Diabetes Prediction

In [1]:
```
import numpy as np
import pandas as pd
import pandera.pandas as pa
import altair as alt
import os
import warnings
from sklearn.preprocessing import StandardScaler
from sklearn.compose import make_column_transformer, make_column_selector
from sklearn.model_selection import train_test_split, GridSearchCV
from sklearn.tree import DecisionTreeClassifier
from sklearn.naive_bayes import BernoulliNB
from sklearn.pipeline import make_pipeline
from ucimlrepo import fetch_ucirepo
from sklearn.metrics import (
    accuracy_score, make_scorer, fbeta_score,
    recall_score, precision_score, ConfusionMatrixDisplay
)
from deepchecks.tabular.checks import FeatureLabelCorrelation, FeatureFeatur
from deepchecks.tabular import Dataset

alt.data_transformers.disable_max_rows()
warnings.filterwarnings("ignore", category=FutureWarning, module="deepchecks

np.random.seed(522)
```

```
/opt/conda/lib/python3.11/site-packages/deepchecks/core/serialization/datafr
ame/html.py:16: UserWarning:

pkg_resources is deprecated as an API. See https://setuptools.pypa.io/en/lat
est/pkg_resources.html. The pkg_resources package is slated for removal as e
arly as 2025-11-30. Refrain from using this package or pin to Setuptools<81.
```

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. In the USA it is the 8th leading cause of death. Globally an estimated 44% of people living with diabetes are undiagnosed. (Snapshot of Diabetes in Canada, 2023; Rios et al., 2017; 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).
No missing values were present and all features were already encoded numerically. The target classes is imbalanced (≈86% non-diabetic, ≈14% diabetic).

Methods and Results

The analysis uses the 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 are heavily imbalanced (≈86% non-diabetic, ≈14% diabetic).

EDA

Group-wise mean differences revealed the strongest risk factors for diabetes:

- PhysHlth (days of poor physical health)
- BMI
- Age
- MentHlth (days of poor mental health)
- GenHlth (self-rated general health)

Weakest factors

- HvyAlcoholConsump
- Fruits
- Veggies
- PhysActivity
- Education
- Income

Box plots of the top five predictors clearly separate the diabetic and non-diabetic groups.

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 more appropriate than accuracy or f1 because we don't want to 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=200
   Best CV f2-score = 0.5908

2. **Bernoulli Naive Bayes** (with StandardScaler preprocessing)
   Hyperparameters: alpha ∈ {1e-3, 1e-2, 1e-1, 1e0, 1e1, 1e2, 1e3, 1e4}
   Best parameters: alpha=1e-3
   Best CV f2-score = 0.4453

Results

Model	Test Accuracy	Test f2-score	Test recall	Test precision
Decision Tree	0.706	**0.587**	**0.783**	0.293
Naive Bayes	**0.814**	0.460	0.489	**0.373**

Table: 1

Load Data

In [2]:
```
# fetch dataset
cdc_diabetes_health_indicators = fetch_ucirepo(id=891)

# data (as pandas dataframes)
X = cdc_diabetes_health_indicators.data.features
y = cdc_diabetes_health_indicators.data.targets
```

Validate Data Before Saving

X Verification

In [3]:
```
"""
Checks verified:
Correct data file format
Correct column names
No empty observations (and by extension Missingness not beyond expected thre
Correct data types in each column
No outlier or anomalous values

Maximum allowable ranges for the numeric_features were determined from
the schema description in https://archive.ics.uci.edu/dataset/891/cdc+diabet
"""

# Check that X is a Pandas DataFrame
if not isinstance(X, pd.DataFrame):
    raise TypeError("X object obtained is not a Pandas Dataframe.")

# Create a list of expected column names
column_names = ["HighBP","HighChol","CholCheck","BMI","Smoker","Stroke","Hea
                "Fruits","Veggies","HvyAlcoholConsump","AnyHealthcare",
                "NoDocbcCost","GenHlth","MentHlth","PhysHlth","DiffWalk","Se

# Create a list of column names that are binary features
binary_features = ["HighBP","HighChol","CholCheck","Smoker","Stroke","HeartD
                "Fruits","Veggies","HvyAlcoholConsump","AnyHealthcare",
                "NoDocbcCost","DiffWalk","Sex"]

# Define allowable ranges for numeric features
numeric_features = {"BMI": (5,256),
                    "GenHlth": (1,5),
                    "MentHlth": (0,30),
                    "PhysHlth": (0,30),
                    "Age": (1,13),
                    "Education": (1,6),
                    "Income": (1,8)}

# Check that all expected columns are present
schema_dict = {}
for col_name in binary_features:
    schema_dict[col_name] = pa.Column(int, pa.Check.between(0,1), nullable =

# Add numeric features to schema with their respective ranges
for col_name in numeric_features.keys():
    schema_dict[col_name] = pa.Column(int, pa.Check.between(numeric_features

schema = pa.DataFrameSchema(schema_dict)

schema.validate(X, lazy = True)
```

Out[3]:

	HighBP	HighChol	CholCheck	BMI	Smoker	Stroke	HeartDiseaseorAttack
0	1	1	1	40	1	0	0
1	0	0	0	25	1	0	0
2	1	1	1	28	0	0	0
3	1	0	1	27	0	0	0
4	1	1	1	24	0	0	0
...	...	...	...	...	...	...	...
253675	1	1	1	45	0	0	0
253676	1	1	1	18	0	0	0
253677	0	0	1	28	0	0	0
253678	1	0	1	23	0	0	0
253679	1	1	1	25	0	0	1

253680 rows × 21 columns

Y Verification

In [4]:
```
# Use same template as X verification, only one column
if not isinstance(y, pd.DataFrame):
    raise TypeError("y object obtained is not a Pandas Dataframe.")


schema_dict = {}

target_name = ["Diabetes_binary"]

for col_name in target_name:
    schema_dict[col_name] = pa.Column(int, pa.Check.between(0,1), nullable =

schema = pa.DataFrameSchema(schema_dict)

schema.validate(y, lazy = True)
```

Out[4]:

	Diabetes_binary
0	0
1	0
2	0
3	0
4	0
...	...
253675	0
253676	1
253677	0
253678	0
253679	1

253680 rows × 1 columns

Save Raw Data

In [5]:
```
# check if raw folder exists
raw_data_path = "../data/raw"

if not os.path.exists(raw_data_path):
    os.makedirs(raw_data_path)

## Save Raw Data
X.to_csv("../data/raw/diabetes_raw_features.csv")
y.to_csv("../data/raw/diabetes_raw_targets.csv")
```

Data Wrangling

In [6]:
```
# No major cleaning needed — dataset is already very clean!
# Combine features and targets to get a overview of the full data set
df = X.copy()
df['diabetes'] = y

# Quick info
df.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 253680 entries, 0 to 253679
Data columns (total 22 columns):
 #   Column                Non-Null Count   Dtype
---  ------                --------------   -----
 0   HighBP                253680 non-null  int64
 1   HighChol              253680 non-null  int64
 2   CholCheck             253680 non-null  int64
 3   BMI                   253680 non-null  int64
 4   Smoker                253680 non-null  int64
 5   Stroke                253680 non-null  int64
 6   HeartDiseaseorAttack  253680 non-null  int64
 7   PhysActivity          253680 non-null  int64
 8   Fruits                253680 non-null  int64
 9   Veggies               253680 non-null  int64
 10  HvyAlcoholConsump     253680 non-null  int64
 11  AnyHealthcare         253680 non-null  int64
 12  NoDocbcCost           253680 non-null  int64
 13  GenHlth               253680 non-null  int64
 14  MentHlth              253680 non-null  int64
 15  PhysHlth              253680 non-null  int64
 16  DiffWalk              253680 non-null  int64
 17  Sex                   253680 non-null  int64
 18  Age                   253680 non-null  int64
 19  Education             253680 non-null  int64
 20  Income                253680 non-null  int64
 21  diabetes              253680 non-null  int64
dtypes: int64(22)
memory usage: 42.6 MB
```

In [7]:
```
df.head()
```

Out[7]:

	HighBP	HighChol	CholCheck	BMI	Smoker	Stroke	HeartDiseaseorAttack	PhysA
0	1	1	1	40	1	0	0	
1	0	0	0	25	1	0	0	
2	1	1	1	28	0	0	0	
3	1	0	1	27	0	0	0	
4	1	1	1	24	0	0	0	

5 rows × 22 columns

In [8]:
```
df.tail()
```

Out[8]:

	HighBP	HighChol	CholCheck	BMI	Smoker	Stroke	HeartDiseaseorAttack
253675	1	1	1	45	0	0	0
253676	1	1	1	18	0	0	0
253677	0	0	1	28	0	0	0
253678	1	0	1	23	0	0	0
253679	1	1	1	25	0	0	1

5 rows × 22 columns

Data Summary

All the features in this dataset were selected by clinician to be relevent to a person having diabetes. We will use all features in our model.

In [9]:
```
df.describe()
```

Out[9]:

	HighBP	HighChol	CholCheck	BMI	Smoke
count	253680.000000	253680.000000	253680.000000	253680.000000	253680.00000
mean	0.429001	0.424121	0.962670	28.382364	0.44316
std	0.494934	0.494210	0.189571	6.608694	0.49676
min	0.000000	0.000000	0.000000	12.000000	0.00000
25%	0.000000	0.000000	1.000000	24.000000	0.00000
50%	0.000000	0.000000	1.000000	27.000000	0.00000
75%	1.000000	1.000000	1.000000	31.000000	1.00000
max	1.000000	1.000000	1.000000	98.000000	1.00000

8 rows × 22 columns

In [10]:
```
'''
These checks ensure data quality by verifying:
- Checking if duplicate rows exist in the dataset, preventing redundant data
  (We are not dropping duplicates automatically to avoid unintentional data
  (For the purpose of this dataset, because we already finished the analysis
- Checking for outlier in ("BMI", "MentHlth", "PhysHlth") columns to see if
  which helps maintain data integrity and model robustness.
  (For the purpose of this dataset, we will accept the outlier value because
- Categorical validation is not applicable for this dataset
'''

def iqr_outliers(series: pd.Series) -> bool:
    """Return True if all values are within 1.5 * IQR (no extreme outliers)"
    Q1 = series.quantile(0.25)
    Q3 = series.quantile(0.75)
    IQR = Q3 - Q1
    lower_bound = Q1 - 1.5 * IQR
    upper_bound = Q3 + 1.5 * IQR
    return series.between(lower_bound, upper_bound).all()


# Define the schema with meaningful checks
diabetes_schema = pa.DataFrameSchema(
    columns={
        "BMI": pa.Column(float, nullable=False),
        "MentHlth": pa.Column(float, nullable=False),
        "PhysHlth": pa.Column(float, nullable=False),
    },
    checks=[
        # 1. No duplicate rows
        pa.Check(
            lambda df: ~df.duplicated().any(),
            error="DUPLICATE_ROWS: Found duplicate observations. Use df.drop
        ),

        # 2. No extreme outliers in continuous variables using IQR rule
        pa.Check(
            lambda df: iqr_outliers(df["BMI"]),
            error="OUTLIERS_IN_BMI: Extreme outliers detected in BMI (beyond
        ),
        pa.Check(
            lambda df: iqr_outliers(df["MentHlth"]),
            error="OUTLIERS_IN_MENTHLTH: Extreme values in MentHlth (beyond
        ),
        pa.Check(
            lambda df: iqr_outliers(df["PhysHlth"]),
            error="OUTLIERS_IN_PHYSHLTH: Extreme values in PhysHlth (beyond
        )
    ]
)

# Validate with lazy=True to see all errors at once
try:
    diabetes_schema.validate(df, lazy=True)
    print("All checks passed! Dataset is clean and ready for modeling.")
except pa.errors.SchemaErrors as e:
    print("Validation failed! See errors below:")
    print(e.failure_cases)  # Shows detailed failure report
```

```
Validation failed! See errors below:
     column failure_case index    schema_context  \
3      None        False  None  DataFrameSchema
4      None        False  None  DataFrameSchema
5      None        False  None  DataFrameSchema
6      None        False  None  DataFrameSchema
0       BMI        int64  None            Column
1  MentHlth        int64  None            Column
2  PhysHlth        int64  None            Column

                                               check  check_number
3  DUPLICATE_ROWS: Found duplicate observations. ...           0.0
4  OUTLIERS_IN_BMI: Extreme outliers detected in ...           1.0
5  OUTLIERS_IN_MENTHLTH: Extreme values in MentHl...           2.0
6  OUTLIERS_IN_PHYSHLTH: Extreme values in PhysHl...           3.0
0                                    dtype('float64')          NaN
1                                    dtype('float64')          NaN
2                                    dtype('float64')          NaN
```

Visualizations

In [11]:
```python
diabetes_count = pd.DataFrame(df['diabetes'].value_counts()).reset_index()

alt.Chart(diabetes_count).mark_bar().encode(
    x=alt.X('diabetes:O', title='Has Diabetes'),
    y="count",
    color="diabetes:N"
).properties(title='Count of Diabetes vs Non-Diabetes Recores in Dataset')
```

Out[11]:

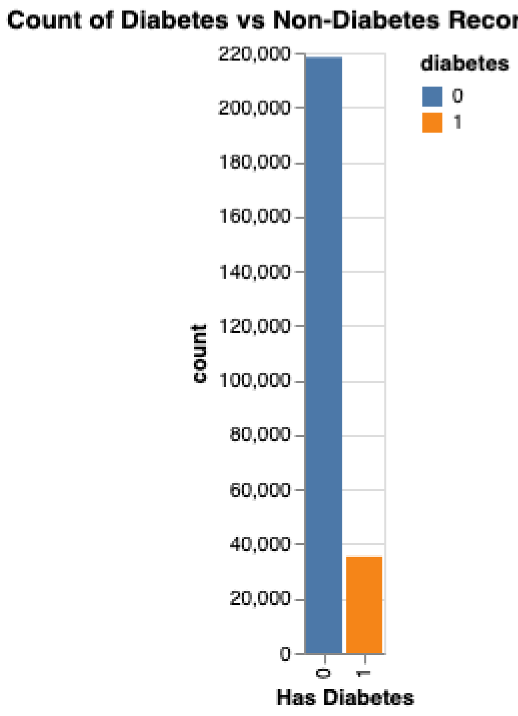
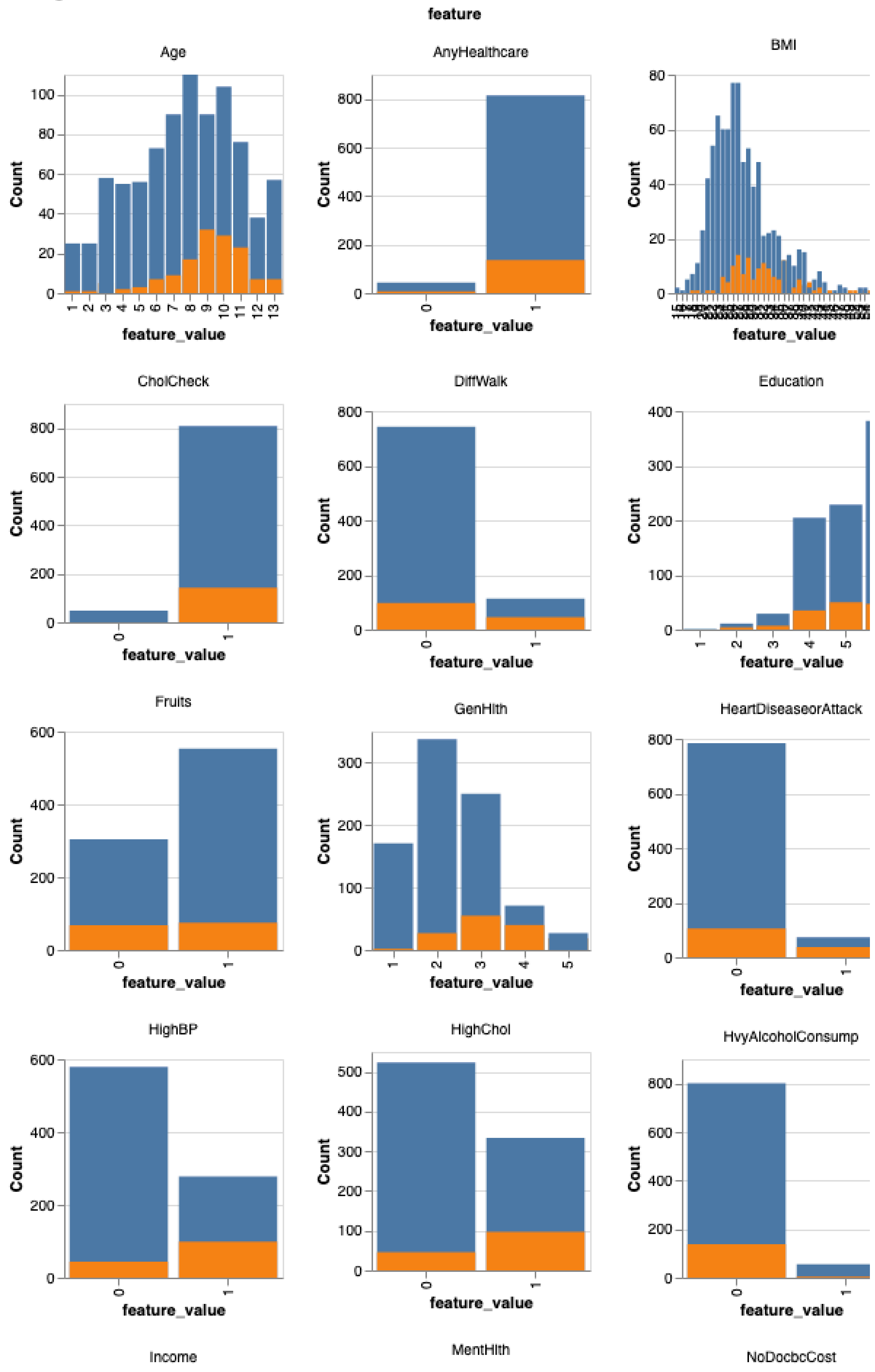


Figure 1

In [12]:
```python
df_sample = df.sample(n=1000, random_state=522)
features = df_sample.columns.to_list()
```

```
df_sample_long = pd.melt(df_sample, id_vars=["diabetes"], value_vars=feature

histograms = alt.Chart(df_sample_long).mark_bar().encode(
    x=alt.X("feature_value:O"), # Chose to use ordinal instead of quantitati
    y=alt.Y("count()", title="Count").stack(False),
    color=alt.Color("diabetes:N"),
).properties(
    width=150,
    height=150,
).facet(
    "feature:N",
    columns=3,
).resolve_scale(
    x="independent",
    y="independent",
).properties(
    title='Histograms of Features',
)

histograms
```

Out[12]: **Histograms of Features**



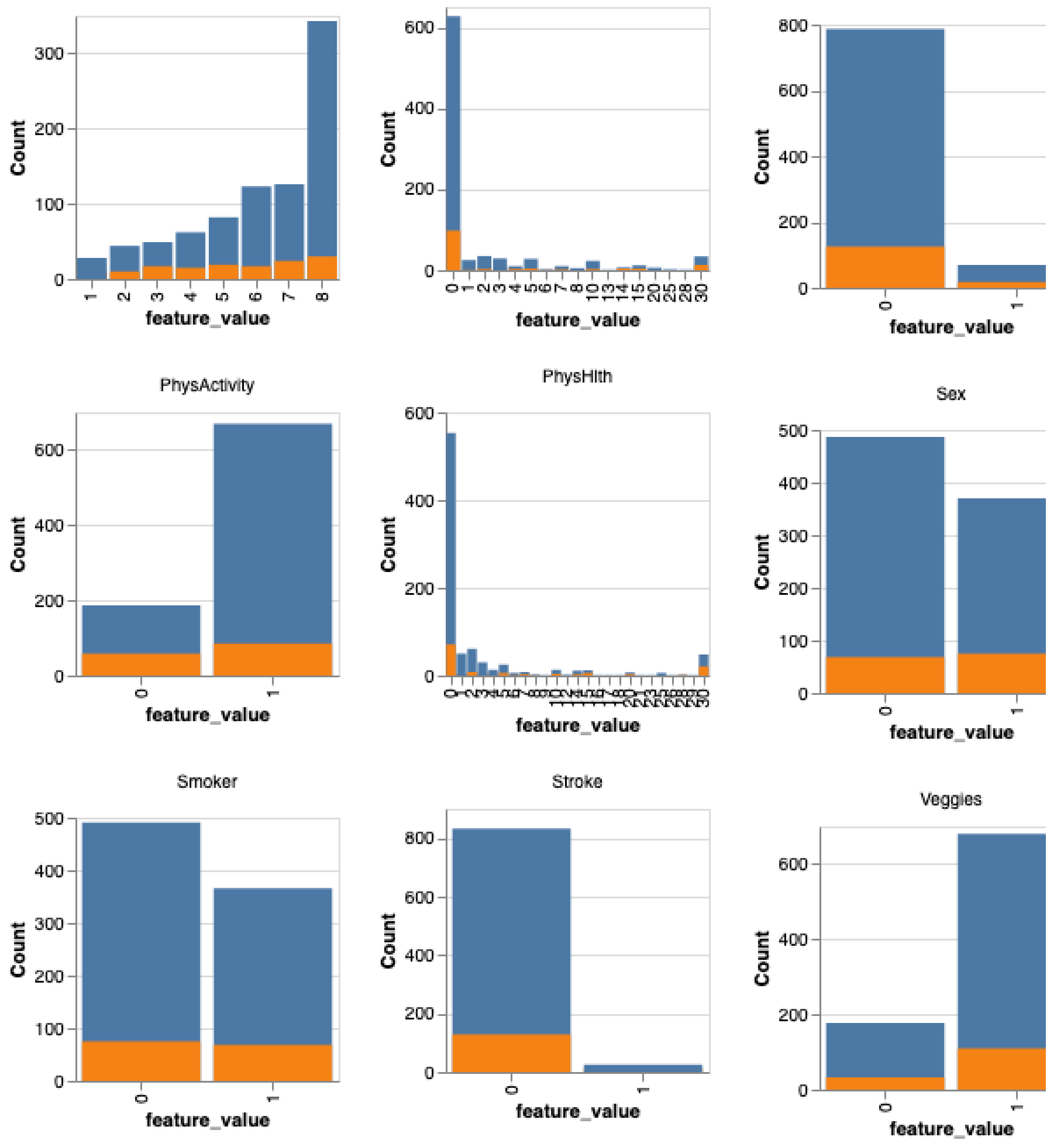


Figure 2

```
In [13]: # For binary features boxplot is not infomative
         non_binary_features = ['BMI', 'GenHlth', 'MentHlth', 'PhysHlth', 'Age', 'Edu
         df_sample_nonbinary = df_sample_long[df_sample_long["feature"].isin(non_bina

         alt.Chart(df_sample_nonbinary).mark_boxplot().encode(
             x='diabetes:N',
             y='feature_value:Q',
             color='diabetes:N'
         ).facet(
             column='feature:N'
         ).properties(
             title='Boxplots for Non-Binary Features',
         ).resolve_scale(
             y="independent"
         )
```

Out[13]:

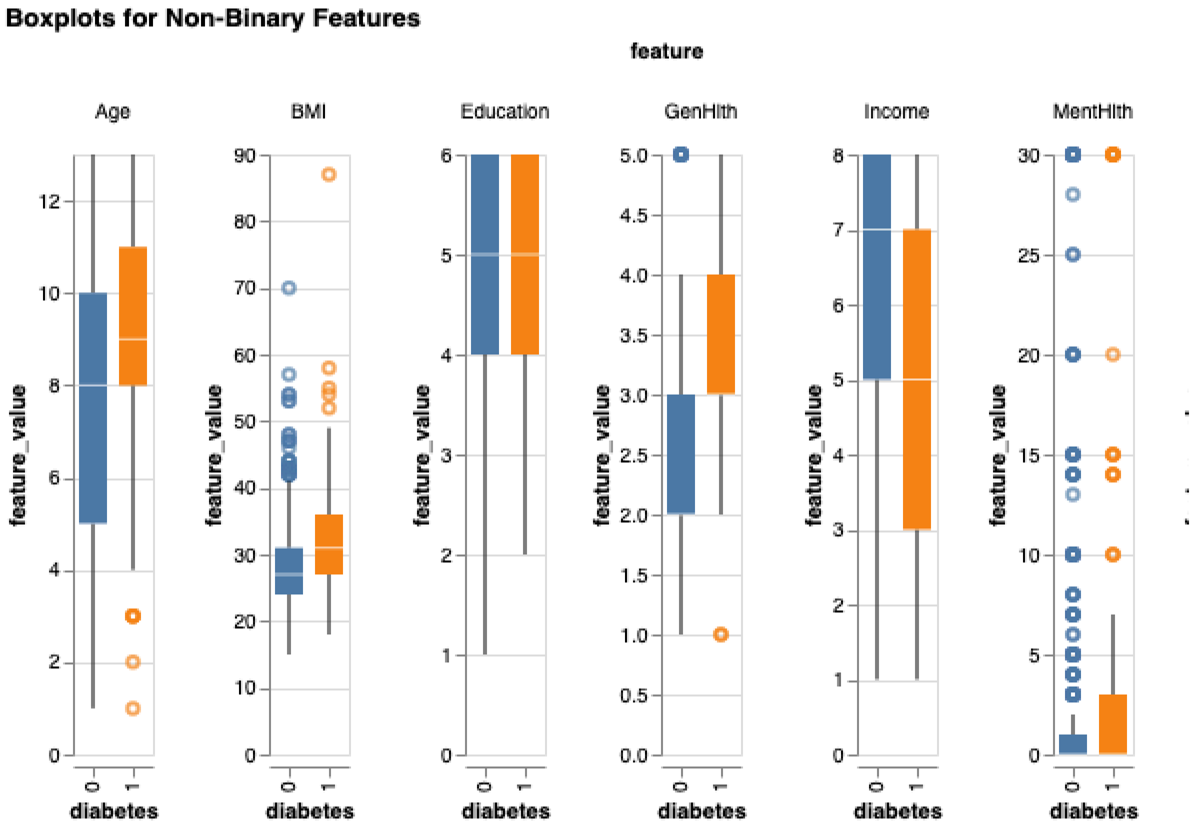


Figure 3

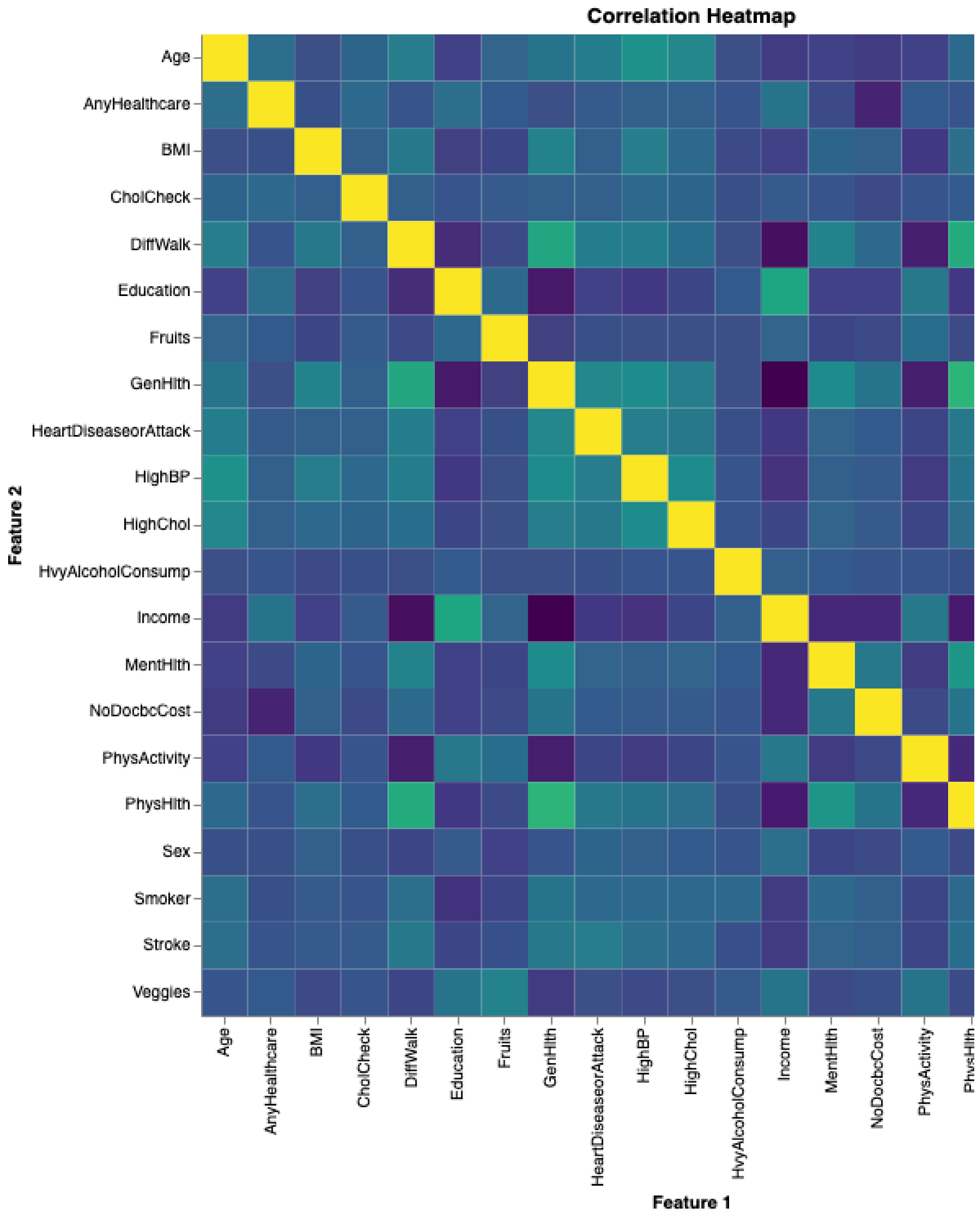
In [14]:
```
# split the data 70-30 split
train_df, test_df = train_test_split(
    df, test_size=0.3, random_state=522, stratify=df['diabetes']
)

# check if processed folder exists
processed_data_path = "../data/processed"

if not os.path.exists(processed_data_path):
    os.makedirs(processed_data_path)

# Save processed data
train_df.to_csv(processed_data_path+"/diabetes_train.csv", index=False)
test_df.to_csv(processed_data_path+"/diabetes_test.csv", index=False)
```

In [15]:
```
X_train = train_df.drop('diabetes', axis=1)
y_train = train_df['diabetes']
X_test  = test_df.drop('diabetes', axis=1)
y_test  = test_df['diabetes']
```

In [16]:
```
# Create correlation chart
correlation_matrix = X_train.corr()
correlation_long = correlation_matrix.reset_index().melt(id_vars='index')
correlation_long.columns = ['Feature 1', 'Feature 2', 'Correlation']
```

```
alt.Chart(correlation_long).mark_rect().encode(
    x='Feature 1:O',
    y='Feature 2:O',
    color=alt.Color('Correlation:Q', scale=alt.Scale(scheme='viridis')),
    tooltip=['Feature 1', 'Feature 2', 'Correlation']
).properties(
    width=600,
    height=600,
    title="Correlation Heatmap"
)
```

Out[16]:



In [17]:
```
'''
- Target/response variable follows expected distribution
  (In the diabetes dataset, we expect the prevalence of diabetes to be arour

Validate training data for anomalous correlations:
- Feature-label correlations (target vs features)
- Feature-feature correlations (between features)

Thresholds set based on domain knowledge.

We perform these checks on training data only because including test data he
and invalidate the evaluation of model generalization.
'''

# Target variable follows expected distribution
# In this dataset: ~13-15% diabetes is normal, >30% or <5% is suspicious

distribution_schema = pa.DataFrameSchema(
    checks=[pa.Check(
        lambda df: df.mean().between(0.05, 0.30),
        error="ANOMALOUS_TARGET_DISTRIBUTION: Diabetes prevalence should be
        )
    ]
)

distribution_schema.validate(train_df[['diabetes']], lazy=True)

# Combine features and target into a dataset for validation
diabetes_train_ds = Dataset(
    df=train_df,
    label="diabetes",
    cat_features=[]
)

# Check that feature-label predictive power score (PPS) is below 0.9
check_feat_lab_corr = FeatureLabelCorrelation().add_condition_feature_pps_le
check_feat_lab_corr_result = check_feat_lab_corr.run(diabetes_train_ds)

# Check that no feature pairs have correlation above 0.92
check_feat_feat_corr = FeatureFeatureCorrelation().add_condition_max_number_
    threshold=0.92, n_pairs=0
)
check_feat_feat_corr_result = check_feat_feat_corr.run(diabetes_train_ds)

# Raise errors if any checks fail
if not check_feat_lab_corr_result.passed_conditions():
    raise ValueError("Feature-Label correlation exceeds the maximum acceptab

if not check_feat_feat_corr_result.passed_conditions():
    raise ValueError("Feature-feature correlation exceeds the maximum accept
```

Classification Analysis

```
In [18]: f2_scorer = make_scorer(fbeta_score, beta=2)
```

```
In [19]: tree = DecisionTreeClassifier(random_state=522, class_weight='balanced')

         tree_params = {
             'max_depth': [6, 8, 10, 12, 14],
             'min_samples_leaf': [175, 200, 225, 250]
         }

         tree_grid = GridSearchCV(tree, tree_params, cv=5, scoring=f2_scorer, n_jobs=
         tree_grid.fit(X_train, y_train)

         best_tree = tree_grid.best_estimator_
         print("Best Decision Tree params:", tree_grid.best_params_)
         print("Best CV f2-score:", tree_grid.best_score_.round(4))
```

```
Best Decision Tree params: {'max_depth': 10, 'min_samples_leaf': 225}
Best CV f2-score: 0.5919
```

```
In [20]: preprocessor = make_column_transformer(
             (StandardScaler(), X_train.columns)
         )

         nb_pipe = make_pipeline(
             preprocessor,
             BernoulliNB()
         )

         nb_params = {'bernoullinb__alpha': [1e-3, 1e-2, 1e-1, 1e0, 1e1, 1e2, 1e3, 1e

         knn_grid = GridSearchCV(nb_pipe, nb_params, cv=5, scoring=f2_scorer, n_jobs=
         knn_grid.fit(X_train, y_train)

         best_nb = knn_grid.best_estimator_
         print("Best NB k:", knn_grid.best_params_)
         print("Best CV f2-score:", knn_grid.best_score_.round(4))
```

```
Best NB k: {'bernoullinb__alpha': 0.001}
Best CV f2-score: 0.4604
```

```
In [21]: models = {
             'Decision Tree': best_tree,
             'Naive Bayes': best_nb
         }

         results = []

         for name, model in models.items():
             y_pred = model.predict(X_test)
             y_prob = model.predict_proba(X_test)[:, 1]

             results.append({
                 'Model': name,
                 'Test Accuracy': round(accuracy_score(y_test, y_pred),3),
                 'Test f2-score': round(fbeta_score(y_test, y_pred, beta=2),3),
                 'Test recall': round(recall_score(y_test, y_pred),3),
                 'Test precision': round(precision_score(y_test, y_pred),3),
             })

         score_df = pd.DataFrame(results)
         score_df
```

Out[21]:

	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	0.460	0.489	0.373

Result Visualizations

In [22]:

```
score_melt = score_df.melt(id_vars='Model', var_name='Metric', value_name='S

alt.Chart(score_melt).mark_bar().encode(
    x='Model:N',
    y='Score:Q',
    color='Model:N',
    column='Metric:N'
).properties(
    title='Decision Tree vs Naive Bayes Performance on Test Set'
)
```

Out[22]:

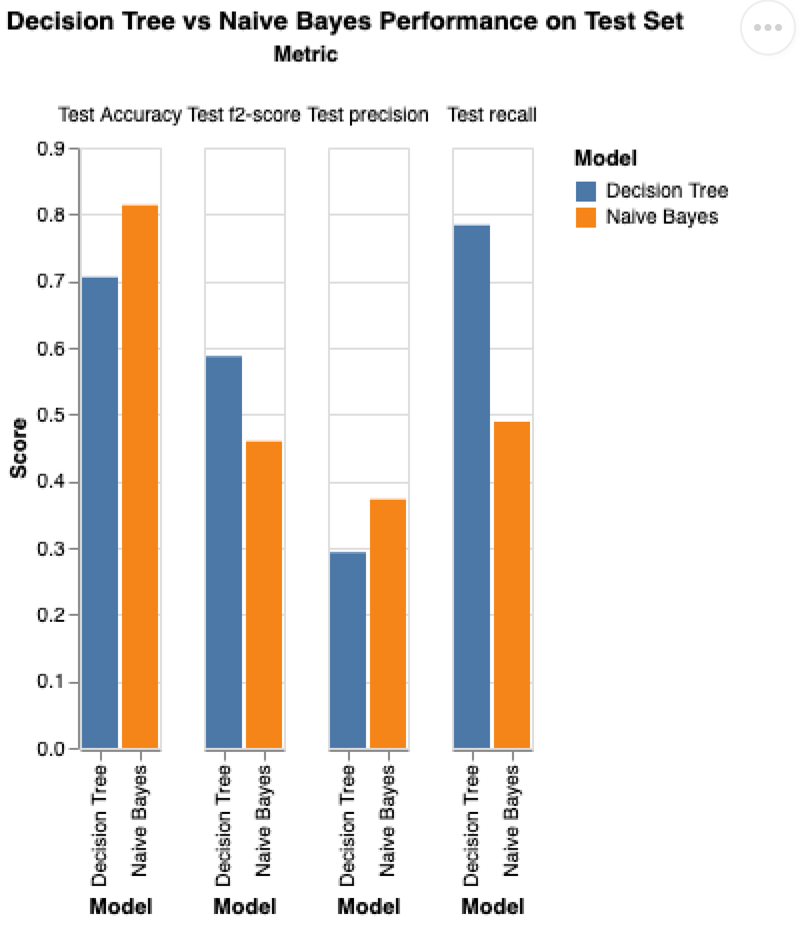


Figure 4

```
In [23]: # Confusion matrix for best model (decision tree)

         ConfusionMatrixDisplay.from_estimator(
             best_tree,
             X_test,
             y_test,
             values_format="d",
         )
```

```
Out[23]: <sklearn.metrics._plot.confusion_matrix.ConfusionMatrixDisplay at 0x7f3fddf
         15a50>
```

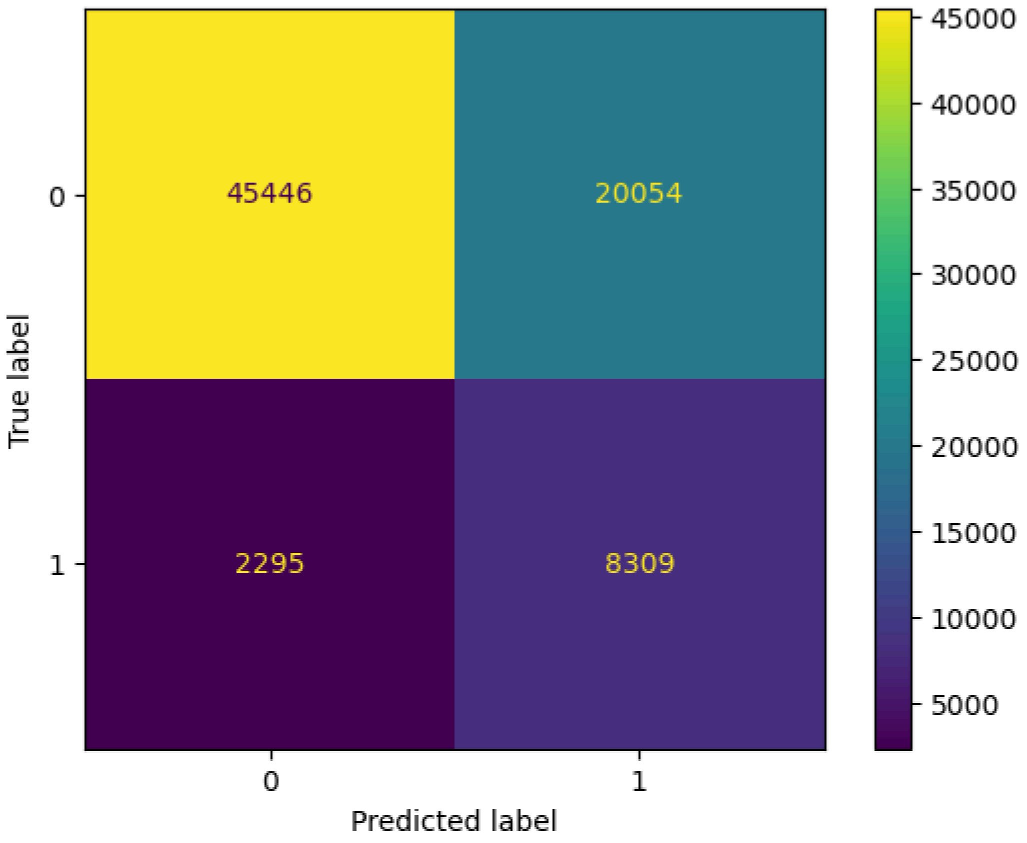


Figure 5

Discussion

The current performance of the tree model is likely already good enough to offer some benefit in the real world given the large number of people with undiagnosed diabetes. However the the recall score likely could be impoved on and the precision score definitely leaves something to be desired.

We were surprised by the high rate of false positives. This might be an indication of how many non-diabetic people are at risk.

Further improvements to predicting diabetes could likely be found by 1) trying a wider veriety of model type and using a wider hyperperameter search 2) possibly through more feature engineering.

A future study could be done to find a smaller set of the most easy to obtain features. Such a model would be more usable by the average person. Some work is needed to determine this smaller number of easy to obtain features that doesn't significantly reduce model performance.

Another question is if a regression model could be made that predicts a persons risk as a percent chance of developing diabetes. Longitudinal data might be required for this type of prediction.

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