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A Comprehensive Analysis of Chinese, Japanese, Korean, US-PIMA Indian, and Trinidadian Screening Scores for Diabetes Risk Assessment and Prediction

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Abstract: Risk assessment and developing predictive models for diabetes prevention is considered an important task. Therefore, we proposed to analyze and provide a comprehensive analysis of the performance of diabetes screening scores for risk assessment and prediction in five populations: the Chinese, Japanese, Korean, US-PIMA Indian, and Trinidadian populations, utilizing statistical and machine learning (ML) methods. Additionally, due to the present COVID-19 epidemic, it is necessary to investigate how diabetes and COVID-19 are related to one another. Thus, by using a sample of the Korean population, the interrelationship between diabetes and COVID-19 was further investigated. The results revealed that by using a statistical method, the optimal cut points among Chinese, Japanese, Korean, US-PIMA Indian, and Trinidadian populations were 6.205 mmol/L (FPG), 5.523 mmol/L (FPG), and 5.375% (HbA1c), 150.50–106.50 mg/dL (FBS), 123.50 mg/dL (2hPG), and 107.50 mg/dL (FBG), respectively, with AUC scores of 0.97, 0.80, 0.78, 0.85, 0.79, and 0.905. The results also confirmed that diabetes has a significant relationship with COVID-19 in the Korean population (p-value 0.001), with an adjusted OR of 1.21. Finally, the overall best ML models were performed by Naïve Bayes with AUC scores of 0.736, 0.75, and 0.83 in the Japanese, Korean, and Trinidadian populations, respectively.

Keywords: risk assessment; prediction model; diabetes; statistical method; screening scores; machine learning

MSC: 62-07; 62G10; 62G15; 62H30; 62P10

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Citation: Fitriyani, N.L.; Syafrudin, M.; Ulyah, S.M.; Alfian, G.; Qolbiyani, S.L.; Anshari, M. A Comprehensive Analysis of Chinese, Japanese, Korean, US-PIMA Indian, and Trinidadian Screening Scores for Diabetes Risk Assessment and Prediction. *Mathematics* **2022**, *10*, 4027. https://doi.org/10.3390/math10214027

Academic Editor: Victor Leiva

Received: 5 October 2022
Accepted: 28 October 2022
Published: 30 October 2022

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1. Introduction

Disease risk assessment has become a major clinical focus in recent decades [1–3]. It is an essential method for the prevention of diseases such as diabetes, cardiovascular disease, and chronic kidney disease [4–6]. Aside from risk assessment, disease prediction model development is also a major area of attention in clinical research since it can help with disease prevention, early detection, and worst-case scenario prevention for people with disorders. In the last decade, most of the previous studies have used risk assessment and predictive models for diabetes prevention, considering that diabetes is one of the leading causes of worldwide mortality and morbidity [7–9], where the number of deaths is around 71% of all global deaths [10–13].

As the cost of medical diagnosis, tests, and treatment has been rising [14], several methods and strategies have been developed to help individuals more easily and cost effectively check their health status. According to the guidelines on the prevention of diabetes, risk assessment and prediction models are solutions that are recommended to be used for those diagnosed as having a high risk of developing diabetes, thus it could help them in preventing the risk of diabetes [15,16]. In recent years, statistical methods and machine learning methods have been successfully and widely used as solutions for diabetes screening programs to assess and predict the risk of diabetes, providing high predictive accuracy [7,8,14–18]. Therefore, in this study, we propose a comprehensive analysis of diabetes screening scores for risk assessment and prediction in numerous national populations by utilizing statistical methods including logistic regression for predictors in the models, and also machine learning (ML) models such as Gaussian Naive Bayes (GNB), logistic regression (LR), decision tree (DT), multi-layer perceptron (MLP), support vector machine (SVM), random forest (RF), extreme gradient boost (XGB), and ensemble learning with 10-folds cross-validation. A statistical method based on logistic regression was used to estimate the odds ratio (OR), 95% confidence interval (CI), and *p*-value for each predictor and outcome, along with the area under the receiver operating characteristic (ROC) curve (AUC). For diagnostic performance, we computed the percent (%) of participants who scored high for sensitivity, specificity, positive predictive value (PPV), negative predictive value (NPV), likelihood ratio positive/negative (LR+/−), Youden index, accuracy, and AUC, along with the ROC curve. For prediction models utilizing ML, several performance metrics including accuracy, precision, recall, f1, AUC, and ROC curves are used to assess the model's performance. We utilized five diabetes publicly available datasets from several nations, including China, Japan, South Korea, the United States, and Trinidad. In addition, due to the present COVID-19 epidemic, it is imperative to look at how diabetes and COVID-19 are related to one another. Thus, in this study, using a sample of the Korean population, the interrelationship between diabetes and COVID-19 is investigated.

The organization of this paper is as follows. In Section 2, we present the related works in diabetes screening programs and diabetes prediction models. Section 3 presents the diabetes data collection and flowchart of the study. Section 4 presents the results of the study and discussion. Finally, in Section 5, the conclusion, limitations, and future challenges are provided.

2. Literature Review

Diabetes is a lifelong disorder that is categorized as a chronic disease caused by insufficient insulin production by the pancreas (type 1 diabetes) and inefficient insulin utilization by the body (type 2 diabetes). Several methods could be used to conduct diabetes screening. They are fasting plasma glucose (FPG) [19–24], hemoglobin A1C (HbA1C) [25–28], capillary fasting blood glucose (CBG) [16,29–31], venous plasma glucose (VPG) [32–34], and oral glucose tolerance test (OGTT) [22,23,35] which checks the 2-h plasma glucose (2hPG). Among these available diabetes screening or diagnostic tests, FPG, HbA1c, and OGTT are the most recommended and useful for population-based screening [36]. According to ADA and WHO recommendations, diabetes diagnosis based on FPG is carried out by checking blood glucose level after not having eaten or drunk anything other than water for at least 8 h before the test, and diabetes could be diagnosed when the blood glucose is larger than 126 mg/dL or larger than 7 mmol [36,37]. The blood glucose level of hemoglobin (HbA1c) is indicated as diabetes when the HbA1c is 6.5% or higher [36]. While using OGTT (blood glucose level after drinking the glucose syrup for 2 h before the test), diabetes is classified when the 2hPG is $\geq$200 mg/dL [36].

It is important to evaluate the diabetes screening scores as they could be used to assess the risk of diabetes and its prediction [25]. Blood glucose screening based on FPG, HbA1C, and 2hPG has been conducted by previous studies for predicting type 2 diabetes, impaired diabetes, and gestational diabetes using statistical methods. The assessment of the diabetes model could be carried out by measuring the sensitivity, specificity, positive pre-

dictive value (PPV), negative predictive value (NPV), likelihood ratio positive (LR+), likelihood ratio negative (LR−), Youden index, and AUC-ROC [16,38,39]. To find the optimal cut point for predicting diabetes, the Youden index is one of the most suitable and commonly used methods to find optimal cut points for each diabetes diagnostic variable. Statistical methods are the best method used to describe population characteristics [16]. Kianpour et al. [14], Meng et al. [16], Nomura et al. [25], and Katulanda et al. [22] analyzed the characteristics of American, Korean, Iranian, Sri Lankan, and Sweden populations for diabetes screening. Using logistic regression, Kianpour et al. [14], Meng et al. [16], Nomura et al. [25], and Katulanda et al. [22] revealed the significance of associations (assessed by OR, CI, and *p*-value) to see the association between risk factors and diabetes and kidney disease. To classify diabetes, FPG, HbA1c, and OGTT were utilized by Meng et al. [16], Nomura et al. [25], and Katulanda et al. [22] as diagnostic measures, while Kianpour et al. [14] utilized CBG and HbA1c as diagnostic measures for diabetes classification. The results showed that FPG, HbA1C, and OGTT are precise diagnostic measures used to predict diabetes. In revealing the optimal cut point which could improve the performance of diabetes prediction models, Meng et al. [16], Zafari et al. [40], Baek et al. [41], Xu et al. [42], and Schisterman et al. [43] applied the Youden index. Wu et al. [44] analyzed the diabetes scores in the Chinese population and found that by using the optimal cut point of FPG, the sensitivity increased by around 0.25%, and the specificity decreased by around 6% with an AUC of 0.93. Cai et al. [45] predicted diabetes based on the optimal cut point of nomogram in the Japanese (NAFLD) population. The results showed that the sensitivity was 77.49% and specificity was 72.36%, with an AUC of 0.811.

To strengthen the analysis of the diabetes prediction model, aside from statistical methods, analyzing the diabetes prediction model utilizing machine learning methods may become another considered solution. This method has been widely used for the classification and prediction of diabetes [40]. Numerous previous studies have developed and analyzed diabetes prediction models utilizing machine learning methods such as multilayer perceptron (MLP) [46–48], logistic regression (LR) [16,49–52], K-neural networks (K-NN) [52–54], decision tree (DT) [55–58], Naïve Bayes (NB) [59–63], random forest (RF) [64–69], and extreme gradient boosting (XGB) [69–72]. Mohapatra et al. [47], Butt et al. [48], and Bani-Salameh et al. [52] utilized a machine learning-based approach for the classification, early-stage identification, and prediction of diabetes. The result of the analysis revealed that MLP outperforms other classifiers in predicting diabetes with an accuracy of 77% to 86%. Rajendra and Latifi [50] developed a diabetes prediction model utilizing LR combined with the ensemble technique—Max-voting and stacking. On the US-PIMA Indian diabetes dataset, the accuracy obtained was around 78% and on Vanderbilt diabetes dataset the accuracy obtained was 93%. In line with Rajendra and Latifi [50], Joshi et al. [51] revealed that the LR-based diabetes prediction model could predict type 2 diabetes for US-PIMA Indian diabetes dataset by up to 78.26%. Diabetes prediction using K-NN also showed good performance applied in US-PIMA Indian diabetes dataset which is conducted by Premamayudu et al. [54] and Sarker et al. [55]. The accuracy achieved 79% and the ROC achieved around 73%. Diabetes prediction based on decision tree and Naïve Bayes looked promising. To the results conducted by Posonia et al. [56] and Dwivedi et al. [58], the accuracy of the diabetes prediction model based on the decision tree model reached 95.8% and 91,2%, respectively. While the diabetes prediction model utilizing Naïve Bayes achieved 92% [57] and 89.9% [61]. Wang et al. [67] utilized random forest combined with SVM-SMOTE and two feature dimensionality reduction methods (logistic stepwise regression and LAASO) to classify the diabetes survey sample data with unbalanced categories and complex related factors. The results showed that the AUC improved by up to 94.80%. Finally, Li et al. [71] and Wang et al. [73] evaluated the prediction of type 2 diabetes risk and its effect on the XGBoost model. The results showed that the accuracy for [71] and [73] reached 81.20% and 89.09%, respectively. All the previous studies have proved that statistical and machine learning methods could be used for analyzing

and predicting diabetes and its risk; therefore, in this study, we utilized both methods in analyzing and predicting the risk of diabetes.

3. Materials and Methods

3.1. Study Populations and Data Sources

In this study, all the study population and data sources were obtained from public diabetes and COVID-19 datasets. We evaluated and compared diabetes screening scores in China, Japan, Korea, the United States, and India, and then analyzed the interrelationship between diabetes and COVID-19 in Korean populations. The detailed study populations and data sources in this study are as follows.

The first study population and data source are from the Rich Healthcare Group in China, which included all medical records for participants who received a health check from 2010 to 2016 [73]. The total number of participants recruited for the study was 211,833, which consisted of 116,123 males and 95,710 females from Shanghai, Beijing, Nanjing, Suzhou, Shenzhen, Changzhou, Chengdu, Guangzhou, Hefei, Wuhan, and Nantong, aged from 20 to 99 years old.

The second study population and data source are from NAFLD in the Gifu Area, Longitudinal Analysis (NAGALA) data, which was based on a population-based longitudinal analysis of a medical examination program at Murakami Memorial Hospital (Gifu, Japan) [74]. The total number of participants was 15,464, ranging from 22 to 70 years old in Gifu, Japan.

The third study population and data source are from the National Health Insurance Sharing Services (NHISS) of Korea, which included all medical records of participants who received a health examination from 2013 to 2014 [6,75]. The participants recruited for the study were aged 20 years old or older, and came from 16 cities and provinces in Korea. The dataset consisted of 43,0335 males and 40,6839 females, which is 83,7174 participants in total.

The fourth study population and data source are from the National Institute of Diabetes and Digestive and Kidney Diseases, United States of America (USA) [76]. All the participants were Pima-Indian women, at least 21 years old and living near Phoenix, Arizona, in the USA. The total number of participants was 768, of which 500 tested negative and 267 tested positive for diabetes.

The fifth study population and data source are from random hospital records in Trinidad, located in the Caribbean [77,78]. The study consists of 121 participants (84 males and 75 females), which consist of 62% of East Indian ethnicity, 28% of African ethnicity, and 10% of mixed ethnicity. There are two groups in this study; the first group is the non-diabetes group (n = 50), and the second group is the diabetes group (n = 71).

The last study population and data source used in this study are from the Korean Center for Disease Control and Prevention (KCDC) COVID-19 dataset [79] which was collected from February to June 2020. The participants recruited for the study ranged from 10 to 70 years of age and came from 16 cities and provinces in Korea. The total number of participants was 5165. Due to missing values, the total number of participants became 3496, which consists of 1604 males and 1892 females. Using this data from the KCDC, COVID-19 cases in Korea could be identified. We followed the procedures from previous studies [80,81] in collecting the sample, conducting the experiment, and identifying it. We used the 3496 patients with COVID-19 diagnoses as the case group. A control group of COVID-19 patients was chosen using stratified random sampling. Based on gender and age (0–9, 10–19, 20–29, 30–39, 40–49, 50–59, 60–69, 70–79, and 80 or more), we used 1:5 matching to choose the control group, which is from the NHISS Korea diabetes dataset. A total of 17,480 subjects were chosen to make up the control group, and the final subject count was 20,976.

3.2. Proposed Study Design

This section explains the proposed study. The proposed study includes five primary goals, which are displayed in Figure 1. To accomplish those goals, we first collected

the diabetes data, which are openly accessible and originate from many nations and ethnic groups, to be used as research samples. Once diabetes data were collected, the population characteristics were analyzed to summarize nationally representative samples. The summary of population characteristics was conducted by using descriptive statistics by measuring the mean and standard error. Furthermore, for the second goal, the diabetes risk factors of all national diabetes data were assessed. We used logistic regression to assess the diabetes risk factors and significant associations by measuring the OR, CI, and *p*-values. We assessed the risk factors of diabetes based on the World Health Organization (WHO) [82,83] and the Centers for Disease Control and Prevention (CDC) of the United States [84] guidelines, where the risk factors consisted of age, gender, BMI, hypertension, cholesterol, triglycerides, smoking, alcohol, physical activity or exercise, and family history of diabetes. To evaluate the association between risk factors and diabetes, the chi-squared test was employed; thus, the diabetes risk factors could be revealed [14,16,85]. Aside from looking into diabetes risk factors, this study looked into the relationship between risk factors and COVID-19, as well as the interrelationship between diabetes and COVID-19 [80,81], utilizing the Korean COVID-19 dataset. For the prediction of diabetes, the proposed study involves two methods. The first prediction method used is the logistic regression-based statistical method. The performance of diabetes and non-diabetes scores using the LR-based statistical method was then measured through the sensitivity, specificity, PPV, and NPV based on diagnostic characteristic cut points for the high-risk group, as well as measured through the AUC and ROC curve for the prediction measure. The Youden index-based cut points were utilized to reveal the optimal cut points used to classify high-risk groups, which were then compared with the results based on ADA and WHO diagnostic characteristic cut point recommendations. Finally, we used machine learning-based prediction methods, such as MLP, LR, KNN, DT, NB, RF, and XGB, combined with a 10-fold cross-validation technique to predict diabetes. All classifiers were subject to the 10-fold cross-validation, with the dataset divided into 10 equal parts. Nine of the portions were utilized for training, and the final portion was utilized for testing. We repeated that process 10 times while rotating the test set. Then, depending on the outcomes across iterations, we chose the performance metrics (precision, recall, f1, and accuracy) in the final phase. The performance of the prediction models across all those employed in this study was then evaluated.

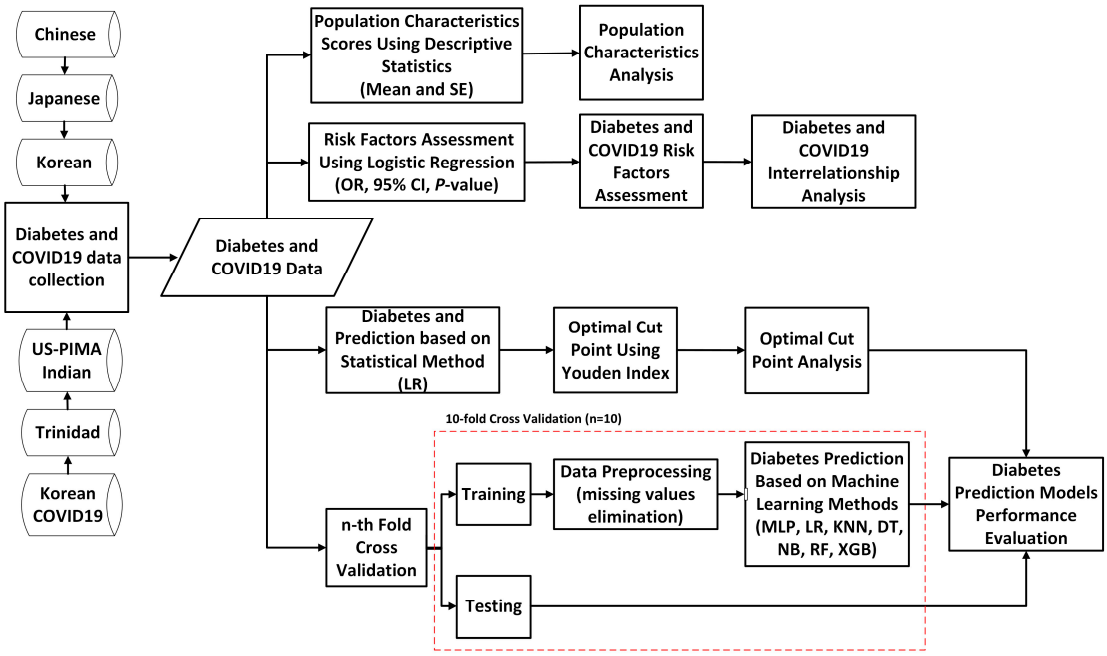


Figure 1. A flowchart of the proposed study design.

3.3. Chi-Squared Test of Association

Using the Statistical Package for the Social Sciences (SPSS) version 25.0, a chi-squared test was utilized in this study to compare the categorical characteristics between the risk factors and diabetes for all population samples. The chi-squared test is a significant statistic and hypothesis testing method to examine independence across two categorical variables or to assess how well a sample fits the distribution of a known population (goodness of fit) [86,87]. The formula for calculating a chi-squared is as follows:

$$x^2 = \sum_{i=1}^{n} \frac{(O_i - E_i)^2}{E_i} \tag{1}$$

where x^2 is chi-squared value, n represents the number of cells, O_i is the observed value, and E_i is expected value. A low value for chi-square represents a high correlation between two categorical variables (sets of data), while a large chi-squared value indicates there is no statistically significant difference between two categorical variables.

3.4. Model Evaluation

We used a confusion matrix to determine the performance of the statistical method-based and machine learning-based prediction models for diabetes. In this study, "diabetes" was defined as a positive event and "non-diabetes" was defined as a negative event. The confusion matrix for two classes was used to extract true positives (TP), true negatives (TN), false positives (FP), and false negatives (FN).

To measure the performance of the statistical method-based prediction model, we used sensitivity, specificity, PPV, NPV, and AUC, while for machine learning-based prediction models, we used accuracy, precision, recall, f1, and AUC. The performance of the classifier can be structured, arranged, and selected using a receiver operating characteristic (ROC) graph. The area under the ROC curve (AUC) measures how likely it is that the classifier would assign a randomly selected positive instance a higher score than a randomly selected negative case. The performance measurements were conducted using SPSS version 25.0 for statistical method-based prediction models, while the machine learning-based prediction models were all implemented in Python version 3.9.7 and Scikit-learn version 1.1.2.

The formulas for calculating sensitivity or recall, specificity, PPV or precision, NPV, f1, accuracy, and AUC [7,88] are as follows.

$$Sensitivity\ or\ Recall = \frac{TP}{TP + FN}, \tag{2}$$

$$Specificity = \frac{TN}{FP + TN}, \tag{3}$$

$$PPV\ or\ Precision = \frac{TP}{TP + FP}, \tag{4}$$

$$NPV = \frac{TN}{FN + TN}, \tag{5}$$

$$F1 = \frac{2 \times precision \times recall}{precision + recall}, \tag{6}$$

$$Accuracy = \frac{TP + TN}{TP + FN + FP + TN}. \tag{7}$$

4. Results and Discussions

4.1. Descriptive Statistics Analysis

As the objective of this research was to analyze as well as evaluate the performance of diabetes screening scores for various diabetes datasets from several countries, we gathered five diabetes datasets from populations of China, Japan, Korea, the US-Indian, and

Trinidad. To analyze the sample of China, Japan, Korea, the US-PIMA Indian, and Trinidad populations, descriptive statistics based on intricate survey designs, such as mean with standard error and percentage, were used. In this study, we examined the demographic and health statistics of the nation, including mean age, gender, health conditions, lifestyle habits, and test results from medical examinations. Design feature weights and clusters were taken into consideration to accurately depict the population's overall health statistics. We conducted the statistical analyses by following the analyses guidelines of the National Health and Nutrition Examination Survey (NHANES), as well as following previous studies [14–16,89–91].

The characteristics of the adult populations in China, Japan, Korea, the US-PIMA Indian, and Trinidad are displayed in Table 1. The number of populations is 211,833, 15,464, 837,174, 768, and 121, respectively. There are only three datasets with age and gender variables included among the five diabetes datasets included in this investigation. These datasets come from China, Japan, and US-PIMA Indian for age, and China, Japan, and Korea for gender. As shown in Table 1, the mean ages of the Chinese and Japanese populations are not significantly different, with the mean ages being 42.1 and 43.7. However, the US-PIMA Indian adult population is seen to have a much lower mean age compared to the Chinese and Japanese populations, with a mean age of 33.25 years. Something interesting was revealed by the BMI information. While the US-PIMA Indian has the lowest mean age, it has the highest mean BMI, followed by Trinidad with the obesity ($30 \leq$ BMI < 40) percentage of 48.70 and 30.58, respectively. Another interesting finding comes from the Trinidadian population. The mean SBP is seen as the highest among other countries' populations, with a mean SBP of 145.12. This indicates that the Trinidadian population is categorized as having high blood pressure or hypertension according to WHO hypertension control guidelines [92]. On the other hand, the mean DBP is regarded as normal (DBP < 90 mmHg). In terms of related outcomes, the Trinidadian population scored the highest FPG (126.24), which indicates the presence of diabetes due to the level of FPG being greater than 125 mg/dL [36]. The HbA1c and OGTT test results are normal (HbA1c < 6.6% and 2hPG < 155 mg/dL) [36] in the Japanese and US-PIMA Indian populations. Not only in the FPG test result but the mean triglyceride was also recorded as high for the Trinidadian population compared to other national populations with a mean triglyceride score greater than 150 mg/dL. This high score is also followed by an LDL level where the mean is greater than 100 mg/dL. In contrast, the mean HDL is seen to be in the normal range. For ALT and AST tests conducted on Chinese and Japanese populations, the results reveal that there was no abnormality detected. Based on laboratory tests to determine whether diabetes is present, the prevalence of diabetes in the Chinese, Japanese, Korean, US-PIMA Indian, and Trinidadian populations were 1.97%, 2.41%, 11.53%, 34.90%, and 58.68%, respectively. The Trinidad diabetes result was recorded as the highest among other nations.

Table 1. Characteristics of the population representing China, Japan, Korea, US-PIMA Indian, and Trinidad.

Characteristic	China Population (n = 211,833)	Japan Population (n = 15,464)	Korea Population (n = 837,174)	US-PIMA Indian Population (n = 768)	Trinidad Population (n = 121)
Age, year	42.1 ± 0.027	43.71 ± 0.072	43.19 ± 0.018	33.25 ± 0.424	-
Male/Female, %	54.82/45.18	45.49/54.51	57.40/42.60	-	-
BMI, kg/m^2	23.24 ± 0.007	22.12 ± 0.025	23.59 ± 0.0036	31.99 ± 0.284	29.18 ± 0.70
Obesity Status, % (WHO/Asia Criteria)					
- BMI < 25/BMI < 23	71.28/49.60	83.68/65.08	68.91/44.91	15.23/7.94	25.62/11.57
- 25 ≤ BMI < 30/23 ≤ BMI < 27.5	25.47/39.64	14.60/29.46	27.33/43.56	23.31/17.97	38.02/33.88
- 30 ≤ BMI < 40/27.5 ≤ BMI < 35	3.23/10.52	1.71/5.30	3.75/11.18	48.70/41.80	30.58/43.80
- BMI ≥ 40/BMI ≥ 35	0.02/0.24	0.01/0.16	0.01/0.35	12.76/32.29	5.79/10.74

Table 1. *Cont.*

Characteristic	China Population (n = 211,833)	Japan Population (n = 15,464)	Korea Population (n = 837,174)	US-PIMA Indian Population (n = 768)	Trinidad Population (n = 121)
SBP/	119.06 ± 0.04/	114.50 ± 0.12/	120.18 ± 0.02/	-/	145.12 ± 1.94/
DBP, mmHg	74.18 ± 0.02	71.58 ± 0.08	74.96 ± 0.01	79.11 ± 0.70	87.24 ± 0.98
Family history of diabetes, %	2.05	-	-	-	-
Exercise, %	-	17.52	-	-	-
Current smoker, %	28.43	41.60	-	-	-
Alcohol intake, %	28.43	23.66	-	-	-
Outcomes-related					
- Fasting Plasma Glucose (FPG), mg/dL	88.47 ± 0.02	-	98.71 ± 0.03	-	126.24 ± 5.19
- Hemoglobin HbA1c,%	-	5.17 ± 0.003	-	-	-
- 2-h plasma glucose (2hPG), mg/dL	-	92.97 ± 0.06	-	120.89 ± 1.15	-
	82.78 ± 0.04	198.20 ± 0.27	-	-	191.09 ± 4.38
- Cholesterol, mg/dL	23.55 ± 0.04	80.79 ± 0.47	-	-	157.46 ± 9.30
- Triglyceride, mg/dL	24.70 ± 0.02	56.54 ± 0.13	-	-	47.08 ± 1.19
- HDL, mg/dL	49.83 ± 0.04	-	-	-	111.73 ± 4.00
- LDL, mg/dL	23.95 ± 0.05	19.99 ± 012	-	-	-
- ALT, U/L	24.08 ± 0.04	18.40 ± 0.07	-	-	-
- AST, U/L	1.97	2.41	11.53	34.90	58.68
Diabetes based on lab tests, %					

4.2. Diabetes Risk Factors and Significant Analysis

A second analysis was conducted in this study to assess the diabetes risk factors and significant associations based on OR, CI, and p-value. According to the diabetes guidelines of WHO [82,83] and the Centers for Disease Control and Prevention (CDC) of the United States [84], the risk factors of diabetes consist of age, gender, BMI, hypertension, cholesterol, triglycerides, smoking, alcohol, physical activity or exercise, and family history of diabetes. We defined diabetes risk factors using WHO and CDC guidelines and assessed their statistical significance of associations by calculating the odds ratio (OR), 95% confidence interval (CI), and p-value as described in [14,16,93,94]. Table 2 shows the OR, CI, and p-value of diabetes risk factors in a Chinese population sample. High OR scores are shown for ages over 45 years and BMI equal to or greater than 27.5 kg/m^2. The scores showed that individuals older than 45 years have an 11.18-fold greater risk of having diabetes and individuals with a BMI equal to or greater than 27.5 kg/m^2 have a 9.56-fold greater risk of having diabetes compared to normal individuals. A 2.91-fold and 3.83-fold greater risk of having diabetes are shown when the individual is 35–44 years of age and has a BMI of 23–27.4 kg/m^2. Other risk factors, such as gender, cholesterol, and family history, were found to have a two times greater association with diabetes, whereas triglycerides, smoking, and alcohol had no strong association with OR scores less than 1. However, even though OR scores vary, all p-values of the risk factor are significant (p-values < 0.001). These scores indicate that age, gender, BMI, hypertension, cholesterol, triglycerides, smoking, alcohol, and family history of diabetes are strongly correlated with diabetes.

Table 2. Chinese adults' diabetes score in the Chinese diabetes dataset (4174 diabetes cases, n = 211,833, AUC = 0.97).

Diabetes Risk Factors	OR (95% CI)	p-Value
Age, year		
35–44	2.91 (2.54–3.34)	<0.001
≥45	11.18 (9.92–12.59)	<0.001
Male, %	2.14 (2.00–2.29)	<0.001
BMI, kg/m^2 (Asia criteria)		
23–27.4	3.83 (3.51–4.17)	<0.001
≥27.5	9.56 (8.72–10.49)	<0.001
Hypertension (based on SBP/DBP)	3.16 (2.96–3.37)	<0.001
Cholesterol, mg/dL	1.99 (1.87–2.12)	<0.001
Triglyceride, mg/dL	0.99 (0.24–4.02)	<0.001
Smoking	0.98 (0.92–1.05)	<0.001
Alcohol	0.98 (0.92–1.05)	<0.001
Family history of diabetes	2.08 (1.78–2.43)	<0.001

Similar to the Chinese population's diabetes scores, the diabetes risk factors in the Japanese population are also shown to have a strong correlation with diabetes. As displayed in Table 3, high scores of OR are shown for ages over 45 years and BMI equal to or greater than 27.5 kg/m^2 with a score of 4.53 and 8.78, respectively. Those scores indicate that individuals older than 45 years of age have a 4.53-fold greater risk of having diabetes and individuals with a BMI equal to or greater than 27.5 kg/m^2 have an 8.78-fold greater risk of having diabetes compared to normal individuals. The striking difference is shown by triglyceride. While triglycerides are shown to not have a strong correlation with diabetes in a Chinese population sample, in a Japanese population sample, it shows a strong correlation with an OR score of 5.10. There were different findings in the relationship between age (between 35 and 44 years) and diabetes and also alcohol intake with diabetes. In a Japanese population sample, diabetes was not affected by age between 35 and 44 years, nor by alcohol, where *p*-values showed 0.230 and 0.534, respectively. The detailed scores of OR, CI, and *p*-value of diabetes risk factors in the Japanese population sample are displayed in Table 3.

Table 3. Japanese adults' diabetes score in the Japanese diabetes dataset (373 diabetes cases, *n* = 15,464, AUC = 0.80).

Diabetes Risk Factors	OR (95% CI)	*p*-Value
Age, year		
35–44	2.65 (1.50–2.58)	0.230
≥45	4.53 (2.58–7.95)	<0.001
Male, %	2.80 (2.20–3.57)	<0.001
BMI, kg/m^2 (Asia criteria)		
23–27.4	2.97 (2.35–3.76)	<0.001
≥27.5	8.78 (6.59–11.68)	<0.001
Hypertension (based on SBP/DBP)	2.81 (2.23–3.53)	<0.001
Cholesterol, mg/dL	1.94 (1.57–2.40)	<0.001
Triglyceride, mg/dL	5.10 (2.07–3.16)	<0.001
Smoking	2.25 (1.82–2.78)	<0.001
Alcohol	1.31 (1.04–1.64)	0.534
Exercise	0.74 (0.55–1.00)	<0.001

Unlike the Chinese and Japanese diabetes datasets, the Korean diabetes dataset (NHIS), US-PIMA Indian, and Trinidadian diabetes datasets only consist of less than five risk factors or predictor attributes (see Tables 4–6). In the Korean population, four risk factors (e.g., gender, age, BMI, and hypertension) were used to evaluate the diabetes scores. As presented in Table 4, the gender results revealed that males and females are equally likely to have a risk of diabetes (OR = 1.11, *p*-value < 0.001). It is very surprising when age is used as the risk factor for diabetes in the Korean population. Individuals aged 45 years old or older have a 24 times higher risk of diabetes, which is more than 2 times higher than China and 6 times higher than Japan. According to OR scores for BMI, individuals with a BMI of between 23 to 27.4 kg/m^2 and a BMI of 27.5 or higher have a two-fold and three-fold higher risk of diabetes than people with a normal BMI, with OR scores are 2.01 (*p*-value < 0.001) and 3.04 (*p*-value < 0.001), respectively. While the Chinese and Japanese populations with hypertension are around three times more likely to develop diabetes, the Korean adult population has a lower score at risk of diabetes with an OR score of 1.98 (*p*-value < 0.001). Interesting findings are shown on OR score age.

Table 4. Korean adults' diabetes Score in the Korean diabetes dataset (96,512 diabetes cases, *n* = 837,174, AUC = 0.85).

Diabetes Risk Factors	OR (95% CI)	*p*-Value
Male, %	1.11 (1.10–1.13)	<0.001
Age, year		
35–44	4.33 (4.16–4.51)	<0.001
≥45	24.11 (23.28–24.96)	<0.001
BMI, kg/m^2 (Asia criteria)		
23–27.4	2.01 (1.98–2.04)	<0.001
≥27.5	3.04 (2.98–3.10)	<0.001
Hypertension (based on SBP/DBP)	1.98 (1.95–2.01)	<0.001

Table 5. US-PIMA Indian adults' diabetes score in the US-PIMA Indian diabetes dataset (268 diabetes cases, n = 768, AUC = 0.79).

Diabetes Risk Factors	OR (95% CI)	p-Value
Age, year		
35–44	3.08 (2.10–4.51)	<0.001
≥45	2.83 (1.91–4.20)	<0.001
BMI, kg/m^2 (WHO criteria)		
25–30	3.45 (1.61–7.43)	0.350
≥30	10.32 (5.10–20.87)	<0.001
Hypertension (based on DBP)	1.69 (1.22–2.35)	0.678

Table 6. Trinidadian adults' diabetes score in the Trinidadian diabetes dataset (71 diabetes cases, n = 121, AUC= 0.905).

Diabetes Risk Factors	OR (95% CI)	p-Value
BMI, kg/m^2 (WHO criteria)		
25–30	1.80 (0.72–4.52)	0.410
≥30	3.69 (1.39–9.78)	0.432
Hypertension (based on SBP/DBP)	1.99 (0.95–4.16)	0.485
Cholesterol, mg/dL	1.04 (0.50–2.17)	0.691
Triglycerides, mg/dL	1.78 (0.84–3.77)	0.601

While the Chinese, Japanese, and Korean adults aged 45 years or older showed a higher possibility of being at risk of diabetes compared to individuals with an age between 35 and 44 years old, the US-PIMA Indian population showed a lower possibility of being at risk of diabetes, with an OR score for individuals aged 45 or older of 2.83 (p-value < 0.001) and 3.08 (p-value < 0.001) for individuals aged between 35 and 44. Surprisingly, the OR score for BMI equal to 30 or higher, leading all nations, showed that individuals with a BMI of equal to 30 or higher have a 10-fold greater risk of having diabetes than normal BMI individuals. However, the possibility of having diabetes for individuals with a BMI of between 25 and 30 kg/m^2 is almost similar among Chinese, Japanese, and Korean adults (OR score = 3.45). For hypertension, the OR score is 1.68, which indicates a low risk of diabetes for individuals with hypertension compared to individuals with normal blood pressure. Even though US-PIMA Indian adults have the highest OR score for BMI among other nations and the overall sample, it showed the lowest OR score for hypertension. The p-values also showed that diabetes is not affected by hypertension or a BMI of between 25 to 30 kg/m^2, which are 0.678 and 0.350, respectively. The detailed scores of OR, 95% CI, and p-value of diabetes risk factors in the US-PIMA Indian population sample are displayed in Table 5. Finally, the diabetes score of the Trinidadian population showed an OR score of 1.80 for a BMI of between 25 and 30 kg/m^2 and 3.69 for a BMI of 30 kg/m^2 or higher. The results also showed that hypertension, cholesterol, and triglyceride did not affect the diabetes risk where the OR scores were 1.99, 1.04, and 1.78, respectively. Based on the results of the p-values shown in Table 6, none of the risk factors (e.g., BMI, hypertension, cholesterol, triglyceride) of the Trinidadian population have a significant association with diabetes (p-values > 0.05), which means that diabetes could not be affected by those risk factors.

Table 7 shows the COVID-19 scores in the Korean population based on the occurrence of diabetes. According to the results when age is used as a predictor of being at risk of COVID-19, subjects with diabetes aged younger than 20 years old has the highest risk of being infected, which is 8.69 times higher (OR, 8.69; 95% CI, 2.53–29.91) than subjects without diabetes in the same age. Subjects aged 60 to 69 years old with diabetes also have a high risk of COVID-19 compared to normal subjects of the same age (OR, 5.18; 95% CI, 4.10–6.55). While sex is used as a predictor for COVID-19 among subjects with diabetes,

males and females with diabetes have a slightly higher risk of COVID-19 compared to normal 1.16 times risk of COVID-19 diabetes (OR, 1.16; 95% CI, 1.20–1.33 for male and OR, 1.28; 95% CI, 1.12–1.47 for female). Furthermore, while all the subjects with diabetes compared to the subjects without diabetes, the adjusted OR showed a slightly higher possibility of being at risk of COVID-19, with the adjusted OR score being 1.21 (95% CI, 1.10–1.34). These findings were in accordance with previous studies [80,81], with the adjusted OR scores not much different from one to another. In this study, we found that all the diabetes-COVID19 scores showed statistically significant (p-value < 0.001), whereas the same finding within [81] even though using a different dataset. Thus, it indicates that age, gender, and diabetes are associated with and related to COVID-19 in the Korean population.

Table 7. Korean diabetes COVID-19 scores in the KCDC COVID-19 dataset (3496 COVID-19 cases, n = 20,976, AUC= 0.52).

Risk Factors	OR (95% CI)	p-Value
Age, year		
<20	8.69 (2.53–29.91)	<0.001
20–29	2.76 (1.26–6.03)	<0.001
30–39	2.43 (1.57–3.75)	<0.001
40–49	1.27 (0.93–1.74)	<0.001
50–59	1.33 (1.08–1.66)	<0.001
60–69	5.18 (4.10–6.55)	<0.001
≥70	3.62 (2.71–4.83)	<0.001
Gender		
Male	1.16 (1.20–1.33)	<0.001
Female	1.28 (1.12–1.47)	<0.001
Diabetes	1.21 (1.10–1.34)	<0.001

As presented in Table 8, screening for diabetes was conducted based on FPG/FBG/FBS, HbA1C, and 2-h plasma glucose (2hPG) as diagnostic measures. The optimal Youden index values were used as cut points for diagnosis of diabetes, measuring sensitivity, specificity, positive predictive value (PPV), negative predictive value (NPV), likelihood ratio positive (LR+), likelihood ratio negative (LR−), area under the curve (AUC), and receiver operating characteristic (ROC) curve [14,16,93,94]. In the five models, the results showed sensitivity from 46.26% to 85.31%, specificity from 74.20% to 100%, PPV from 7.97% to 100%, and NPV from 67.12% to 99.37%. For prediction measured by AUC, the results showed that the models on Chinese, Japanese, Korean, US-PIMA Indian, and Trinidadian adult population samples performed robust measures with an AUC of 0.97, 0.80 (based on FPG), and 0.78 (based on HbA1c), 0.85, 0.79, and 0.905, respectively.

Table 8. Performance of diabetes score in the Chinese, Japanese, Korean, US-PIMA Indian, and Trinidadian adult populations.

Model Population	**Chinese**	**Japanese**		**Korean**	**US-PIMA Indian**	**Trinidadian**
Diagnostic Test	**FPG**	**FPG**	**HbA1C**	**FBS**	**2hPG**	**FBG**
Cut point as recommended by ADA and WHO	≥7 mmol/L	≥5.6 mmol/L	≥5.7%	≥126 mg/dL	≥140 mg/dL	≥126 mg/dL
Optimal cut point	6.205	5.523	5.375	105.50–106.50	123.50	107.50
Percentage of high risk, ADA and WHO/optimal cut points (%)	1.96/4.09	16.94/20.37	6.38/32.13	7.47/20.70	25.65/41.93	35.59/50.85
Sensitivity, ADA, and WHO/optimal cut points (%)	81.93/88.95	61.66/67.29	36.19/76.26	46.26/72.69	50.37/70.15	65.22/81.16
Specificity, ADA, and WHO/optimal cut points (%)	100/97.44	84.16/80.79	94.35/68.91	97.59/86.07	87.60/73.20	100/91.84
PPV, ADA, and WHO/optimal cut points (%)	100/41.07	8.78/7.97	13.68/5.57	71.41/40.48	68.53/58.39	100/93.33
NPV, ADA, and WHO/optimal cut points (%)	99.64/99.77	98.89/99.01	98.36/99.09	93.31/96.03	76.71/82.06	67.12/77.59
LR+, ADA, and WHO/optimal cut points	~/34.75	3.89/3.50	6.41/2.39	19.17/5.22	4.06/2.62	~/9.942

Table 8. *Cont.*

Model Population	Chinese	Japanese		Korean	US-PIMA Indian	Trinidadian
Diagnostic Test	**FPG**	**FPG**	**HbA1C**	**FBS**	**2hPG**	**FBG**
LR−, ADA, and WHO/optimal cut points	0.18/0.11	0.46/0.40	0.68/0.37	0.55/0.32	0.57/0.41	0.35/0.205
Youden index, ADA, and WHO/optimal cut points (%)	81.92/86.39	45.82/48.08	30.55/43.17	43.85/58.76	37.97/43.35	65.22/73.00
AUC	0.97	0.80	0.78	0.85	0.79	0.905
SE	0.002	0.012	0.013	0.001	0.017	0.028
95% CI	0.965–0.972	0.782–0.828	0.752–0.804	0.847–0.850	0.755–0.822	0.850–0.960
p-value	<0.001	<0.001	<0.001	<0.001	<0.001	<0.001

In the Chinese adult population, the optimal cut point of FPG was found to be 6.205 mmol/L with a Youden index of 86.39% (see Table 8). As shown in Figure 2, by using the optimal cut point, the sensitivity increases, and the specificity decreases from 81.93% to 88.95% and 100% to 97.44%, respectively. The increment of sensitivity represents 7.02% of new population samples with a high risk of developing diabetes, and the 2.56% decrement of specificity represents the healthy subjects who undertook unnecessary clinical tests (false positive) [14]. The ROC curve in Figure 3 shows that the diagnostic measure can accurately determine the optimal cut point and the model can accurately classify the Chinese adult population samples between subjects with diabetes and those without diabetes, with an AUC score of 0.97.

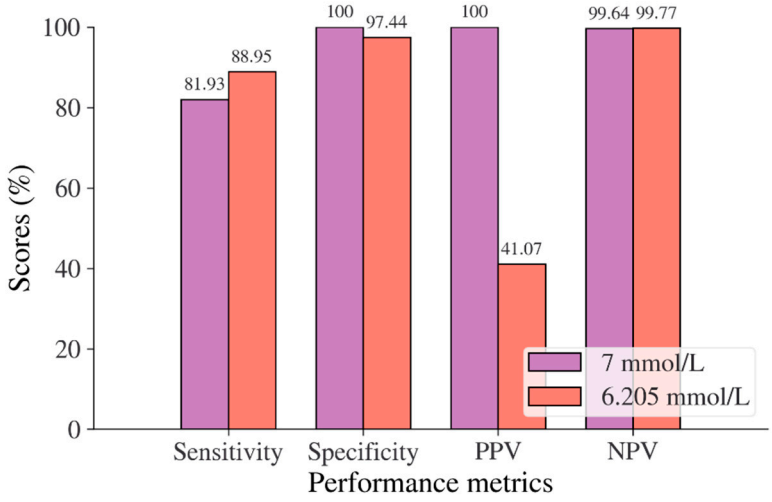


Figure 2. Sensitivity, specificity, PPV, and NPV for FPG in the Chinese adult population based on ADA and WHO cut point recommendations compared to the optimal cut point.

In this study, diabetes diagnosis (FPG 7 mmol/L, HbA1c 6.5%, and 2hPG 200 mg/dL) was not found in the Japanese and Korean adult populations. Thus, we used the cut point of pre-diabetes for diabetes diagnosis, where the cut points are 5.6 mmol/L for FPG, 5.7% for HbA1c, and 140 mg/dL for 2hPG as recommended by ADA and WHO [36,37]. According to the results of the ROC analysis, new cut points were found for diabetes screening tests based on FPG/FBG/FBS, HbA1C, and 2hPG. As displayed in Table 8, the new cut point for the Japanese adult population, which is the optimal cut point based on the Youden index [38,39,95], is 5.523 mmol/L (FPG) and 5.375% (HbA1c), with an optimal Youden index of 48.08% and 43.17%, respectively. The sensitivity and specificity of FPG and HbA1c increase and decrease by using the optimal cut point, respectively, from 61.66% to 67.29% for FPG and 36.19% to 74.26% for HbA1c, and from 84.16% to 80.79% for FPG and 94.35% to 68.91% for HbA1c (see Figure 4). The sensitivity increased by 5.63% for FPG and 38,07% for HbA1c, indicating that 5.63% and 38,08% of population samples previously

classified as healthy changed into pre-diabetes and may have a high risk of developing diabetes in the future. In contrast, a significant decrement was shown in specificity, with degradation values of FPG and HbA1c being 3.37% and 25.44%, respectively. This means that the subjects in the population sample who have negative pre-diabetes test results where they are healthy (false positive) decreased by 3.37% and 25.44%. By using an optimal cut point, as shown in Figure 5, the ROC curve showed the model can accurately classify the population samples between subjects with diabetes and those without diabetes on optimal AUC scores of 0.80 and 0.78.

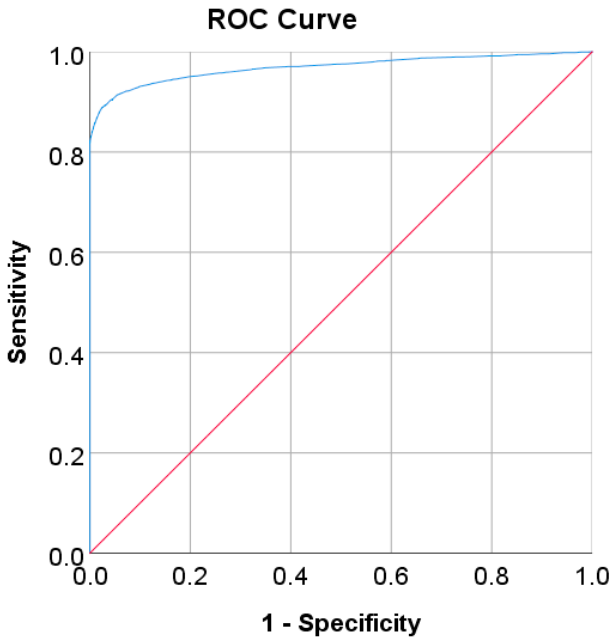
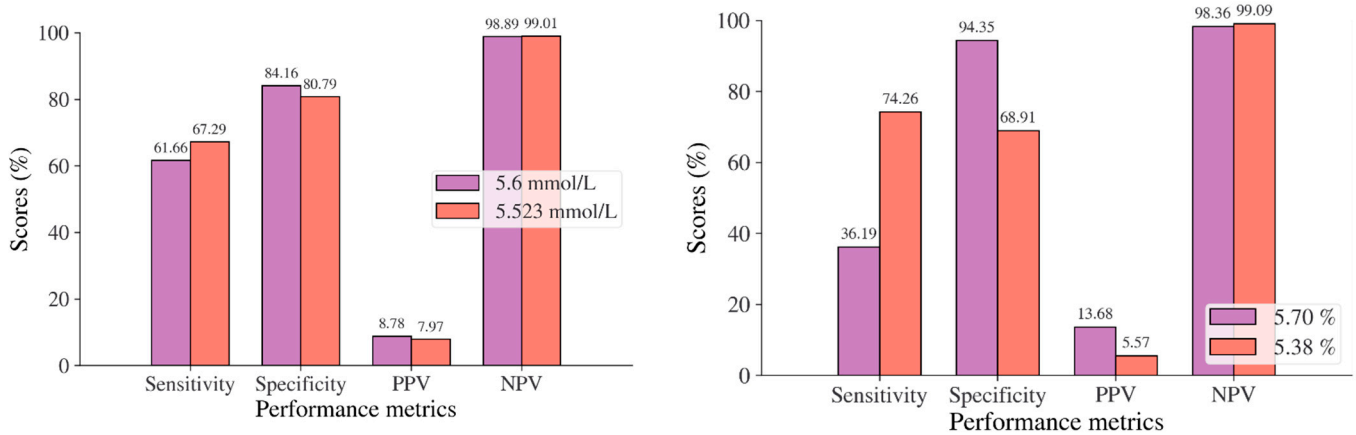
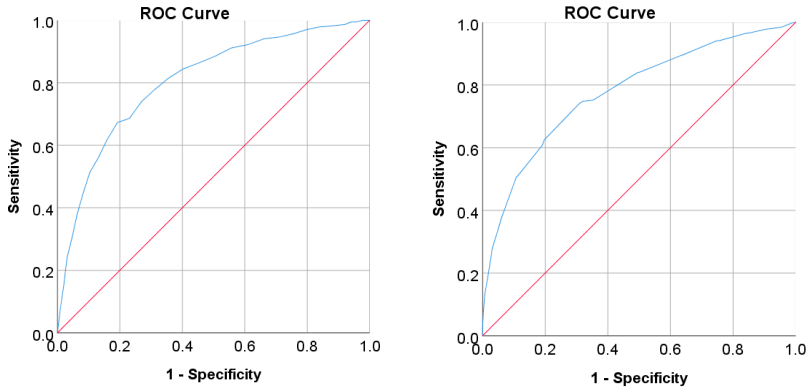


Figure 3. ROC curve for FPG values as a screening test on the Chinese diabetes dataset. FPG was used as the gold standard; the straight line represents the reference line.



(**a**) (**b**)

Figure 4. Sensitivity, specificity, PPV, and NPV for (**a**) FPG and (**b**) HbA1c in the Japanese adult population based on ADA and WHO cut point recommendations compared to the optimal cut point.



(**a**) (**b**)

Figure 5. ROC curve for (**a**) FPG and (**b**) HbA1c values as a screening test on the Japanese diabetes adult population; FPG and HbA1c were used as the gold standard; the straight line represents the reference line.

In the Korean adult population, the new cut point of FBS was found to be optimal in the range of 105.50 to 106.50 mg/dL (see Table 8), with a Youden index of 58.76%. We used 105.50 mg/dL as the FBS's new (optimal) cut point for diabetes screening in the Korean adult population. As shown in Figure 6, the result revealed that by using 105.50 mg/dL, the sensitivity of FBS improved from 46.26% to 72.69% and the specificity decreased from 97.59% to 86.07%. In the US-PIMA Indian adult population, diabetes screening was carried out using 2hPG. The new cut point was found to be optimal at 123.50 mg/dL with a Youden index of 43.35% (see Table 8), which produced an improvement in sensitivity and a decrement in specificity compared to the cut point as recommended by ADA and WHO (140 mg/dL). As presented in Figure 7, the result showed that, when the 2hPG new cut point of 123.50 mg/dL was applied to the US-PIMA Indian population, the sensitivity improved from 50.37% to 70.15% and the specificity fell from 87.50% to 73.20%. The improvement in sensitivity and the decrement in specificity were also found in the Trinidadian adult population, where a new cut point of FBG (107.50 mg/dL) was applied. As shown in Figure 8, sensitivity significantly improved from 65.22% to 81.16% and specificity fell from 100% to 92.84%. When using optimal cut points based on the maximum Youden index, the sensitivity and specificity of Korean, US-PIMA Indian, and Trinidadian adult populations increased and decreased, which represented an increment as high-risk population samples had diabetes and a decrement of healthy subjects in the populations. The ROC curves shown in Figures 9–11 show that the diagnostic measures (FBS, 2hPG, and FBG) can accurately determine optimal cut points and the model can accurately classify the population samples between subjects with diabetes and those without diabetes, with AUC scores of 0.85, 0.79, and 0.905 for the Korean, US-PIMA Indian, and Trinidadian dataset, respectively.

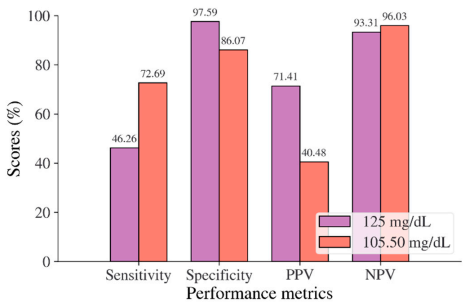


Figure 6. Sensitivity, specificity, PPV, and NPV for FBS in the Korean adult population based on ADA and WHO cut point recommendations compared to the optimal cut point.

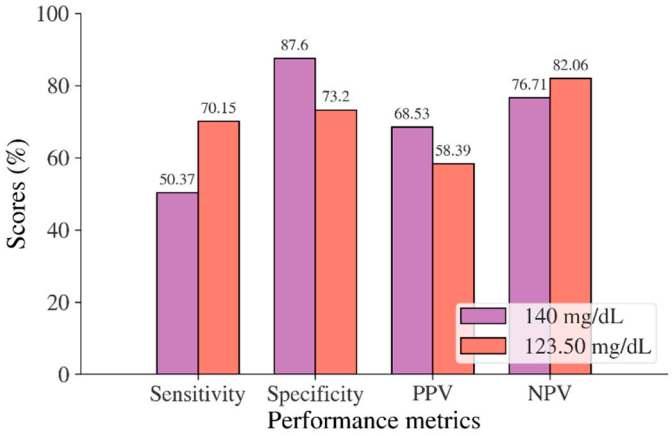


Figure 7. Sensitivity, specificity, PPV, and NPV for 2hPG in the US-PIMA Indian adult population based on ADA and WHO cut point recommendations compared to the optimal cut point.

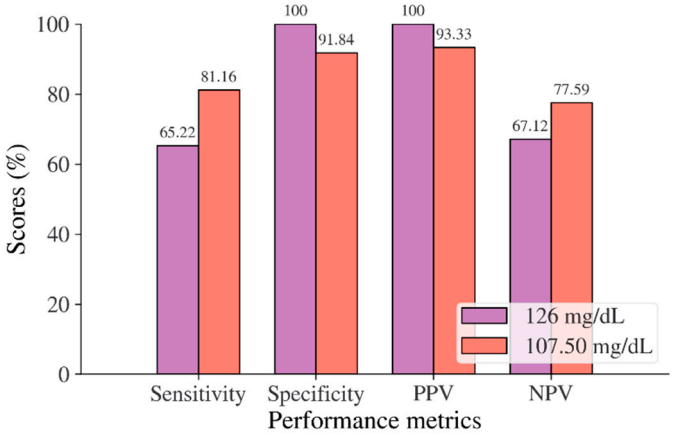


Figure 8. Sensitivity, specificity, PPV, and NPV for FBS in the Trinidadian adult population based on ADA and WHO cut point recommendations compared to the optimal cut point.

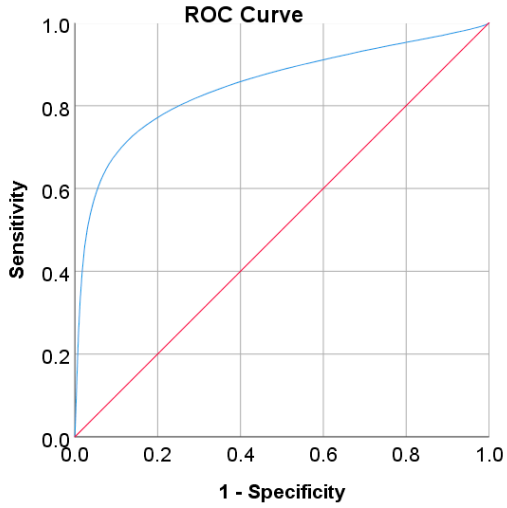


Figure 9. ROC curve for FBS values as a screening test on the Korean adult population; FBS was used as the gold standard; the straight line represents the reference line.

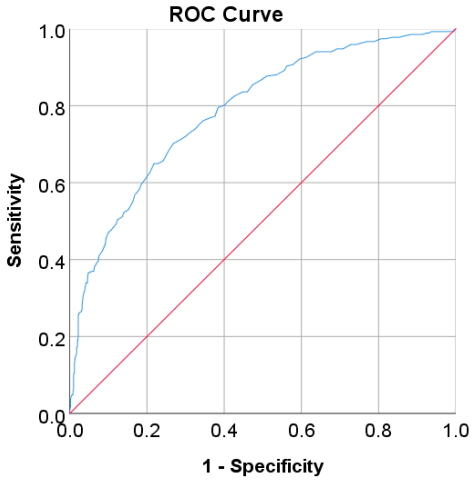


Figure 10. ROC curve for 2hPG values as a screening test on the US-PIMA Indian adult population; 2hPG was used as the gold standard; the straight line represents the reference line.

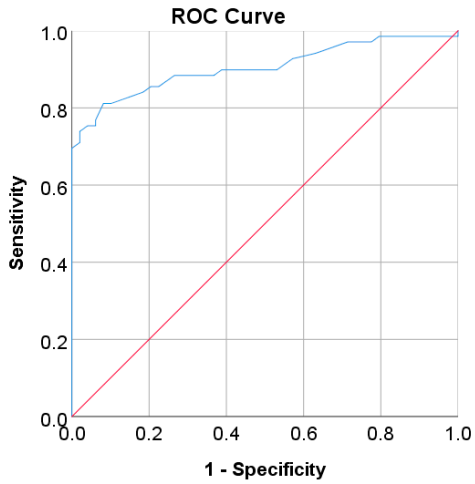


Figure 11. ROC curve for FBG values as a screening test on Trinidadian adult population; FBG was used as the gold standard; the straight line represents the reference line.

According to the results above, the sensitivity and specificity values among all population samples (Chinese, Japanese, Korean, US-PIMA Indian, and Trinidadian) increased and decreased because sensitivity and specificity are inversely related to one another [96]. Thus, as sensitivity rises, specificity falls, and vice versa. All the diagnostics measures and the models also showed good accuracy in determining optimal cut points and classifying the population samples, as proved by high AUC scores.

4.3. Diabetes Prediction Based on Machine Learning Methods

Additional analysis was also carried out in this study to evaluate the performance of the diabetes models based on machine learning methods in predicting the risk of diabetes. The performance evaluation metrics including accuracy, precision, recall, f1, and AUC were used to evaluate the models. The result in Figure 12a showed that the diabetes models on the Chinese adult population sample performed very robustly in terms of accuracy, with an accuracy of 99.37%, 98.73%, 99.15%, 95.37%, 99.59%, and 99.55% for MLP, LR, KNN, DT, NB, RF, and XGB, respectively. The best accuracy was achieved by RF, with an accuracy of 99.59%. In terms of AUC, DT reached the highest value of 0.9002. Following the diabetes models on the Chinese diabetes dataset, the diabetes models on the Japanese adult population sample also performed well in terms of accuracy (see Figure 12b), with an accuracy of 82.36%, 96.50%, 88.23%, 85.11%, 78.91%, 95.39%, and 92.65% for MLP, LR,

KNN, DT, NB, RF, and XGB, respectively. The LR performed best among other methods in terms of accuracy, and NB performed best in terms of AUC, with an AUC score of 0.7361. For the diabetes models on the Korean adult population sample (see Figure 12c), the accuracy varied from 34.65% to 91.77%. While DT, RF, and XGB showed an accuracy of less than 50%, LR and NB showed high accuracy, with accuracy rates of 89.42% and 91.77%, respectively. All the machine learning method performance was shown to be low in terms of AUC, with 0.7525 recorded as the highest achieved by NB. The accuracy and AUC scores of all diabetes models showed not much difference from one another on the US-PIMA Indian adult population sample (see Figure 12d), achieving a model's accuracy of 70.96% to 77.08% and AUC of 0.6755 to 0.7201 performed by MLP as the highest. Along with that, in the Trinidadian adult population sample (see Figure 12e), the models performed with the highest accuracy of 82.80% and AUC of 0.8289, where NB was the best performer. According to the performance evaluation results utilizing machine learning methods, the diabetes prediction model based on NB dominated as the best prediction model in the majority of performance evaluation metrics.

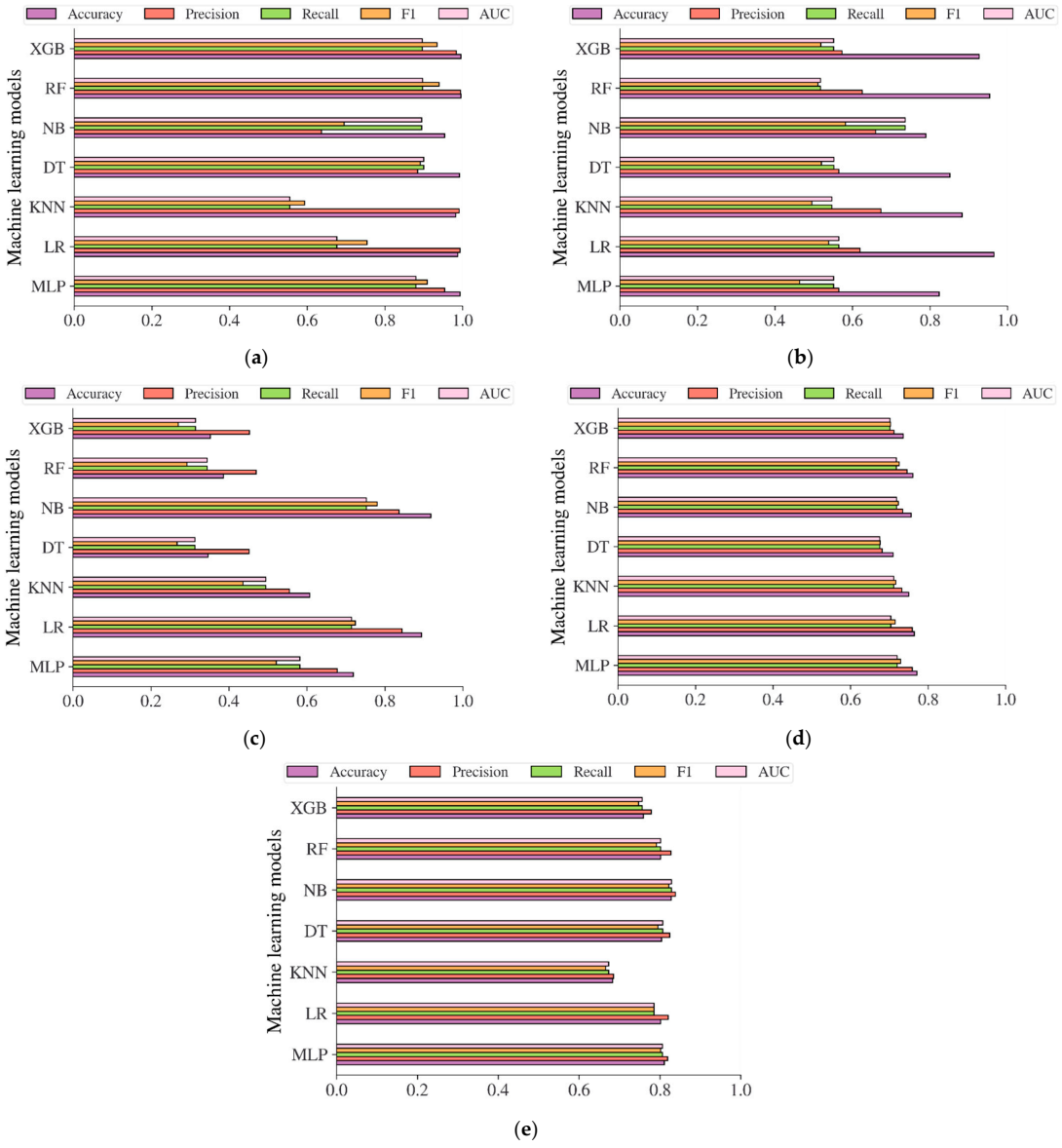


Figure 12. The results of diabetes prediction based on machine learning models on (**a**) Chinese, (**b**) Japanese, (**c**) Korean, (**d**) US-PIMA Indian, and (**e**) Trinidadian adult population samples.

4.4. Comparison with Earlier Works

We further investigated the results of our study with earlier works that utilized the same dataset. Table 9 shows the performance of the proposed study which utilized a statistical-based LR model compared to previous studies across all datasets. Due to the limited number of previous studies that utilized the same datasets, we compared our proposed study to one previous study for the Chinese, Japanese (NAFLD), Korean (NHISS), and Trinidadian datasets. Using the Chinese diabetes dataset for predicting diabetes, our proposed study, which utilized the LR model, outperformed the previous study [44] (XGBoost) with an AUC score of 0.97. While using the Japanese (NAFLD) dataset, our proposed study has the same performance as the previous study [45] that utilized the Cox regression model with an AUC score of 0.80. By using the Korean (NHISS) and US-PIMA Indian datasets, our proposed study performed better than the previous studies [6,49,52,55] with an AUC of 0.85 and 0.79, respectively. Finally, using the Trinidadian dataset, our proposed study provided significant performance compared to the previous study [85] with an AUC score of 0.905.

Table 9. Performance of proposed study as compared to earlier works for diabetes prediction in Chinese, Japanese, Korean, US-PIMA Indian, and Trinidadian datasets.

Dataset	Author	Year	Method	AUC
Chinese	Wu et al. [44]	2021	XGBoost	0.93
	Proposed study	2022	LR	0.97
Japanese (NAFLD)	Cai et al. [45]	2021	Cox regression	0.80
	Proposed study	2022	LR	0.80
Korean (NHISS)	Alfian et al. [6]	2020	DNN + RFE	0.80
	Proposed study	2022	LR	0.85
US-PIMA Indian	Sarker et al. [55]	2018	Optimal KNN	0.73
	Aiswarya and Vakula [49]	2019	LR	0.736
	Bani-Salameh et al. [52]	2021	MLP	0.77
	Proposed study	2022	LR	0.79
Trinidadian	Ramnansingh and Nayak [85]	2019	Binomial LR	0.72
	Proposed study	2022	LR	0.905

5. Conclusions

In this study, we conducted a comprehensive analysis of diabetes screening scores to investigate the nationally representative sample summaries, risk factors, optimal cut points, and prediction models. The risk factors for diabetes revealed in this study involved age equal to or older than 45 years old, being male, obesity (BMI > 27.5 kg/m^2), smoking, no exercise, and a family history of diabetes. If those risk factors are present, diabetes is very likely to occur in the subject. Using the optimal Youden index, the cut points across all the population samples were found to be optimal at 6.205 mmol/L for FPG in the Chinese adult population, 5.523 mmol/L for FPG, and 5.375% for HbA1C in the Japanese adult population, 105.50 to 106.50 mg/dL for FBS in the Korean adult population, 123.50 mg/dL for 2hPG in the US-PIMA Indian adult population, and 107.50 mg/dL for FBG in the Trinidadian adult population. By using those optimal cut points, the sensitivity and specificity of the models increased and decreased in all prediction models that utilized statistical methods, e.g., LR. We also found that diagnostic measures, such as FPG/FBS/FBG, HbA1C, and 2hPG could accurately determine the optimal cut points and the model could accurately classify the population samples between subjects with diabetes and those without diabetes, with an AUC score of 0.97 for FPG, 0.80 for FPG, 0.78 for HbA1C, 0.85 for FBS, 0.79 for 2hPG, and 0.905 for FBG, respectively, in Chinese, Japanese, Korean, US-PIMA Indian, and Trinidadian adult populations. While the LR-based statistic method was used to identify the relationship between diabetes and COVID-19 in the Korean population, a statistically significant score (p-value < 0.001) was found, and it showed that subjects with diabetes have

a slightly higher risk of COVID-19 compared to the non-diabetic subjects, with the adjusted OR of 1.21 (95% CI, 1.10–1.34). Furthermore, in predicting diabetes using ML methods with employed 10-fold cross-validation, the prediction models could also accurately detect diabetes, with the highest accuracy rate of up to 99.59% performed by RF, 96.50% performed by LR, 91.77% performed by NB, 77.08% performed by MLP, and 82.80% performed by NB in Chinese, Japanese, Korean, US-PIMA Indian, and Trinidadian adult populations. Among all machine learning methods applied in this study, NB performed better in the majority of performance evaluation metrics, such as accuracy, precision, recall, f1, and AUC. By conducting this ML-based prediction methods analysis, the information of the best model for predicting diabetes was revealed, as well as the information regarding the most suitable model for real-world healthcare data and requirements.

Even though the diabetes screening scores showed robust results in revealing risk factors, determining cut points, and assessing the risk of diabetes or predicting diabetes, this study has limitations that should be noted. The first limitation of this study is that we generalized some multiple-categorical variables in the dataset into binary categorical variables, so it may result in different findings. For example, we categorized the smoking variable into two categories: smoking and not smoking, where there are four levels of smoking. Thus, it may result in different findings, and analysis of using multiple categories could be investigated in future work. The second limitation is that this study only used one dataset to investigate the interrelationship between diabetes and COVID-19. To reveal a strong and robust interrelationship between diabetes and COVID-19, the utilization of numerous datasets is recommended, especially datasets across various nations. Therefore, in future work, the utilization of numerous datasets in order to investigate and reveal a strong interrelationship between diabetes and COVID-19 will be challenging.

Author Contributions: Conceptualization, N.L.F. and M.S.; methodology, N.L.F. and S.L.Q.; software, M.S. and G.A.; validation, G.A., M.A. and S.M.U.; formal analysis, M.S., S.L.Q. and N.L.F.; investigation, S.L.Q. and S.M.U.; resources, S.L.Q. and S.M.U.; data curation, M.A. and S.L.Q.; writing—original draft preparation, N.L.F.; writing—review and editing, N.L.F. and M.S; visualization, M.S. and N.L.F.; supervision, G.A. and M.A.; project administration, G.A. and M.A.; funding acquisition, N.L.F. and M.S. All authors have read and agreed to the published version of the manuscript.

Funding: This work was funded by the Sejong University Industry-Academic Cooperation Foundation (Grant No. 20220208).

Institutional Review Board Statement: Not applicable.

Informed Consent Statement: Not applicable.

Data Availability Statement: Not applicable.

Conflicts of Interest: The authors declare no conflict of interest.

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