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ORIGINAL RESEARCH

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The utility of a machine learning model in identifying people at high risk of type 2 diabetes mellitus

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ABSTRACT

Background: According to previous reports, very high percentages of individuals in Saudi Arabia are undiagnosed for type 2 diabetes mellitus (T2DM). Despite conducting several screening and awareness campaigns, these efforts lacked full accessibility and consumed extensive human and material resources. Thus, developing machine learning (ML) models could enhance the population-based screening process. The study aims to compare a newly developed ML model's outcomes with the validated American Diabetes Association's (ADA) risk assessment regarding predicting people with high risk for T2DM.

Research design and methods: Patients' age, gender, and risk factors that were obtained from the National Health Information Center's dataset were used to build and train the ML model. To evaluate the developed ML model, an external validation study was conducted in three primary health care centers. A random sample ($N = 3400$) was selected from the non-diabetic individuals.

Results: The results showed the plotted data of sensitivity/100-specificity represented in the Receiver Operating Characteristic (ROC) curve with an AROC value of 0.803, 95% CI: 0.779–0.826.

Conclusions: The current study reveals a new ML model proposed for population-level classification that can be an adequate tool for identifying those at high risk of T2DM or who already have T2DM but have not been diagnosed.

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Machine learning; type-2 diabetes mellitus; high risk; health informatics; Saudi Arabia

1. Background

Type 2 diabetes mellitus (T2DM) is a global healthcare burden and the most common type of diabetes, representing 90% of all diabetes cases [1]. T2DM has developed gradually over the years due to several modifiable (e.g. weight and physical activity status) and non-modifiable (age and genetic variations) risk factors [2]. In addition, it is described as one of the progressive diseases that could lead to cardiovascular and neurological complications, especially in the absence of an adequate treatment plan [3,4].

According to the International Diabetes Federation (IDF), in 2021, 541 million people already have impaired glucose tolerance, and 643 million are likely to be diagnosed with diabetes by 2023 [5]. Among adults, the global prevalence of diagnosed diabetes was 10.5% in 2021, expected to exceed 12% by 2045 [6].

Efficient detection of diabetes in clinical settings is considered important to initiate evidence-based care. Multiple approaches have been proposed to screen and detect people at high risk of T2DM [7,8]. In addition, various self-assessment questionnaires were established, aiming to select individuals at high risk of T2DM for further examination and early detection. However, having difficult tradeoffs between accepting either modest sensitivity or modest specificity are some of the approaches' issues. One of the major disadvantages of risk assessment questionnaires is their reliance on self-reported data [9–11].

The American Diabetes Association (ADA) risk assessment is an acceptable and validated tool to detect people with a high probability of developing T2DM or who already have T2DM but have not been diagnosed. It is based on a simple questionnaire consisting of 8 questions for males and 9 for females. Based on the questionnaire's answers, an individual is given

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a score ranging from 0 to 10; a score of ≥ 5 indicates the individual is recognized as at high risk of developing T2DM [12,13]. Although people with high risk based on the ADA risk assessment may not have T2DM or prediabetes, they might be genuinely at high risk of developing the disease within a few years, especially when the modifiable risk factors were neglected [14].

Machine learning (ML) has been described as a branch of artificial intelligence (AI) that enables computers to make successful predictions by using statistical algorithms that may learn from data and apply their knowledge to new, unseen data, enabling the computers to accomplish jobs without needing explicit instructions. It exhibited an impressive development recently with the help of the rapid increase in the storage capacity and processing power of computers. Together with many other disciplines, ML methods have been widely employed in medical fields by assist in the diagnosis of chronic diseases [15–17]. Several previous studies utilized single or multiple ML algorithms, including naïve Bayes (NB), logistic regression (LR), and random forest (RF), based on demographic, clinical, and genetic data to determine new diagnostic models to predict chronic diseases, such as diabetes, depression, and stroke [18–20]. So far, numerous ML models have been assessed for their ability to predict T2DM and its complications (e.g. diabetic retinopathy and diabetic neuropathy) [21–23]. However, limited studies focused on developing a ML model to detect people with high risk of T2DM. Despite the availability of validated questionnaires (e.g. ADA risk assessment) that assist in detecting people with high risk for T2DM, these tools are time-consuming and have the drawback of not capturing all possible risk factors [12,13]. Therefore, this paper introduces a novel ML model developed by the Saudi Ministry of Health and Lean Business Service (the digital partner of the Saudi Ministry of Health), to classify a large proportion of the population and detect those at high risk for T2DM. The developed ML model can be integrated into electronic medical records, provide clinical decision support within short a time, and could improve clinical workflows.

The current study aimed to evaluate the ML model's validity and utility as a classification method to identify people at high risk of T2DM and determine the most appropriate cutoff points. Besides, the study targeted comparing the ML models' outcomes with the validated ADA risk assessment regarding predicting people with high risk for T2DM. We evaluated the manuscript's adherence to the TRIPOD-AI checklist to improve clarity and provide details of the ML prediction model.

2. Patients and methods

2.1. Data source

The National Health Information Center's dataset was used to train the ML model. The National Health Information Center is a Saudi centralized and comprehensive source of information and analyses on health activities. Patients' demographics (age and gender) and clinical data (using the International Classification of Disease (ICD-10)) have been used to build the model. The training dataset consisted of 6,714,518 non-diabetic and 688,099 individuals with diabetes (4,428,929 males and 2,973,688 females).

2.2. Risk factors

An initial literature review and the data-driven approach were used to identify highly correlating risk factors (represented as ICD-10 codes) with T2DM in the dataset. Table 1 shows the ICD-10 codes, which were used as independent variables.

The risk factors used to build the ML model were based on the frequency of their occurrence and their correlation with T2DM. Several studies confirmed that the risk factors used in the ML models, including hypertension, dyslipidemia, cardiovascular disorders, obesity, hyperplasia of the prostate, ophthalmic disorders, connective tissue disorders, thyroid disorders, gastrointestinal disorders, CKD, spondylopathies, refractive errors, nutritional deficiencies, gestational diabetes, genitourinary infections, and polyneuropathies, are highly correlated with T2DM [24–34]. These variables were derived from the National Health Information Center.

Table 1. List of risk factors (represented as ICD-10) used in the ML model as independent variables highly correlated with T2DM.

ICD-10	Description
I10	Essential hypertension
E78	Disorders of lipid metabolism
I67,I25	Arterial dissections
E66	Obesity
N40	Hyperplasia of prostate
H25,H26	Cataract and other lens disorders
M15,M17, M19	Osteoarthritis
H04,H10, H01	Cornea and external disease
H43,H35	Retinal and vitreous conditions
M79,M25	Musculoskeletal pain, not low back pain
E03	Thyroid disorders
I11,I50	Heart failure
K21	Oesophageal disorders
M47,M50, M51	Spondylopathies/spondyloarthropathy (including infective)
H52	Refractive error
R73	Abnormal findings without diagnosis (Impaired fasting glucose)
N18	Chronic kidney disease
E79	Other specified and unspecified nutritional and metabolic disorders
H40	Glaucoma
M75,M77	Other specified connective tissue disease
O24	Diabetes in pregnancy or abnormal glucose tolerance complicating pregnancy; childbirth; or the puerperium (without the preexisting diabetes)
M54	Low back pain
M10	Gout
H53	Blindness and vision defects
R07	Nonspecific chest pain
M81	Osteoporosis
K29	Gastritis and duodenitis
K76	Other specified and unspecified liver disease
D29	Benign neoplasms
I20	Coronary atherosclerosis and other heart disease
G61,G62	Polyneuropathies
N39,R35	Genitourinary signs and symptoms
M13	Other specified joint disorders
E55	Nutritional deficiencies

2.3. Internal validation and algorithm selection

Data derived from the National Health Information Center was imported and loaded in Python version 3.10.9. The patients' age, gender, and risk factors (represented as ICD-10 codes in Table 1) were recognized as features (x) and used as nominal variables. Although no missing data was detected regarding gender and age variables, risk factor variables were either not actually presented or could be missed for some patients. The Class weights feature in Python was used to assign weights to patient-related data (age, gender, and risk factors) according to their degree of correlation with T2DM. Features variables with large weight include older ages, male gender, retinal and vitreous conditions, polyneuropathies, obesity, genitourinary signs and symptoms, essential hypertension, disorders of lipid metabolism, abnormal blood glucose findings without diagnosis, and diabetes in pregnancy. The target variable (y) is described as continuous data with a range of 0 to 1. A higher score indicates that the person has a high risk for T2DM. The data was split using the split-sample method at a split ratio of 80/20. Specifically, 80% of the data from 1 January 2022, to 30 June 2022, was allocated for training purposes, while the remaining 20% of the data from 1 July 2022, to 31 December 2022, was reserved for internal validation. Model training was based on six different ML algorithms, including Logistic Regression, Random Forest, Linear Support Vector Classification (SVC), Decision Tree, Gradient-Boosted Decision Trees (GBT), and Naïve Bayes. The choice of these algorithms was made based on their favorable performance demonstrated in terms of evaluation metrics reported by numerous prior studies in predicting diabetes [35]. Given that the models prioritized initial screening of T2DM through specific risk variables and to avoid the potential health risks of missed T2DM cases, the cost of additional testing for false positives is often considered a lesser concern. Therefore, no calibration approaches were employed for the models that were used. The performance of the trained models was assessed using the evaluation metrics, including accuracy, precision, recall, F1 Score, true negative, true positive, false negative, false positive, and area under Receiver Operating Characteristic (AROC).

2.4. External validation of the model

To evaluate the ML model, an external validation study was conducted from January to February 2023 in Unaizah, Al-Qassim, Saudi Arabia. We selected three sentinel sites, which represent the main primary health care centers (PHCs) dealing with chronic diseases in Unaizah. This study only included non-diabetic adults registered at any of the three selected sites (PHCs). People with documentation of any type of diabetes were excluded using particular ICD-10 codes that related to diabetes (Table 2). The inclusion/exclusion criteria yielded 19,400 individuals. The sample size was calculated using OpenEpi, version 3.01 [36], considering a precision of 4%, a confidence level of 95%, and a design effect of 1. Since the prevalence of high-risk T2DM in Saudi Arabia is not well-known, we used 50% as the hypothesized prevalence of high-risk T2DM. This hypothesized prevalence was approximately related to the prevalence of three risk factors for T2DM in Saudi Arabia, including prehypertension (40.6%), dyslipidemia (43%), and overweight (68.2%) (range 40.6–68.2%) [24,25,37–39]. Accordingly, the minimum estimated sample size should be at least 583 adults. To account for non-respondents, we randomly targeted 3400 individuals who were selected, and their likelihood of having diabetes was estimated using the ML model.

Table 2. Clinical data (represented as ICD-10) list used in the ML model as independent variables that were used to exclude patients with diabetes.

ICD10	Description
E10-E14	diabetes mellitus (type1, type2, specified, unspecified)
N08.3	Glomerular disorders in diabetes mellitus
O24.0	Pre-existing diabetes mellitus, Type 1, in pregnancy
O24.1	Pre-existing diabetes mellitus, Type 2, in pregnancy
O24.11-O24.14	Pre-existing diabetes mellitus, Type 2, in pregnancy, (specified conditions)
O24.19	Pre-existing diabetes mellitus, Type 2, in pregnancy, unspecified
O24.2	Pre-existing diabetes mellitus, other specified type, in pregnancy
O24.21-O24.24	Pre-existing diabetes mellitus, other specified type, (specified conditions)
O24.29	Pre-existing diabetes mellitus, other specified type, in pregnancy, unspecified
O24.3	Pre-existing diabetes mellitus, unspecified, in pregnancy
O24.31-O24.34	Pre-existing diabetes mellitus, unspecified, in pregnancy, (specified conditions)
O24.39	Pre-existing diabetes mellitus, unspecified, in pregnancy, unspecified
H36.0	Diabetic retinopathy
H28.0	Diabetic cataract
M14.2	Diabetic arthropathy
T38.3	Insulin and oral hypoglycemic [antidiabetic] drugs
Y42.3	Insulin and oral hypoglycemic [antidiabetic] drugs causing adverse effects in therapeutic use
G63.2	Diabetic polyneuropathy

2.5. Data collection

A short text message was sent to 3400 individuals via their mobile numbers, asking them to complete and submit the Arabic-validated version of the reliable ADA risk assessment questionnaire [40,41]. Before filling out the questionnaire, all individuals were asked to declare whether they had previously been diagnosed with diabetes. If they answered 'yes,' they were transferred to an exit page and received a follow-up short message service (SMS) thanking them for participating and asking them to continue their care plan with their designated doctors. If they answered 'no,' they were directed to fill out the ADA survey, and their scores were documented. If the score was below 5, they received an assurance SMS with wishes to maintain their health. If the score equals 5 or above, they are directed to schedule an appointment with the nearest participating PHC using 'Sehhaty,' the Ministry of Health patient portal app (Figure 1).

2.6. Data analysis

Microsoft Excel 2016 program was used to organize and analyze the data. We used Python version 3.10.9 to train and test the model. Based on the outcomes of the ML model's scores that were compared with the validated and reliable ADA risk assessment scores, the values of specificity, sensitivity, 100-

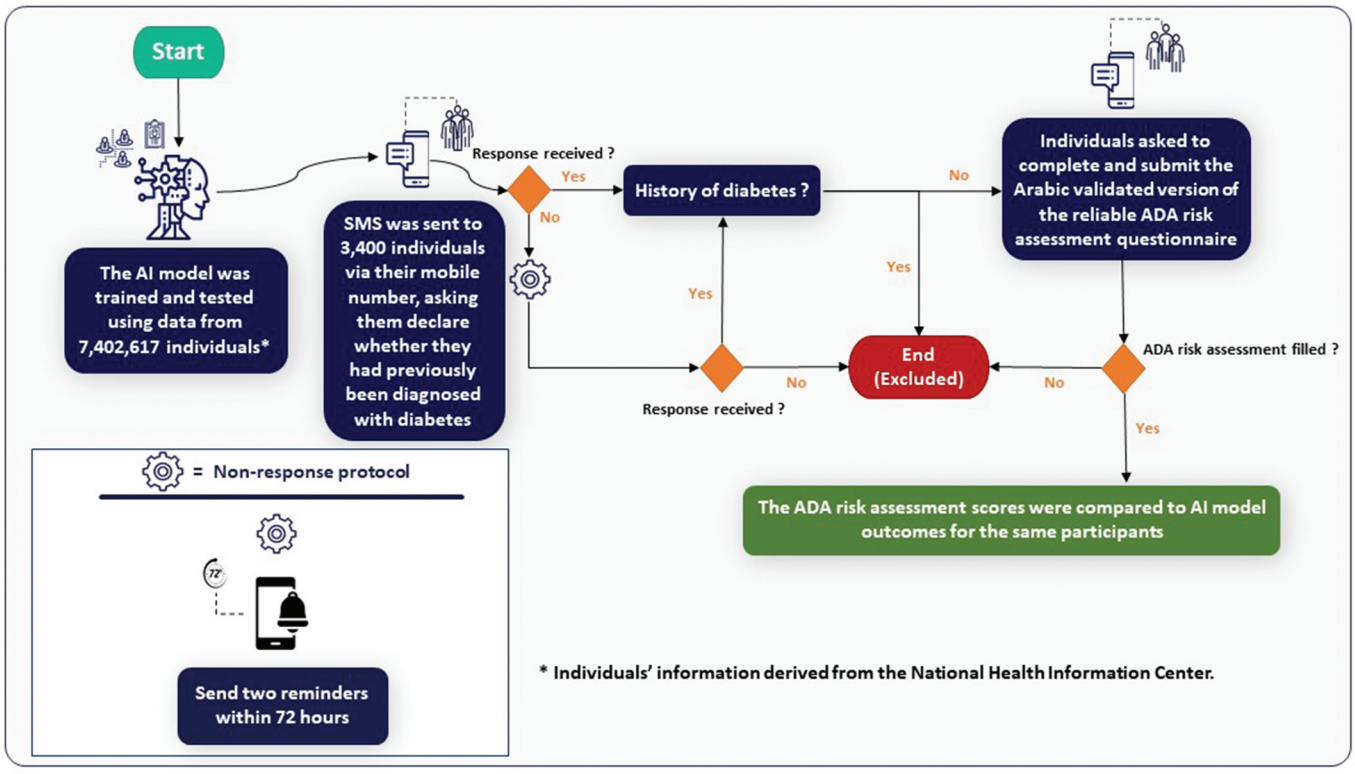

Figure 1. The steps of the applied protocol for T2DM high risk screening through ML model and compare the results with ADA risk assessment scores.

Table 3. Results of logistic regression, random forest, linear support vector, decision tree classifier, gradient-boosted decision trees classifier, and Naïve Bayes algorithms.

Model Name	Accuracy	Precision	Recall	F1 Score	TN	TP	FN	FP	AROC [95% CI]
Logistic Regression	0.808802	0.258695	0.763599	0.386463	1086110	87368	27048	250358	0.788 [0.787-0.789]
Random Forest Classifier	0.718052	0.198138	0.845205	0.321021	945105	96705	17711	391363	0.776 [0.775-0.777]
Linear SVC	0.807191	0.257625	0.767943	0.385818	1083275	87865	26551	253193	0.789 [0.788-0.790]
Decision Tree Classifier	0.771424	0.225891	0.782277	0.350555	1029742	89505	24911	306726	0.776 [0.775-0.777]
GBT Classifier	0.756439	0.221376	0.829709	0.349501	1002573	94932	19484	333895	0.790 [0.789-0.791]
Naïve Bayes	0.771201	0.205911	0.665632	0.314525	1042764	76159	38257	293704	0.723 [0.722-0.724]

TN: True negative; TP: True positive; FN: False negative; FP: False positive; AROC: Area under ROC; Linear SVC: Linear support vector classification; GBT: Gradient-boosted decision trees.

specificity, Receiver Operating Characteristic (ROC) curve, area under ROC (AROC), and Youden's index were determined. These measures were used to evaluate the accuracy of the ML model in identifying people at high risk of T2DM and to assess the suitability of different cutoff points.

2.7. Ethical consideration

The study was reviewed and approved by the Central Institutional Review Board (IRB) at the Saudi Ministry of Health (IRB log no: 23–31 M). Informed consent was obtained from participants to participate in the study. Participants' confidentiality and anonymity were also assured by assigning each participant a code number for the purpose of analysis only, and their participation was completely voluntary.

3. Results

After testing multiple algorithms, we found that logistic regression reached an accuracy of 81%, a recall of 76%, and an AROC of 0.788 (95% CI: 0.787–0.789), which outperforms other algorithms in identifying the high risk of T2DM in the dataset; hence, it was used (Table 3).

A total of 859 subjects responded to the SMS; 180 participants were excluded as they declared that they had already been diagnosed with T2DM. The remaining 679 subjects filled out the ADA risk assessment questionnaire and were included in the analysis. The SMS response percentage was 25.2%; most (68.1%) responded to the first SMS, while the others responded to the first and second SMS reminders (23.6% and 8.3%, respectively). Table 4 shows the characteristics of SMS respondents. Out of the 679 included participants, 46.8% were classified as people at high risk of T2DM when the ML model cutoff point of ≥ 0.5 was used. Based on the ADA risk assessment, 41.4% of the same participants were identified as having a high risk of T2DM, as they scored ≥ 5.

Figure 2 reveals the ROC curve with an AROC value of 0.803, 95% CI: 0.779–0.826 based on the ML model's scoring results (range 0–1). These generated data from the results were classified into different categories as follows: (<0.1),

Table 4. The characteristics of SMS respondents and those who completed the ADA risk assessment questionnaire.

Variable	Total ($N = 859$)
Age (median [range])	48 [35–57]
Age range N (%)	
<35	223 (25.9)
35-49	264 (30.8)
50-59	265 (30.8)
≥ 60	107 (12.5)
Male N (%)	412 (47.9)
History of diabetes N (%)	180 (20.9)
No history of diabetes N (%)	679 (79.1)
Response round N (%)	
1st SMS	585 (68.1)
1st reminder	203 (23.6)
2nd reminder	71 (8.3)
Body mass Index (BMI) N (%)*	
<25 kg/m^2	169 (24.9)
25-30 kg/m^2	260 (38.3)
31-40 kg/m^2	226 (33.3)
> 40 kg/m^2	24 (3.5)
Family history*	447 (65.8)
History of gestational diabetes*‡ N (%)	36 (10)
History of Hypertension* N (%)	196 (28.8)
Physically inactive* N (%)	136 (20)
ADA risk assessment score ≥ 5* N (%)	281 (41.4)
ML model score ≥ 0.5* N (%)	318 (46.8)

*Out of 679 (non-diabetic people).
‡Out of non-diabetic female participants ($N = 359$).

(0.10–0.19), (0.2–0.29), (0.3–0.39), (0.4–0.49), (0.5–0.59), (0.6–0.69), (0.7–0.79), (0.8–0.89), (0.9–0.99), and > 0.99-1). In the ROC curve, the true positive rate (sensitivity) is plotted as a function of 100 minus the false positive rate (100-specificity) at different ML model cutoff points.

Table 5 presents the sensitivity, specificity, and Youden's index at different cutoff points of the ML model. Youden's index of 0.531 and 0.556 were detected at the cutoff points ≥ 0.5 and ≥ 0.4, respectively. However, the cutoff point at ≥ 0.5 showed more balanced sensitivity and specificity (77.94% and 75.13%, respectively) for detecting people at high risk of T2DM than the cutoff point at ≥ 0.4. Other cutoff points showed Youden's indexes of less than 0.5.

Figure 3 reveals a confusion matrix with its evaluation measures representing the true and predictive values of ADA diabetes risk scores and ML model scores, respectively.

4. Discussion

The current study developed a new ML model estimated to classify a large number of people and identify those with a high risk of T2DM in simple and rapid manners with lower costs and resources, making it a potential opportunity for a national T2DM early identification program. After the ML model was compared to the validated ADA risk assessment, its sensitivity and specificity reached acceptable levels, according to the outcomes of the AROC and Youden's index measures [42]. The selection of the ADA risk assessment tool as a comparator was based on multiple studies demonstrating a considerable correlation between the tool's scores and hemoglobin A1c (HbA1c) and blood glucose levels [43–46]. In addition, the ADA risk assessment tool has a high sensitivity (83%) in detecting people with a high risk of T2DM or who already have T2DM but have not been diagnosed [47]. Although the tool's specificity is low (57%), it can still be considered an adequate noninvasive predictor for such a progressive disease with the risk of several serious complications [47].

The newly formulated ML model to identify people at high risk of T2DM was evaluated among 679 participants in Saudi Arabia who had never been diagnosed with T2DM. The results of the validated and reliable ADA risk assessment were compared to ML model outcomes for the same participants.

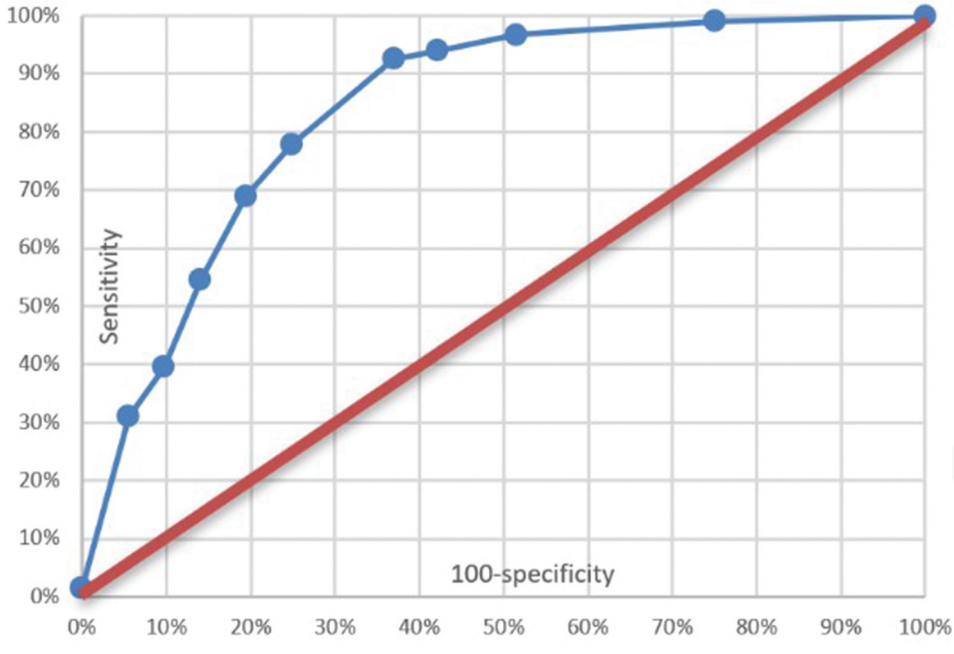

Figure 2. Receiver Operating characteristic (ROC) curve and the area under ROC based on ML model's scoring results. Red line: reference line; Blue line: ROC curve.

Table 5. The sensitivity, specificity, AROC, and Youden's index at different cutoff points.

Cut-off point	Specificity	Sensitivity	100-specificity	Youden's index	AROC [95% CI]
≥1	100.00%	1.42%	0.00%	0.0142	0.803 [0.779-0.826]
≥0.9	94.47%	30.96%	5.53%	0.2543	
≥0.8	90.20%	39.50%	9.80%	0.297	
≥0.7	85.93%	54.45%	14.07%	0.4038	
≥0.6	80.65%	68.84%	19.35%	0.4949	
≥0.5	75.13%	77.94%	24.87%	0.5307	
≥0.4	63.07%	92.53%	36.93%	0.556	
≥0.3	57.79%	93.95%	42.21%	0.5174	
≥0.2	48.49%	96.80%	51.51%	0.4529	
≥0.1	24.87%	98.93%	75.13%	0.238	
≥0.0	0.00%	100.00%	100.00%	0	

AROC: Area under ROC. CI: Confidence Interval.

a

	Predictive negative AI model scores < 0.5	**Predictive positive** AI model scores ≥ 0.5
True negative ADA diabetes risk scores < 5	299 β	99 δ
True positive ADA diabetes risk scores ≥ 5	62 Ω	219 α

α: True positive. β: True negative. δ: False positive. Ω: False negative.

b

Measure	Value
Sensitivity	0.7794
Specificity	0.7513
Negative Predictive value	0.8283
False Positive Rate	0.2487
False Negative Rate	0.2206
Accuracy	0.7629
F1 Score	0.7312

Figure 3. (a) A confusion matrix representing true (ADA diabetes risk scores) and predictive values (ML model scores). (b) Evaluation measures from the confusion matrix.

After reviewing the results regarding the plotted data of sensitivity/100-specificity represented in the ROC curve, the AROC value was within the acceptable range (AROC = 0.803, 95% CI: 0.779–0.826). Additionally, when considering the sample size, the ML model demonstrated a power of at least 80% for risk stratification, as evidenced by its comparable outcomes with the ADA risk assessment. Therefore, the ML model could be an adequate tool to identify people at high risk of developing T2DM or who already have T2DM but have not been diagnosed [48,49].

Moreover, two cutoff points of the ML model (≥0.5 and ≥ 0.4) were generally recognized as acceptable in accuracy based on the results of Youden's index, which were above 0.5 [50]. The option to choose one of these cutoffs depends on the T2DM prevalence and the financial condition in a specific country or region [51]. A lower cutoff point could be considered to capture more people at high risk of T2DM in the targeted population. However, such decisions should be balanced thoroughly to ensure the cost-effectiveness of the tool.

With a cutoff value of ≥ 0.1, the classification of people at high risk of T2DM using the current population-based ML model might be tuned to have a 99% sensitivity. In this case, the majority of enrolled individuals will need to undergo one or more T2DM diagnostic measures (oral glucose tolerance tests (OGTTs), HbA1c tests, or fasting blood glucose (FBG) tests) in order to confirm the diagnosis. Yet, because of the low specificity (25%) at that cutoff point (≥0.1), these diagnostic tests may place an unnecessary burden on patients and healthcare resources.

Strategies like multi-stage screening and risk factor assessment can help manage the number of false positives while ensuring early detection of T2DM. Besides, compared to the potential health risks of missed T2DM cases, the cost of additional testing for false positives is often considered a lesser

concern. While the best-performing models do not outperform currently available screening strategies at certain risk thresholds, one advantage is that an optimal trade-off between sensitivity and specificity can be chosen [52,53]. For instance, if the cutoff point ≥ 0.5 is applied, which has a sensitivity of 78%, nearly 47% of the enrolled people will have to visit the primary healthcare centers. These visits will likely be beneficial and warranted, as 78 out of 100 individuals may be diagnosed with T2DM or prediabetes. Those who are confirmed to be negative should be evaluated for T2DM-related risk factors, which they most likely have. Early identification and management of those risk factors could delay or prevent T2DM.

One difficult component of clinical usefulness is figuring out an appropriate cutoff point with acceptable true positive and true negative rates. The burden of T2DM diagnostic methods and associated costs are among the criteria that influence the choice of a certain cutoff point with particular sensitivity and specificity for screening individuals at high risk for T2DM [54,55].

Several AI models with different formulations have been studied and implemented to either predict or diagnose diabetes. Polak & Mendyk developed a diagnostic Artificial Neural Network (ANN) model to detect pregnant women with gestational diabetes mellitus (GDM) based on their demographics and specific risk factors for GDM, such as smoking and hypocholesteraemia. The sensitivity of their ANN model was around 70% [56]. Also, Moreira et al. developed another ANN model to detect GDM, but with a higher sensitivity (≈79%). However, these two studies did not clearly show the ANN models' specificity [57].

The current study was not the first to develop an AI model to identify people at high risk of T2DM; for instance, Wang et al. established an ANN model that considered the individuals' lifestyle status, particular characteristics, and body-specific measurements [58]. Compared to our developed AI model, the Wang et al. ANN model is somewhat superior in specificity (75.1% vs. 79.1%, respectively) and sensitivity (77.9% vs. 86.9%, respectively). However, the validation method of our ML model reported in this study was validated by comparing the outcomes of the ADA risk assessment scores with the ML model's scores, whereas Wang et al.'s ANN model was compared using multivariate logistic regression models [58].

On the other hand, considering the ADA risk assessment, 41.4% of the non-diabetic participants in the current study were at high risk of T2DM. This percentage was somewhat closely related to the percentage determined by the current ML model (46.8%) at the cutoff point of ≥ 5. Two studies with larger numbers of participants showed that the prevalence of high-risk T2DM was 23% and 22.7%, respectively [59,60]. The high prevalence reported in this study could be related to the inclusion of participants in the ML model who have risk factors highly correlated with T2DM, which are not present in the ADA risk assessment. Despite several risk factors used in the ML model, such as CKD and heart failure, which would have been tested for their diabetes status, this could only applied under ideal circumstances and in ideal clinics. Several studies reported a high prevalence of undiagnosed diabetes among patients diagnosed with CKD and heart failure [61–63].

In contrast to some previous studies that examined the use of AI in diabetes, this current research employs a machine learning model that was trained on a vast dataset. The study also utilized easily accessible data points such as age, gender, and existing risk factors, which can be seamlessly integrated into existing healthcare workflows.

Nevertheless, there were several limitations recognized in this study. The ML model was trained to discriminate between people without diabetes and persons with diabetes, while the study aims to evaluate the new ML model as a classification tool for high risk T2DM. This issue was related to the utilization of electronic medical records regarding the limitation of prediabetes related ICD-10 codes (e.g. R73) entered and used by physicians. Yet, prediabetes (high risk of diabetes) and T2DM share almost all of the same risk factors.

Another possible limitation is related to the validation of the developed ML model, which relied on the ADA risk assessment tool rather than the actual outcomes of T2DM diagnostic measures in the study population.

Besides, the developed ML model did not exclude some subjects diagnosed with T2DM. This issue could be because several patients were diagnosed and treated in hospitals and clinics not linked with the Saudi National Health Information Center's dataset. Therefore, the ICD-10 codes were missed, and the ML model was not able to notify those patients of their diabetes status. In addition, the ML model utilized the common list of diagnostic codes that exist in Saudi Arabia. Thus, some risk factors for T2DM were not included.

Moreover, the study's voluntary recruitment technique certainly contributed to the non-responder rate of almost 75%. Previous research has consistently shown that, as compared to mandated recruitment techniques, voluntary recruiting is a significant contributor to non-response bias in demographic and health-related data [64]. This type of bias can be readily identified for particular variables in the current study (i.e. gestational diabetes and level of physical activity). However, other significant factors such as age, gender, BMI, and family history of T2DM remained mostly unaffected or had no impact. This limitation may be influenced, particularly in relation to the ML model's ability to accurately identify patients with some T2DM risk factors, including history of gestational diabetes and status of physical activity. Therefore, reduced generalizability and overestimation of the ML model's accuracy are anticipated.

Furthermore, using non-calibrated logistic regression to develop the ML model instead of a neural network might be considered a limitation, as ML models based on neural networks are superior at differentiating between abnormal and normal cases [65].

In addition, another possible limitation of this study could be related to ICD-10 code R73 (Abnormal findings without diagnosis (Impaired fasting glucose)), which may affect the clinical usefulness of the current ML model as it should not depend on lab investigations. However, only one of the included subjects had this code in its history. Thus, the R73 code has a minimal impact on identifying high risk for T2DM in the study.

5. Conclusions

The current study developed a new ML model that was estimated to classify a large number of people and identify those with a high risk of T2DM. Compared to the ADA risk assessment tool, the current ML model could be recognized as a time-saving screening method that can be integrated into electronic medical records in a simple and rapid process with lower costs and resources. In addition, the results point to possible ways to find people with a high risk of T2DM or those who haven't been diagnosed yet. This could help health care providers make early decisions about treatment and lower the risk of diabetes complications. Further improvements to the developed model could potentially boost the effectiveness of this approach, facilitate the program's expansion to wider geographic areas, and concurrently lessen the strain of conventional T2DM screening programs on the healthcare system.

List of abbreviations

ADA	American Diabetes Association.
AI	Artificial Intelligence.
AROC	Area under ROC.
BMI	Body Mass Index.
FN	False negative.
FP	False positive.
GBT	Gradient-boosted decision trees.
Linear SVC	Linear support vector classification.
ML	Machine Learning.
ROC	Receiver-operating characteristic.
SMS	Short Message Service.
T2DM	Type-2 Diabetes Mellitus.
TN	True negative.
TP	True positive.

Declaration of interest

The authors have no relevant affiliations or financial involvement with any organization or entity with a financial interest in or financial conflict with the subject matter or materials discussed in the manuscript. This includes employment, consultancies, honoraria, stock ownership or options, expert testimony, grants or patents received or pending, or royalties.

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Ethics statement

The study was reviewed and approved by the institutional review board committees of the Saudi Ministry of Health (IRB log no: 23–31 M). Informed consent was taken from participants to participate in the study. Participants' confidentiality and anonymity were also assured by assigning each participant with a code number for the purpose of analysis only, and their participation was completely voluntary.

Data availability statement

The data that support the findings of this study are available from the corresponding author upon reasonable request. The data are not publicly available due to containing information that could compromise the privacy of research participants.

Authors' contributions

AK and AZ mainly contributed in conceptualization, design of methodology, and data curation. AK, AZ, FS, AY, RN, and RS mainly contributed in formal analysis. MM, DA, NM, RJ, FD, MH, AH, and AS contributed in writing – original draft preparation. AF, EK, AF, AF, NR, and EG mainly contributed in writing – review and editing. AK, AZ, and NR mainly contributed in resources. All authors substantially contributed to the conception and design of the article, interpreting the relevant literature, and been involved in writing and revising the article for intellectual content. All authors have read and agreed to the published version of the manuscript and accountable for the contents of the article and to share responsibility to resolve any questions raised about the accuracy or integrity of the published work.

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