# Diabetes Prediction

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### Summary

In this project we attempt to build a model to predict diabetes disease. We compared a decision tree model and naive bayes model and found the decision tree is stronger in this context. We used f2-score as our scoring function because detecting diabetes is the priority: a false negative could be much worse then a false positive.

In the test dataset: the decision tree model correctly detected 8283 of 10604 positive cases (recall rate is about 78%). This result does come at a fairly significant cost in terms of false positives (precision rate is about 30%) with 19650 false positives. Depending on the actual cost of false positive this may need significant improvement to be a viable screening model.

### Introduction

In Canada and the USA approximately 10% of people are living with diabetes. In Canada in 2023 approximately 3.7 million people were living with diabetes and in the USA in 2021 approzimately 38.4 million people were living with diabetes. ("Snapshot of Diabetes in Canada, 2023" (2023)) In the USA it is the 8th leading cause of death. (Rios et al. (2017)) Globally an estimated 44% of people living with diabetes are undiagnosed. (Stafford et al. (2025))

In this project we try to predicted diabetes disease based on common health factors. A reliable model could help to prescreen people and recommend following up with a physician for people who are at risk. Given the large number of people living with undiagnosed diabetes this could potentially have a significant positive impact of world health.

The analysis uses the American CDC Behavioural Risk Factor Surveillance System (BRFSS) 2015 Diabetes Health Indicators dataset (UCI ID 891), containing 253,680 survey responses with 21 health-related features and a binary diabetes outcome (0 = no diabetes/pre-diabetes, 1 = diabetes). (Dane and Teboul (2021))

No missing values were present and all features were already encoded numerically. The target classes is imbalanced ( 86% non-diabetic, 14% diabetic).

## Methods

This analysis was performed in Python 3.11.6 (*Python 3.11.6 Documentation* 2021-2025). Additionally, here is a list of the Python packages used within the analysis with brief explanation:

| Package | Version | Use case | Reference |
|---|---|---|---|
| `numpy` | `1.26.4` | General analysis use | *NumPy Documentation* (2008-2022) |
| `pandas` | `2.1.2` | Data management/processing | team (2020), McKinney (2010) |
| `pandera` | `0.27.0` | Data valiadion | Bantilan (2020) |
| `altair` | `5.1.2` | Generating plots | VanderPlas et al. (2018), Satyanarayan et al. (2017) |
| `scikit-learn` | `1.3.2` | Model creation and evaluation | Pedregosa et al. (2011) |
| `ucimlrepo` | `0.0.7` | Data extraction | Kelly, Longjohn, and Nottingham (2021) |
| `deepchecks` | `0.18.1` | Data validation | Chorev et al. (2022) |
| `click` | `8.3.1` | Script tool | Pallets (2020) |
| `quarto` | `1.8.26` | Report creation | Allaire et al. (2025) |
| `tabulate` | `0.9.0` | Table formatting | Astanin (2025) |

### Modeling Approach

### Results

## EDA

### Data Summary

Table 2: Description of the training data.

| Unnamed: 0 | count | mean | std | min | 25% | 50% | 75% | max |
|---|---|---|---|---|---|---|---|---|
| HighBP | 177576.0 | 0.4293 | 0.495 | 0.0 | 0.0 | 0.0 | 1.0 | 1.0 |
| HighChol | 177576.0 | 0.4228 | 0.494 | 0.0 | 0.0 | 0.0 | 1.0 | 1.0 |
| CholCheck | 177576.0 | 0.9627 | 0.1896 | 0.0 | 1.0 | 1.0 | 1.0 | 1.0 |
| BMI | 177576.0 | 28.385 | 6.5916 | 12.0 | 24.0 | 27.0 | 31.0 | 98.0 |
| Smoker | 177576.0 | 0.4433 | 0.4968 | 0.0 | 0.0 | 0.0 | 1.0 | 1.0 |
| Stroke | 177576.0 | 0.0407 | 0.1976 | 0.0 | 0.0 | 0.0 | 0.0 | 1.0 |
| HeartDiseaseorAttack | 177576.0 | 0.094 | 0.2919 | 0.0 | 0.0 | 0.0 | 0.0 | 1.0 |
| PhysActivity | 177576.0 | 0.7563 | 0.4293 | 0.0 | 1.0 | 1.0 | 1.0 | 1.0 |
| Fruits | 177576.0 | 0.6351 | 0.4814 | 0.0 | 0.0 | 1.0 | 1.0 | 1.0 |
| Veggies | 177576.0 | 0.8122 | 0.3905 | 0.0 | 1.0 | 1.0 | 1.0 | 1.0 |
| HvyAlcoholConsump | 177576.0 | 0.0563 | 0.2305 | 0.0 | 0.0 | 0.0 | 0.0 | 1.0 |
| AnyHealthcare | 177576.0 | 0.9513 | 0.2153 | 0.0 | 1.0 | 1.0 | 1.0 | 1.0 |
| NoDocbcCost | 177576.0 | 0.0845 | 0.2782 | 0.0 | 0.0 | 0.0 | 0.0 | 1.0 |
| GenHlth | 177576.0 | 2.5128 | 1.0685 | 1.0 | 2.0 | 2.0 | 3.0 | 5.0 |
| MentHlth | 177576.0 | 3.1833 | 7.4056 | 0.0 | 0.0 | 0.0 | 2.0 | 30.0 |
| PhysHlth | 177576.0 | 4.2542 | 8.7248 | 0.0 | 0.0 | 0.0 | 3.0 | 30.0 |
| DiffWalk | 177576.0 | 0.1682 | 0.374 | 0.0 | 0.0 | 0.0 | 0.0 | 1.0 |
| Sex | 177576.0 | 0.4408 | 0.4965 | 0.0 | 0.0 | 0.0 | 1.0 | 1.0 |
| Age | 177576.0 | 8.0321 | 3.0558 | 1.0 | 6.0 | 8.0 | 10.0 | 13.0 |
| Education | 177576.0 | 5.049 | 0.9863 | 1.0 | 4.0 | 5.0 | 6.0 | 6.0 |
| Income | 177576.0 | 6.0514 | 2.0729 | 1.0 | 5.0 | 7.0 | 8.0 | 8.0 |
| diabetes | 177576.0 | 0.1393 | 0.3463 | 0.0 | 0.0 | 0.0 | 0.0 | 1.0 |

Table 2 displays a numerical distribution of the dataset, where as Table 3 lists the first 5 rows transposed of the training dataset as example observations used. Both tables have been transposed from their original form for more syntactical presentation. All features of the dataset consist entirely of integer values, and by all `count` values being identically 177576 (the number of observations in the training dataset), there exist no null values, making the preprocessing step of the analysis relatively simple.

Table 3: First few rows of the training data as example observations.

| | 0 | 1 | 2 | 3 | 4 |
|---|---|---|---|---|---|
| HighBP | 0 | 0 | 1 | 0 | 1 |
| HighChol | 1 | 0 | 1 | 0 | 0 |
| CholCheck | 1 | 1 | 1 | 1 | 1 |
| BMI | 23 | 25 | 28 | 25 | 30 |
| Smoker | 0 | 0 | 0 | 0 | 1 |
| Stroke | 0 | 0 | 0 | 0 | 0 |
| HeartDiseaseorAttack | 0 | 0 | 0 | 0 | 0 |
| PhysActivity | 1 | 1 | 1 | 0 | 1 |
| Fruits | 1 | 1 | 0 | 1 | 1 |
| Veggies | 1 | 1 | 1 | 1 | 1 |
| HvyAlcoholConsump | 0 | 0 | 0 | 0 | 0 |
| AnyHealthcare | 1 | 1 | 1 | 1 | 1 |
| NoDocbcCost | 0 | 0 | 0 | 0 | 1 |
| GenHlth | 1 | 3 | 2 | 2 | 4 |
| MentHlth | 0 | 0 | 15 | 0 | 30 |
| PhysHlth | 0 | 30 | 2 | 0 | 15 |
| DiffWalk | 0 | 0 | 0 | 0 | 0 |
| Sex | 0 | 0 | 1 | 0 | 0 |
| Age | 10 | 12 | 6 | 8 | 8 |
| Education | 6 | 6 | 5 | 5 | 4 |
| Income | 8 | 7 | 6 | 7 | 4 |
| diabetes | 0 | 0 | 0 | 0 | 0 |

### Visualizations

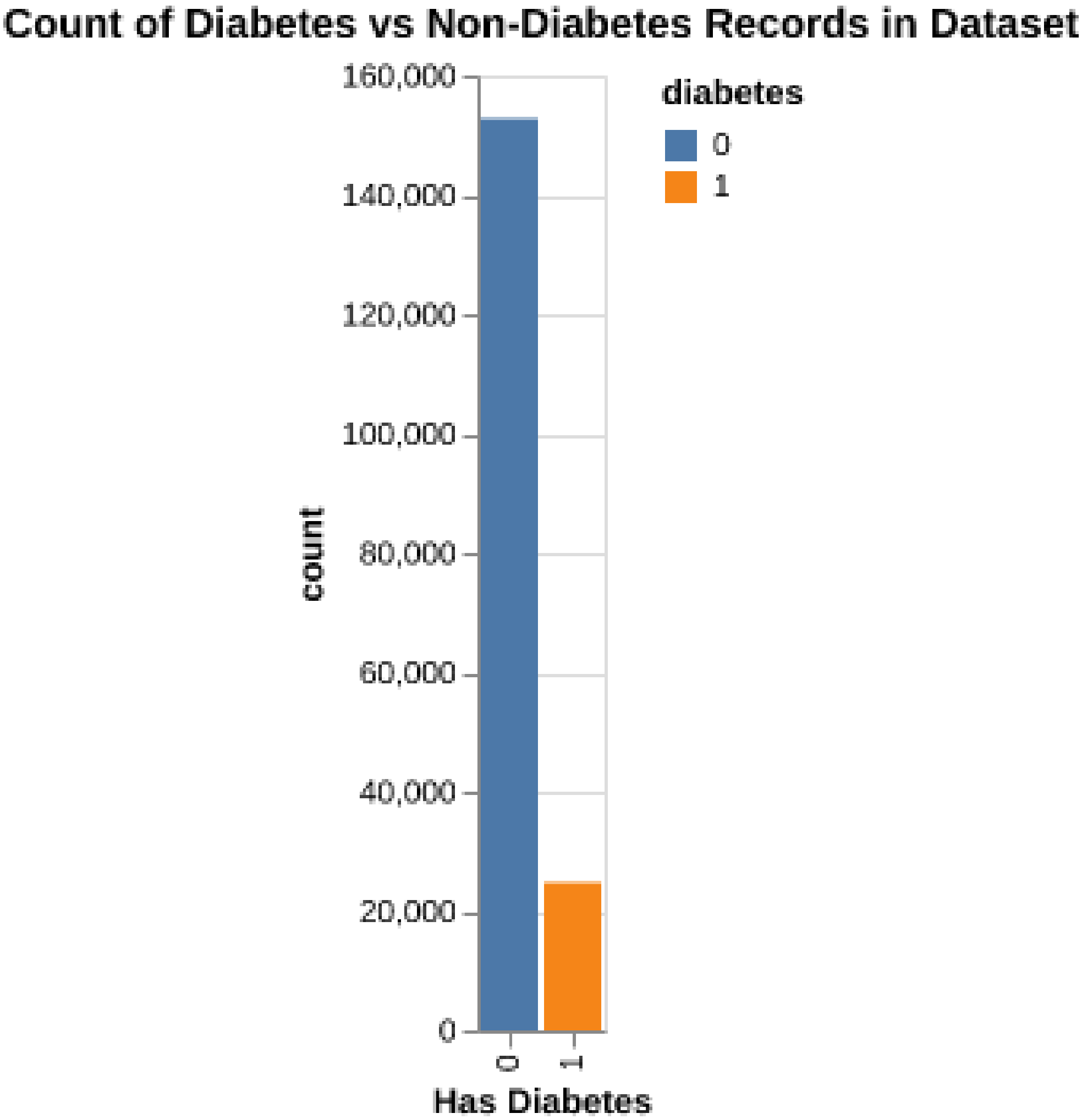

Figure 1: Frequency bar graph of the labels.

Figure 1

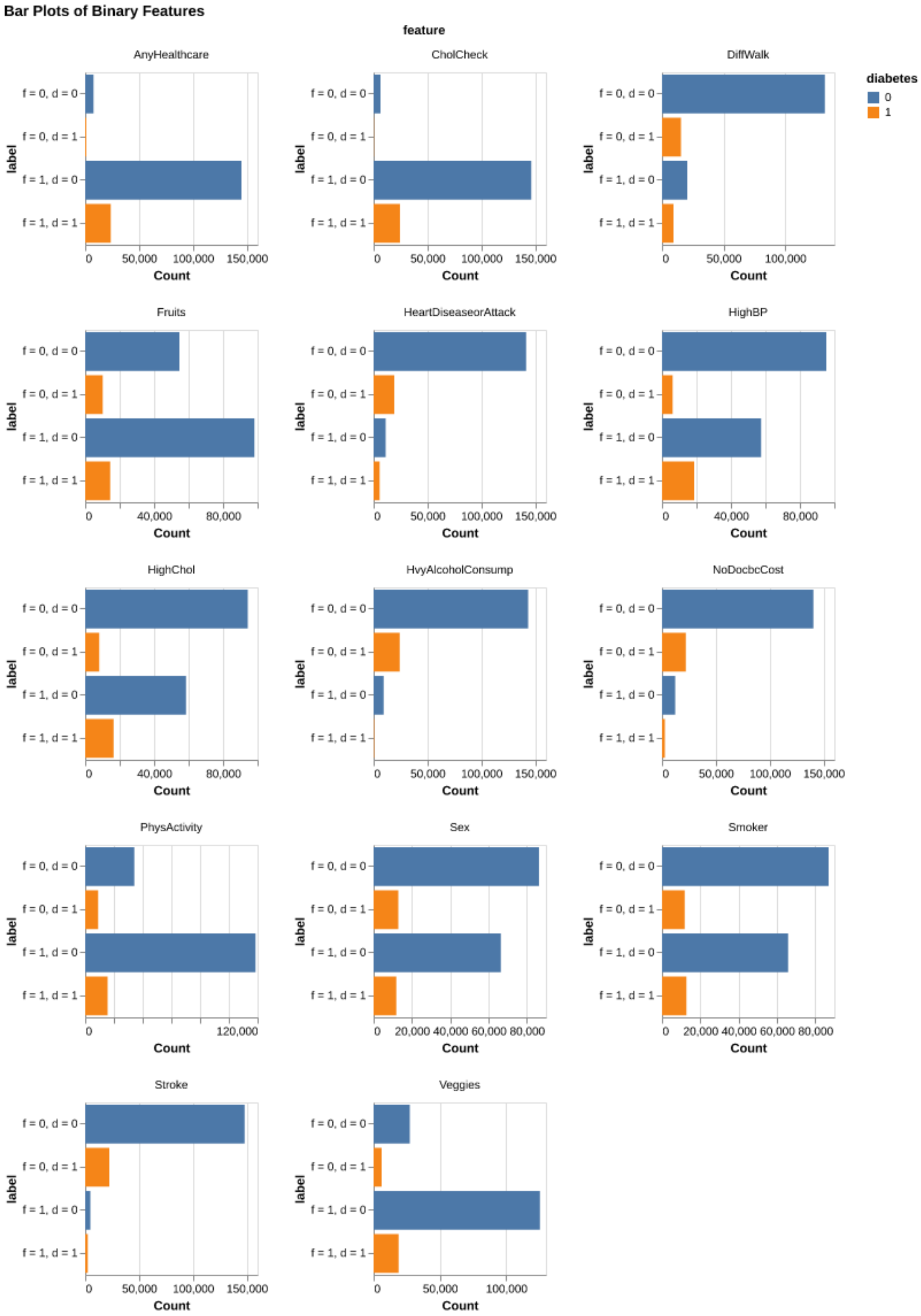

Figure 2: Frequency bar graphs of the binary features.

Figure 2

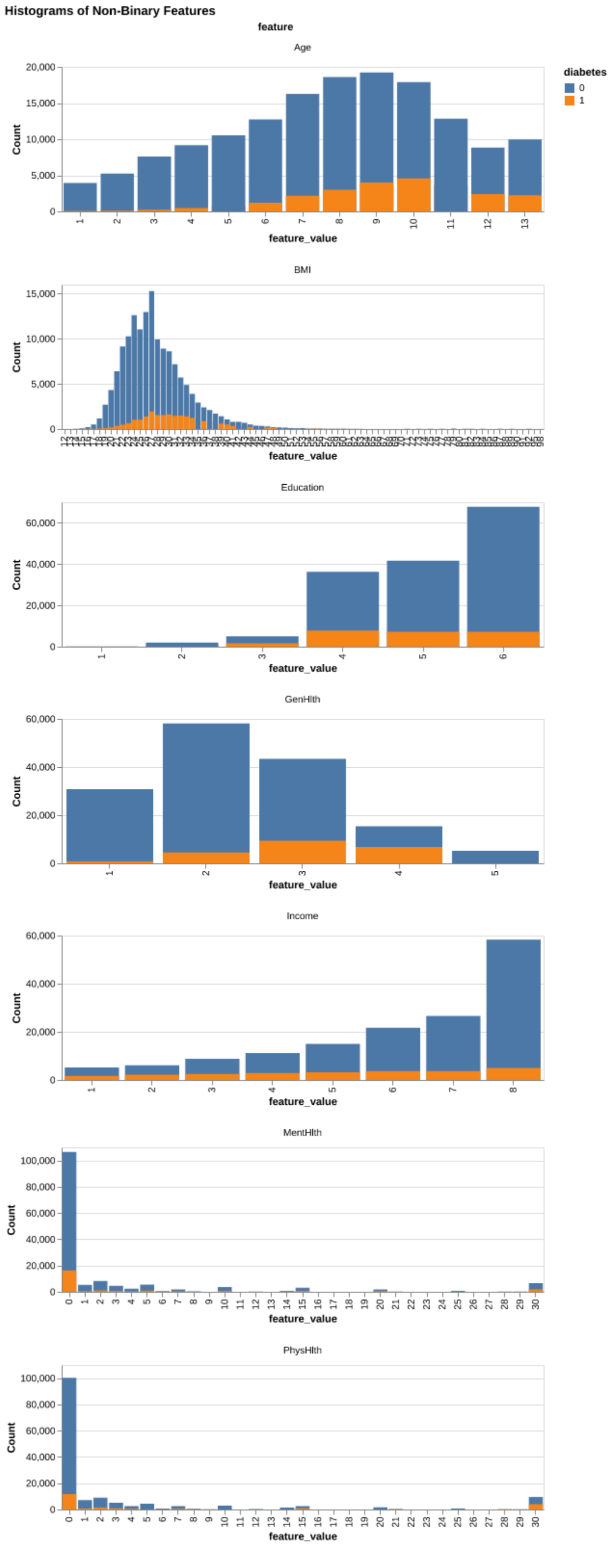

Figure 3: Histograms of the non-binary numeric features.

Figure 3

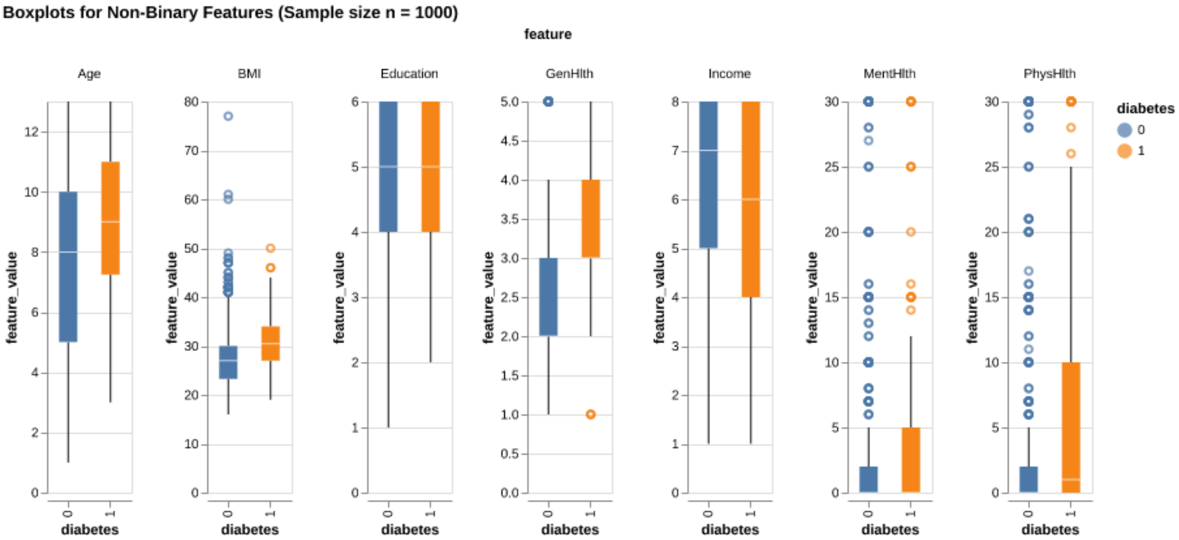

Figure 4: Boxplots of the non-binary numeric features.

Figure 4

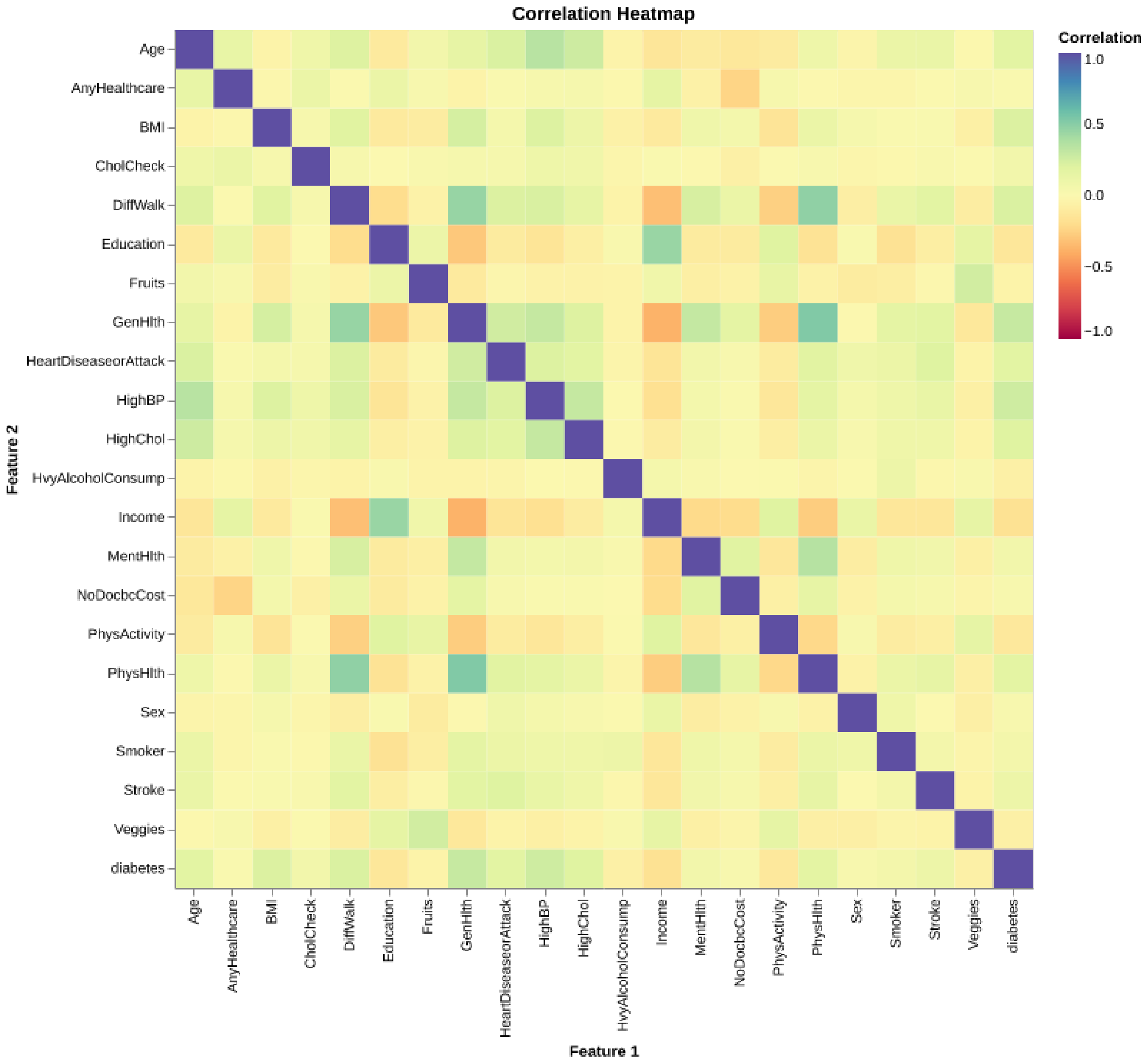

Figure 5: Feature-feature correlation plot of all features.

Figure 5

## Modeling

### Classification Analysis

### Result Visualizations

## Discussion

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