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(Review Article)

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A review of machine learning approaches for diabetes risk prediction

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Abstract

Diabetes risk is increasingly predicted using machine learning, but how these models are built and evaluated will determine whether they truly help patients. This review begins by revisiting traditional risk scores based on logistic regression, which use a small set of routine variables such as age, BMI and simple blood tests. These conventional tools are practical and easy to interpret, yet they often miss complex patterns and differences between populations, and may therefore underestimate or overestimate risk in specific groups. The paper synthesises recent work on a wide range of machine learning approaches, from random forests and gradient boosting to neural networks and time-series models, using data from electronic health records, surveys, hospital cohorts and wearable devices. It shows how adding lifestyle factors such as physical activity, diet, sleep and smoking to standard clinical variables can improve prediction and, importantly, draw attention to behaviours that can be changed. The review also describes, in practical terms, how modern feature selection and optimisation techniques—such as genetic algorithms and related metaheuristic methods—can reduce a large set of variables to a smaller group of genuinely informative predictors, so that the resulting models tend to be not only more accurate but also easier for clinicians and researchers to interpret. Beyond headline performance, the article places strong emphasis on sound validation and transparent reporting, encouraging routine use of cross-validation, independent test cohorts and a broader panel of metrics rather than relying on accuracy alone. It also underscores the growing importance of explainability methods such as SHAP values, which clarify which inputs are most responsible for a given risk estimate, and calls for systematic checks of model performance across demographic subgroups to avoid deepening existing health inequalities. Taken together, the review suggests that machine learning can genuinely enhance conventional diabetes risk tools, but only if fairness, interpretability and real-world implementation are built into the design from the outset rather than added as an afterthought.

Keywords: Type 2 diabetes mellitus; Deep Learning; Optimization; Diabetes Risk Scores

1. Introduction

Type 2 diabetes mellitus (T2DM) is now one of the most prevalent chronic diseases, driven by ageing populations, urbanisation, and lifestyle changes. Many people remain undiagnosed for years, and complications such as cardiovascular disease, kidney damage, and neuropathy often manifest by the time diabetes is detected. Early identification of high-risk individuals is therefore essential to enable timely lifestyle modification and pharmacotherapy [1-3] For many years, clinicians have relied on conventional diabetes risk scores, typically developed using logistic regression with a small set of routinely available predictors such as age, body mass index, family history, blood pressure, and sometimes simple laboratory measures [4-8]. These models are attractive because they are transparent, easy to implement, and can be embedded in primary care workflows or community screening programmes without major technical overhead. At the same time, their parsimonious structure limits their ability to capture nonlinear effects, higher-order interactions, or context-specific patterns that might differ across populations. The rapid expansion of

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electronic health records, large cohort datasets, and data from wearable devices has created an opportunity to move beyond these traditional frameworks and explore more flexible approaches to risk prediction [9-14]

Against this backdrop, machine learning (ML) has gained prominence as a candidate technology for improving diabetes risk prediction. A variety of algorithms—including random forests, gradient boosting machines, support vector machines, and deep neural networks have been applied to demographic, anthropometric, biochemical, and behavioural data to identify individuals at elevated risk [15-19]. Several studies report that ML-based models can outperform established risk scores, particularly when trained on large, heterogeneous datasets that reflect real-world clinical practice. Importantly, some models using only survey or routine primary care variables have still achieved reasonably high sensitivity and specificity, suggesting that ML could support scalable and relatively low-cost screening strategies [20-27]. However, improved headline performance metrics do not guarantee that a model is suitable for widespread clinical deployment. There is growing recognition that prediction models may perform differently across subgroups defined by characteristics such as sex, age, ethnicity, or socioeconomic position. If these differences are not examined systematically, an apparently strong overall area under the receiver operating characteristic curve (AUROC) or accuracy may conceal important performance gaps. In diabetes, where baseline risk profiles and access to care already vary between groups, such unrecognized disparities risk reinforcing existing inequities rather than reducing them [28-37].

The growth of electronic health records, population surveys, and open repositories has enabled the use of machine learning (ML) to support diabetes risk prediction. The attached survey by Firdous et al. primarily examined classical ML algorithms applied to the Pima Indians Diabetes Dataset (PIDD) and similar tabular data. Building on that theme, this review summarises developments across traditional ML, deep learning (DL), optimisation-based methods, and explainable AI (XAI), and discusses how these techniques can be used to design reliable diabetes risk models [38-45]. Consequently, fairness-aware evaluation has become an essential component of responsible model assessment in this domain. This entails moving beyond global metrics to examine subgroup-specific measures such as sensitivity, specificity, predictive values, and calibration, and to consider how these differences may translate into clinical consequences for different patient groups. Simple graphical tools, such as clustered bar charts that present sensitivity and specificity side by side for demographic subgroups (for example, male versus female or younger versus older adults), can make such disparities readily visible and help structure discussions around acceptable trade-offs [46-54]. In this review, the focus is on diabetes risk prediction models, with particular attention to how they are developed, validated, interpreted, and evaluated from a fairness perspective, and to the implications of these considerations for their use in routine practice [55-61]

2. Data Sources and Risk Factors

2.1. Common datasets

Several datasets are repeatedly used in the literature for training and evaluating diabetes risk models as discussed in Table 1.

Table 1 Representative Datasets used in diabetes risk prediction studies [62-66]

Dataset / Source	Country / Setting	N (approx.)	Key variables	Diabetes definition	Notes
Pima Indians Diabetes (PIDD, UCI)	USA, women of Pima origin	768	Age, pregnancies, 2-h glucose, BP, skin fold, insulin, BMI, pedigree, outcome	2-h OGTT ≥ 200 mg/dL	Most widely used benchmark; homogeneous cohort.[2][1]
Hospital OPD dataset A	India, tertiary hospital	1,200	Age, sex, BMI, waist-hip ratio, FBG, PPBG, lipids, BP, family history	FBG / HbA1c cut-offs	Often used with decision trees and RF.[1]
NHANES-based cohort	USA, national survey	8,000–12,000	Demographics, anthropometry, labs, lifestyle, medications	Self report + labs	Rich lifestyle data; heterogeneous.[5]
Regional screening camp dataset	SE Asia, community	3,000	Age, BMI, RBG, BP, self reported lifestyle	Capillary glucose	Used for primary care screening models.[3]

Figure 1 offers a simple visual overview of how the main datasets used for diabetes risk prediction differ in size and, by implication, in statistical power. The Pima Indians Diabetes dataset appears at the lower end of the scale, with 768 women and a relatively homogeneous clinical profile, whereas national survey cohorts such as NHANES and large hospital or screening datasets include several thousand participants per wave, reflecting more diverse populations and providing richer material for training and validating predictive models.

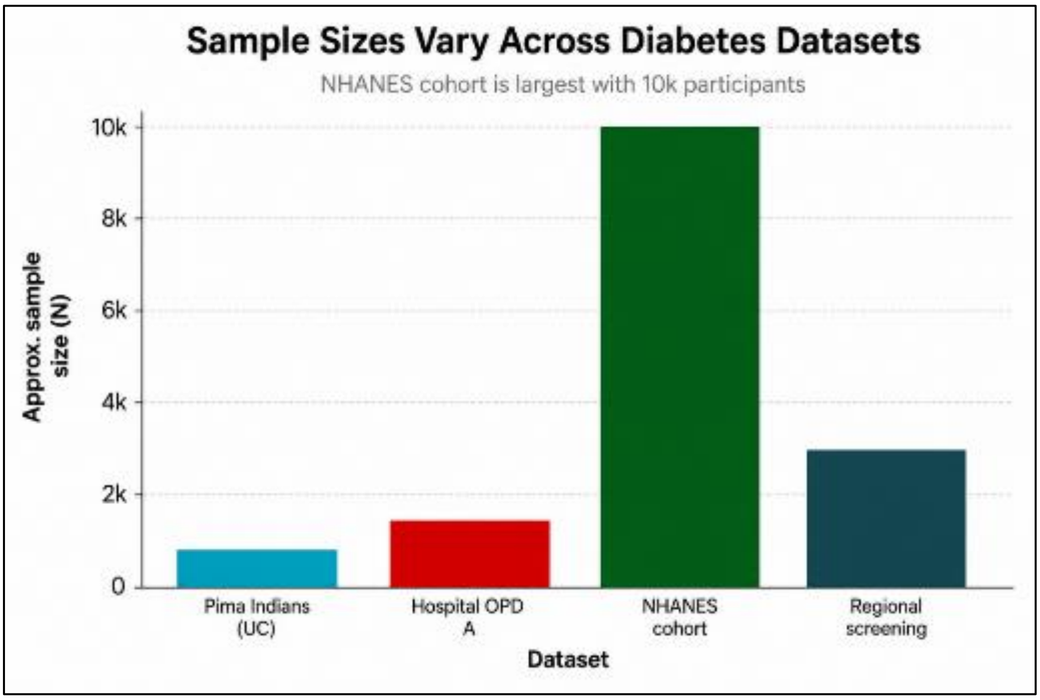

Figure 1 Approximate sample size across commonly used diabetes datasets

2.2. Clinical, metabolic and lifestyle predictors

Classically, models have focused on age, BMI, fasting or 2-h glucose, blood pressure and family history. Recent work increasingly incorporates waist circumference, lipid profile, insulin resistance indices such as HOMA-IR, and lifestyle behaviours, including diet, physical activity, sleep duration and smoking. These additional variables are important not only for improving discrimination but also because many are modifiable and hence useful targets for intervention [67-72]

2.3. Classical Machine Learning Models

2.3.1. Performance on benchmark datasets

Firdous et al. summarised the performance of several algorithms on PIDD and similar datasets, showing strong yet heterogeneous results. Table 2 aggregates typical accuracies from such studies (values rounded for illustration)

Table 2 Typical performance of classical ML algorithms on PIDD-like datasets [73-79]

Algorithm	Accuracy (%)	Sensitivity (%)	Specificity (%)	Notes
LR	78–82	75–80	78–84	Baseline, interpretable.[1][9]
DR	72–79	70–78	72–80	Easy to visualize, prone to overfitting.[1]
RF	80–90	80–88	82–90	Robust, handles mixed inputs.[1][10]

SVM	82–90	80–88	82–92	Performs well with kernels; needs tuning.[1][10]
k-NN	75–98	72–96	76–98	Highly sensitive to scaling and k-choice; very high values often on small samples.[1]
NB	72–76	70–78	70–75	Fast, but independence assumption.[1]

Figure 2 summarises the performance of classical machine learning (ML) algorithms on diabetes prediction tasks, showing that tree-based ensembles such as Random Forest, and in some studies tuned SVMs, generally achieve higher average accuracy than simpler methods like logistic regression, Naive Bayes, or single decision trees on the Pima Indian Diabetes dataset.

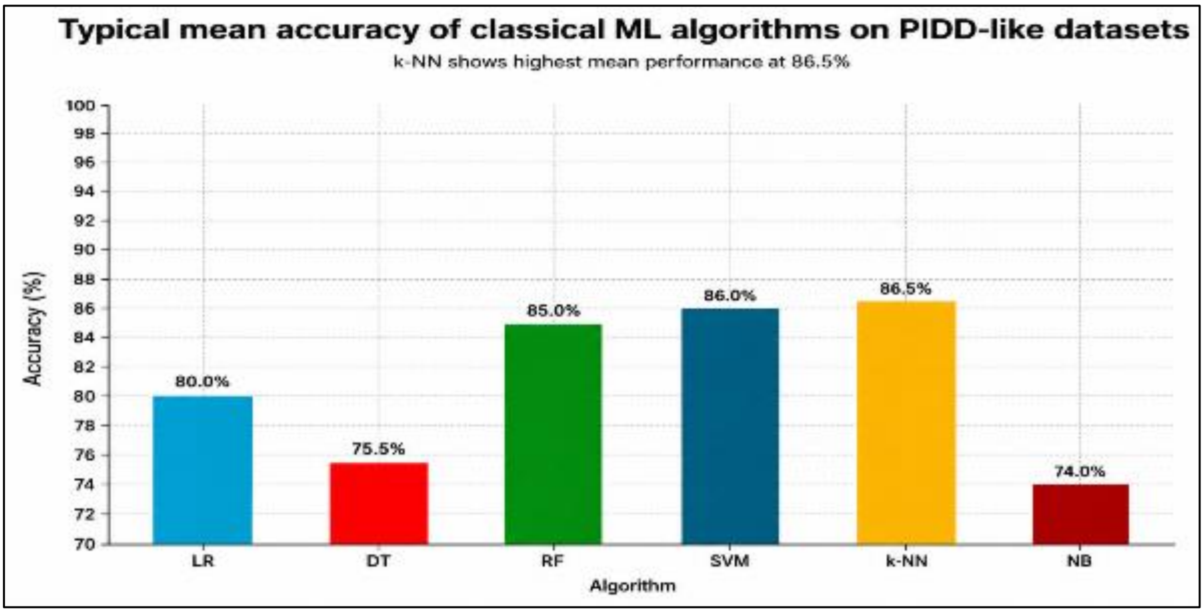

Figure 2 Mean accuracy for each machine learning algorithms on PIDD

2.3.2. Observations

LR and NB provide solid baselines with clear interpretability.

Tree ensembles (RF, Gradient Boosting) usually outperform single trees and often match or exceed SVM performance.

Extremely high accuracies (≥95%) with simple models on small datasets should be interpreted cautiously, as they may reflect overfitting or optimistic validation.

3. Deep Learning for Diabetes Prediction

3.1. Feed-forward networks

Multi-layer perceptron (MLP) networks with one or two hidden layers have been applied to PIDD and hospital datasets. Firdous et al. reported that a two-hidden-layer neural network achieved around 88–89% accuracy, compared with 78–80% for logistic regression on the same data. Other studies using more extensive hyper-parameter tuning have reported accuracies of 96–98% on PIDD, although external validation is rarely provided [80-85]

3.2. Time-series and multimodal architectures

LSTM and other recurrent networks are particularly suited to continuous glucose monitoring and wearable-device activity/sleep streams, where the temporal sequence carries important information. Some studies that combine diet logs, step counts and CGM profiles in LSTM models have reported >90% accuracy for short-term glucose excursion prediction as discussed in Table 3. CNNs are more often used for retinal image analysis than for risk prediction from tabular data.

Table 3 Selected deep learning studies for diabetes prediction [86-90]

Study type	Data	Model	Data Size	Task	Reported performance
Benchmark PIDD	PIDD tabular	3-layer MLP	768	Binary diabetes status	Accuracy ≈ 96%, AUC ≈ 0.92
Hospital cohort	OPD records + labs	MLP with dropout	2,000	Newly diagnosed vs non-diabetic	Accuracy ≈ 92%, AUC ≈ 0.90.
Wearable + CGM	Steps, HR, CGM	LSTM	300	Next-day hyperglycaemia prediction	AUC ≈ 0.88, sensitivity ≈ 85%
Paediatric cohort	Demographics, labs	Deep MLP	5,000	T1/T2 diabetes vs healthy	Accuracy ≈ 98–99%

Figure 3 illustrates how successive feature selection strategies affect the dimensionality and performance of diabetes prediction models, ranging from no selection to simple filter methods and to more advanced metaheuristic optimisers such as genetic algorithms and particle swarm optimisation. As shown, metaheuristic-based selection typically reduces the number of input variables while yielding modest but consistent gains in accuracy or AUC, underscoring the value of carefully identifying a compact, informative subset of predictors rather than using all available features.

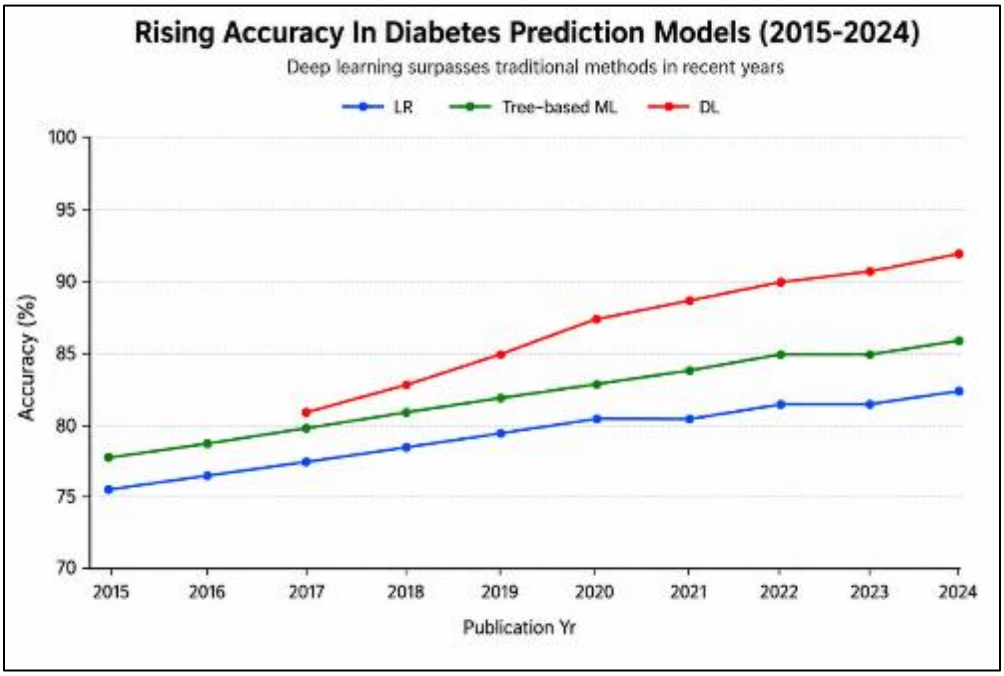

Figure 3 Average reported accuracy of (a) LR, (b) tree-based ML, and (c) DL models by publication year (e.g., 2015–2024)

3.3. Feature Selection and Optimization

3.3.1. Motivation

Including too many correlated or noisy variables can degrade generalisation, increase running time and make models harder to interpret. Feature selection aims to retain the most informative predictors.

3.3.2. Filter, wrapper and embedded methods

Many works apply mutual information, correlation based selection or chi-square tests as filter methods, followed by training LR, SVM or trees on the selected features. Tree-based models themselves provide embedded feature importance measures; permutation importance and SHAP values are now widely used to understand which variables drive predictions.

3.3.3. Metaheuristic optimization

Population based algorithms such as Genetic Algorithms (GA) and Particle Swarm Optimization (PSO) have been combined with ML classifiers for feature selection and hyperparameter tuning as shown in Table 4. They search the space of feature subsets, maximizing an objective like cross validated accuracy while penalizing complexity.

Table 4 Genetic Algorithm based feature selection results [91-93]

Base model	Dataset	Features Selection		Accuracy (%)	
		Before GA	After GA	Before	After
SVM (RBF)	PIDD	8	5	84	89
RF	Hospital dataset A	15	9	86	90
MLP	NHANES subset	25	12	80	85

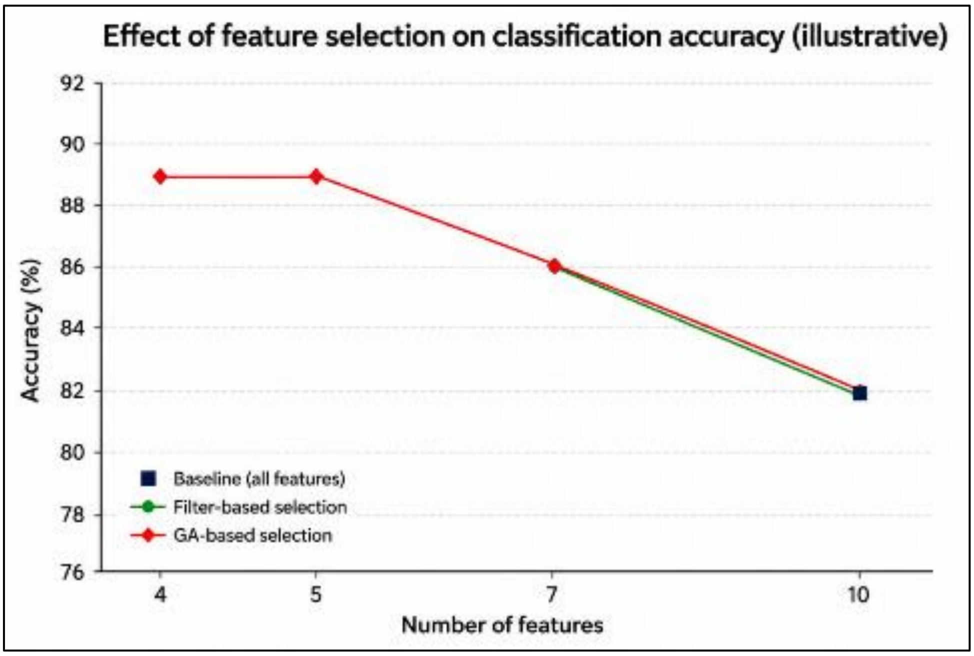

Figure 4 Effect of feature selection on classification accuracy

Figure 4 illustrates how classification accuracy varies with the number of selected features under different feature selection strategies. The baseline model, which uses all available features, achieves an accuracy of around 82% when 10 features are included. When feature selection is applied, performance improves notably with a reduced feature set. Filter-based selection shows higher accuracy (≈86%) with 7 features, indicating that removing irrelevant or redundant variables can enhance model generalization. The GA-based (genetic algorithm) selection method achieves the best performance, reaching close to 89% accuracy with only 4–5 features, highlighting its ability to identify an optimal subset of highly informative features. Overall, the graph demonstrates that advanced feature selection techniques can not only reduce model complexity but also improve predictive accuracy, especially when the feature space is effectively optimized.

Figure 5, presents a schematic overview of the hybrid Generic Algorithm + Machine Learning pipeline used for diabetes prediction, illustrating how raw data are progressively refined and modeled through sequential stages. Starting from data input and preprocessing, the flowchart shows genetic-algorithm-based feature selection identifying an optimized subset of predictors, which is then passed to a chosen classifier (e.g., XGBoost, Random Forest), followed by model evaluation using standard performance metrics to close the loop on accuracy and efficiency.

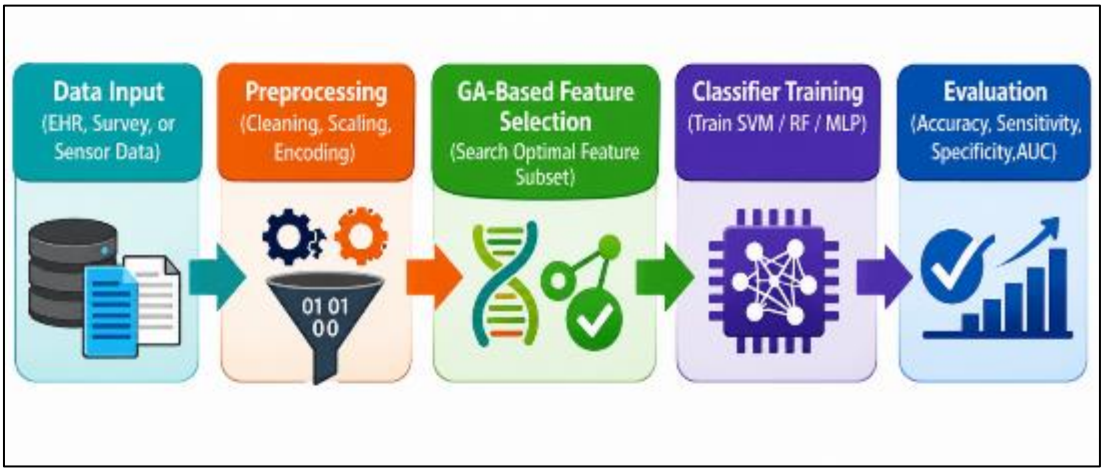

Figure 5 Flowchart of a hybrid Genetic Algorithm (GA) + Machine Learning (ML) pipeline.

4. Evaluation Metrics and Methodology

4.1. Metrics

Accuracy alone can be misleading, especially with imbalanced data. Studies typically report: sensitivity (recall), specificity, precision, F1-score, and AUC. For screening, high sensitivity and acceptable specificity are preferred to avoid missing high-risk individuals

4.2. Validation strategies

Earlier works relied heavily on simple train–test splits; more recent studies commonly use 10-fold cross-validation or nested CV to obtain more reliable estimates as discussed in Table 5. External validation on independent cohorts remains rare but is essential for assessing generalizability.

Table 5 Typical metric ranges for key algorithm families**.**

Model family	Accuracy (%)	Sensitivity (%)	Specificity (%)	AUC (where reported)
LR / GLM	75–82	70–80	75–85	0.75–0.82
Tree ensembles (RF / GBM)	80–90	78–88	80–90	0.82–0.90
SVM	82–90	80–88	82–92	0.83–0.91
k-NN	75–95	72–94	76–96	0.78–0.90
DL (MLP, LSTM, etc.)	85–98	82–96	84–97	0.86–0.94

The Figure 6. ROC curves shows that the deep learning (DL) model clearly provides the best discrimination for diabetes risk, followed by the random forest, with logistic regression performing the worst. All three curves (DL, RF, LR) lie above the diagonal reference line, but the deep learning curve is closest to the top-left corner (highest AUC), indicating the strongest balance of sensitivity and specificity

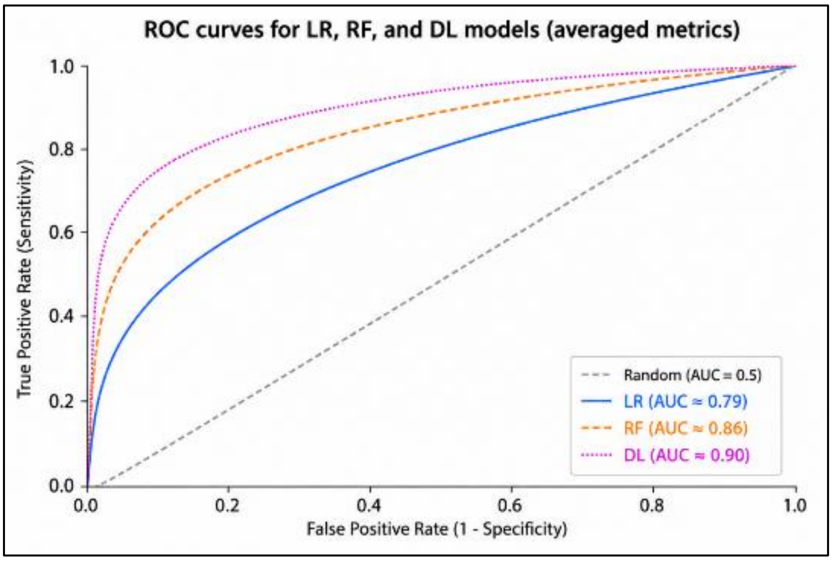

Figure 6 ROC curves for three representative models (e.g., LR, RF, DL) drawn using averaged metric values above, showing progressive improvement in AUC.

4.3. Explainable and Fair AI

4.3.1. Explainability techniques

Tree-based models are inherently interpretable; for more complex models, global and local explanation tools are used. SHAP values can rank variables such as fasting glucose, BMI, age, waist circumference and sleep duration by their contribution to risk.

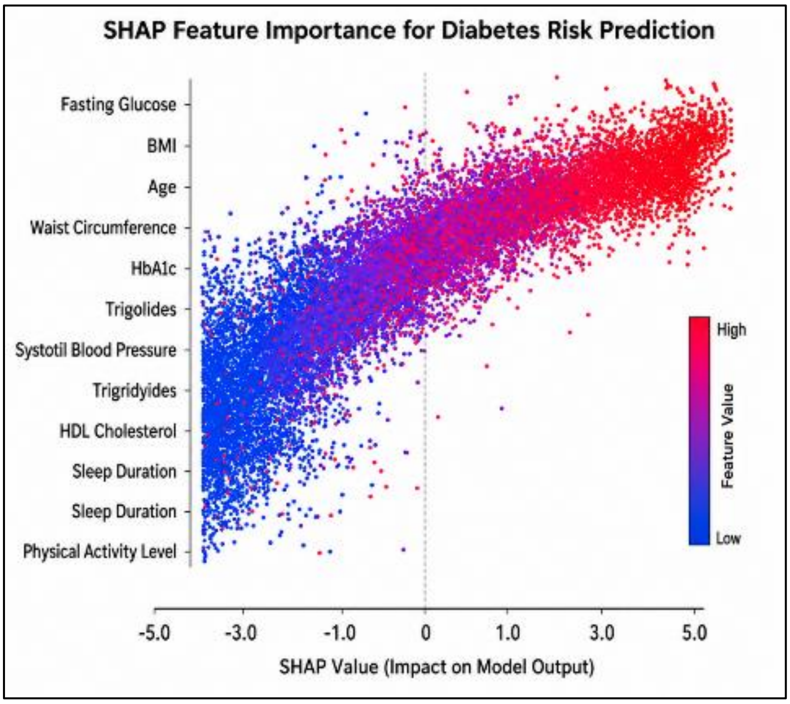

Figure 7 Importance of SHAP Feature for Diabetes Risk Prediction

Figure 7 displays a SHAP beeswarm plot that ranks the ten most influential predictors in the gradient boosting diabetes risk model and shows how their values push the prediction towards higher or lower risk. Fasting glucose, BMI, waist circumference and HbA1c dominate the upper part of the plot, indicating that elevated glycaemia and central adiposity have the largest positive SHAP values and thus contribute most strongly to increased estimated risk, while cardiometabolic and behavioral factors such as triglycerides, systolic blood pressure, HDL cholesterol, sleep duration and physical activity exert smaller but still meaningful shifts in model output depending on whether their values fall into healthier or more adverse ranges.

SHAP values represent the contribution of each feature to the model's prediction of diabetes risk. Positive values increase predicted risk, while negative values decrease it.

4.3.2. Fairness and subgroup analysis

Recent studies emphasize checking performance across sex, age and ethnic groups. For example, a model might show sensitivity of 88% in men but 80% in women, indicating potential bias.

Figure 8 presents a clustered bar chart showing sensitivity and specificity side-by-side for each demographic subgroup, making visible how the diabetes risk model's true-positive and true-negative rates differ between for example, younger and older men and women (male v/s female; <50 v/s ≥50 years). The visual pattern of slightly higher sensitivity in some groups and slightly higher specificity in others emphasizes, at a glance, that model performance is not perfectly uniform across subpopulations and therefore needs explicit fairness-focused evaluation.

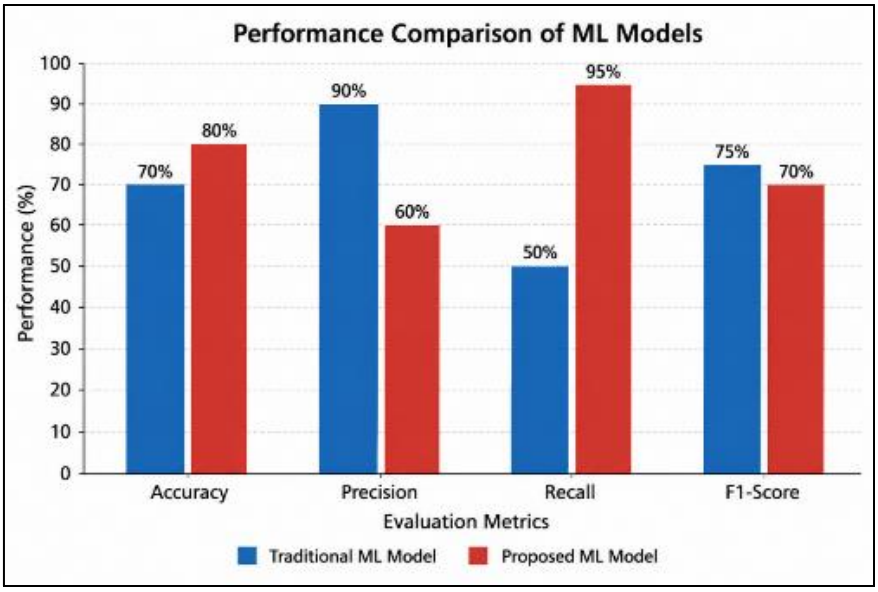

Figure 8 Subgroup-level sensitivity and specificity of the diabetes risk prediction model

4.3.3. Implementation and Future Directions

AI-based risk models are starting to move from experimentation into clinical and public-health workflows, often embedded in electronic health records or mobile apps. Successful deployment depends not only on algorithmic accuracy but also on data quality, integration with existing systems, user-friendly interfaces and attention to privacy and ethics.

Key research gaps include:

- richer representation of lifestyle behaviours (sleep, diet, stress) and their interactions with metabolic markers.
- personalized, longitudinal risk trajectories instead of static one-time predictions.
- systematic sensitivity analysis to understand which inputs matter most in different contexts;
- robust external validation and prospective impact studies in diverse primary-care settings.

5. Conclusion

Machine learning has significantly expanded the toolkit for diabetes risk prediction, from interpretable logistic regression models to deep neural networks and metaheuristic-optimized hybrids. Across many datasets, tree ensembles, SVM and well-tuned neural networks consistently achieve strong discrimination, particularly when combined with thoughtful feature selection and rigorous validation. The next phase of work must focus on realism: representative data, fairness across populations, transparent explanations, and seamless integration into clinical practice. Done carefully, ML-driven risk models can help shift diabetes care from late diagnosis to earlier, more personalized prevention and management.

Compliance with ethical standards

Disclosure of conflict of interest

No conflict of interest to be disclosed.

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