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

**by**

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# Introduction (background of the prj) (each section write 160-200)

Diabetes is a chronic disease in which the human body cannot utilize insulin generated by the body or produce enough insulin [16]. In other words, it affects the body's function and causes the body function to not work properly because of disordered metabolism.

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Figure 1: Diabetes around the world in 2021 & prediction in 2030 & 2045 [17]

Nowadays, Diabetes becomes a significant health issue in the world, which has been increasingly prevalent across the world for the past several years. In Fig 1, it shows the prediction that the number of patients with Diabetes will increase in 2030 and 2045, of which Africa will increase to 134 percent. In addition, the World Health Organization [18] estimated that 830 million people exhibit symptoms of Diabetes, which comprises approximately 10% of the world's population. In addition, IDF Diabetes Atlas [19] found that 537 million adults were having Diabetes and 6.7 million people died because of Diabetes in 2021.

In view of the growing popularity of technologies, machine learning has become one of the approaches used to predict if a person is likely to develop Diabetes. The main advantage of machine learning is that it can generate the corresponding prediction based on datasets and preprocessing, which enables experts to make decisions based on the prediction. Two famous Diabetes datasets were used for the research: the Pima Indian Diabetes dataset [20] and the NHANES dataset [21]. All these datasets come from people who truly lived in the world.

## Overview

### Motivation (why u want to do this project?(want to know how machine learning operate in diabetes prediction / NHANES dataset are rarely used in research paper (most paper rather used Pima Indian dataset/ )

Oxx

### Objective (what do you want to achieved in this project? (e.g. proof that xx is more better / try to used another method that is rarely used in research paper to see the result is better or not)

xx

# Related Work (List how machine learning works on Diabetes prediction in tradition / List how neural network work on Diabetes prediction (Maybe can write it?) /List the method used in reference paper (baseline) )

Before the widespread of Gradient Boosting, there were studies based on traditional machine learning algorithms to do the classification task. For example, Abdillah and Suwarno [22] used a Support Vector Machine to predict Diabetes in 2016.

This final year project is based on two research papers that used the Pima Indian Diabetes dataset and the 2013-2014 NHANES dataset, respectively. They proposed two different approaches to the classification.

Tasin et al. [23] proposed a method based on eXtreme Gradient Boosting (XGBoost) on the Pima Indian Diabetes dataset. XGBoost is a robust machine-learning algorithm good at classification and regression tasks. In the preprocessing, they used ADASYN to process the class imbalance problem. In addition, they merged the extra dataset called the RTML private dataset with the Pima Indian Diabetes dataset. They replaced the missing values of features besides Insulin and Age with the mean value. Moreover, they used Polynomial Regression, a form of regression analysis, to model the relationship between input variables (x) and output variables (y) by fitting a polynomial equation to the data [24] to predict the missing value of Insulin. It is noted that some research on Diabetes prediction had also used Polynomial Regression to predict the missing values and brought gains to the experiment results. For example, Aditya Shastry et al. [25] applied polynomial regression to predict the missing value of the features in data preprocessing, which improved model performance. This method gave them 81% accuracy and an AUC of .84.

Qin et al. [26] proposed a method based on CatBoost on the 2013-2014 NHANES dataset. In the preprocessing, they used ADASYN and One-Hot encoding to solve the class imbalance and categorical features, respectively. Also, they compared five machine learning models, which were XGBoost, CatBoost, Support Vector Machine. Random Forest and Logistic Regression, of which CatBoost performs well with 82.1% accuracy and an AUC of 0.83.

# Methodology

## Random Forest

Random Forest is an ensemble machine learning algorithm combining multiple Decision trees for classification and regression tasks. Compared with the Decision Tree algorithm, Random Forest can provide better performance that improves the model's accuracy, especially for complex datasets. For example, Chen et al. [27] commented that Random Forest was the most effective algorithm compared to Naïve Bayes Tree and Alternating Decision Tree, which provided higher accuracy and can handle complex datasets like historical flood data and geographical factors.

## XGBoost

XGBoost is an ensemble machine learning algorithm based on the gradient boosting framework and decision tree to process the tasks like classification and regression [28]. In other words, it is an optimized gradient boosting framework and is widely used in competitions like Kaggle. The main feature of XGBoost is that it provides higher performance and speed to handle large datasets because of parallel processing. Also, it can learn and handle the missing values during the training to save time for preprocessing, which is suitable for situations in which datasets have many missing values.

## CatBoost

CatBoost is a machine learning algorithm based on a gradient boosting framework and decision tree, similar to XGBoost. Compared with XGBoost, CatBoost is better at handling categorical features because it uses ordered encoding to encode categorical variables [29], which can handle overfitting and improve the model performance. In addition, Hancock and Khoshgoftaar [30] commented that CatBoost is good at processing categorical and heterogeneous data. Therefore, it is suitable for datasets with categorical features.

## Proposed Framework (My proposed framework (how it works) ; why choose that component in the proposed framework?(e.g. improve acc? / Convenient? / haven’t used in research paper? (most of paper use polynomial regression) )

Figure 2: Proposed Framework

As shown in Fig. 2, the Pima Indian Diabetes dataset and the 2013-2014 NHANES dataset are the target datasets in the proposed framework. Before splitting the data for training and testing, it is necessary to preprocess the datasets because there are raw data in the datasets that have not been processed. Also, most of the datasets have null values or missing values, which negatively affect the overall result, such as generating abnormal model performance, leading to biased parameter estimates and incorrect conclusions on the experiment result [31]. Therefore, filling in the missing values is important to prevent the situations above.

In “Missing Value”, polynomial regression and the imputation of missing values by mean are used to fill the missing values in the Pima Indian Diabetes dataset and the 2013-2014 NHANES dataset. In “Feature Importance,” a correlation matrix is created to view the relationship between features and output and select the key features as input.

In “Split data”, the data will be split into an 80:20 ratio, in which 80 is the training set, and 20 is the testing set. In “Feature Scaling,” Feature Scaling can ensure fair treatment of all features [32], in which Standardization will be applied in normalizing the input features. After the training and testing in “Train” and “Test,” the evaluation will be conducted to review the results and make adjustments if the results do not meet the expectation.

# Dataset

## Pima Indian Diabetes Dataset

|  |  |
| --- | --- |
| Pima Indian Diabetes Dataset | |
| **Features** | Pregnancies |
| Glucose **(2 hours in an oral glucose tolerance test (mg/dL))** |
| Blood Pressure **(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

Nine variables are provided in the Pima Indian Diabetes Dataset. They are Pregnancies, Glucose, Blood Pressure, Insulin, BMI, DiabetesPedigreeFunction, Age and Outcome. In the experiment, Outcome will be defined as a target variable because its variable indicates a person who is diagnosed with having Diabetes or not directly (“1” means having Diabetes and “0” means not having Diabetes), and the rest are classified into Features because they are the risk factors of having Diabetes or not. Here is the information about each feature below:

Pregnancies: it means the number of times a female is pregnant or not, and the median value of Pregnancies is 3. There was the study explored the relationship between pregnancy and Diabetes. Buchanan et al. [4] commented that there is a higher risk of having Diabetes if a female has Gestational diabetes mellitus (GDM) during pregnancy.

Glucose (Blood Sugar): it is a group of carbohydrates [5] that provides energy for the human body that is important to body function. Eyth et al. [6] commented that it is considered a moderate level if the glucose level is lower than 140 mg/dL in the oral glucose tolerance test. The median value of Glucose is 117, which means that the typical glucose level for the participants in the dataset is relatively moderate. Generally, Glucose is directly related to Diabetes as the body cannot regulate blood glucose levels generally if a person is diagnosed with having Diabetes. For example, the Mayo Clinic [7] noted that Diabetes can cause excessive Glucose in the blood, which cannot be properly regulated and results in serious health issues.

BloodPressure: it means the heart beats and pumps blood into the arteries [8] that deliver oxygen and nutrients into the body. It is considered moderate if systolic and diastolic pressure are less than 120 and 80 [9]. In the dataset, BloodPressure used diastolic blood pressure as the unit to measure blood pressure. The median value of BloodPressure is 72, which means that the typical blood pressure level for the participants in the dataset is relatively normal. Several organizations explored the relationship between blood pressure and Diabetes. For example, the probability of getting high pressure is higher than a person without Diabetes if a person has Diabetes [10].

SkinThickness: In general, it measures body fat on thighs and limbs. In the dataset, triceps (the back of the upper arm) was used to estimate the body fat. The average triceps skin thickness of human and women are 18.7 ± 8.5 mm and 23.6 ± 7.5 mm respectively [11]. It is noteworthy that all the participants in the dataset are females and the median value of SkinThickness before preprocessing is 23 mm, which is similar to the measurement on triceps skin thickness above. In addition, Särnblad et al [12] found that the skin thickness with a person with Diabetes is higher than a health person, even they have a similar BMI.

Insulin: it regulates blood sugar levels and is important for energy production and storage. The average insulin level (2-hour Serum insulin (µh/ml)) of a human is between 16 and 166 [13], and the median value of Insulin before preprocessing is 30.5. Moreover, Insulin is related to glucose and Diabetes. Better Health Channel [14] states that Diabetes will cause the body not to have enough Insulin and result in high blood glucose levels.

BMI: it measures body fat based on Height and Weight. The median BMI in the dataset is 32, which is considered obesity, and 18.5 to 24.9 is also considered a healthy body [15].

DiabetesPedigreeFunction: it is a function that scores the probability of Diabetes based on Family history. Smith et al. [16] defined that the value of DiabetesPedigreeFunction would be higher if more people had Diabetes in the family and vice versa.

Age: the age of all patients is at least 21 years old, and the median age is 29.

Outcome: it is a target variable that diagnosed Diabetes or not.

## 2013-2014 NHANES Dataset

The National Health and Nutrition Examination Survey (NHANES)

|  |  |
| --- | --- |
| NHANES Dataset (Raw data) | **Features (selected)** |
| **Demographic** | SEQN (ID of participant)  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

Five raw data sets are in the 2013-2014 NHANES Dataset: Demographics, Diet, Examination, Labs and Questionnaire.

Demographic is the characteristics of the participants, which describe personal information and social status. For example, it collects income, education, and marital status. Generally, these variables are used to analyze the relationship between health and socioeconomic factors to help researchers understand the health disparity between populations. Three variables in demographics are captured as the selected features in data preprocessing, which are SEQN (ID of the participant), RIAGENDR (Gender of the participant), and RIDAGEYR (Age of the participant). The reason that these 3 variables are the selected features in the experiment is that they are similar to the features provided in the Pima Indian Diabetes Dataset to make a comparison of two different datasets (Pima Indian Diabetes Dataset and 2013-2014 NHANES Dataset)' model performances. This approach will be applied to other raw data sets in the following experiment to make the results more comparable.

Diet collects the participants’ intake of food and drink. The purpose of gathering these attributes is to evaluate the nutrition and dietary habits of the participants to understand the relationship between Diet and physical disease (e.g., Obesity, Diabetes, Cardiovascular disease). Two variables in Diet are captured as the selected features in the data preprocessing, which are DR1DAY (Intake day of the week) and DR1TKCAL (Energy (kcal) taken in 1 day). These two variables are the selected features in the experiment because calorie intake is a key factor in preventing and managing type 2 diabetes [1].

Examination is the physical and physiological measurements. The purpose of collecting these measurements is to reflect the health data about the participants and enable the researchers to explore the relationship between the measurements and other NHANES raw data sets (e.g., Diet and Labs). In the experiment, BMXBMI (BMI) and BPXDI1 (Blood Pressure) are the selected features in the data preprocessing, as these selected features are the same as those provided in the Pima Indian Diabetes dataset.

Labs means the laboratory tests performed on biological samples collected from the participants. Collecting these biological samples aims to provide objective and quantifiable measures of health and nutrition to enable the researchers to understand participants’ nutritional status and health conditions. LBXGLT (Glucose) and LBXIN (Insulin) were selected features in the experiment. They are used in data preprocessing since these selected features are the same as those provided in the Pima Indian Diabetes dataset.

Questionnaire collects information from a series of interviews and questionnaires. The questions are related to family or individual-level information [2]. The questionnaire aims to collect information (e.g. health behaviors, medical history, and lifestyle choices) from participants to provide a critical context for understanding health outcomes and risk factors. In addition, it helps researchers to study risk factors for diseases such as Diabetes and Hypertension. In the experiment, DIQ010 (Diabetes Diagnosis) and ALQ120Q (alcoholic drinks taken per day/ months) will be taken as the selected features in the data preprocessing as DIQ010 indicates whether a participant is diagnosed with Diabetes or not (which is similar to "Outcome" in Pima Indian Diabetes dataset). Also, there was a study that explored the relationship between alcohol consumption and Diabetes. For example, Koppes et al. [3] commented that moderate alcohol consumption could reduce the risk of getting type 2 Diabetes.

# Experiment (study the dataset [e.g. have null value / what is it?]

## Data Preprocessing on Pima Indian Diabetes dataset:

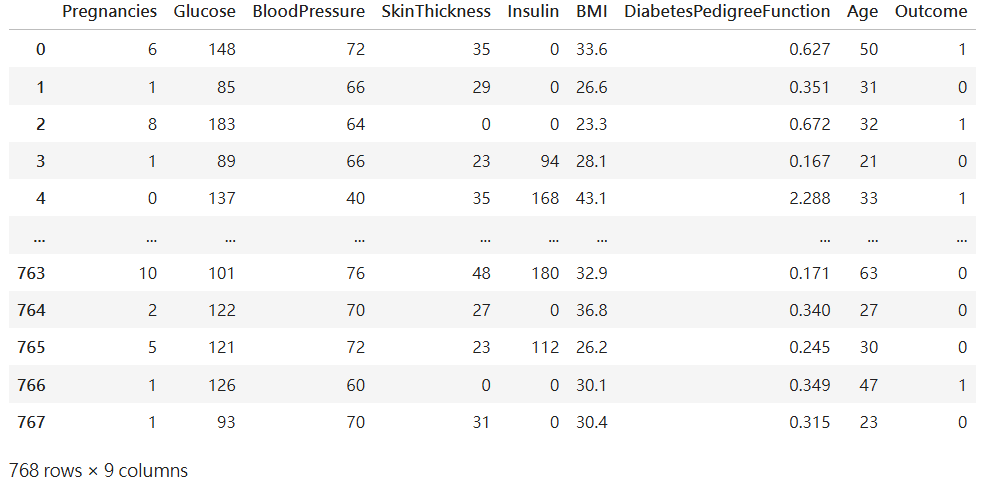


Figure 3: Information of Pima Indian Diabetes dataset

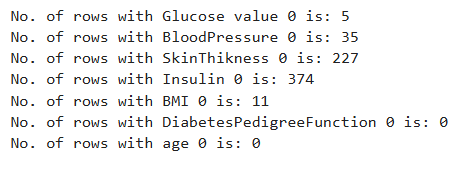


Figure 4: Missing value count on the Pima Indian Diabetes dataset

In Fig. 3, 768 entries were collected in the dataset, including eight features and the target variable. In addition, some features like “Glucose” and “BloodPressure” exist the missing values in Fig.4, in which “SkinThickness” and “Insulin” have 227 (approximately 30% of total entries in the dataset) and 374 (approximately 49% of total entries in the dataset) missing value respectively. There is no null value on the dataset. To fill in the missing values, the features “Glucose”, “Blood Pressure,” and “BMI” will be filled by their mean value as they are a minority of missing values in the dataset. For the features “SkinThickness” and “Insulin,” Polynomial Regression is applied to predict the missing values, and the predicted values will replace them.

|  |  |
| --- | --- |
|  | **Parameter settings** |
| degree | 2 |
| include\_bias | False |

Table 3: Settings on Polynomial features

|  |  |  |  |
| --- | --- | --- | --- |
| Feature(s) selected to predict “SkinThickness” | | | |
| Glucose | BMI | Age | BloodPressure |

Table 4: Feature(s) selected to predict “SkinThickness”

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Feature(s) selected to predict “Insulin” | | | | |
| Glucose | BMI | Age | BloodPressure | SkinThickness |

Table 5: Feature(s) selected to predict “Insulin”

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Figure 5: Correlation Matrix of Pima Indian Diabetes dataset

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Figure 6: The predicted values on “SkinThickness”

Before the Polynomial Regression, it is necessary to identify the features for predicting “SkinThickness” and “Insulin”. In Table 4 and Table 5, the common features are “Glucose”, “BMI”, “Age” and “BloodPressure”. The reason for choosing four features is based on the Correlation Matrix, as shown in Fig. 5. In the prediction of  “Insulin,” the reason for selecting “BloodPressure” and “SkinThickness” instead of “DiabetesPedigreeFunction” is to test the performance under the same four common features. In addition, two research papers mentioned in the Related Work section did not use the predicted values by using Polynomial Regression in another prediction of the features that exist missing values. The experiment combines linear regression and polynomial features to form the Polynomial Regression. The degree of the polynomial features is set to 2, and a bias is not included in the polynomial features, as shown in Table 3. Next, fit\_transform is applied to the non-zero values features to find the metrics like mean value and standard deviation in overall statistics. Then, the non-zero values are normalized by transforming them afterward. Then, the values will be predicted based on the features of non-zero values in Fig. 6 and replace zero values with predicted values.

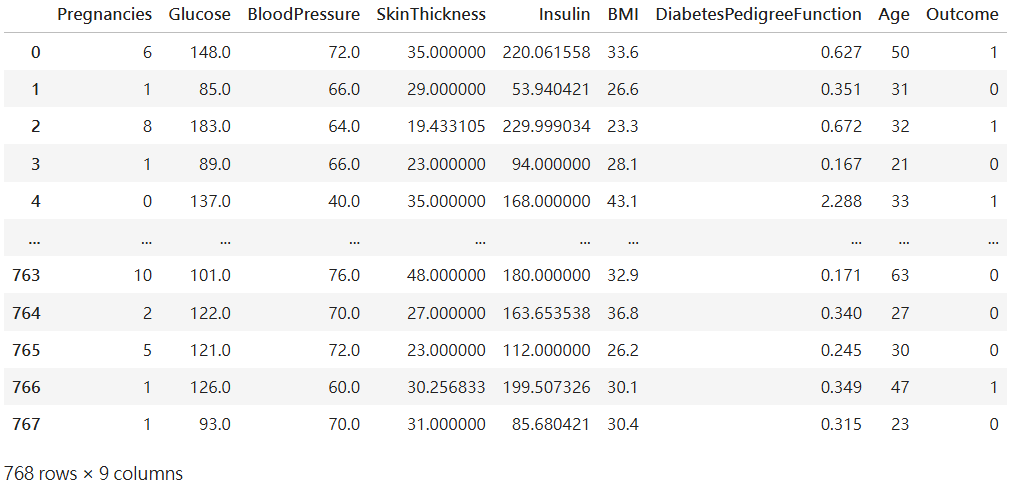


Figure 6: Pima Indian Diabetes dataset (Predicted value filled)

Fig.6 shows that all the predicted values were inserted into the corresponding features when the Polynomial Regression was done. Also, these predicted values were inserted based on the values of other features instead of randomly inserted the predicted values, which preserved the characteristic of the dataset that these values were learned from other features to make the prediction and predicted with a rational value. Therefore, they would not harm the experiment environment and make the results more comparable.

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AI 產生的內容可能不正確。Figure 7: Q-Q Plot of each feature (after the Polynomial Regression)

Q-Q Plot (Quantile-Quantile Plot) reflects the distribution of the features, whether they are normal or not. In Fig.7, features “Glucose,” “BloodPressure,” “SkinThickness,” and “BMI” were displayed in a normal distribution form as they roughly followed the red slope on the plot. On the other hand, the q-q plots of features “Insulin,” “Age,” and “DiabetesPedigreeFunction” were displayed in a curved pattern, which means they are not the normal distribution. For example, most of the spots in the feature “Age” are approximately concentrated on those above 20, which is in line with the description of the dataset that the participants are at least 21 years old.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **The combinations of Key Features** | | | | | |
| **Key Features** | Glucose | Insulin | BMI | Age |  |
| Glucose | Insulin | BMI | SkinThickness |  |
| Glucose | Insulin | BMI | Age | BloodPressure |
| Glucose | Insulin | BMI | Age | SkinThickness |

Table 5: The combination of key features

To define the key features and target variable in the prediction, choosing the features as input is important in the experiment. Four combinations of key features were tested in the experiment to compare the different key features in the result, as shown in Table 5. Most of the key features are selected in order of the score in Correlation Matrix besides “Pregnancies” and “DiabetesPedigreeFunction”. The reason there are no “Pregnancies” and “DiabetesPedigreeFunction” in the combinations is that “Pregnancies” is only related to females, and it will affect the experiment result. Therefore, it will affect the prediction of Diabetes in a male if “Pregnancies” counted as a key feature. In addition, the score of “BloodPressure” and “DiabetesPedigreeFunction” are the same, but “BloodPressure” is directly related to the body, especially Diabetes, which is mentioned in the section Dataset – Pima Indian Diabetes Dataset. On the other hand, “DiabetesPedigreeFunction” is a mathematical function that represents the probability of Diabetes based on Family history, and it is hard to directly link to the human body. Therefore, “Pregnancies” and “DiabetesPedigreeFunction” are not selected as the prediction's key features.

## Data Preprocessing on 2013-2014 NHANES dataset:

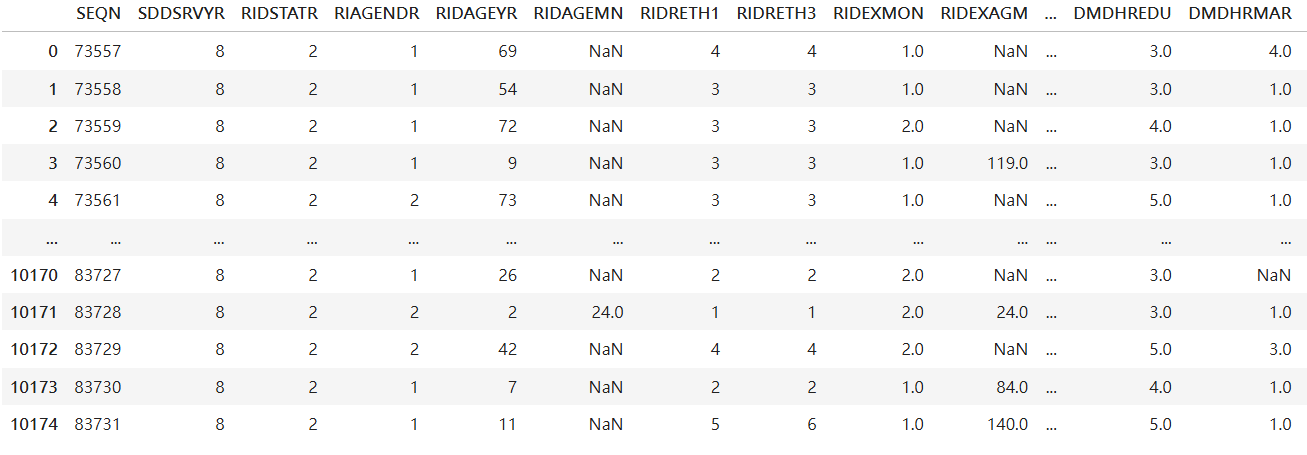


Figure 8: Information of Raw data Demographic

|  |  |  |
| --- | --- | --- |
| NHANES Dataset (Selected Raw data) | **Features in code** | **Renamed Features** |
| **Demographic** | SEQN (ID of participant)  RIAGENDR (Gender)  RIDAGEYR (Age) | ID  Gender  Age |
| **Examination** | SEQN (ID of participant)  BMXBMI (BMI)  BPXDI1 (Blood Pressure) | ID  BMI  BloodPressure |
| **Labs** | SEQN (ID of participant)  LBXGLT (Glucose)  LBXIN (Insulin) | ID  Glucose  Insulin |
| **Questionnaire** | SEQN (ID of participant)  DIQ010 (Diabetes Diagnosis) | ID  Outcome |

Table 6: Abstract of Selected Raw data and Features

In the experiment, five raw data will be merged into one. In Fig.8, there are too many variables in each raw data. It is necessary to select relevant variables from each raw data to make the dataset readable to people. The features were selected as shown in Table 2. In the 2013-2014 NHANES dataset, all the features were written in code, which was not readable to the public. Therefore, the key features are renamed, as shown in Table 6. Also, to create a similar environment to the Pima Indian Diabetes dataset and make the results more comparable, the raw data Diet and ALQ120Q in the questionnaire were removed from the dataset as there were no features that matched the Pima Indian Diabetes dataset.

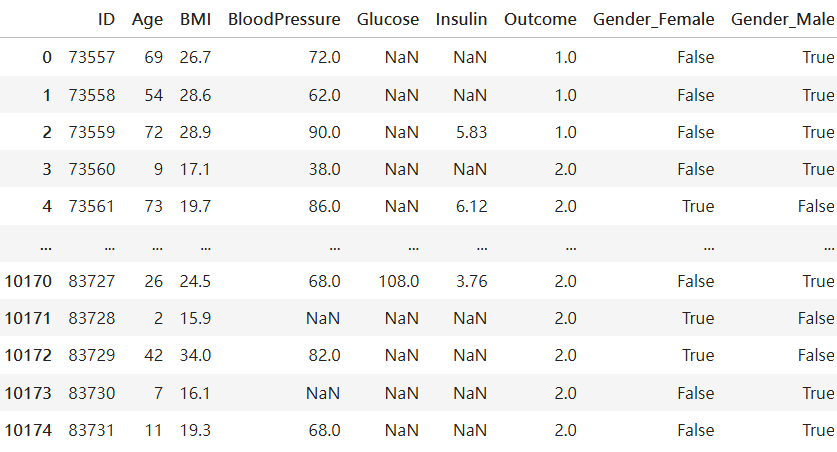


Figure 9: Information of Merged data (Not preprocessed)

To merge the raw data into one, ID is the common feature in each raw data, and ID is used to combine all the raw data. Despite the merged data, null and missing values exist in Fig.9. In this situation, the mean fills all the null and missing values in each feature. Also, there are two types of values in Outcome, which 1.0 is “Diagnosed with Diabetes” and 2.0 is “No Diabetes”. The values in Outcome are renamed 1 and 0, respectively, similar to the Pima Indian Diabetes dataset. Moreover, some work is done on the merged data, such as removing the columns “Gender\_Female” and “Gender\_Male” and removing the rows where “Glucose” and “Insulin” are less than 0.

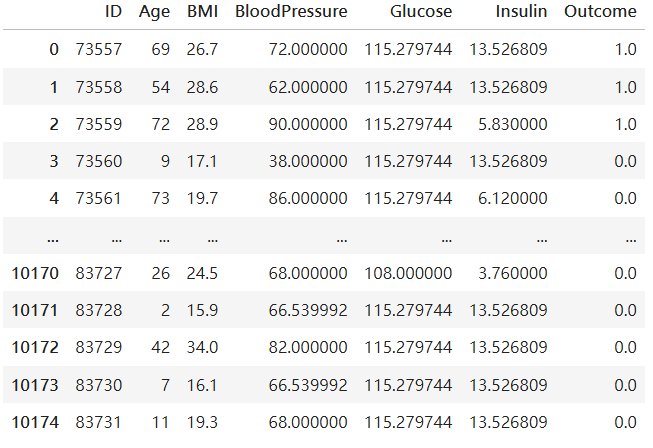


Figure 10: Merged data (Processed)

In Fig.10,

## Split data & Feature Scaling ‘

dd

# Result (list the result [acc/auc/precision..] / list the hyperparameters used/adjusted in the experiment in TWO dataset)

# Discussion (what u find/observe in the experiment)

# Conclusion (summarize what u achieved in the prj & any improvements / future work)

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