

# Diabetes Prediction

Alexander Wen, Raymond Wong, Michael Eirikson

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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 than 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 approximately 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:

Table 1: Table of Python packages used

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

## Modeling Approach

The data were split 70/30 into training and test sets with stratification on the target. Two classifiers were trained and tuned using 5-fold cross-validated grid search with **f2-score** as the scoring metric. We chose to use f2-score because it is most important to not miss true positives.

1. **Decision Tree** (class\_weight='balanced')  
Hyperparameters: max\_depth: {6,8,10,12,14}, min\_samples\_leaf: {175, 200, 225, 250}  
**Best parameters:** max\_depth=10, min\_samples\_leaf=225  
**Best CV f2-score** = 0.587
2. **Bernoulli Naive Bayes** (with StandardScaler preprocessing)  
Hyperparameters: alpha: {1e-3, 1e-2, 1e-1, 1e0, 1e1, 1e2, 1e3, 1e4}  
**Best parameters:** alpha=0.001  
**Best CV f2-score** = 0.46

## Modeling Results

Table 2: Scores for models.

Unnamed:						
0	Model	Test Accuracy	Test f2-score	Test recall	Test precision	
0	Decision Tree	0.706	0.587	0.784	0.293	
1	Naive Bayes	0.814	0.46	0.489	0.373	

## EDA

### Data Summary

First, here is a sample of the training data showing the first few entries and last few entries in the dataset in Table 3 and Table 4.

Table 3: First few rows of the training data.

Unnamed:																							
0	HighBP	HighChol	HighFats	HighSug	HeartDisease	PhysActivity	Age	Gender	Smoker	AlcoholConsumption	Insulin	Glucose	BodyMassIndex	PhysHealth	PhysHealth2	PhysHealth3	PhysHealth4	PhysHealth5	PhysHealth6	PhysHealth7	PhysHealth8	PhysHealth9	PhysHealth10
0	0	0	1	1	23	0	0	0	1	1	1	0	1	0	1	0	0	0	10	6	8	0	
1	1	0	0	1	25	0	0	0	1	1	1	0	1	0	3	0	30	0	12	6	7	0	
2	2	1	1	1	28	0	0	0	1	0	1	0	1	0	2	15	2	0	1	6	5	6	0

Table 3: First few rows of the training data.

Unnamed:																							
0	HighBP	HighChol	HighFPG	HighLDM	HighS	Stroke	HeartDisease	Angiogram	Angiogram	Angiogram	Angiogram	Angiogram	Angiogram	Angiogram	Angiogram	Angiogram	Angiogram	Angiogram	Angiogram	Angiogram	Angiogram	Angiogram	
3	3	0	0	1	25	0	0	0	1	1	0	1	0	2	0	0	0	0	8	5	7	0	
4	4	1	0	1	30	1	0	0	1	1	1	0	1	1	4	30	15	0	0	8	4	4	0

Table 4: Last few rows of the training data.

Unnamed:																								
0	HighBP	HighChol	HighFPG	HighLDM	HighS	Stroke	HeartDisease	Angiogram	Angiogram	Angiogram	Angiogram	Angiogram	Angiogram	Angiogram	Angiogram	Angiogram	Angiogram	Angiogram	Angiogram	Angiogram	Angiogram	Angiogram	Angiogram	
0	1775	71	1	1	29	0	0	0	1	1	1	0	1	0	2	0	2	0	0	4	6	5	0	
1	1775	72	0	1	22	0	0	0	0	1	1	0	1	0	3	0	0	1	0	13	4	1	0	
2	1775	73	1	1	25	1	0	0	1	1	1	0	1	0	2	0	0	0	1	6	5	7	0	
3	1775	74	1	1	24	1	0	0	1	1	1	0	1	0	3	2	1	0	0	4	4	8	0	
4	1775	75	1	1	31	1	0	0	0	1	1	0	1	0	2	0	2	0	0	8	4	4	0	

All features of the dataset are numeric, and further EDA shows there are no null values in the dataset.

Table 5: Description of the training data.

Unnamed:																					
0	HighBP	HighChol	HighFPG	HighLDM	HighS	Stroke	HeartDisease	Angiogram	Angiogram	Angiogram	Angiogram	Angiogram	Angiogram	Angiogram	Angiogram	Angiogram	Angiogram	Angiogram	Angiogram	Angiogram	Angiogram
0	count	1775	1775	1775	1775	1775	1775	1775	1775	1775	1775	1775	1775	1775	1775	1775	1775	1775	1775	1775	1775
1	mean	0.42	0.27	0.76	0.68	0.54	0.34	0.70	0.30	0.73	0.33	0.85	0.22	0.56	0.29	0.42	0.82	0.54	0.79	0.33	0.50
2	std	0.49	0.49	0.18	0.59	0.64	0.67	0.72	0.31	0.72	0.30	0.43	0.53	0.42	0.27	0.78	0.40	0.57	0.34	0.63	0.59
3	min	0	0	0	12	0	0	0	0	0	0	0	0	0	1	0	0	0	0	1	1
4	25%	0	0	1	24	0	0	0	1	0	1	0	1	0	2	0	0	0	0	6	4
5	50%	0	0	1	27	0	0	0	1	1	1	0	1	0	2	0	0	0	0	8	5
6	75%	1	1	1	31	1	0	0	1	1	1	0	1	0	3	2	3	0	1	10	6
7	max	1	1	1	98	1	1	1	1	1	1	1	1	1	5	30	30	1	1	13	6

Table 5 displays a numerical distribution of the dataset. Most features are binary in nature, with the exceptions of To better visualize we then plotted frequency counts of the target labels:

## Visualizations

### Count of Diabetes vs Non-Diabetes Records in Dataset

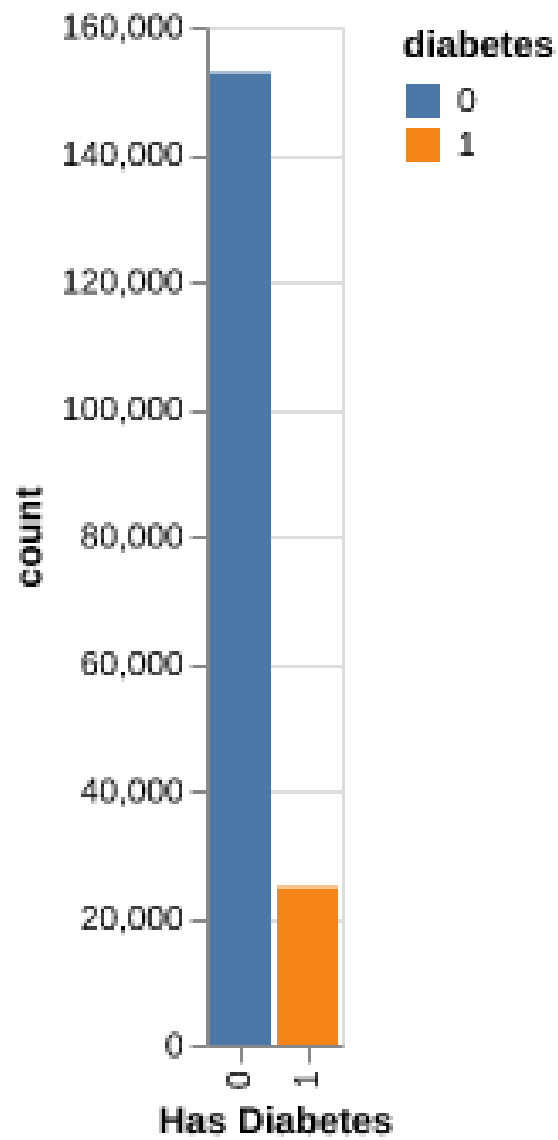


Figure 1: Frequency bar graph of the labels.

Figure 1

### Bar Plots of Binary Features

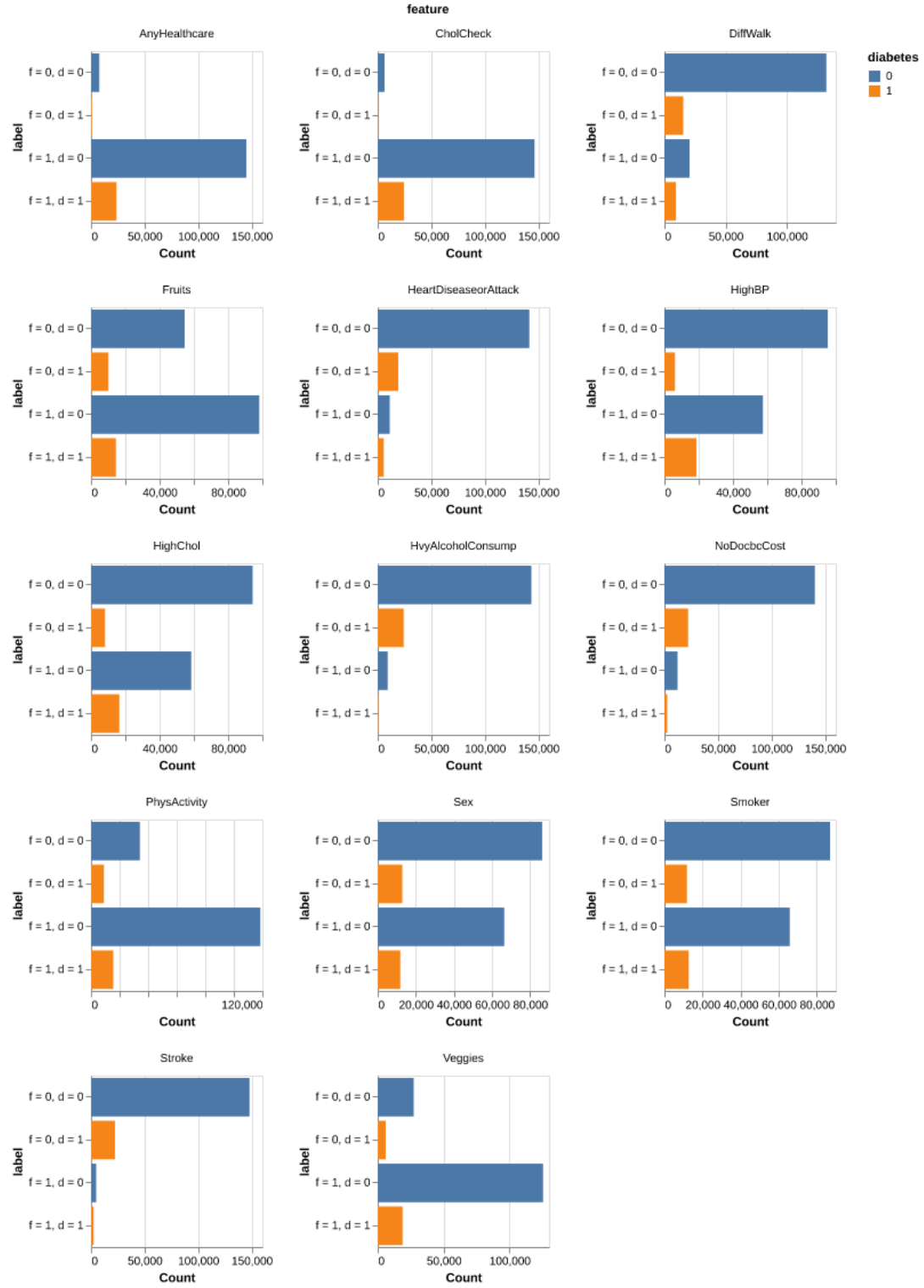


Figure 2: Frequency bar graphs of the binary features.

Figure 2

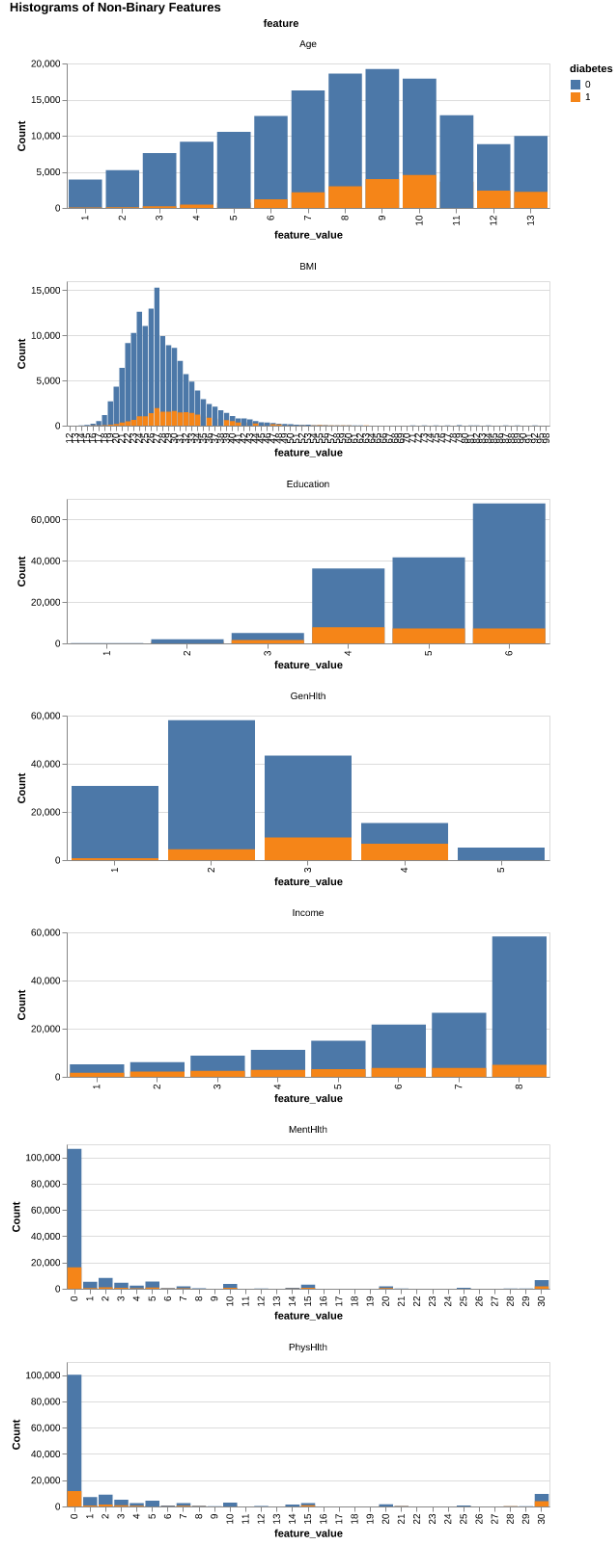


Figure 3: Histograms of the non-binary numeric features.



Figure 3

Boxplots for Non-Binary Features (Sample size n = 1000)

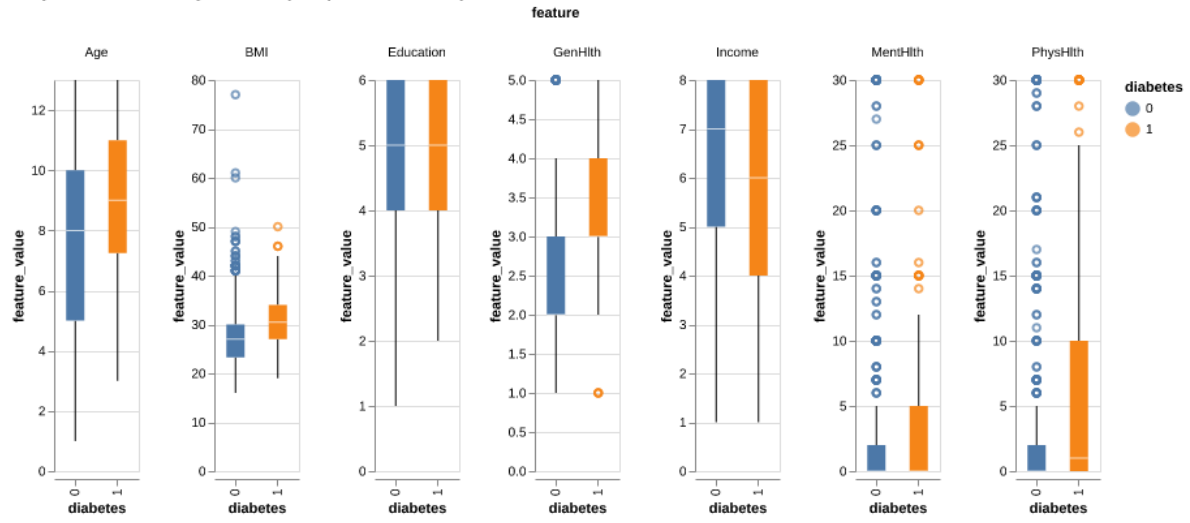


Figure 4: Boxplots of the non-binary numeric features.

Figure 4

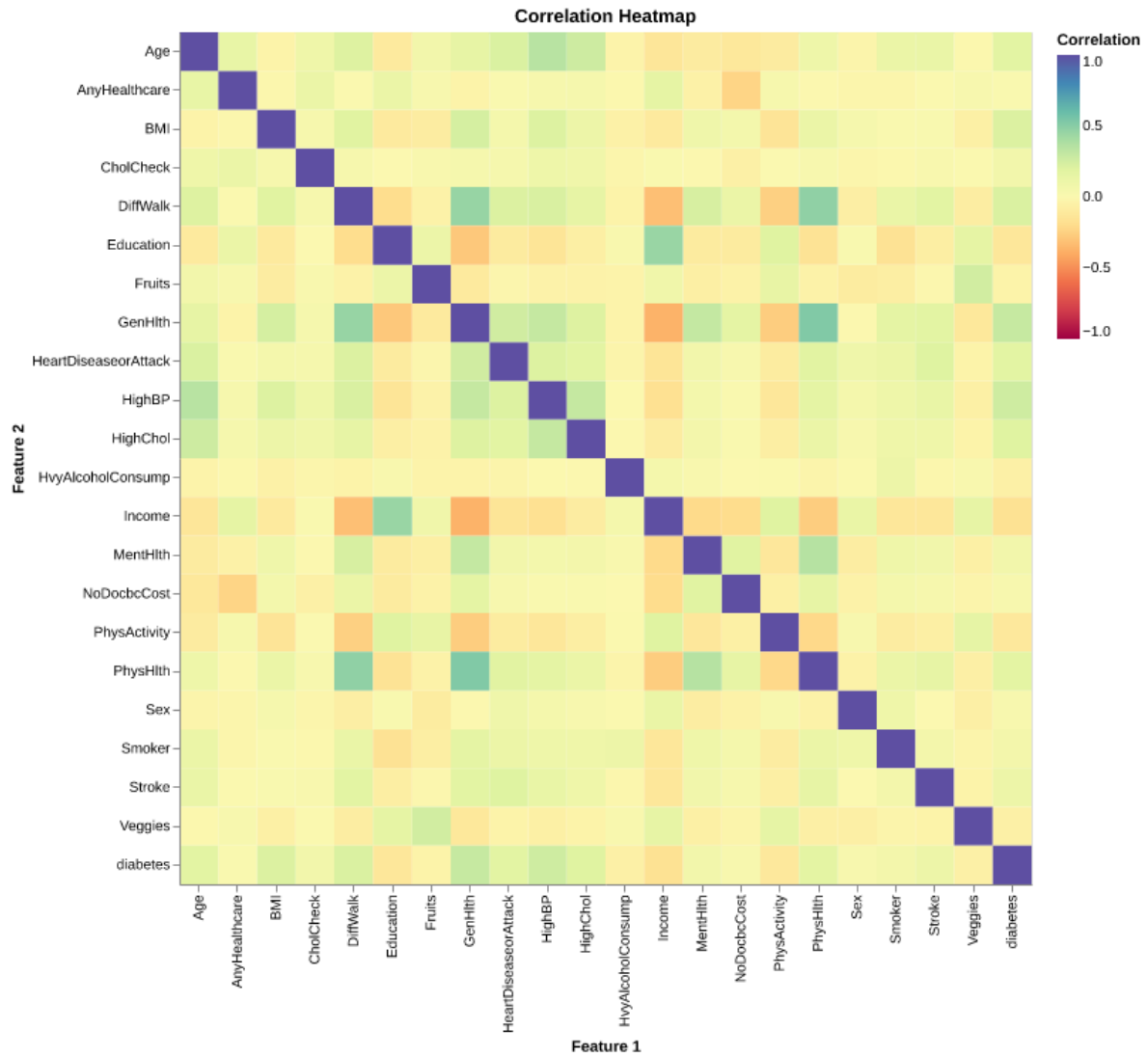


Figure 5: Feature-feature correlation plot of all features.

Figure 5

## Modeling

## Classification Analysis

## Result Visualizations

## Discussion

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