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**Machine learning model to predict the risk of diabetes**

**by**

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Abstract

Diabetes has become a noteworthy social issue in the world, where more and more people have been diagnosed with diabetes in recent years. To find out the problem, machine learning is one of the approaches used to predict diabetes. This project introduces two datasets, the Pima Indian Diabetes dataset and the NHANES dataset. In addition, a machine learning framework proposed by Tasin et al. [4] is the baseline model in this model. Moreover, polynomial regression and SMOTE are applied to predict missing values and class imbalance problems. Furthermore, Random Forest and XG Boost are used for the prediction of diabetes in this project, and Random Forest and XG Boost have the highest accuracy in the Pima Indian Diabetes dataset and the NHANES dataset, respectively. In the future, exploring other key features and preprocessing methods will be the major options to get better results for this project.

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# INTRODUCTION

Diabetes has been increasingly prevalent across the world for the past several years. It is estimated that currently, in 2022, around 8.3 million people [1] exhibit symptoms of diabetes, which comprises approximately 10.4% of the world's population, which makes ignoring diabetes impossible. Modern people have a fast life that we can hardly spare time to exercise, which leads to unhealthy living habits, such as obesity, sleep deprivation, etc. There are two main categories of common diabetes: Type 1 and Type 2. The former is congenital, hereditary, etc. [2], and the latter is its own acquired poor eating habits, lack of exercise, etc. [2]. Machine learning has been applied in diabetes prediction for years to predict if a patient is likely to develop diabetes. One of the advantages of machine learning is that it can generate the corresponding prediction based on the dataset's content. It allows people to make suitable decisions based on the predictions generated by machine learning algorithms. This project explores machine learning algorithms and applies them to diabetes predictions.

## Overview

### Background

One of the most significant issues in the world is Diabetes. As mentioned earlier, many people, whether adults, youth, or children, have had diabetes in recent years. Early for diabetes, people used to do blood glucose measurements to check their blood glucose levels to see if they had diabetes or not. In the past, a blood glucose meter was used. With the evolution of science and technology, another approach that is put forth is the identification of diabetes by using machine learning algorithms. People can view the predicted output generated by machine learning algorithms to check if they are at risk for diabetes. It saves time for people who are allowed to check their health conditions without viewing the indices from the body. Moreover, it decreases the probability of misjudgment due to human factors.

### Problem Statement

Although diabetes prediction with machine learning has been implemented recently, much research on diabetes prediction with machine learning algorithms has indicated different results. For example, Mujumdar and Vaidehi [3] indicated that Logistic Regression and Adaboost perform well with high accuracy in diabetes prediction. Tasin et al. [4] commented that XGBoost with the ADASYN approach performs well in diabetes prediction. It is difficult for people to judge whether machine learning models are the most suitable for diabetes prediction. Furthermore, much research has been done on diabetes prediction using machine learning algorithms and different datasets (NHANES and Pima Indian Diabetes) and data preprocessing methods. Making the same topic on diabetes prediction with machine learning algorithms has caused different results. Therefore, this project is a good research topic to work on. The results will be determined by collecting data from different sources, implementing the methodology, and comparing different methodologies.

# Dataset

## Pima Indian Diabetes Dataset

|  |  |
| --- | --- |
| Pima Indian Diabetes Dataset | |
| **Features** | Pregnancies |
| Glucose **(2 hours in an oral glucose tolerance test (mg/dL))** |
| BloodPressure **(Diastolic blood pressure (mm Hg))** |
| SkinThickness |
| Insulin **(2-Hour Serum insulin (µh/ml))** |
| BMI |
| DiabetesPedigreeFunction |
| Age |
| **Target** | Outcome |

Table 1: Information on Pima Indian Diabetes Dataset

The Pima Indian Diabetes Database provided information about the patients who have Diabetes or not. The dataset source comes from the National Institute of Diabetes and Digestive and Kidney Diseases [5]. A total of 768 patients were recorded in the Pima Indian Diabetes Database, which are Pima Indians that are at least 21 years old females.

A total of 9 variables were listed in the dataset, which included eight features and one target variable. Here is the explanation of these variables:

Pregnancies: It means the number of times pregnant

Glucose (Blood Sugar): It is a group of carbohydrates [6] that provides energy for the body, and mg/dL is the measuring unit of glucose. If the glucose is lower than 140 mg/dL, it is considered normal [7].

BloodPressure: It means heart beats and pumps blood into the arteries [8]. Lack of exercise and obesity would result in Higher blood pressure, and it would cause health risks such as headache and dizziness.

SkinThickness: It estimates the body fat on thighs and limbs.

Insulin: It helps regulate blood sugar levels and is important for energy production and storage.

BMI: It measures body fat based on Height and Weight. 18.5 to 23 is considered a healthy weight and a normal body level.

DiabetesPedigreeFunction: It is a function that scores the probability of Diabetes based on Family history.

Age: The age of all patients is at least 21 years old.

Outcome: A variable that diagnosed Diabetes or not.

## 2013-2014 NHANES Dataset

The National Health and Nutrition Examination Survey (NHANES) is a project that the National Center for Health Statistics implemented. This project aims to collect data from American adults and children through interviews and body checks. NHANES collected dietary intake, physical examinations, and laboratory tests. Also, this project uses population-based sampling that includes the entire American population. This dataset is available for open access and widely used for health research and public health initiatives. Here is the abstract of the dataset:

|  |  |
| --- | --- |
| NHANES Dataset | **Features** |
| **Demographic** | SEQN (ID of interviewee)  RIAGENDR (Gender)  RIDAGEYR (Age) |
| **Diet** | DR1DAY (Intake day of the week)  DR1TKCAL (Energy (kcal) take in 1 day) |
| **Examination** | BMXBMI (BMI)  BPXDI1 (Blood Pressure) |
| **Labs** | LBXGLT (Glucose)  LBXIN (Insulin) |
| **Questionnaire** | DIQ010 (Diabetes\_Diagnosis)  ALQ120Q (alcoholic drinks taken per day/ months) |

Table 2: Abstract of NHANES Dataset

NHANES Dataset is divided into five parts, which are demographic, diet, examination, labs and questionnaire.

Demographic: it means the characteristics of a population, which include gender, age and marital status, etc.

Diet: it means the dietary intake information collected from the interviewees. Nutrient information like Energy taken, Vitamins, fats and carbohydrates are recorded in the database.

Examination: it means the physical examinations and medical tests conducted on the interviewees, such as BMI and blood pressure.

Labs: it means the laboratory tests performed on biological samples collected from the interviewees, such as glucose levels and Insulin.

Questionnaire: it means the self-reported information collected from the interviewees through structured interviews and surveys. It covers the topics that related to health and lifestyle like physical activity and health conditions. The details of the data processing would be explained in the following section.

# CURRENT PROGRESS

For this project, machine learning is a suitable approach to diabetes prediction because diabetes prediction belongs to a classification task that determines whether or not the patients are diagnosed with diabetes. The process includes data preprocessing, feature selection, training, testing, and performance evaluation. All the work is done on Jupyter Notebook, a web-based application that provides an interactive computing notebook environment to describe the data analysis.

Tasin et al. [4] proposed a machine-learning framework that acquired 81% accuracy using XGBoost. The preprocessing methods are extreme gradient boosting techniques for filling the missing value; SMOTE and ADASYN are applied to address the class imbalance issue. In addition, it collected the samples from 203 people called RTML, which is used for filling “Insulin” and is the merged dataset. In this project, it will be the baseline model for the reference.

## Data Preprocessing on Pima Indian Diabetes dataset:

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Figure 1: Pima Indian Diabetes Dataset (raw data)

The dataset has 768 rows (participants) with nine columns (features) before preprocessing. As shown in Figure 1, there are some values of zero in columns “SkinThickness” and “Insulin.” There are no null values on the dataset, so filling in zero is unnecessary.

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Figure 2: Check missing value on Pima Indian Diabetes Dataset

In Figure 2, many missing values existed in columns “SkinThickness” and “Insulin,” which count for about 30% and 50% of the dataset. Other columns “Glucose”, “BloodPressure” and “BMI” with value 0 will be filled by their mean as they are only a tiny minority of the whole dataset. To identify the rows where column “SkinThickness” is zero, variables “zero\_SkinThickness\_rows” and “non\_zero\_SkinThickness\_rows” are defined to find the rows where it is zero and non-zero, respectively. To predict column “SkinThickness” become more reliable, columns “Glucose”, “BloodPressure” and “BMI” and “Age” are used to assist the prediction of column “SkinThickness”.

Polynomial Regression is applied to predict the missing value of column “SkinThickness”. Aditya Shastry et al. [9] applied polynomial regression to predict the missing value in data preprocessing and it was helpful to improve the model performance. First, the degree of the polynomial features is set to 2 and a bias column is not included in the polynomial features. Next, fit\_transform() is applied to find the metrics of overall statistical properties (mean, standard deviation). Then, linear regression will be applied to train and predict the column “SkinThickness.”

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Figure 3: Fill the missing values on “SkinThickness”

In Figure 3, the predicted values of the column “SkinThickness” are based on the input features (the columns “Glucose,” “Blood Pressure,” “Age,” and “BMI”). The reason for not using the column “Insulin” as the input feature for the prediction of the column “SkinThickness” is that “Insulin” has lots of missing values, and it affected the predicted result that some of the predictions would generate negative values. Therefore, the approach that uses the column without missing value as the input feature is appropriate for predicting the features with the missing values.

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Figure 4: Fill the missing values on “Insulin”

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Figure 5: Check if there have missing value (0) or not

Figure 4 uses columns “Glucose,” “Blood Pressure,” “Age,” “BMI,” and “SkinThickness” as the input features for the prediction of “Insulin,” which are the missing value. As shown in Figure 4, polynomial regression did not generate negative values after the input features were used. After the polynomial regression, replace all the predicted values with all the missing values. As shown in Figure 5, there is no missing value in each column, which means all the predicted values are successfully replaced.一張含有 文字, 螢幕擷取畫面, 數字, 字型 的圖片

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Figure 6: All the missing values are replaced by the predicted values

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Figure 7: Quantile-Quantile Plot of all features (Pima Indian Diabetes Dataset)

As shown in Figure 7, there are the normal distribution of all features which are displayed in Q-Q plot form. Spots in features “Glucose,” “Blood Pressure,” “SkinThickness,” and “BMI” roughly follow the straight red line on the plot. Also, the spots on the features “Insulin”, “Age,” and “DiabetesPedigreeFunction” are deviated from the red straight line. For example, most of the spots in the feature “Age” are concentrated on 20, meaning most participants are about 21 years old.

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Figure 8: Correlation matrix of all features and outcome (Pima Indian Diabetes Dataset)

Figure 8 shows the correlation coefficient between all the features and the outcome. Based on the ranking in descending order, the relationship between the features and the outcome are “Glucose”, “Insulin”, “BMI”, “SkinThickness”, “Age”, “Pregnancies” and “BloodPressure”, which the highest score and lowest score are “Glucose” and “BloodPressure” respectively. Cleveland Clinic [10] reported that glucose level and diabetes are strongly correlated. According to ranking, features “Glucose”, “Insulin”, “BMI” and “SkinThickness” are selected as the key features for the prediction of diabetes.

After defining the key features and “Outcome” as a class, the data will split into 80:20, 80% for training, and the rest for testing. Next, feature scaling is applied to split data. Standardization is used in the feature scaling to normalize the data. In the standardization process, the scaler will be defined and fit into the training data. Then, the testing data will be transformed to finish the feature scaling.

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Figure 9: Feature Importance (Pima Indian Diabetes dataset)

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Figure 10: Balanced data (Pima Indian Diabetes Dataset)

As shown in Figure 9, “Glucose” has the highest rank in feature importance after standardization. Furthermore, the features rank the same as the correlation matrix. Then, SMOTE is applied to process imbalance data, which can significantly improve model performance, especially for weak learners [11]. In Figure 10, all the data are balanced at 50:50 after applying SMOTE.

## Data Preprocessing on NHANES dataset:

Since the NHANES dataset has five raw data sets, it is necessary to preprocess the data to ensure that it is readable and understandable to people because there are many features in each raw data set. Originally, medication (not mentioned in Table 1) was one of the raw data of the NHANES dataset, but no complete description can be found on the NCHS official website. In addition, diet does not have similar features compared to Pima Indian Diabetes dataset. Therefore, medication and diet will not be used in data preprocessing.

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Figure 11: Information about demographic (NHANES dataset)

In Figure 11, each feature is complex to read for people as they are named in terms. To make the data more readable and understandable features similar to the Pima Indian Diabetes dataset are selected and relabeled. For example, “SEQN”, “RIAGENDR” and “RIDAGEYR” are relabeled as “ID”, “Gender” and “Age” respectively. After the relabeling, all the data are merged on the "ID” and uses a left join. Then, category mapping is created for gender and split into Male and Female, and categorical variables are converted into dummy variables.

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Figure 12: Merged dataset (NHANES dataset)

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Figure 13: Total number of each row with value 0

In Figure 12, the merged dataset collects the key features and is renamed. Despite the conversation, many null values are still on the merged dataset. Therefore, fill the null values with zero in the entire dataset and apply polynomial regression to predict these values. In this situation, it is not suitable to use means or median to replace the null values as there are many null values in Figure 13, and this will negatively influence the prediction of diabetes if applied.

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Figure 14: Merged dataset after Polynomial Regression applied (NHANES dataset)

After the polynomial regression applied, the predicted values replace the null values in the merged dataset and it looks understandable. In column “Outcome”, there are five values (1 for Yes, 2 for No, 3 for Borderline, 7 for Refused, and 9 for Do not know). Values 1 and 2 are retained, and the rest are removed because of their unclear result. Furthermore, the proportion of “Outcome” larger than two in the dataset is 2%; consequently, removing these will not significantly impact the prediction of diabetes.

In addition, it is counterintuitive to use values 1 and 2 to represent having diabetes and not having diabetes, especially since the value 2 will mistake people for invalid. Accordingly, it is necessary to use 1 and 0 to represent having diabetes and no diabetes instead of 1 and 2.

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Figure 15: Quantile-Quantile Plot of all features (NHANES dataset)

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Figure 16: Correlation matrix of all features and outcome (NHANES dataset)

In Figure 15, “Blood pressure,” “Glucose,” and “Insulin” are the normal distribution, and most of the spots on these features follow the red straight line. Additionally, “Age” looks like an inverse z shape. Most spots deviate from two ranges and can be considered a bimodal distribution.

In Figure 16, put the relationship between features and “Outcome” in descending order are "Age", "BMI", "Insulin", "BloodPressure", "Glucose" and "ID". “ID” will not be used as the input feature because it is a negative for “Outcome”. In addition, “ID” is used to assign the numeric labels to each entry, which means it does not have a meaningful relationship with “Outcome”. Moreover, the result of the correlation matrix is different from the Pima Indian Diabetes dataset in that “Age” is the highest score in the NHANE dataset, but "Glucose" is the highest score in the Pima Indian Diabetes dataset.

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Figure 17: Feature Importance (NHANES dataset)

In Figure 17, “Glucose” has the highest feature importance after standardization, the same rank as the Pima Indian Diabetes dataset. Also, it is worthy to note that “Insulin” is at the bottom of the feature importance. In the preprocessing, “Glucose”, “Age”, “BMI”, “BloodPressure” and “Insulin” are selected as input features in order to make a similar environment to make the comparison.

## Preliminary Result

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Figure 18: Reproduce Result (XGB+ADASYN)

Figure 19: Paper Result (XGB+ADASYN)

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Figure 20: Reproduce Result (AUC)

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Figure 21: Paper Result (AUC)

Despite the same dataset and environment, it is found that the results of the XG Boost Classifier are different, as shown in the figures above.

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Figure 23: Preliminary Result (Random Forest) (Pima Indian Diabetes dataset)`

Figure 22: Preliminary Result (XG Boost) (Pima Indian Diabetes dataset)

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Figure 24: Preliminary Result (XG Boost) (NHANES dataset)

Figure 25: Preliminary Result (Random Forest) (NHANES dataset)

Since the referenced paper proposed a machine learning framework that used XG Boost with ADASYN and other machine learning models like random forest for the comparison in the paper, XG Boost and Random Forest are used to predict diabetes in this project. For the Pima Indian Diabetes dataset, Random Forest obtains 77.9% accuracy, and XG Boost is the highest. It has 86.1% accuracy for the NHANES dataset. Adjustments have been implemented in the Pima Indian Diabetes dataset, such as the input features change to “Glucose”, “Insulin”, “BMI”, “BloodPressure” and “Age”, which are the same as the input features in the NHANES dataset. The reason for the different results in the two datasets can be the number of entries in the NHANES dataset, which is around ten thousand.

# CHALLENGES

Data preprocessing for the NHANES dataset is challenging as it includes five different data sources. Also, each data has lots of features whether it is useful for diabetes prediction or not. Therefore, I need to read the description of the features to ensure that I can remove the redundancy and get the key features from each data and merge them into a new data frame with filtered.

Moreover, there are many missing values with 0 and null values on the Pima Indian Diabetes dataset and NHANES dataset. For example, a number of rows with “LBXGLT” and “LBXIN” (value 0) have 7830 and 7082, respectively, which comprises approximately 77% and 70% of the whole NHANES dataset. The approach of filling value zero with the means is used to predict the missing value but it performs poorly in the q-q plot as both are not the normal distribution. Therefore, polynomial regression approach is used in this situation to predict the missing value and it is better than filling value zero with the means.

# FUTURE WORKS

1. Try to use other preprocessing methods

Standardization and SMOTE are applied as the data preprocessing approaches in this stage. For feature scaling, methods like min-max scaling and mean normalization will be the options to transform the data to fit within a specific range or scale. For the class imbalance in datasets, techniques like ADASYN will be the possible choice to ensure that the model will not lead to poor performance in the minority class.

2. Try to select other key features for comparison

In this stage, “Glucose”, “Insulin”, “BMI”, “SkinThickness” are the selected features in the Pima Indian Diabetes dataset. The criteria for selecting the input features are based on the correlation matrix, which is lower than 0.2, to ensure that no more redundancy features as the input features affect the model performance. For the NHANES dataset, “Glucose”, “Insulin”, “BMI”, “Age” and “BloodPressure” are the input features in the dataset. In the future, it is possible to explore more features as input features and make comparisons to review which performs better under the same preprocessing method.

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Appendices

## Appendix 1: Pima Indian Diabetes dataset

https://www.kaggle.com/datasets/uciml/pima-indians-diabetes-database

## Appendix 2: 2013-2014 NHANES dataset

https://www.kaggle.com/datasets/cdc/national-health-and-nutrition-examination-survey/data?select=diet.csv