Predicting the Onset of Diabetes

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Abstract

This study analyzes the Pima Indians Diabetes Database to develop predictive models for diagnosing diabetes based on diagnostic measurements such as glucose, BMI, insulin levels, and number of pregnancies. The dataset includes medical data from female patients of Pima Indian heritage aged 21 or older. We explored multiple predictive techniques, including logistic regression, regularized regression, tree-based methods, k-nearest neighbors, quadratic discriminant analysis, and dimensionality reduction approaches. The models were evaluated using accuracy, ROC-AUC and other metrics, cross-validation ensuring robustness. Key predictors like glucose and BMI were consistently significant across models. Random Forest and logistic regression emerged as top performers in overall predictive accuracy and interpretability. The study underscores the importance of data-driven approaches in healthcare and highlights actionable insights for improving diabetes diagnostics.

1. INTRODUCTION

Diabetes Mellitus is a group of diseases characterized by chronic hyperglycemia. Type I is due to a lack of the hormone used to control blood glucose levels, insulin, as a result of damage to the pancreas, the organ that secretes insulin. Type II diabetes is much more common and is caused by insulin resistance and impaired secretion of insulin. The chronic hyperglycemia of diabetes can lead to widespread damage across virtually all parts of the body; it can cause or lead to increased risk of immunosuppression, retinopathy, cardiovascular disease, kidney disease, neuropathy, diabetic ketoacidosis, and life-threatening disease such as diabetic ketoacidosis.

Diabetes has become a significant public health concern due to its increasing prevalence and substantial economic impact. The number of adults living with diabetes worldwide has surpassed 800 million, more than quadrupling since 1990 [4]. In the United States, the total annual cost of diabetes reached $412.9 billion in 2022, including $306.6 billion in direct medical costs and $106.3 billion in indirect costs [3]. This growing incidence and associated financial burden underscore the urgent need for effective public health interventions and policies to address the diabetes epidemic. The combination of a high prevalence of disease and the existence of good treatments to prevent or slow complications means that early detection of diabetes can have significant benefits.

The Pima Indians Diabetes Database, developed by the National Institute of Diabetes and Digestive and Kidney Diseases, provides an opportunity to explore predictive models for diabetes diagnosis using clinical and demographic data. Despite its extensive use in machine learning research, there is limited focus on comparing diverse predictive techniques tailored to healthcare settings.

This study aims to evaluate and compare multiple modeling approaches, including logistic regression, tree-based methods, and dimensionality reduction techniques, to identify key predictors and optimize diagnostic accuracy.

2. METHODS

2.1 Pre-processing

To begin the analysis, we first examined the dataset, including the distributions of each predictor as seen in (Figure 1). This clearly demonstrated a lack of any degenerate distributions, but showed a concerning trend of zero values for predictors that physiologically should not be zero such as glucose or BMI. To correct these values, we converted them into missing values (Figure 2) and performed predictive mean matching using the MICE package in R [2] (Figure 3). Afterwards, the data was checked for correlation (Figure 4) and for multicolinearity. Using a correlation threshold of 0.75 and VIF threshold of 10, no offending predictors were found, and thus we could proceed.

After completion of imputation, we proceeded to center and scale the data set. Cook's distance was used to identify outliers, and then any influential points with a cook's distance of $4/(n-k-1)$ were removed.

2.2 Models

The models chosen were logistic regression with all predictors, stepwise logistic regression using the AIC criteria, random forests, QDA, and KNN from k=1 to k=20. We chose to optimize the AUC and accuracy metrics and used 10 fold cross-validation.

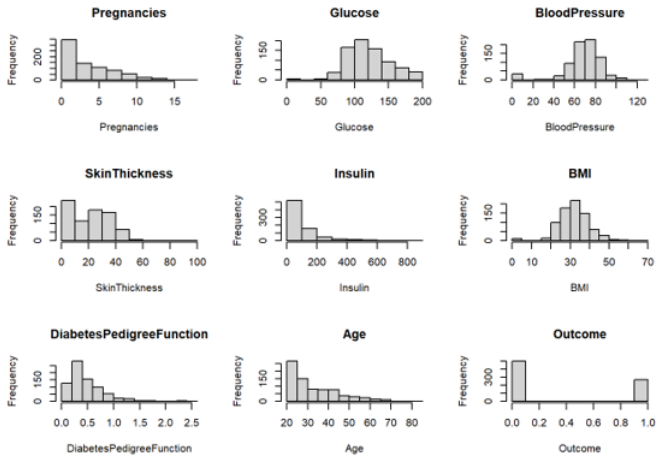


Figure 1: Histogram of each predictor before preprocessing.

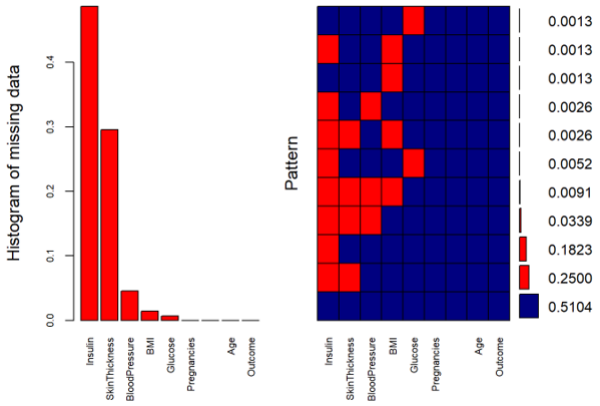


Figure 2: MICE output showing a histogram of missing data by predictor on the left and a graph on the left showing combinations of missing values, with the missing values in red for each.

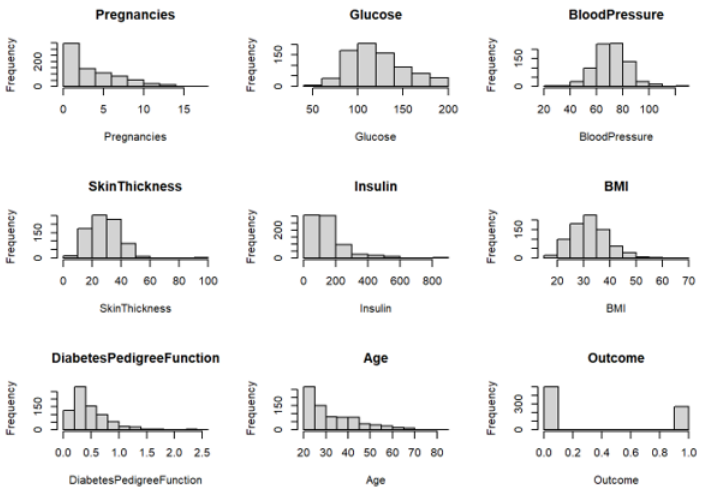


Figure 3: Histogram of each predictor after performing imputation.

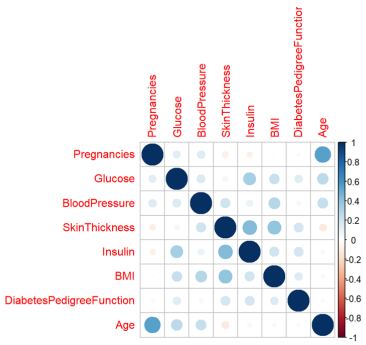


Figure 4: Correlation plot of all predictors in the dataset. Of note, the highest correlation is between age and pregnancy at 0.6, less than the threshold of 0.75

3. RESULTS

We tested several predictive models on the Pima Indians Diabetes Database, including logistic regression, stepwise logistic regression, k-nearest neighbors (kNN), quadratic discriminant analysis (QDA), and Random Forest. Model performance was assessed using metrics such as accuracy, ROC-AUC, precision, recall, and F1-score, with 10-fold cross-validation ensuring reliability. We paid special attention to AUC due to its importance to physicians.

The full logistic regression model, incorporating all predictors, achieved an accuracy of 81.1% and an AUC of 0.892, with significant predictors including glucose, BMI, pregnancies, and diabetes pedigree function (Figure 6).

Stepwise logistic regression reduced the model to these key predictors while maintaining an AUC of 0.893 and an accuracy of 80.3%, providing a more interpretable yet robust solution(Figure 7).

Random Forest demonstrated strong performance with an AUC of 0.879 and an accuracy of 79.8%. It identified glucose, BMI, insulin, and pregnancies as the most influential predictors, further validating their importance in diabetes prediction (Figure 8).

KNN achieved an accuracy of 79.4% and an AUC of 0.751. Performance improved as the number of neighbors increased, with k=10 striking a balance between overfitting and underfitting (Figure 10).

QDA provided competitive performance with an AUC of 0.864 and an accuracy of 80.2%. The model effectively captured non-linear relationships, as illustrated by its curved decision boundaries (Figure 9).

4. DISCUSSION

Key predictors like glucose and BMI were consistently significant across all models, highlighting their strong asso-

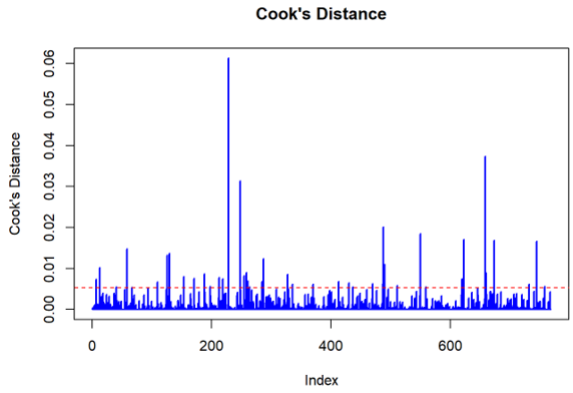


Figure 5: Plot of cook's distance for all points in the dataset, with the threshold of $4/(n-k-1)$ depicted with the red line.

Model	Accuracy	AUC	F1
KNN	0.794	0.751	0.668
Logistic (full)	0.811	0.892	0.705
Logistic (stepwise)	0.803	0.893	0.694
QDA	0.802	0.864	0.688
Random Forest	0.798	0.879	0.679

Table 1. Table showing a comparison of accuracy, AUC, and F1 scores for each model.

```
##
## Call:
## glm(formula = Outcome ~ ., family = binomial, data = diabetes.complete)
##
## Coefficients:
##                           Estimate Std. Error z value Pr(>|z|)
## (Intercept)              -1.06818    0.12052  -8.863  < 2e-16 ***
## Pregnancies               0.73329    0.13799   5.314 1.07e-07 ***
## Glucose                   1.54771    0.17070   9.067  < 2e-16 ***
## BloodPressure            -0.07534    0.13079  -0.576    0.565
## SkinThickness            -0.06767    0.15328  -0.441    0.659
## Insulin                   0.49179    0.16569   2.968    0.003 **
## BMI                       0.91598    0.17793   5.148 2.63e-07 ***
## DiabetesPedigreeFunction  0.51566    0.11873   4.343 1.40e-05 ***
## Age                      -0.00367    0.13418  -0.027    0.978
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 928.12  on 720  degrees of freedom
## Residual deviance: 510.99  on 712  degrees of freedom
## AIC: 528.99
##
## Number of Fisher Scoring iterations: 6
```

Figure 6: Output from the summary function in R when called on the full logistic regression model.

```
## Call:
## glm(formula = Outcome ~ Glucose + BMI + Pregnancies + DiabetesPedigreeFunction,
##     family = binomial, data = diabetes.complete)
##
## Coefficients:
##                           Estimate Std. Error z value Pr(>|z|)
## (Intercept)              -1.0695     0.1176  -9.093  < 2e-16 ***
## Glucose                   1.7020     0.1468  11.596  < 2e-16 ***
## BMI                       0.8522     0.1263   6.749 1.49e-11 ***
## Pregnancies               0.6683     0.1125   5.939 2.87e-09 ***
## DiabetesPedigreeFunction  0.5025     0.1152   4.361 1.30e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
##     Null deviance: 926.82  on 720  degrees of freedom
## Residual deviance: 531.33  on 716  degrees of freedom
## AIC: 541.33
##
## Number of Fisher Scoring iterations: 5
```

Figure 7: Output from the summary function in R when called on the stepwise logistic regression model.

```
##                           MeanDecreaseGini
## Pregnancies                       22.71057
## Glucose                           90.51467
## BloodPressure                     20.52261
## SkinThickness                     30.62870
## Insulin                           49.26548
## BMI                               44.23437
## DiabetesPedigreeFunction          31.13513
## Age                               32.69667
```

Figure 8: Output from R showing the mean decrease of Gini impurity, which is a measure of feature importance.

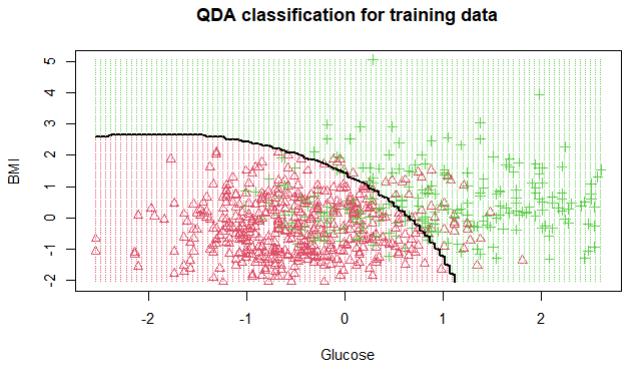
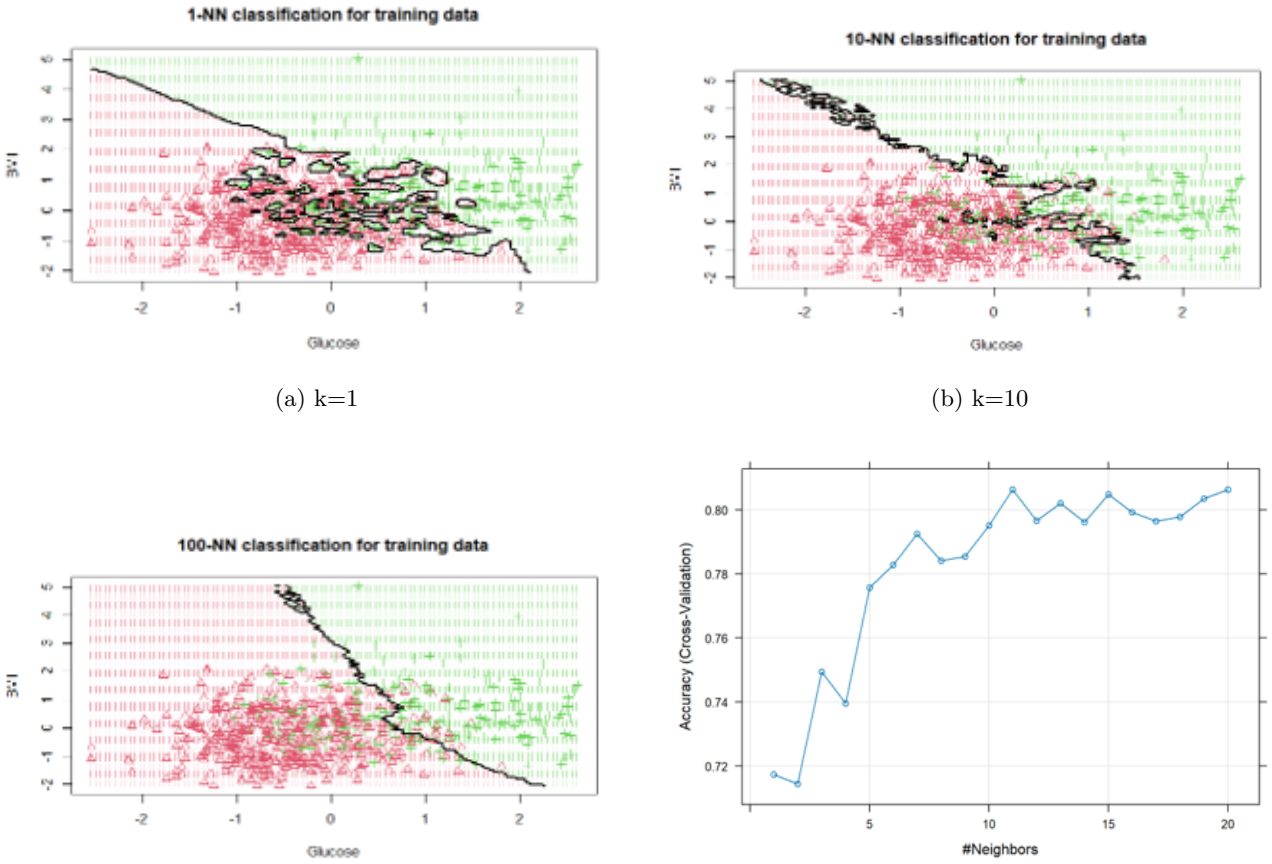


Figure 9: Distribution boundary for the QDA model for glucose vs. BMI.



(a) k=1

(b) k=10

(c) k=100

(d) Accuracy Graph

Figure 10: Plots of decision boundaries for different K values (k=1, k=10, k=100) alongside a graph showing the accuracy for each KNN model by their k value.

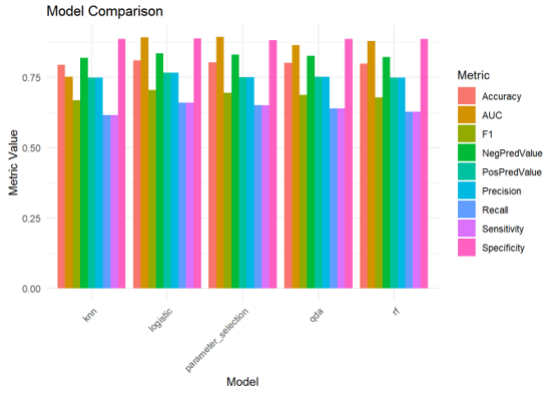


Figure 11: Graph showing a comparison of accuracy, AUC, F1, negative predictive value, positive predictive value, precision, recall, sensitivity, and specificity of each model.

ciation with diabetes outcomes. Random Forest further emphasized the importance of insulin and pregnancies, while logistic regression provided a clear ranking of feature significance.

Logistic regression and Random Forest emerged as the top-performing models, balancing predictive accuracy and interpretability. While Random Forest captured complex relationships between predictors, logistic regression offered greater transparency for identifying key factors associated with diabetes.

While Random Forest identified insulin as an important predictor, logistic regression did not include it as statistically significant. This discrepancy likely arises from the difference in how these models handle relationships within the data—Random Forest captures non-linear interactions, whereas logistic regression relies on linear associations and statistical significance. If glucose and BMI already explain most of the variance, the additional predictive power of insulin becomes negligible for the logistic regression model.

Moreover, insulin is not a primary diagnostic criterion for diabetes. Diabetes is typically diagnosed based on: Fasting blood glucose levels (126 mg/dL), HbA1c levels (6.5%), and Oral glucose tolerance test (OGTT) [1].

Insulin levels are rarely included because they vary widely within and among individuals, increasing increasing after meals and decreasing during fasting periods. This variability makes it challenging to obtain a single measurement that accurately reflects an individual's typical insulin status.

5. CONCLUSION

By applying robust evaluation metrics and prioritizing model interpretability, this study provides actionable insights for clinicians and researchers seeking effective diabetes screening strategies. Our results emphasize the importance of glucose and BMI as key predictors of diabetes across all models.

Future work should explore additional preprocessing techniques, such as **winsorization** to address extreme outliers and **principal component analysis (PCA)** to reduce multicollinearity among predictors. Advanced modeling approaches, including **support vector machines (SVM)** and **neural networks**, could be investigated to potentially improve predictive accuracy and better handle complex, non-linear relationships in the data. Furthermore, incorporating external datasets and addressing potential biases specific to the Pima Indian population could enhance the generalizability of the findings.

This study highlights the value of data-driven approaches in healthcare and underscores the need for continuous improvement in diabetes screening, ensuring more precise and actionable outcomes for clinical applications.

REFERENCES

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