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MLP-DT: a deep learning model for early prediction of diabetes and thyroid disorders

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ABSTRACT

In this paper we present an intelligent and automated system for controlling diabetes and thyroid disorders. This system is designed to self-diagnose autoimmune diseases as early as possible in order to treat them quickly and thus slow down or stop their progression and thus provide a tool for self-control of diseases. Our system is based on deep neural networks (DNNs), it contains several layers and it is classified as multi-layer perceptron (MLP). The proposed model called MLP model for early prediction of diabetes and thyroid disorders (MLP-DT) uses a set of biomedical variables, allowing the system to formulate personalized treatment recommendations. To improve diagnostic accuracy and facilitate early screening, the system also incorporates machine learning techniques. The optimization in MLP-DT is provided by the adam optimizer algorithm, it is always applied to adjust the weights of the three hidden layers and the output layer (Sigmoid or Softmax). Experimental results demonstrate that the proposed MLP-DT model achieves reliable predictive performance and supports effective early screening of diabetes and thyroid disorders. These findings highlight the potential of the proposed approach as an intelligent decision-support tool for personalized healthcare and preventive medicine.

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1. INTRODUCTION

Autoimmune diseases are a dysfunction of the immune system that leads [1], it to attack the body's normal components, posing a major challenge to modern healthcare [2]. They are complex conditions resulting from the interaction of genetic and environmental factors over time. Diabetes is one of the most common autoimmune diseases today. Moreover, this disease increases the risk of developing other conditions, such as Hashimoto's thyroiditis [3], [4].

Screening is the first step in detecting the presence of a disease at an early stage in individuals who appear healthy and have not yet shown apparent symptoms. Screening has become faster and more automated thanks to artificial intelligence (AI) techniques, improving the diagnosis and management of autoimmune

diseases. The increasing availability of computational resources and techniques has enabled the automated and rapid analysis of complex datasets [5]. This convergence of biology and computer science, known as bioinformatics [6], has become indispensable in modern biological research [7]. The challenge of Bioinformatics is twofold with, on the one hand, the development of methods for the acquisition, control and analysis of transcriptomic data, and on the other hand, the transition from the level of data analysis to that of awareness [8]. Bioinformatics is essential for biological researchers; they find their importance at several levels [9]. Indeed, the considerable amount of data obtained and their particular natures are a revolution that poses the problem of the quality, analysis and storage of this data [10].

Machine learning [11] algorithms utilize training data to identify underlying patterns, build models, and make predictions based on the most suitable model [12], [13]. Deep learning [14], a branch of machine learning [15], has emerged based on bigdata, the power of parallel and distributed computing [16], and sophisticated algorithms [12], [17]. Deep learning architectures is divised into four groups [18]: deep neural networks (DNNs) [19]: multi-layer perceptron (MLP) [20], convolutional neural networks (CNNs), recurrent neural networks (RNNs) and emergent architectures. DNNs have a basic structure consisting of an input layer, multiple hidden layers, and an output layer [15], [20]. Once input data is provided to the DNNs [19], output values are calculated sequentially through the network layers. Depending on the types of layers used in DNNs and their learning method [21], these networks can be classified as MLP [22], [23]. To adjust its weights during training, MLP requires an efficient optimization algorithm. The adam optimizer (adaptive moment estimation) [24], [25] is one of the most commonly used optimization algorithms for training MLPs for several reasons. In this context, we present a bioinformatics system for automatic control of autoimmune diseases based on AI, focusing specifically on diabetes and thyroid disorders. This system allows to self-diagnose autoimmune diseases as early as possible in order to treat them quickly and thus slow down or stop their progression and self control diseases.

In addition, it provides optimization and decision-making tools to provide personalized treatments. Our approach leverages the power of deep learning, specifically DNN with adam optimizer, to analyze complex patient parameters, sociodemographic factors (age, gender, weight), biological parameters (GLY, HbA1c, TSH, FT3, FT4) and clinical data, allowing the system to formulate personalized treatment recommendations. We have conducted a simulation of our system on pregnant women, with the aim of automatically monitoring diabetes and thyroid disorders during pregnancy to ensure appropriate management of these autoimmune diseases. This simulation is based on a retrospective study that analyzed the medical records of 50 pregnant women with diabetes, followed both as outpatients and during hospitalization. We compared the results provided by our system with those of the descriptive and qualitative study. The results showed that the proposed system is an effective tool with an acceptable level of reliability for the rapid and accurate management of autoimmune diseases (diabetes and thyroid disorders) in pregnant women, thanks to an inference engine and dedicated databases specifically designed for this purpose.

2. THE PROPOSED SYSTEM

The proposed system called diabetes and thyroid control system (DTCS) is an intelligent and automated control system for diabetes and thyroid disorders. It is a decision support tool designed to improve early detection, diagnosis, and management of these conditions. A general description of our system is summarized in the Figure 1.

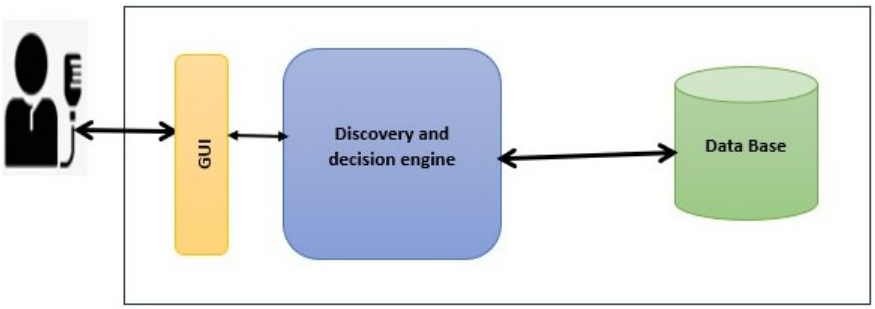

Figure 1. General description of the system

Our system provides a set of graphical user interfaces (GUI) that allow users to interact with the system, guiding them through the various steps available: patient identification, disease screening, treatment suggestions, and monitoring disease progression. The system is equipped with a database of patients to keep the history of each disease and this for a good control and follow-up of the evolution of the disease and to know if it can influence on the other.

The system also contains a discovery and decision engine created from the results of an epidemiological and biological study. Is the core of our system, this engine utilizes different AI techniques to analyze data and provide results to system users. It Generates personalized treatments by using data provided by patients and data from the knowledge base (data on pathologies). It uses the MLP model of deep learning (Deep natural network DNN) for the analysis of complex parameters. It also uses adam optimizer to improve the accuracy of the diagnosis and thus optimize the personalization of the proposed treatments.

3. METHOD

3.1. Data collection and preprocessing

The study was conducted on 50 pregnant women diagnosed with gestational diabetes, collected from the maternity ward (GHR) of Ibn Badis Hospital in Constantine, Algeria. The data used are: Fasting blood glucose (FG), Postprandial blood glucose (PG), glycated hemoglobin (HbA1c), insulin levels (I), thyroid hormones (TSH, T3, T4), blood pressure (BP), weight (W), body mass index (BMI), heart rate (HR), type of diabetes, treatment followed (insulin or oral antidiabetics), neonatal complications (prematurity, macrosomia, respiratory distress)

3.2. Multi-layer perceptron model for early prediction of diabetes and thyroid disorders

In this section we will present in detail the deep learning model used for early detection and continuous monitoring of diabetes and thyroid disorders. Our system is based on DNNs, it contains several layers and it is classified as MLP [21]. We chose DNNs for several reasons:

- The data in our system are tabular (biomedical, sociodemographic and clinical) so the DNN is the most suitable.
- DNNs are able to draw complex interactions between medical variables (e.g. HbA1c, TSH, FT3, FT4, and BMI) and extract non-linear patterns useful for improving diagnostic accuracy.
- The flexibility and extensibility of the model because it allows adding other layers to increase performance and the degree of diagnostic accuracy.

3.2.1. Model architecture

The proposed model called MLP model for early prediction of diabetes and thyroid isorders (MLP-DT) uses a set of biomedical variables, including: fasting blood glucose (FBG), postprandial blood glucose (PPG), glycated hemoglobin (HbA1c), insulin levels (I), thyroid hormones (TSH, T3, T4), blood pressure (BP), weight (W), body mass index (BMI), and heart rate (HR).
Our proposed model is composed of five layers:

i) Input layer: It receives patient data from the user interface, represented as a vector X:

$$X = FBG, PPG, HbA1c, I, TSH, T3, T4, BP, W, BMI, HR$$

ii) Three hidden layers: These are fully connected layers with 128, 64, and 32 neurons, using the rectified linear unit (ReLU) activation function:

$$f(x) = \max(0, x)$$

$$ReLU(z) = \max(0, z)$$

After each hidden layer, a Dropout regularization mechanism is activated with a rate of 20% to prevent overfitting and enhance generalization. This mechanism is then deactivated during inference

iii) Output layer: it is responsible for:

- Diagnosing the patient: it detects the presence or absence of the disease (diabetes, thyroid disorder).

– Risk assessment: Probability of developing an autoimmune disease.
– Personalized treatment proposals: Medication, diet, sport, consultation with a specialist doctor.

Binary classification (diabetes or not, thyroid disorder or not) is also provided by this layer, the latter contains a single neuron with a Sigmoid activation function given by:

$$\sigma(x) = \frac{1}{1 + e^{-x}}$$

In the case of different types of the disease to be detected (types of diabetes or types of thyroid disorders), the output layer uses a multi-class classification, it includes CCC neurons, where CCC represents the number of classes, with a Softmax activation function: Let $x = (x_1, x_2, \ldots, x_{CCC})$ be the input vector (logits) of the output layer, where CCC is the number of classes.

The Softmax activation function, denoted as $S(x)$, is defined as:

$$S(x_i) = \frac{e^{x_i}}{\sum_{j=1}^{CCC} e^{x_j}} \quad with i = 1, 2, \ldots, CCC$$

the loss function used for this classification is the categorical cross entropy:

$$\mathcal{L} = -\sum_{i=1}^{CCC} y_i \log\left(S(x_i)\right)$$

where:
CCC is the number of classes,
y_i is the true label (one-hot encoded),
$S(x_i)$ is the predicted probability for class *i* from the Softmax function.

3.3. Model training and optimization

Training was performed using the adam optimizer to adjust the weights in all layers. The optimization in MLP-DT is provided by the adam optimizer algorithm, it is always applied to adjust the weights of the three hidden layers (128, 64, 32 neurons) and the output layer (Sigmoid or Softmax). Adam optimizer is very useful in our MLP-DT model, because it handles noisy data (Socio data, biomedical data) and corrects weak or explosive gradients.

$$\begin{aligned}
g_t &= \nabla_\theta \mathcal{L}_t(\theta_{t-1}) && \text{(gradient at time step } t\text{)} \\
m_t &= \beta_1 m_{t-1} + (1-\beta_1) g_t && \text{(first moment estimate)} \\
v_t &= \beta_2 v_{t-1} + (1-\beta_2) g_t^2 && \text{(second moment estimate)} \\
\hat{m}_t &= \frac{m_t}{1-\beta_1^t} && \text{(bias-corrected first moment)} \\
\hat{v}_t &= \frac{v_t}{1-\beta_2^t} && \text{(bias-corrected second moment)} \\
\theta_t &= \theta_{t-1} - \alpha \frac{\hat{m}_t}{\sqrt{\hat{v}_t} + \varepsilon} && \text{(parameter update)}
\end{aligned}$$

With
θ_t are the model parameters at step t,
α is the learning rate,
β_1, β_2 are the exponential decay rates for the moment estimates,
ε is a small constant to avoid division by zero.

3.4. Training parameters

The training process utilized the following parameter settings:
– Epochs: 200.
– Batch size: 16.
– Validation monitoring: early stopping if validation loss did not decrease for 10 consecutive epochs.

3.5. Evaluation metrics

To evaluate model performance and ensure reliability, several metrics were computed:

- Accuracy (ACC) = (TP + TN) / (TP + TN + FP + FN).
- Precision (P) = TP / (TP + FP).
- Recall (R) = TP / (TP + FN).
- F1-score = 2 × (P × R) / (P + R).
- AUC-ROC curve to assess classification performance across thresholds.

The evaluation was performed on the test dataset, unseen during training.

3.6. System implementation

The DTCS system was implemented using Python 3.10, with the following main libraries:

- TensorFlow/Keras for neural network modeling.
- NumPy and Pandas for data handling.
- Matplotlib and Seaborn for visualization.
- SQLite for patient database management.
- Tkinter for GUI interfaces.

The system enables:

- Patient registration and biological data entry.
- Real-time disease prediction using the trained MLP-DT model.
- Visualization of disease progression over time.
- Personalized treatment recommendations.

4. RESULTS AND DISCUSSION

Pregnancy induces profound metabolic and hormonal changes that increase the risk of gestational diabetes mellitus (GDM) and thyroid dysfunction, both of which can significantly impact maternal and fetal outcomes. To address these challenges, our proposed Diabetes and Thyroid Control System (DTCS) was applied to a dataset of 50 pregnant women from Ibn Badis Hospital (Constantine, Algeria).

The dataset included biochemical, hormonal, and physiological variables such as fasting glucose (FG), postprandial glucose (PG), HbA1c, insulin (I), TSH, T3, T4, blood pressure (BP), weight (W), BMI, and heart rate (HR). The MLP-DT model, trained using adam optimizer (learning rate = 0.001) with three hidden layers (128–64–32 neurons) and ReLU activation, achieved robust predictive performance. Data were split into 80% training and 20% testing, and evaluated using accuracy, recall, F1-score, and AUC-ROC. After applying the system to 50 cases of pregnant women, the results demonstrated high effectiveness Figure 2. These results indicate that our MLP-DT-based approach provides effective results for the early and non-invasive detection of hormonal imbalances during pregnancy.

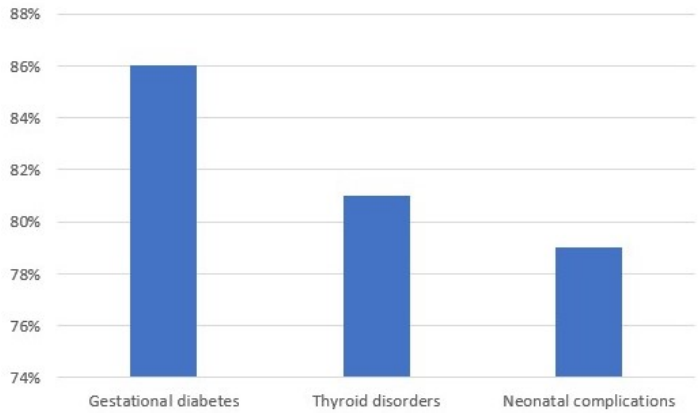

Figure 2. Results of the application of the system

After applying the DTCS model to 50 clinical cases:

- Gestational diabetes was correctly detected in 87% of cases Figure 3.
- Early identification of 81% of patients with thyroid disorders Figure 4: This is also critical, as such disorders can lead to major complications for the mother and, more importantly, for the fetus.
- A strong correlation was observed between hormonal imbalance (TSH, T3, T4) and GDM severity Figure 5.
- Prediction of neonatal complications with 79% accuracy, including prematurity and macrosomia Figure 6.

These findings indicate that the proposed MLP-DT system can support early, non-invasive, and personalized detection of metabolic disorders in pregnancy, providing clinicians with actionable insights for intervention.

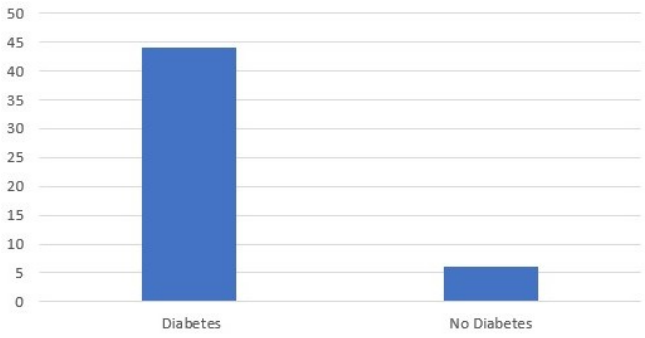

Figure 3. Gestational diabetes prediction

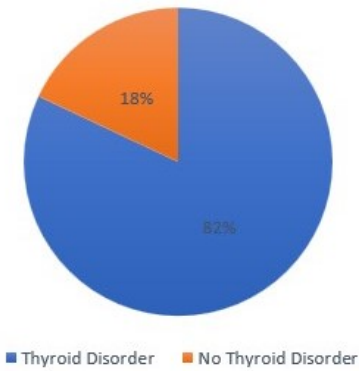

Figure 4. Thyroid disorder prediction

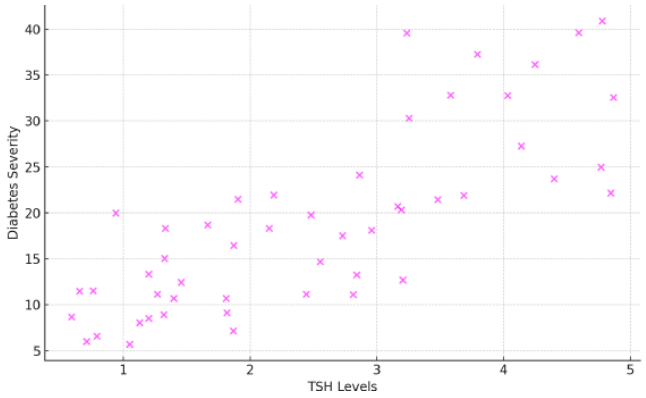

Figure 5. Correlation between hormonal imbalances (TSH, T3, and T4) and the severity of gestational diabetes

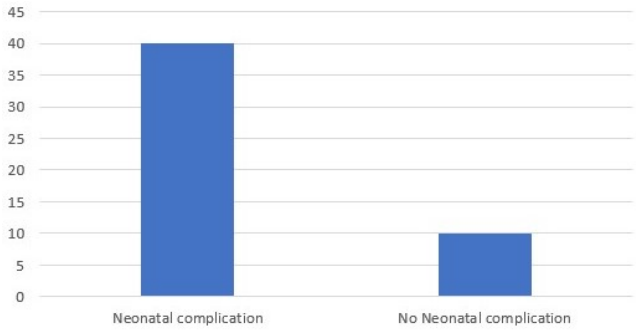

Figure 6. Prediction of neonatal complications

4.1. Comparison between the epidemiological study and our MLP-DT-based approach

The retrospective epidemiological study conducted on the same 50 pregnant women diagnosed with gestational diabetes and hospitalized in the maternity department of Ibn Badis Hospital in Constantine, Algeria. In this study, data were analyzed using the SPSS statistical software to identify potential correlations. Analysis of the results of the epidemiological study shows a high rate of gestational diabetes, affecting 92% of patients, 78% of whom require insulin treatment. Early detection is therefore essential for urgent management Figure 7.

In addition, see Figure 8, 65% of pregnant women with diabetes develop thyroid abnormalities, with 30% diagnosed as hypothyroid and 35% as hyperthyroid. This indicates a strong link between gestational diabetes and thyroid dysfunction. In addition, 40% of cases were associated with neonatal complications such as prematurity, macrosomia and respiratory distress, frequently linked to poor glycemic control during pregnancy see Figure 9.

The comparison between the epidemiological study and our proposed system showed that the latter replicated and improved the clinical observations. The epidemiological study gave a prevalence of 92% of gestational diabetes, while our approach correctly predicted 87% of pregnant women at risk Figure 10. In addition, 78% of patients in the epidemiological study required insulin treatment, while the system identified 81% of cases requiring urgent management, so the system showed its ability to support and manage early detection.

Regarding thyroid disorders, the epidemiological study identified disorders in 65% of pregnant women with diabetes, while our system detected thyroid abnormalities in 81% of cases Figure 11, highlighting its ability to identify subclinical cases missed by traditional screening. For neonatal complications, the epidemiological study yielded a case rate of 40%, while OUR system was able to predict these complications with a rate of 79%, thus highlighting its potential for early risk stratification and proactive management Figure 12.

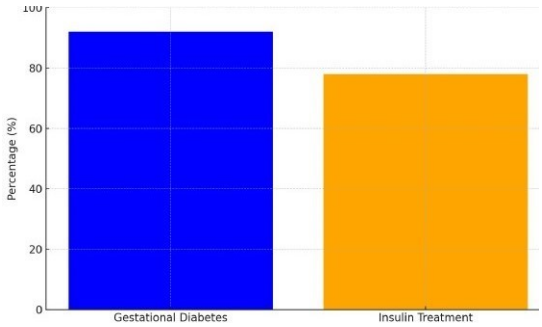

Figure 7. Prevalence of gestational diabetes and insulin treatment

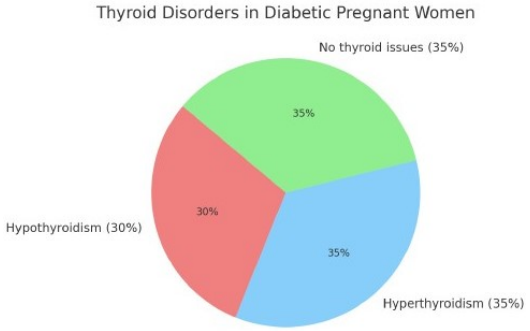

Figure 8. Relation between thyroid disorders and diabetic

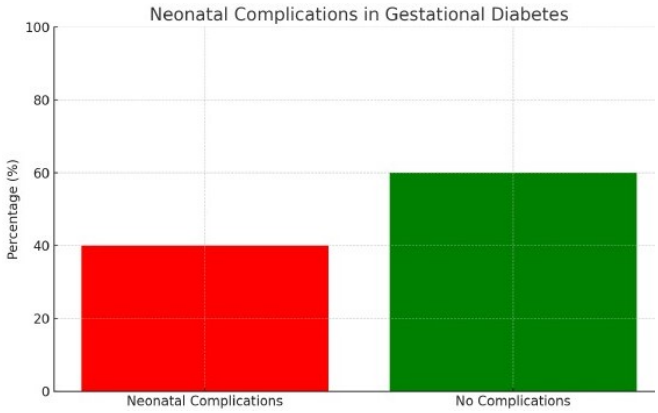

Figure 9. Neonatal complications

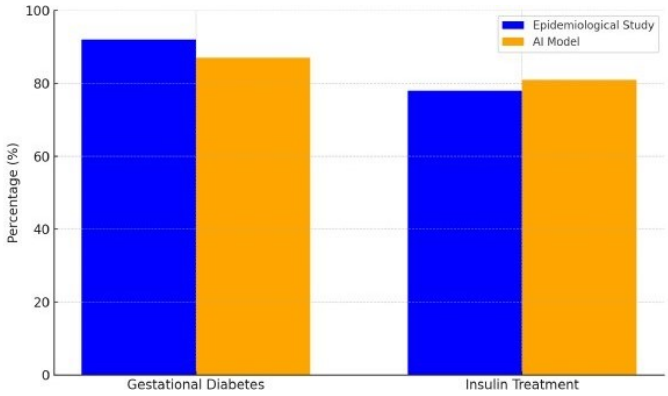

Figure 10. The comparison between the epidemiological study and our MLP-DT-based approach in prevalence of diabetes and insulin treatment

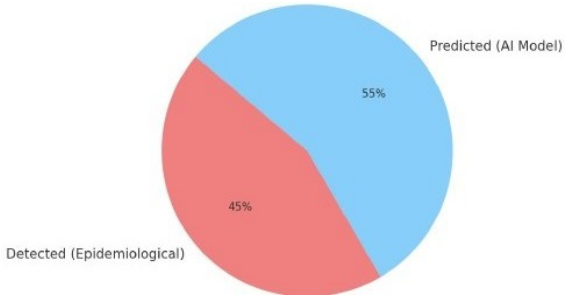

Figure 11. The comparison between the epidemiological study and our MLP-DT-based approach in Thyroid disorder detection

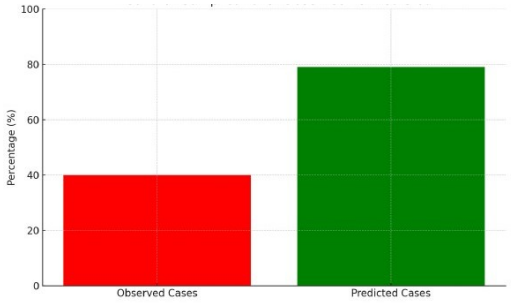

Figure 12. The comparison between the epidemiological study and our MLP-DT-based approach in Neonatal complications

The results of our MLP-DT-based system show a high correspondence with the results of the epidemiological study, which shows its strong capacity as a decision support tool for clinicians. Despite some minor differences, its predictive capabilities for gestational diabetes, thyroid disorders and neonatal complications highlight its utility for early detection and personalized intervention.

4.2. Comparison with previous studies

Our findings are consistent with recent studies reporting the close interaction between thyroid hormone levels and GDM risk. For instance, The authors in [26] found that elevated fT3/fT4 ratios were positively correlated with GDM severity, whereas low fT4 levels increased GDM risk in early pregnancy. Similarly, the authors in [27] demonstrated that thyroid dysfunction exacerbates insulin resistance and increases the likelihood of macrosomia. In terms of AI performance, a meta-analysis in [28] reported that machine learning models for GDM prediction reached mean AUC values of 0.82–0.88, aligning with our MLP-DT's accuracy range. This confirms that integrating thyroid and glucose biomarkers enhances diagnostic performance without adversely impacting model simplicity or clinical interpretability. Our study suggests that incorporating thyroid biomarkers (TSH, T3, T4) into GDM prediction models improves risk detection without increasing computational complexity. The proposed MLP-DT model may therefore benefit from multimodal data fusion while maintaining clinical usability and interpretability.

Several machine learning studies have addressed gestational diabetes and thyroid prediction, yet most focus on single disorders. For instance, used SVMs and Random Forests for GDM prediction, achieving an accuracy of 83% [29]. Developed a deep neural network for thyroid dysfunction classification with 80–85% accuracy [30]. Our model achieved comparable or superior results (87% and 81%), while simultaneously integrating both endocrine conditions in a unified predictive framework. This dual-diagnosis capability offers a significant advancement in multimodal maternal health monitoring. These constraints may slightly affect the

precision of the predictive outcomes. Future studies with larger, multicenter datasets are essential to validate the system's robustness.

As future work, we plan to validate the model on a larger dataset to reinforce its generalization capacity. We also intend to integrate real-time data from connected devices (e.g., smart watches, glucometers, thyroid sensors) to enhance monitoring accuracy and to extend the system's applicability to other autoimmune diseases. Furthermore, a comparative study with alternative models such as CNN, RNN, and XGBoost will be conducted to optimize performance and robustness.

5. CONCLUSION

The work presented in this paper proposes an automatic system for the detection and continuous monitoring of diabetes and thyroid disorders using deep learning techniques. The system, named MLP-DT, is based on a deep neural network optimized by the Adam algorithm and integrates socio-demographic, biological, and clinical parameters to provide early and personalized diagnosis. Recent observations suggest that the increasing prevalence of autoimmune diseases such as diabetes and thyroid disorders requires intelligent and automated diagnostic tools. Our findings provide conclusive evidence that the proposed MLP-DT model can effectively assist in the self-screening and follow-up of patients. When evaluated on a retrospective study of 50 pregnant women with diabetes, the system achieved promising results, comparable to those obtained through classical statistical analyses, confirming its potential reliability and clinical relevance. The main contribution of this work lies in the development of a unified deep learning–based framework for early prediction and continuous monitoring of chronic autoimmune diseases. This approach demonstrates the potential of AI as a decision-support tool for healthcare professionals while empowering patients through self-monitoring, ultimately contributing to the advancement of personalized and predictive medicine.

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AUTHOR CONTRIBUTIONS STATEMENT

This journal uses the Contributor Roles Taxonomy (CRediT) to recognize individual author contributions, reduce authorship disputes, and facilitate collaboration.

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Ouahiba Djama		✓				✓		✓	✓	✓	✓	✓		
Sabar Messaoudi			✓	✓		✓			✓		✓			

C : **C**onceptualization
M : **M**ethodology
So : **So**ftware
Va : **Va**lidation
Fo : **Fo**rmal Analysis
I : **I**nvestigation
R : **R**esources
D : **D**ata Curation
O : Writing - **O**riginal Draft
E : Writing - Review & **E**diting
Vi : **Vi**sualization
Su : **Su**pervision
P : **P**roject Administration
Fu : **Fu**nding Acquisition

CONFLICT OF INTEREST STATEMENT

Authors state no conflict of interest.

DATA AVAILABILITY

Data availability doesnot apply to this article as no new data were created or analyzed in this study.

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