Predicting Diabetes Based on Various Factors Using Decision Tree Analysis

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Abstract

Each year, many patients learn that they have diabetes and are left wondering what could have done to prevent the diagnosis. This paper uses decision tree modeling to investigate which predictors of the Healthcare Diabetes dataset from kaggle are important in predicting an outcome of diabetes. In this study, after exploratory data analysis, the data was split into a training and testing set that will be used to build a decision tree. The performance was evaluated using standard classification metrics, including accuracy, precision, recall, and F1 score. Our results provided that glucose level emerged as a robust predictor of diabetes. This study contributed to the growing body of literature on diabetes prediction. These findings allow for early intervention measures, that can be used to provide a foundation for future research in diabetes risk assessment.

Keywords

Decision Trees, Diabetes, Machine Learning,

1 Introduction

According to the American Diabetes Association, about 11.3 percent of Americans, or about 37.3 million people, have diabetes. Of those 37.3 million people, about 28.7 million were actually diagnosed with diabetes, while the remaining 8.6 million were left undiagnosed (Diabetes). Those left undiagnosed are at risk for even more serious illness if left untreated. Diabetes is a disease where your body does not create enough insulin, or use it properly, in order to get glucose into your cells and use it for energy (Diabetes Overview).

There are two types of diabetes that the majority of patients have: type 1 or 2. The bodies of people that have type 1 diabetes do not make any insulin so they must take a daily insulin shot. Whereas individuals who have type 2 diabetes produce insulin, but their bodies do not use it properly so they are treated either by exercise, taking on a diet, or in some cases use of various medicines and/or insulin (Difference). Therefore, it is very important that your body has a normal glucose level. In this paper, I will be working to determine the pre-existing factors that can be used in order to predict if a person may have diabetes. Establishing the predictors is very important to me as many of my family members have a long history of suffering from this disease. Therefore, this information could directly allow myself and my family members to be proactive in terms of prevention and care. It is important to better predict this disease to save people from unnecessary suffering.

Previously, the prediction of diabetes has been studied using alternative machine learning models. Specifically in Sisodia's paper, it focused on the "Prediction of Diabetes using Classification Algorithms", they worked through the topic by producing results using support vector machine and Naive Bayes classifier. In Sisodia's paper they were able to get to an accuracy level of 76.3 percent, which I hope to exceed using a different machine learning model (Deepti Sisodia (2018)). In this paper, I will be continuing the investigation with a different data set using decision trees to better understand the predictors of diabetes.

In this paper the specific research question that I will be focusing on is: how can we use machine learning models, specifically decision trees, in order to identify individuals that may have already been or are at risk at developing diabetes? This will be researched using a data set that contains various metrics on one's health that will be described in the next section of the paper.

The rest of the paper is organized as follows. The data will be presented in Section 2. The methods are described in Section 3. The results are reported in Section 4. A discussion concludes in Section 5.

2 Data

In order to study the proposed research question on the topic of diabetes, I searched through many databases in order to find a set that had all of the information I was looking for. I was searching for a data set including health metrics that included correlations to diabetes such as weight or glucose levels. This led me to further research on the impact of BMI on diabetes patients. This then became a predictor for my data set. After exploration, I was able to find a data set entitled "Healthcare Diabetes Data set" on the website Kaggle. The data set was originally sourced from the National Institute of Diabetes and Digestive and Kidney Diseases. The data encompasses eight different predictors including: pregnancies, glucose, blood pressure, skin thickness, insulin, BMI, diabetes pedigree function, and age. In Table 1 I will provide the first few lines of the data set in order to provide more information on these predictors and their values.

Table 1: Head of the Dataset

Pregnancies	Glucose	BloodPressure	SkinThickness	Insulin	BMI	DiabetesPedigreeFunction	Age	Outcome
6	148	72	35	0	33.60	0.63	50	1
1	85	66	29	0	26.60	0.35	31	0
8	183	64	0	0	23.30	0.67	32	1
1	89	66	23	94	28.10	0.17	21	0
0	137	40	35	168	43.10	2.29	33	1
5	116	74	0	0	25.60	0.20	30	0

The predictors listed above will be represented in my research as the following variables. 'Pregnancies' will provide the number of times an entry has been pregnant. 'Glucose' will provide the plasma glucose concentration over two hours using the results of an oral glucose tolerance test on a entry. 'BloodPressure' gives the diastolic blood pressure in mm Hg of an entry. 'SkinThickness' will provide the triceps skin fold thickness in mm. 'Insulin' will include a test on two hour serum insulin in mu U/ml. 'BMI' will provide a calculation of weight (kg) divided by height (m^2). 'DiabetesPedigreeFunction' will provide a genetic score of diabetes. 'Age' will simply be the entry's age at the time of the collection. Following this paragraph, I will provide the link to the dataset that I will be using as well as including some descriptive statistics as seen in Table 2 including the mean, standard deviation, and median.

Dataset link: Healthcare Diabetes

Table 2: Descriptive Statistics of Healthcare Diabetes Dataset

Variable	Mean	SD	Median
Pregnancies	3.74	3.32	3.00
Glucose	121.10	32.04	117.00
BloodPressure	69.13	19.23	72.00
SkinThickness	20.82	16.06	23.00
Insulin	80.13	112.30	37.00
BMI	32.14	8.08	32.20
DiabetesPedigreeFunction	0.47	0.33	0.38
Age	33.13	11.78	29.00

Another valuable piece of information for understanding our patients is seeing the range of the dataset. In Figure 1, we are able to see the spread of each predictor in our dataset. We can see that the majority of our patients are in the 20 to 30 year old range and that the distribution is skewed to the right. The blood pressure predictor provides us with a slightly normal distribution with the average being around 70 beats per minute. The BMI distribution is somewhat normal as well, with a slight right skew. The diabetes pedigree function, however, is very skewed to the right. Glucose levels appear to be normal. Insulin levels appear to be very skewed to the right with the majority of values being 0. The outcome distribution is exactly as expected with only values of 0 or 1. The number of pregnancies predictor also supplied a right skew but we know this to be valid as most people are not having four or more children, but there are some outliers. The final predictor graphed was the skin thickness, this predictor displayed a right skew.

3 Methods

Various methods will be used to complete the analysis necessary for this paper. I have begun by exploring basic descriptive statistics in the previous section in order to gain an understanding of my data set. Next, we will move on to model testing, where we will perform both decision tree analysis in order to determine what predictors prove to be necessary in predicting if a patient will have the outcome 1 of having diabetes.

Figure 1: Each variable represented as a histogram

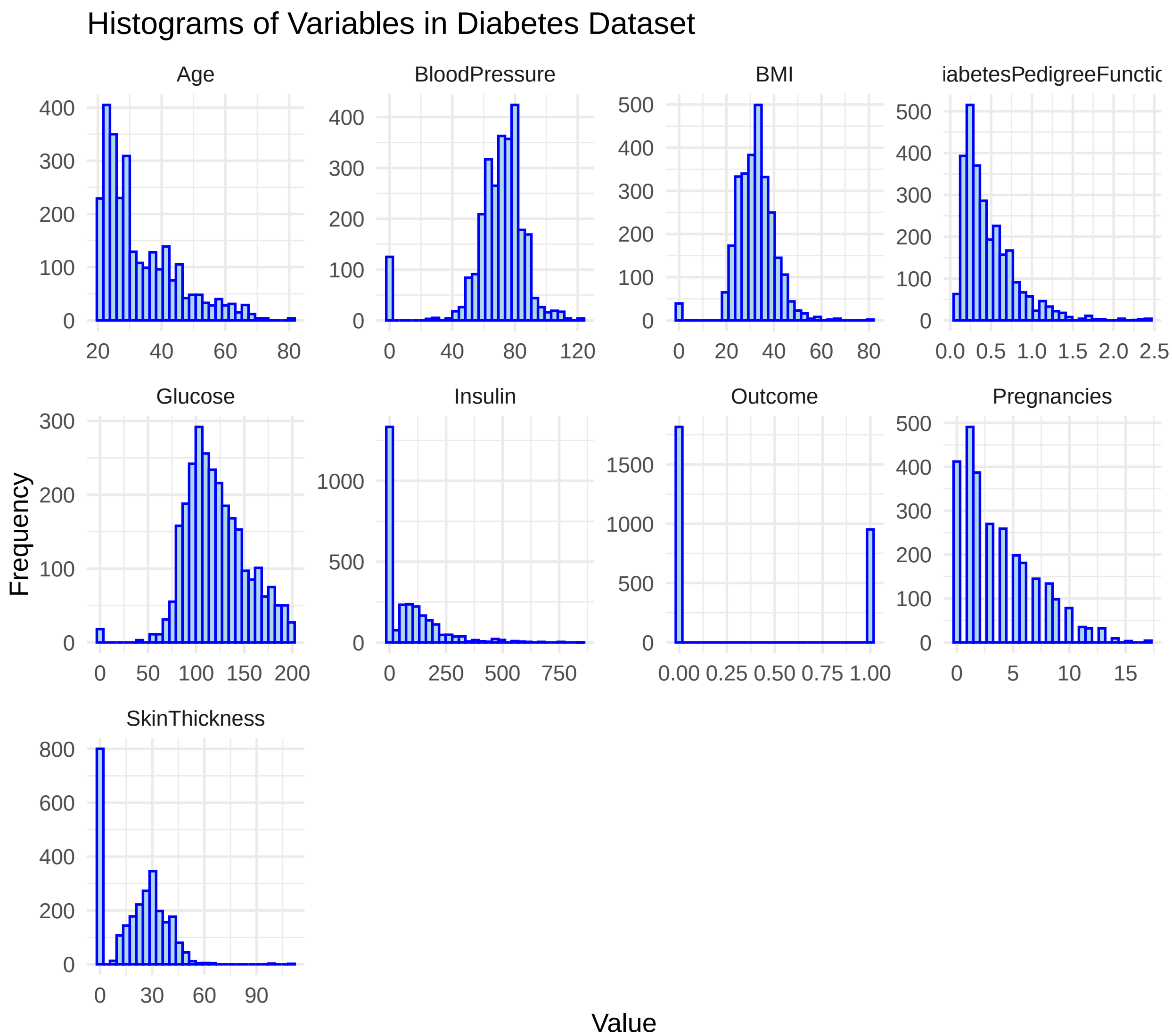
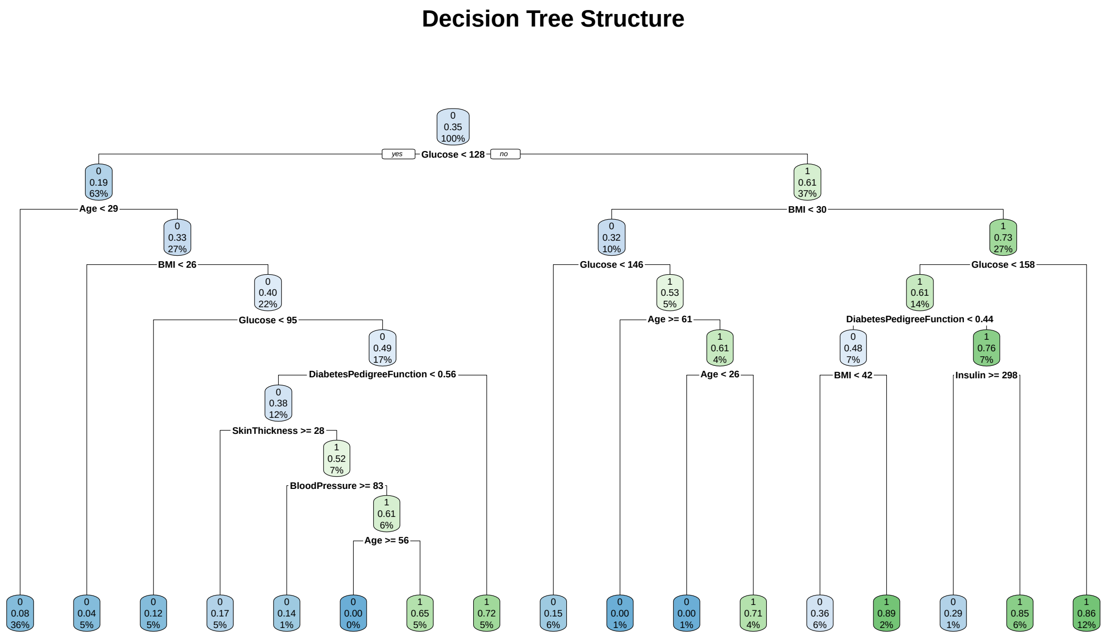


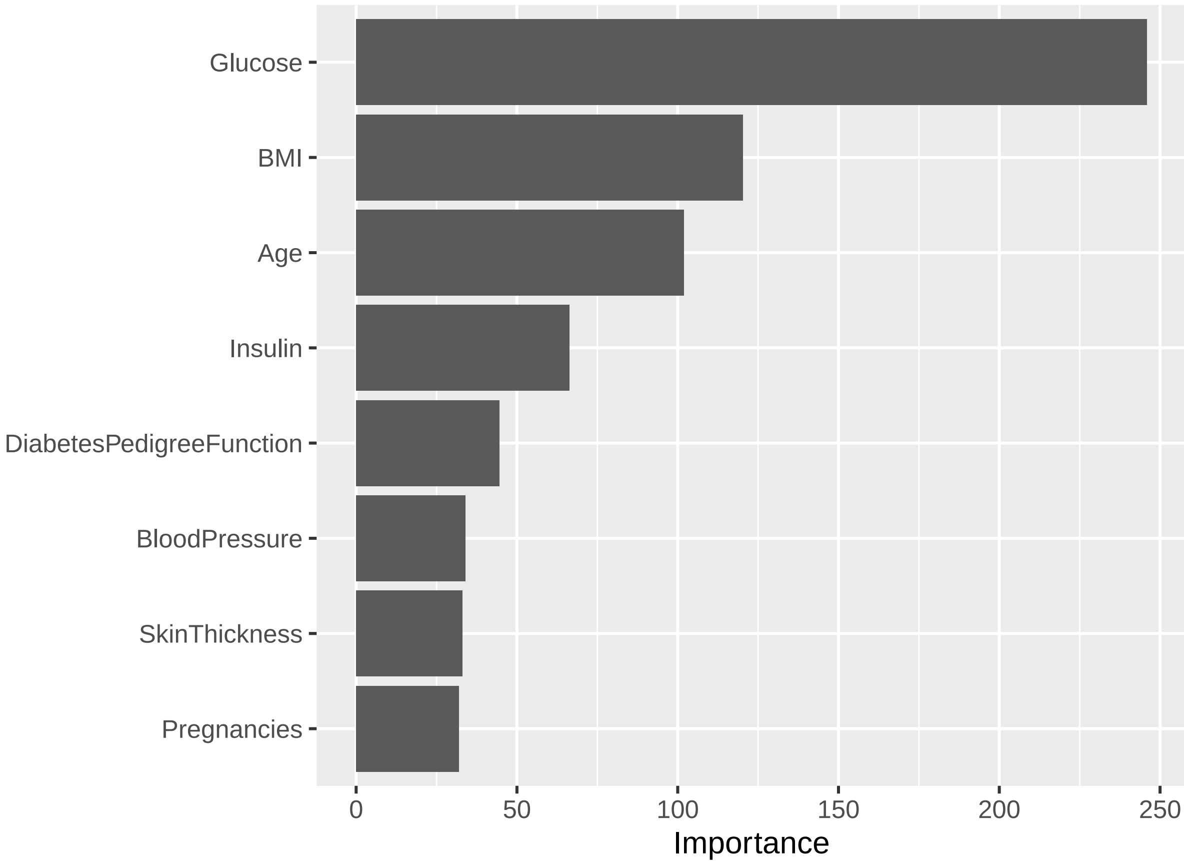
Figure 2: Decision Tree Structure



To begin, I will provide an explanation of what a decision tree is and why it is useful in this case. A decision tree is considered to be an example of supervised learning used for regression and classification. Through my analysis I will present a tree, this tree will begin at the top with a decision root node, which is the point where you make a decision. Following down there are subsequent sub trees that have other decision nodes. Finally, at the bottom of each tree you reach a leaf node, where it is the output of the decision and there are no further branches off of this.

I will then begin to create my model for my decision tree by splitting the data into a test and training set. The training set will encompass 80 percent of the data whereas the test set will only have 20 percent. This method of splitting will help to prevent any biases that may be attributed from imbalances in the distribution of critical features. After creating these two sets I will now be ready to build the model. This will be done by using the rpart function in R, where the method will be 'class' as this is a binary model. We will then see in Figure 2 the structure of the decision tree created. Starting at the root node at the top of the graph, it shows the overall probability of having diabetes in this dataset. 35 percent of the patients were classified as having diabetes (or the outcome of 0). The node then asks if the the glucose level of the patient is less than 128. If yes, then it moves down to the left child node. 63 percent have glucose level less than 128 with a diabetes outcome of 0 probability of 19 percent. The child node then asks if the patients age is less than 29 years old. If yes, the chance of not having diabetes is eight percent. The rest of the tree is described similiarly but with different values of probability, predictors, and outcomes.

Figure 3: Variance Importance Plot



4 Results

After completing our methods section, we can now move on to talk about the results of our model. Based on Figure 3, we can see that the top three predictors are glucose, BMI, and age. The result of glucose being of the greatest importance makes complete sense with medical knowledge of diabetes as a patient that has high amounts of glucose in their bloodstream could have type 2 diabetes. This is known due to glucose not being absorbed by insulin as these patients do not use insulin properly. We can see that almost all of the outcomes are explained by glucose. The next predictor that is successful in predicting a large amount of the data is the patient's BMI. This aligns on a medical standpoint as patients who have larger BMI values are more susceptable to getting type 2 diabetes as they are considered to be obese. Based on my results, BMI was able to predict about half of the outcomes. The last predictor that proved to be valuable in predicting if someone has diabetes is age. This result is somewhat medically backed but not entirely a result that I expected. Often times people that are older have diabetes due to numerous factors but it is not as common for younger patients.

Looking at Table 3, we can see that the accuracy of our model is 0.82, which is high so it will be satisfactory. This tells me that we classify correctly 82 percent of the time out of the total instances. The next metric we will look at is precision. We were able to get to 72 percent. This is the ratio of correctly predicted positive observations to the total predicted positives. Looking at recall, we were able to correctly identify about 74 percent of the actual positive instances. This is pretty strong and will be considered satisfactory. The final metric that we have is the F1 score, which is the harmonic mean of precision and recall, which we were able to get a value of 0.73. This indicates a balanced performance.

Table 3: Decision Tree Results

Metric	Value
Accuracy	0.82
Precision	0.72
Recall	0.74
F1 Score	0.73

Finally we can now look at Figure 4, to see the confusion matrix heatmap for our decision tree analysis. Out of the 371 patients that had an outcome of not having diabetes, the model correctly identified 318 of them. The model only incorrectly missed a positive diagnosis 53 times. In terms of predicting that the patients had diabetes, the model predicted 136 patients had diabetes out of the 183 that actually did. In turn it predicted that 47 of the patients did not have diabetes when in fact they did. This shows that the model does a pretty good job in identifying if the patient has diabetes but does an even better job identifying when the patient does not have diabetes.

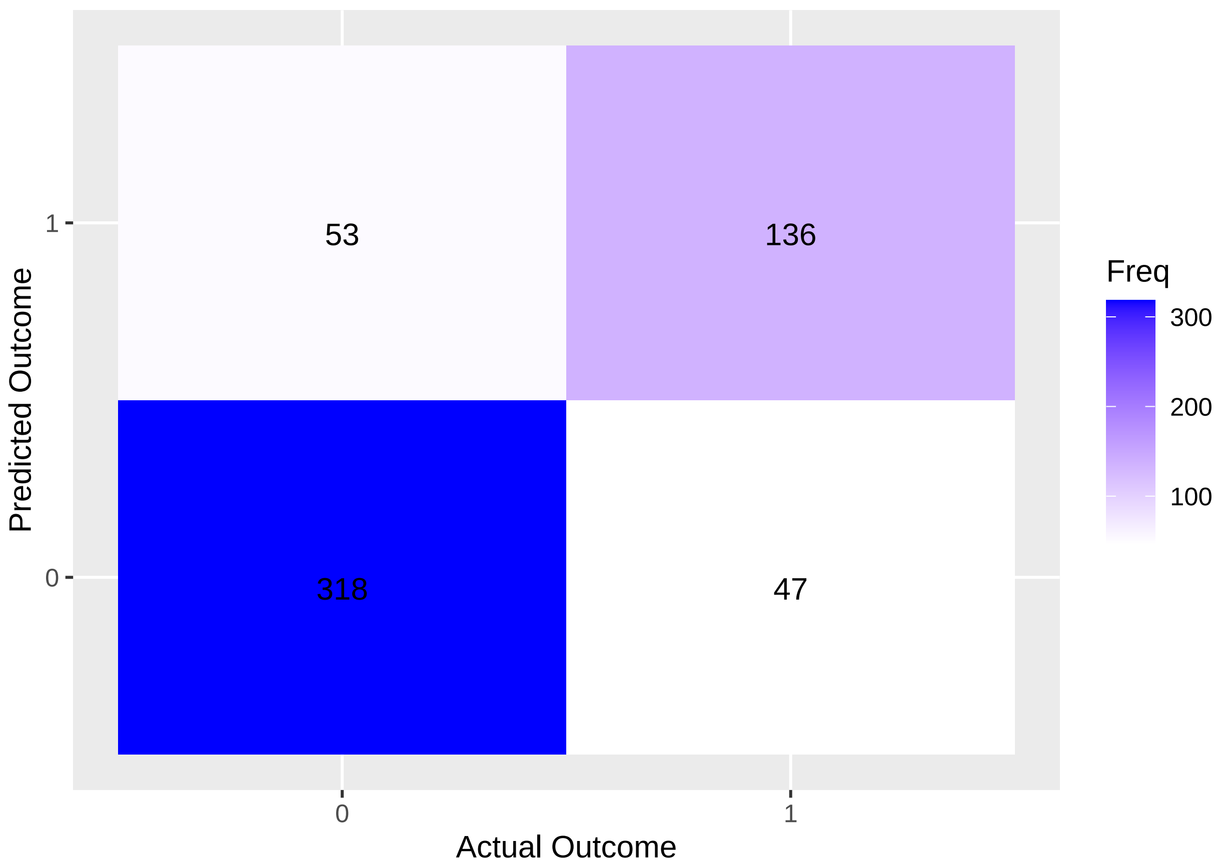
5 Discussion

Currently, this study is limited as we are set within the bounds of this data set. In future studies I can include more predictors in order to see if there are any other factors that could be used to predict diabetes. Moreover, I can have an even larger data set in order to ensure my accuracy. Other data sets may suggest that certain predictors are not helpful in predicting diabetes that my model did not pick up on due to the metrics of my data.

This study can be expanded further by using other machine learning techniques to study the data. This can be used to cross-validate my results to ensure that I am are providing the most accurate information. Other machine learning techniques could include random forest and logistic regression to give even more understanding of the data.

As this is a paper dealing with sensitive medical data, I have many limitations in order to be ethical as well as respecting patient privacy. Based on the data set collected I should be able to ensure full patient privacy as names or any very unique identifiers are not listed with each entry. I simply have age for each entry so I do not have to worry as much for the sake of privacy as this cannot be traced back to a particular person. In terms of our direct models I may have to disregard some assumptions as they may not fit with real world data. If something unexpected happens, I may have to reconsider the data set used and consider finding a new one. This will be done by a case-by-case scenario and will be investigated thoroughly before making any decisions.

Figure 4: Confusion Matrix Heatmap



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