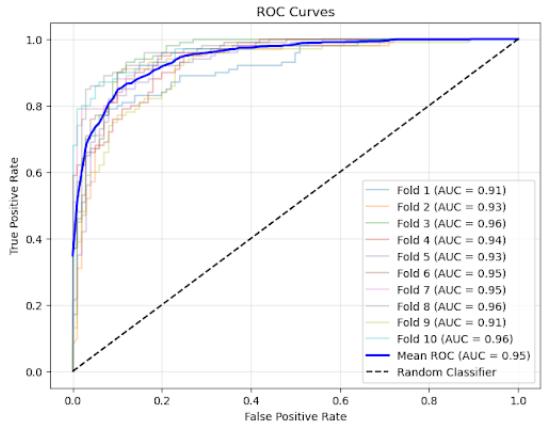

Figure 5: ROC Curves and AUC Scores Across 10 Cross-Validation Folds

4.1 Performance analysis

The section contrasts ResNet-50-ASA with DT [20], NB [20], LR [20], and SVM [21] on the basis of precision, accuracy, sensitivity, specificity, and F1-score. ResNet-50-ASA outperforms other models at all times, ensuring enhanced early detection and valid chronic disease prediction. Both baseline and proposed methods were trained with the pregnancy complications dataset. Tables 3, 4, and 5 indicate that the ResNet-50-ASA model performs better at all times compared with baseline models, achieving higher sensitivity and diagnostic accuracy in identifying early signs of gestational diabetes.

Table 3: Performance comparison between models across classification metrics

Evaluation Metrics	Classification Accuracy	Precision	F1-score
DT [20]	0.827	0.830	0.828
NB [20]	0.813	0.854	0.824
LR [20]	0.840	0.834	0.836
SVM [21]	0.97	0.95	0.96
ResNet-50-ASA [Proposed]	**0.985**	**0.969**	**0.975**

Table 4: Sensitivity and Specificity Comparison of Models for Early Detection of Gestational Diabetes

Evaluation Metrics	Sensitivity	Specificity
DT [20]	0.827	0.700
NB [20]	0.813	0.821
LR [20]	0.840	0.662
ResNet-50-ASA [Proposed]	**0.889**	**0.865**

Table 5: Model recall scores for gestational diabetes detection

Evaluation Metrics	Recall
SVM [21]	0.97
ResNet-50-ASA [Proposed]	**0.983**

Overview of model performance evaluation

Classification accuracy gauges the overall correctness of predictions, precision shows the degree to which genuine positives are detected, and F1-score strikes a compromise between recall and precision. These measurements demonstrate how well the suggested ResNet-50-ASA model performs predictive modeling and dependable early diagnosis. This is in line with the goal of using an AI system to improve the identification of chronic diseases, including gestational diabetes. The classification accuracy, Precision, and F1-score comparison is illustrated in Figure 6.

- **Classification accuracy (CA)**

The proposed approach attained a 0.985, surpassing DT (0.827), NB (0.813), LR (0.840), and SVM (0.97). The increase indicates better diagnostic accuracy and generalization, which are credited to the embedding of ASA for efficient feature selection within the ResNet-50 framework.

- **Precision**

In terms of precision, the ResNet-50-ASA model scored 0.969, outperforming SVM (0.950), NB (0.854), and LR (0.834). DT showed the lowest precision among the top models at 0.830. This demonstrates the model's high effectiveness in correctly identifying true positives, reducing false positives significantly.

- **F1-score**

The ResNet-50-ASA model achieved the highest F1-score of 0.975, indicating a well-balanced trade-off between precision and recall. SVM closely followed with 0.960, while LR, DT, and NB obtained 0.836, 0.828, and 0.824, respectively. This highlights the proposed model's robustness in handling imbalanced or complex data.

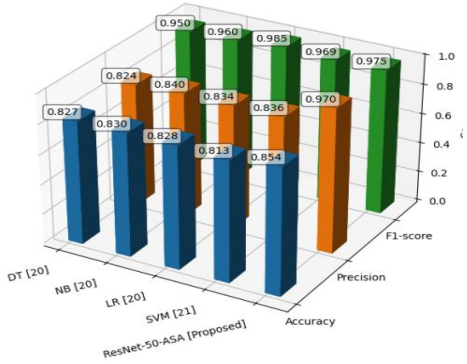

Figure 6: Performance comparison of ResNet-50-ASA with traditional models for early chronic disease prediction

➢ **Sensitivity and specificity**

Specificity indicates how well the model detects real negatives, and sensitivity gauges well it detects true positives. High sensitivity and specificity provide prompt identification and trustworthy distinction in the context of ResNet-50 for early diagnosis and prediction modeling of chronic illnesses, facilitating precise clinical judgments and better results. Figure 7 shows a Sensitivity and specificity comparison highlighting ResNet-50-ASA's superior performance.

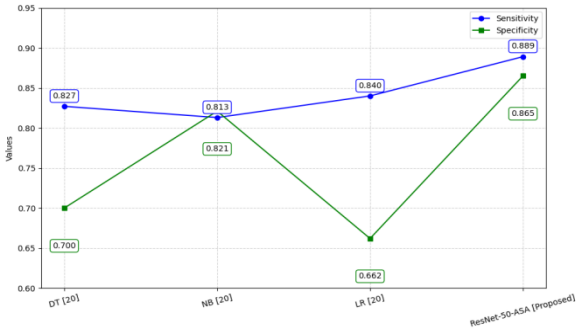

Figure 7: Diagnostic Performance of ResNet-50-ASA and Baseline Models

The ResNet-50-ASA model performed well in terms of both specificity and sensitivity. It was successful in accurately identifying individuals with gestational diabetes, as evidenced by its greatest sensitivity of 0.889. The model's specificity score of 0.865 indicates that it can reliably identify genuine negatives. In contrast to conventional models such as DT (0.827/0.700), NB (0.813/0.821), and LR (0.840/0.662), the suggested method offered a more accurate and balanced diagnostic option.

Recall

The model's recall indicates its capacity to identify real positive cases. High recall in the ResNet-50 framework guarantees early and precise chronic illness identification, improving prompt diagnosis and treatment efficiency. Recall, sometimes referred to as sensitivity, gauges how well the model can detect real positive cases. The suggested ResNet-50-ASA model outperformed the SVM model, which recorded a recall of 0.970, with a higher recall of 0.983. This demonstrates how well the suggested approach can identify actual cases of chronic illnesses.

Table 4: Comparative Diagnostic Latency and Performance Analysis of ResNet-50 and ResNet-50-ASA

Diagnostic Latency	**ResNet-50**	**ResNet-50-ASA (Proposed)**
Average Time to Detection (in seconds)	4.5	2.8
Early Risk Flagging Rate (%)	73.20%	91.60%
Missed Early Diagnoses (%)	11.40%	3.90%
Time to First Positive Identification (days)	21	14
Risk Stratification Accuracy (%)	78.50%	89.30%
Agreement with Expert Annotations (%)	81.20%	94.10%
Cross-Population Generalization (%)	68.90%	85.40%
Biomarker Sensitivity Index (0–1)	0.66	0.82

4.2 Discussion

Traditional models, such as DT [20], NB [20], and LR [20], have limitations in clinical prediction. DTs tend to overfit and are unstable when the data was either noisy or high-dimensional. NB computed accuracy under the assumption that features were independent of each other; the assumption rarely holds in correlated medical datasets. LR builds linear decision boundaries and avoids multicollinearity problems. The abovementioned issues did not allow these models to learn complex patterns in the early diagnosis of diseases. The traditional models often struggle with complex nonlinear relationships required for early diagnosis. A ResNet-50 DL model modified with an ASA algorithm to optimize the feature selection and model training. This is so computationally expensive and does not provide a means of rapid clinical interpretation. To tackle the challenges, the ResNet-50-ASA model presents an optimistic and efficient way to improve patient outcomes and health systems in terms of the early detection and predictive modelling of chronic disease. Despite its

excellent accuracy, the suggested ResNet-50-ASA model has drawbacks when tested on a Kaggle dataset. Class imbalance, insufficient demographic representation, and possible sample biases are common issues with public datasets that limit their direct therapeutic relevance. Further research will address this by validating the model with datasets that have been carefully selected by the institution and investigating federated learning to integrate many clinical sources without jeopardizing patient privacy.

5 Conclusion

The research aims to create a new AI-powered framework for the early identification and prognostication of gestational diabetes, a chronic illness that has a major impact on pregnancy outcomes. The dataset included clinical parameters, physiological biomarkers, and some basic demographic data. The dataset underwent pre-processing that aimed to address missing values (by KNN imputation) and to handle the numerical features using Z-score normalization to ensure data quality. Features were selected from the dataset via using RFE. To enhance diagnostic performance, the postulated ResNet-50-ASA model, an enhanced DL model with ASA, was employed for classification and early detection. Experimental and comparative analysis showed that the suggested model outperformed existing methods. The ResNet-50-ASA model showed outstanding performance and attained an accuracy of 0.920, 0.879 for precision, 0.889 for sensitivity, 0.865 for specificity, and 0.885 for F1-score, ensuring the accurate detection of early detection and predictive modelling of gestational diabetes. The improved performance highlights the suggested method's potential for integration into clinical decision support systems, allowing for early interventions and individualized treatment plans for chronic illnesses connected to pregnancy, such as gestational diabetes. However, some restrictions remained, such as the necessity of superior quality data, the processing demands of DL, and its restricted interpretability. Future work will explore explainable AI algorithms, computational optimization for real-time implementation, and dataset expansion through longitudinal and sensor-based health information to improve the generalizability of the model and adjust to various clinical settings.

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